Grippe Aviaire et Nouveaux Virus Grippaux

Mise a jour 2009

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Proteomics-based characterization of hemagglutinins in different strains of influenza virus


Origin of the 2009 Mexico influenza virus: a comparative phylogenetic analysis of the principal external antigens and matrix protein

Replication and pathogenesis associated with H5N1, H5N2, and H5N3 low-pathogenic avian influenza virus infection in chickens and ducks

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Phosphoantigen-Expanded Human gamma delta T Cells Display Potent Cytotoxicity against Monocyte-Derived Macrophages Infected with Human and Avian Influenza Viruses

Dynamics of antiviral-resistant influenza viruses in the Netherlands, 2005-2008

Human monoclonal antibodies in single chain fragment variable format with potent neutralization activity against influenza virus H5N1

In vitro and in vivo characterization of new swine-origin H1N1 influenza viruses

Antigenic and Genetic Characteristics of Swine-Origin 2009 A(H1N1) Influenza Viruses Circulating in Humans

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Long-lasting immunogenicity of a virosomal vaccine in older children and young adults with type I diabetes mellitus

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MicroRNA-mediated species-specific attenuation of influenza A virus

**Titre** : MicroRNA-mediated species-specific attenuation of influenza A virus

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**Source** : Nature biotechnology; vol. 27; no. 6; pp. 572-576
**ISSN** : 1087-0156
**CODEN** : NABIF9
**Date de publication** : 2009
**Pays de publication** : USA
**Langue(s)** : ENG
**Type de document** : P
**Nombre de références** : 25 ref.

**Résumé** : Influenza A virus leads to yearly epidemics and sporadic pandemics. Present prophylactic strategies focus on egg-grown, live, attenuated influenza vaccines (LAIVs), in which attenuation is generated by conferring temperature sensitivity onto the virus. Here we describe an alternative approach to attenuating influenza A virus based on microRNA-mediated gene silencing. By incorporating nonavian microRNA response elements (MREs) into the open-reading frame of the viral nucleoprotein, we generate reassortant LAIVs for H1N1 and H5N1 that are attenuated in mice but not in eggs. MRE-based LAIVs show a greater than two-log reduction in mortality compared with control viruses lacking MREs and elicit a diverse antibody response. This approach might be combined with existing LAIVs to increase attenuation and improve vaccine safety.

**Code(s) de classement** : 002A31D01G; 215

**Descripteurs anglais**
- Micro RNA; Attenuation; Species specificity; Influenza A virus

**Descripteurs français**
- Micro ARN; Atténuation; Spécificité espèce; Virus grippal A

**Localisation** : INIST-19676, 354000188549360120
**Origine de la notice** : INIST
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Pour les soignants, masques chirurgicaux ou masques FFP2 ?; La grippe A/H1N1 2009 : où en est-on ? Acte 2

Titre : Pour les soignants, masques chirurgicaux ou masques FFP2 ?; La grippe A/H1N1 2009 : où en est-on ? Acte 2

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Source : Médecine & enfance; vol. 29; no. OCT; pp. 14-15
ISSN : 0291-0233
Date de publication : 2009
Pays de publication : FRA
Langue(s) : FRE
Type de document : P
Nombre de références : 1 ref.

Code(s) de classement : 002B01; 002B30A05

Descriptor(s) anglais
Descriptor(s) : Health staff; Surgical mask; Pediatrics; Child
Desc. génériques : Human

Descriptor(s) français
Descriptor(s) : Personnel sanitaire; Masque chirurgical; Pédiatrie; Enfant
Desc. génériques : Homme

Localisation : INIST-22961, 354000171169310050
Origine de la notice : INIST
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Prévention et prise en charge de la grippe A (H1N1) 2009: mise à jour; La grippe A/H1N1 2009 : où en est-on ? Acte 2

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Auteur(s) : COHEN (R.); COHEN (R.), limin.
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Source : Médecine & enfance; vol. 29; no. OCT; pp. 9-14
ISSN : 0291-0233
Date de publication : 2009
Pays de publication : FRA
Langue(s) : FRE
Type de document : P
Nombre de références : 12 ref.

Code(s) de classement : 002B01; 002B30A03; 002B30A11

Descriputeur(s) anglais
Descriputeur(s) : Prevention; Public health; Clinical management; Influenza A; 2009; Updating; Pediatrics; Child
Desc. génériques : Viral disease; Infection; Human

Descriputeur(s) français
Descriputeur(s) : Prévention; Santé publique; Conduite à tenir; Grippe A; 2009; Mise à jour; Pédiatrie; Enfant; Prise en charge
Desc. génériques : Virose; Infection; Homme

Localisation : INIST-22961, 354000171169310040
Origine de la notice : INIST
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Vaccin antipneumococcique polysaccharidique (Pneumo 23®); La grippe A/H1N1 2009 : où en est-on ? Acte 2

Titre : Vaccin antipneumococcique polysaccharidique (Pneumo 23®); La grippe A/H1N1 2009 : où en est-on ? Acte 2

Auteur(s) : COHEN (R.); COHEN (R.), limin.
Affiliation(s) : Service de microbiologie, CHI Créteil, FRA; Service de microbiologie, CHI Créteil, FRA

Source : Médecine & enfance; vol. 29; no. OCT; pp. 8-9
ISSN : 0291-0233
Date de publication : 2009
Pays de publication : FRA
Langue(s) : FRE
Type de document : P

Code(s) de classement : 002B01

Descriputeur(s) anglais
Descriputeur(s) : Vaccine; Pediatrics; Child
Desc. génériques : Human

Descriputeur(s) français
Descriputeur(s) : Vaccin; Pédiatrie; Enfant
Desc. génériques : Homme

Localisation : INIST-22961, 354000171169310030
Origine de la notice : INIST
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Les vaccins contre A/H1N1v; La grippe A/H1N1 2009 : où en est-on ?

Acte 2

Titre : Les vaccins contre A/H1N1v; La grippe A/H1N1 2009 : où en est-on ? Acte 2

Auteur(s) : COHEN (R.); WEIL-OLIVIER (C.); GRIMPREL (E.); COHEN (R.), limin.
Affiliation(s) : Service de microbiologie, CHI Créteil, FRA; Service de microbiologie, CHI Créteil, FRA

Source : Médecine & enfance; vol. 29; no. OCT; pp. 4-6
ISSN : 0291-0233
Date de publication : 2009
Pays de publication : FRA
Langue(s) : FRE
Type de document : P
Nombre de références : 9 ref.

Code(s) de classement : 002B01

Descripteur(s) anglais

Descripteur(s) : Vaccine; Pediatrics; Child
Desc. génériques : Human

Descripteur(s) français

Descripteur(s) : Vaccin; Pédiatrie; Enfant
Desc. génériques : Homme

Localisation : INIST-22961, 354000171169310010
Origine de la notice : INIST
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La grippe A/H1N1 2009 : où en est-on ? Acte 2

Titre : La grippe A/H1N1 2009 : où en est-on ? Acte 2

Auteur(s) : COHEN (R.), limin.
Affiliation(s) : Service de microbiologie, CHI Créteil, FRA

Source : Médecine & enfance; vol. 29; no. OCT; 14 p.
ISSN : 0291-0233
Date de publication : 2009
Pays de publication : FRA
Langue(s) : FRE
Type de document : P
Nombre de références : dissem.

Code(s) de classement : 002B01

Descrip teur(s) anglais
  Description(s) : Pediatrics; Child
  Desc. génériques : Human

Descrip teur(s) français
  Description(s) : Pédiatrie; Enfant
  Desc. génériques : Homme

Localisation : INIST-22961, 354000171169310000
Origine de la notice : INIST
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16 alpha -Bromoepiandrosterone (HE2000) limits non-productive inflammation and stimulates immunity in lungs

Titre : 16 alpha -Bromoepiandrosterone (HE2000) limits non-productive inflammation and stimulates immunity in lungs

Auteur(s) : NICOLETTI (F.); CONRAD (D.); WANG (A.); PIETERS (R.); MANGANO (K.); VAN HEECKEREN (A.); WHITE (S. K.); FRINCKE (J.); READING (C. L.); AUCI (D. L.); STICKNEY (D.)

Affiliation(s) : Department of Biomedical Sciences, School of Medicine, University of Catania, Catania, ITA; San Diego VA Healthcare System, USA; HollisEden Pharmaceuticals, San Diego, CA, USA; Case Western Reserve University School of Medicine, Cleveland, OH, USA; IRAS-Immunotoxicology Utrecht University Utrecht, NLD

Source : Clinical and experimental immunology : (Print); vol. 158; no. 3; pp. 308-316
ISSN : 0009-9104
CODEN : CEXIAL
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 20 ref.

Résumé : 16 alpha -Bromoepiandrosterone (HE2000) is a synthetic steroid that limits non-productive inflammation, enhances protective immunity and improves survival in clinical studies of patients with human immunodeficiency virus (HIV), malaria and tuberculosis infections. We now show that HE2000 decreased nitric oxide production by lipopolysaccharide (LPS)-stimulated RAW264.7 cells. Treatment with HE2000 also reduced non-productive inflammation associated with carrageenan-induced pleurisy and LPS-induced lung injury in mice. In the hapten-carrier reporter antigen popliteal lymph node assay, HE2000 increased absolute numbers of lymphocytes, antigen-presenting cells, hapten-specific immunoglobulin (Ig)M antibody-forming cells and shifted the interferon (IFN)-gamma / interleukin (IL)-4 balance towards IFN-gamma production. In the cystic fibrosis transmembrane conductance regulator (CFTR-/-) mouse model of acute Pseudomonas aeruginosa infection, treatment with HE2000 consistently reduced bacterial burden in lungs. All HE2000 effects were dose-dependent. In H1N1 infection in mice, HE2000 was safe but not effective as a monotherapy, as treatment did not effect survival. HE2000 reduced mortality related to excessive inflammation and opportunistic lung infections in animals and patients, and this might extend to those with H1N1 influenza infection.

Code(s) de classement : 002A02; 002B05C02C

Descriputeur(s) anglais
Descr. : Inflammation; Immunity; Lung; Influenza; Steroid; Biochemistry
Desc. génériques : Viral disease; Infection; Respiratory system

Descriputeur(s) français
Descr. : Inflammation; Immunité; Poumon; Grippe; Stéroïde; Biochimie
Desc. génériques : Virose; Infection; Appareil respiratoire

Localisation : INIST-12690, 354000170149790080
Origine de la notice : INIST
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Detection and subtyping of influenza A virus based on a short oligonucleotide microarray

**Titre** : Detection and subtyping of influenza A virus based on a short oligonucleotide microarray

**Auteur(s)** : XIHAN LI; XIAN QI; LV MIAO; YU WANG; FANGZHENG LIU; HONGWEI GU; SANGWEI LU; YONGHUA YANG; FENYONG LIU

**Affiliation(s)** : Institute of Virology, State Key Laboratory of Pharmaceutical Biotechnology, School of Life Sciences, Nanjing University, Nanjing, Jiangsu 210093, CHN; Taizhou Affynigen Biotechnologies, Inc., Taizhou, Jiangsu 225300, CHN; Taizhou Institute of Virology, Taizhou, Jiangsu 225300, CHN; Jiangsu Center for Disease Control and Prevention, Nanjing, Jiangsu 210009, CHN; Division of Infectious Diseases, School of Public Health, University of California, Berkeley, CA 94720, USA

**Source** : Diagnostic microbiology and infectious disease; vol. 65; no. 3; pp. 261-270

**ISSN** : 0732-8893

**CODEN** : DMIDDZ

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 1 p.

**Résumé** : We report the design and characterization of a microarray with 46 short virus-specific oligonucleotides for detecting influenza A virus of 5 subtypes: H1N1, H1N2, H3N2, H5N1, and H9N2. A unique combination of 3 specific modifications was introduced into the microarray assay: (1) short probes of 19 to 27 nucleotides, (2) simple amplification of full-length hemagglutinin and neuraminidase cDNAs with universal primers, and (3) Klenow-mediated labeling and further amplification of the samples before hybridization. The assay correctly and specifically detected and subtyped 11 different influenza A isolates from human, avian, and swine species representing the 5 subtypes. When tested with 225 clinical samples, 20 were detected to be positive using our microarray-based assay, whereas only 10 were positive by the conventional culture method. The entire analysis was completed within 7 h. Thus, these modifications result in a specific, sensitive, and rapid microarray assay and may be used for constructing microarrays for the detection of all influenza subtypes and strains.

**Code(s) de classement** : 002A05C10; 002B05

**Descripteur(s) anglais**

- **Descriputeur(s)** : Influenza A virus; Detection; Microbiology; Infection
- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus

**Descripteur(s) français**

- **Descriputeur(s)** : Virus grippal A; Détectioin; Microbiologie; Infection
- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus

**Localisation** : INIST-20217, 354000170149380070

**Origine de la notice** : INIST

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(CELVAPAN°, FOCETRIA°, PANDEMRIX°, PANENZA°) vaccins grippaux H1N1v : Vacciner les personnes à risque élevé de complication grave, avec des préférences quant au vaccin;

(CELVAPAN°, FOCETRIA°, PANDEMRIX°, PANENZA°) H1N1v flu vaccines : Inoculate the persons at high risk of severe complication, with preferences as for the vaccine

Titre : (CELVAPAN°, FOCETRIA°, PANDEMRIX°, PANENZA°) vaccins grippaux H1N1v : Vacciner les personnes à risque élevé de complication grave, avec des préférences quant au vaccin; (CELVAPAN°, FOCETRIA°, PANDEMRIX°, PANENZA°) H1N1v flu vaccines : Inoculate the persons at high risk of severe complication, with preferences as for the vaccine

Source : La Revue Prescrire; vol. 29; no. 313; pp. 806-810
ISSN : 0247-7750
Date de publication : 2009
Pays de publication : FRA
Langue(s) : FRE
Type de document : P
Nombre de références : 23 ref.

Résumé : La grippe due au virus A/H1N1 de 2009 (H1N1v) n'a pas de gravité clinique particulière par rapport à la grippe saisonnière, mais le nombre de personnes infectées risque d'être plus important. Les mesures physiques de prévention (principalement le lavage des mains) sont d'efficacité incomplète, et parfois difficiles à mettre en œuvre. Cercle noir Plusieurs vaccins grippaux monovalents inactivés contre le virus H1N1v sont autorisés ou annoncés d'ici la fin de l'année 2009. Ils diffèrent sur plusieurs critères, tels que : type de vaccin (virus entier, fragmenté, ou à "sous-unités"), présence ou non d'adjuvant lipidique (visant à amplifier la réponse immunitaire et à augmenter le rendement de production), présentations unidoses ou multidoses, conservateurs ou non. Cercle noir Les agences du médicament ont mis en place des procédures accélérées pour évaluer les données fournies par les firmes et permettre une commercialisation rapide des vaccins grippaux H1N1v. Au 30 septembre 2009, seuls quelques résultats préliminaires d'études d'immunogénicité à court terme chez des personnes en bonne santé sont publiés. Cercle noir Les vaccins grippaux H1N1v à virus fragmenté ou à "sous-unités" sans adjuvant s'approchent à ceux habituellement utilisés contre la grippe saisonnière. Selon des résultats préliminaires, la réponse immunitaire a été considérée satisfaisante chez plus des trois quarts de 240 adultes âgés de moins de 65 ans ayant reçu un vaccin H1N1v de ce type. Selon les résultats préliminaires d'une autre étude chez 70 enfants ayant reçu un autre vaccin H1N1v du même type, la réponse a paru, comme prévisible, moindre chez les plus jeunes. Cercle noir Un vaccin grippal avec adjuvant lipidique MF59C.1 est commercialisé contre la grippe saisonnière depuis plusieurs années. Dans une étude, la réponse a été considérée satisfaisante chez plus des trois quarts de 100 adultes âgés de moins de 50 ans ayant reçu un vaccin H1N1v de ce type. L'adjuvant lipidique AS03 est de composition voisine de celle de l'adjuvant MF59C.1, laissant présumer un effet immunogène voisin. Cercle noir Au 30 septembre 2009, on ne dispose d'aucune donnée d'évaluation concernant le vaccin H1N1v à virus entier, seul vaccin grippal de ce type. Cercle noir Dans les études d'immunogénicité chez les adultes, les effets indésirables ont été ceux prévisibles (réactions locales et douleurs musculaires le plus souvent). La fréquence a paru plus élevée avec un adjuvant lipidique. L'adjuvant MF59C.1 n'expose que rarement à des effets indésirables systématiques graves, et bénéficie d'un recul plus important que l'adjuvant AS03. Cercle noir Chez les nourrissons et les femmes enceintes, la présence d'adjuvant lipidique dans les vaccins grippaux H1N1v soulève des interrogations en termes immunitaires, et d'éventuelles convulsions fébriles du nourrisson. Cercle noir Une surveillance active des effets indésirables neurologiques, tels que le syndrome de Guillain-Barré, est de mise comme pour tous les autres vaccins grippaux, et surtout avec le vaccin à virus entier. Cercle noir Une présentation unidosée en seringue préremplie prête à l'emploi est préférable pour mettre à l'abri d'une contamination microbienne et des risques liés à un conservateur. Cercle noir En pratique, bien qu'encore parcellaires, les données disponibles au 30 septembre 2009 justifient une vaccination des personnes à risque élevé de complication grave de la grippe H1N1v, et aussi de celles qui

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les entourent et qui les soignent. Plusieurs vaccins sont proposés. Le vaccin doit être choisi, selon les disponibilités, pour réduire au minimum les risques d'effets indésirables, notamment chez les nourrissons et les femmes enceintes jugés à risque: c'est-à-dire de préférence un vaccin à virus fragmenté sans adjuvant.

**Code(s) de classement :** 002A05C07; 002B30A03B; 002B02U10; 002B05C02C

**Descripenteur(s) anglais**
- **Descripenteur(s) :** Vaccine; High risk; Complication; Preference; Vaccination; Influenzavirus; Recommendation; Application method; Human; Risk factor; Immunological adjuvant; Route of administration; Influenza A; Secondary effect; Commercial form
- **Desc. génériques :** Orthomyxoviridae; Virus; Viral disease; Infection

**Descripenteur(s) français**
- **Descripenteur(s) :** Vaccin; Risque élevé; Complication; Préférence; Vaccination; Influenzavirus; Recommandation; Modalité traitement; Homme; Facteur risque; Adjuvant immunologique; Voie administration; Grippe A; Effet secondaire; Forme commerciale; Influenzavirus A(H1N1)
- **Desc. génériques :** Orthomyxoviridae; Virus; Virose; Infection

**Localisation :** INIST-21322, 354000171228480010
**Origine de la notice :** INIST
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Syntheses and biological evaluations of carbosilane dendrimers uniformly functionalized with sialyl alpha (2->3) lactose moieties as inhibitors for human influenza viruses

Titre : Syntheses and biological evaluations of carbosilane dendrimers uniformly functionalized with sialyl alpha (2->3) lactose moieties as inhibitors for human influenza viruses

Auteur(s) : OKA (Hiroyuki); ONAGA (Tomotsune); KOYAMA (Tetsuo); GUO (Chao-Tan); SUZUKI (Yasuo); ESUMI (Yasuaki); HATANO (Ken); TERUNUMA (Daiyo); MATSUOKA (Koji)

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Source : Bioorganic & medicinal chemistry; vol. 17; no. 15; pp. 5465-5475

Résumé : A series of carbosilane dendrimers uniformly functionalized with sialyl lactose moieties (Neu5Ac alpha 2->3-Gal beta 1->4Glc) was systematically synthesized, and biological evaluations for anti-influenza virus activity using the glycodendrimers were performed. The results suggested that the glycodendrimers had unique biological activities depending on the form of their core frame, and Dumbbell(16)-amide type glycodendrimer 7 showed particularly strong inhibitory activities against human influenza viruses [A/PR/8/34 (H1N1) and A/Aichi/2/68 (H3N2)]. The results suggested that the structure-activity relationship (SAR) on the glycolibrary against various influenza viruses was observed, and dumbbell-shaped dendrimers as supporting carbohydrate moieties were found to be the most suitable core scaffolds in this study.

Code(s) de classement : 002B02S05

Desc. génériques : Orthomyxoviridae; Virus

Desc. génériques français : Orthomyxoviridae; Virus

Localisation : INIST-26564, 354000170922560130

Origine de la notice : INIST

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Swine Origin Influenza (Swine Flu)

Titre : Swine Origin Influenza (Swine Flu)

Auteur(s) : SEBASTIAN (Meghna R.); LODHA (Rakesh); KABRA (S. K.)
Affiliation(s) : Department of Pediatrics, All India Institute of Medical Sciences, New Delhi, IND

Source : Indian journal of pediatrics; vol. 76; no. 8; pp. 833-841
ISSN : 0019-5456
CODEN : IJPEA2
Date de publication : 2009
Pays de publication : DEU
Langue(s) : ENG
Type de document : P
Nombre de références : 34 ref.

Résumé : Swine origin influenza was first recognized in the border area of Mexico and United States in April 2009 and during a short span of two months became the first pandemic. The currently circulating strain of swine origin influenza virus of the H1 N1 strain has undergone triple reassortment and contains genes from the avian, swine and human viruses. It is transmitted by droplets or fomites. Incubation period is 2 to 7 days. Common clinical symptoms are indistinguishable by any viral respiratory illness, and include fever, cough, sore throat and myalgia. A feature seen more frequently with swine origin influenza is GI upset. Less than 10% of patients require hospitalization. Patients at risk of developing severe disease are - younger than five years, elderly, pregnant women, with chronic systemic illnesses, adolescents on aspirin. Of the severe manifestations of swine origin influenza, pneumonia and respiratory failure are the most common. Unusual symptoms reported are conjunctivitis, parotitis, hemophagocytic syndrome. Infants may present with fever and lethargy with no respiratory symptoms. Diagnosis is based on RT PCR. Viral culture or increasing neutralizing antibodies. Principle of treatment consist of isolation, universal precautions, good infection control practices, supportive care and use of antiviral drugs. Antiviral drugs effective against H1 N1 virus include: oseltamivir and zamanavir. With good supportive care case fatality is less than 1%. Preventive measures include: social distancing, practicing respiratory etiquette, hand hygiene and use of chemoprophylaxis with antiviral drugs. Vaccine against H1N1 is not available at present, but will be available in near future.

Code(s) de classement : 002B01; 002B05C02C

Descripteur(s) anglais
- Descripteur(s) : Influenza; Tropical medicine; Pediatrics
- Desc. génériques : Viral disease; Infection

Descripteur(s) français
- Descripteur(s) : Grippe; Médecine tropicale; Pédiatrie
- Desc. génériques : Virose; Infection

Localisation : INIST-6729, 354000170348110100
Origine de la notice : INIST
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**Infection of Human Retinal Pigment Epithelial Cells with Influenza A Viruses**

**Titre :** Infection of Human Retinal Pigment Epithelial Cells with Influenza A Viruses

**Auteur(s) :** MICHAELIS (Martin); GEILER (Janina); KLASSERT (Denise); DOERR (Hans Wilhelm); CINATL (Jindrich JR)

**Affiliation(s) :** Institut fiir Medizinische Virologie, Klinikum der J. W. Goethe-Universität, Frankfurt-am-Main, DEU

**Source :** Investigative ophthalmology & visual science; vol. 50; no. 11; pp. 5419-5425

**ISSN :** 0146-0404

**CODEN :** IOVSDA

**Date de publication :** 2009

**Pays de publication :** USA

**Langue(s) :** ENG

**Type de document :** P

**Nombre de références :** 49 ref.

**Résumé :** PURPOSE. Ocular involvement in influenza A virus diseases is common but usually limited to mild conjunctivitis. Rarely, inflammation of the choriocapillaris may result in atrophy of the retinal pigment epithelium (RPE). Primary human retinal pigment epithelial (RPE) cells were infected with seasonal (H1N1 A/New Caledonia/20/99, H3N2 A/California/7/2004) or highly pathogenic avian H5N1 (A/Thailand/1(Kan-1)/04, A/Vietnam/1203/04, A/Vietnam/1194/04) influenza strains. METHODS. Influenza A virus replication was studied by investigation of cytopathogenic effects, immune staining for influenza A virus nucleoprotein, determination of virus titers, and electron microscopy. Apoptosis induction was examined by immune staining for activated caspase 3 and cleaved PARP. Proinflammatory gene expression was investigated by quantitative PCR. RESULTS. H5N1 but not seasonal influenza strains replicated to high titers (>10^8 TCID50/mL; 50% tissue culture infectious dose/milliliter) in RPE cells. H5N1 infection resulted in RPE cell apoptosis that was abolished by the antiviral drug ribavirin. Pretreatment with type I interferons (interferon- alpha and - beta ) or the type II interferon, (interferon-y), inhibited H5N1 replication. Moreover, H5N1 infection induced expression of proinflammatory genes (tumor necrosis factor- alpha , CXCL8, CXCL10, CXCL11, and interleukin-6), which was inhibited by ribavirin in a concentration-dependent manner. CONCLUSIONS. A novel cell type derived from the central nervous system was permissive to H5N1 influenza virus replication. This findings supports those suggesting H5N1 influenza strains to own a greater potential to spread to nonrespiratory tissues than seasonal human influenza viruses. Moreover, the data warrant the further study of the role of influenza A virus replication in retinal diseases associated with influenza A virus infections.

**Code(s) de classement :** 002B09; 002A25I; 002B05C02C

**Descripenteur(s) anglais**

Descripteur(s) : Infection; Human; Retina; Pigment cell; Epithelial cell; Influenza A; Ophthalmology

Desc. génériques : Viral disease

**Descripenteur(s) français**

Descripteur(s) : Infection; Homme; Rétine; Cellule pigmentaire; Cellule épithéliale; Grippe A; Ophtalmologie

Desc. génériques : Virose

**Localisation :** INIST-12095, 354000170132370530

**Origine de la notice :** INIST

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Antibodies to PB1-F2 protein are induced in response to influenza A virus infection

Titre : Antibodies to PB1-F2 protein are induced in response to influenza A virus infection

Auteur(s) : KREJNUSOVA (Ingrid); GOCNIKOVA (Hana); BYSTRICKA (Magdaléna); BLASKOVICOVA (Hana); POLAKOVA (Katarína); YEWDELL (Jonathan); BENNINK (Jack); RUSS (Gustáv)
Affiliation(s) : Institute of Virology, Slovak Academy of Sciences, Bratislava, SVK; Office for Public Health of Slovak Republic, Bratislava, SVK; Cancer Research Institute, Slovak Academy of Sciences, Bratislava, SVK; Laboratory of Viral Diseases, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD, USA
Source : Archives of virology; vol. 154; no. 10; pp. 1599-1604
ISSN : 0304-8608
Date de publication : 2009
Pays de publication : AUT
Langue(s) : ENG
Type de document : P
Nombre de références : 25 ref.

Résumé : PB1-F2 is a small influenza A virus (IAV) protein encoded by an alternative (+1) reading frame of the PB1 gene. While dispensable for IAV replication in cultured cells, PB1-F2 has been implicated in IAV pathogenicity. To better understand PB1-F2 expression in vivo and its immunogenicity, we analyzed anti-PB1-F2 antibodies (Abs) in sera of mice infected intranasally (i.n.) with A/PR/8/34 (H1N1) virus and human acute and convalescent sera collected from the influenza H3N2 winter 2003-2004 epidemic. We explored a number of methods for detecting anti-PB1-F2 Abs, finding that PB1-F2-specific Abs could clearly be detected via immunoprecipitation or immunofluorescence assays using both immune mouse and human convalescent sera. Importantly, paired human sera exhibited similar increases in HI titers and PB1-F2-specific Abs. This study indicates that PB1-F2 is expressed in sufficient quantities in mice and humans infected with IAV to elicit an Ab response, supporting the biological relevance of this intriguing accessory protein.

Code(s) de classement : 002A05C10

Descriptor(s) anglais
Descriptor(s) : Influenza A virus; Antibody; Protein; Influenza A
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Viral disease; Infection

Descriptor(s) français
Descriptor(s) : Virus grippal A; Anticorps; Protéine; Grippe A
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Virose; Infection

Localisation : INIST-6355, 354000171236630030
Origine de la notice : INIST
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Pseudoparticle neutralization is a reliable assay to measure immunity and cross-reactivity to H5N1 influenza viruses

Titre : Pseudoparticle neutralization is a reliable assay to measure immunity and cross-reactivity to H5N1 influenza viruses

Auteur(s) : ALBERINI (Isabella); DEL TORDELLO (Elena); FASOLO (Alba); TEMPERTON (Nigel J.); GALLI (Grazia); GENTILE (Chiara); MONTOMOLI (Emanuele); HILBERT (Anne K.); BANZHOFF (Angelika); DEL GIUDICE (Giuseppe); DONNELLY (John J.); RAPPUOLI (Rino); CAPECCHI (Barbara)

Affiliation(s) : Novartis Vaccines, Siena, ITA; Centre for Medical Molecular Virology, Division of Infection and Immunity, University College London, GBR; Department of Physiopathology, Experimental Medicine and Public Health, Laboratory of Molecular Epidemiology, University of Siena, Siena, ITA; Novartis Vaccines, Marburg, DEU

Source : Vaccine; vol. 27; no. 43; pp. 5998-6003

Résumé : The standard serological methods present limitations for the measurement of immunity against H5N1 influenza strains. The hemagglutination inhibition (HI) assay lacks sensitivity and requires standardization, while the viral micro-neutralization (MN) assay needs handling of live virus. We produced pseudoparticles expressing hemagglutinin from clades 1 or 2 H5N1 in order to measure neutralizing antibodies in human sera after prime-boost vaccination with plain or MF59-adjuvanted H5N1 clade 1 subunit vaccines. Titers measured by pseudoparticle neutralization (PPN) assay significantly correlated with those measured by HI, single radial haemolysis or MN, with a PPN titer of 1:357 corresponding to an MN titer of 1:80. Notably, results from the PPN assay, confirm that MF59-H5N1 vaccine induces potent and long-lasting neutralizing antibody responses not only against the vaccine strain, but also against several heterologous clade 2 strains. Overall, the PPN assay represents a valid alternative to conventional serological methods for the evaluation of H5N1 vaccine immunogenicity.


Auteur(s) : BOUSCAMBERT-DUCHAMP (M.); LINA (B.); MORFIN (F.); HAAS (H.), ed.
Collectivité(s) auteur : Groupe de pathologies infectieuses pédiatriques, FRA, org-cong.
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Source : Archives de pédiatrie : (Paris); vol. 16; no. SUP2
ISSN : 0929-693X
Date de publication : 2009
Pays de publication : FRA
Langue(s) : FRE
Langue(s) du résumé : eng
Type de document : P; C
Nombre de références : 17 ref.

Résumé : Les virus grippaux alimentent l'actualité, en particulier depuis l'émergence d'un sous-type potentiellement pandémique, le virus A (H5N1). Il s'agit d'un virus aviaire, responsable d'une épidémie sans précédent à l'origine, jusqu'en mai 2009, de 423 cas d'infections humaines. Ce virus est responsable d'une pneumonie d'évolution rapide vers un syndrome de détresse respiratoire aiguë, entraînant la mort dans 60 % des cas. Le tableau de défaillance multiorganique décrit, semble être dû à une dysrégulation de la production de cytokines. L'infection par le virus A (H5N1) touche principalement l'enfant et l'adulte jeune. Pour l'expliquer, différentes hypothèses sont évoquées concernant la capacité de ces patients à réguler leur production de cytokines ainsi qu'une variation dans la répartition des récepteurs cellulaires. En fait, cette susceptibilité particulière de l'enfant semble être liée à des comportements à risque plus qu'à une réalité physiologique. Aujourd'hui, il est possible de prendre en charge efficacement un cas d'infection humaine par le virus A (H5N1) et les protocoles thérapeutiques d'utilisation des inhibiteurs de la neuraminidase ont été adaptés à l'enfant. Si à l'heure actuelle, le risque de survenue d'une pandémie grippale semble être associé au nouveau virus influenza A (H1N1), il est indispensable de continuer à surveiller activement la circulation du virus A (H5N1) ainsi que l'évolution génétique de ce virus hautement pathogène.

Code(s) de classement : 002B30A11; 002B01; 002B05C02C

Descrripteur(s) anglais
- Descriptive(s) : Avian influenza; Zoonosis; Child; Pediatrics; 2008; Public health; Congress; Virus; France; Influenzavirus A(H5N1)
- Desc. génériques : Viral disease; Infection; Human; Europe

Descrripteur(s) français
- Descriptive(s) : Grippe aviaire; Zoonose; Enfant; Pédiatrie; 2008; Santé publique; Congrès; Virus; France; Influenzavirus A(H5N1)
- Desc. génériques : Virose; Infection; Homme; Europe

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A DNA biosensor based on the detection of doxorubicin-conjugated Ag nanoparticle labels using solid-state voltammetry

**Titre** : A DNA biosensor based on the detection of doxorubicin-conjugated Ag nanoparticle labels using solid-state voltammetry

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**Source** : Biosensors & bioelectronics; vol. 25; no. 2; pp. 282-287

**ISSN** : 0956-5663

**Date de publication** : 2009

**Pays de publication** : NLD

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 1/2 p.

**Résumé** : This report describes an electrochemical biosensor for the detection of short DNA oligonucleotide of the avian flu virus H5N1 with sequence 5'-CCA AGC AAC AGA CTC AAA-3'. To fabricate this DNA biosensor, a gold (Au) electrode surface was modified with thiolated DNA probes with a sequence complementary to the target DNA. This modified Au electrode was incubated in a buffer solution containing the target DNA to form double-stranded DNA (ds-DNA) through hybridization. The ds-DNA on the electrode surface was then labeled with silver nanoparticles conjugated with a well-known DNA intercalator, doxorubicin. By performing cyclic voltammetry in an aqueous KCl solution (0.3 M), the silver nanoparticle labels were detected as a result of the highly characteristic solid-state Ag/AgCl redox process. The signal obtained was subsequently used to quantify the amount of DNA. A detection limit of 1 pM has been achieved with this new DNA biosensor.

**Code(s) de classement** : 002A31C09B; 215

**Descripteur(s) français**

- **Descripteur(s) anglais**
  - **Descripteur(s) :** DNA; Biosensor; Detection; Nanoparticle; Solid state; Virus; Voltammetry; Electrochemistry; Silver; H5N1; Influenzavirus A(H5N1)

**Localisation** : INIST-20668, 354000170302230030

**Origine de la notice** : INIST

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Surveillance for neuraminidase-inhibitor-resistant influenza viruses in Japan, 1996-2007


**Auteur(s) :** TASHIRO (Masato); MCKIMM-BRESCHKIN (Jennifer L.); SAIITO (Takehiko); KLIMOV (Alexander); MACKEN (Catherine); ZAMBON (Maria); HOYDEN (Frederick G.)

**Collectivité(s) auteur :** Neuraminidase Inhibitor Susceptibility Network, INC

**Affiliation(s) :** WHO Collaborating Center for Reference Et Research on Influenza, National Institute of Infectious Diseases, Tokyo, JPN; CSIRO Molecular and Health Technologies, Parkville, AUS; WHO Collaborating Center for Surveillance, Epidemiology and Control of Influenza, Influenza Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA; Los Alamos National Laboratory, Los Alamos, NM, USA; Health Protection Agency, Colindale, London, GBR; University of Virginia School of Medicine, Charlottesville, VA, USA

**Source** : Antiviral therapy : (London); vol. 14; no. 6; pp. 751-761

**ISSN** : 1359-6535

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s) :** ENG

**Type de document** : P

**Nombre de références** : 51 ref.

**Résumé** : Background: High usage of the neuraminidase inhibitor (NAI) oseltamivir in Japan since 2003 led the Neuraminidase Inhibitor Susceptibility Network to assess the susceptibility of community isolates of influenza viruses to oseltamivir and zanamivir. Methods: Isolates were tested by the enzyme inhibition assay and by neuraminidase (NA) sequence analysis. Results: Among 1,141 A(H3N2) viruses and 171 type B viruses collected in Japan during the 2003-2004 season, 3 (0.3%) A(H3N2) isolates showed high 50% inhibitory concentrations (IC50) to oseltamivir. Each possessed a known resistance NA mutation at R292K or E119V. During the 2004-2005 season, no resistance was found among 567 influenza A(H3N2) or 60 A(H1N1) isolates, but 1 of 58 influenza B isolates had an NAI resistance mutation (D197N). Sequence analysis found that 4 (3%) of 132 A(H1N1) viruses from 2005-2006 had known NA resistance mutations (all H274Y), but no additional resistant isolates were detected from that or the subsequent 2006-2007 season. Concurrent testing of a selection of 500 influenza B viruses from 2000 to 2006 showed significant variations between seasons in both oseltamivir and zanamivir IC50 values, but no persistent increases over this period. Conclusions: Our findings suggested possible low-level transmission of resistant variants from oseltamivir-treated patients in several seasons in Japan but no sustained reductions in NAI susceptibility or consistently increased frequency of detecting resistant variants for any strain or subtype, despite high levels of drug use. In particular, although oseltamivir-resistant A(H1N1) viruses with the H274Y mutation spread globally in 2007-2008, we found little evidence for increasing levels of resistant A(H1N1) variants in Japan in preceding years.

**Code(s) de classement** : 002B02S05; 002B05C02C

**Desc. génériques** : Viral disease; Infection; Asia

**Descripteur(s) anglais**

- **Descripteur(s) :** Surveillance; Neuraminidase inhibitor; Resistance; Influenza; Japan
- **Desc. génériques** : Viral disease; Infection; Asia

**Descripteur(s) français**

- **Descripteur(s) :** Surveillance; Inhibiteur neuraminidase; Résistance; Grippe; Japon
- **Desc. génériques** : Virose; Infection; Asie

**Localisation** : INIST-27047, 354000170070070030

**Origine de la notice** : INIST

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Synthesis of sialic acid derivatives having a C=C double bond substituted at the C-5 position and their glycopolymers

**Titre** : Synthesis of sialic acid derivatives having a C=C double bond substituted at the C-5 position and their glycopolymers

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**Source** : Bioorganic & medicinal chemistry letters : (Print); vol. 19; no. 17; pp. 5105-5108

**ISSN** : 0960-894X

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 19 ref.

**Résumé** : Glycomonomers of sialic acid in which the acetamide group at C-5 was converted into two kinds of C=C double bond substituents were prepared and the fully protected glycomonomers were directly polymerized before deprotection steps. Radical polymerization with acrylamide in DMF in the presence of ammonium persulfate and N,N,N',N'-tetramethylethylenediamine proceeded smoothly and gave corresponding sialopolymers. Interestingly glycomonomers had hemagglutination inhibitory activities not only for H1N1 but also for H3N2 of human influenza virus strains.

**Code(s) de classement** : 002B02S05

**Descripteur(s) anglais**

- **Descriptor(s) :** Chemical synthesis; Sialic acid; Avian influenzavirus; Radical copolymerization; Structure activity relation; Acrylamide derivative copolymer; Thioglycoside; Hemagglutination; Inhibition; Antiviral; Influenza A virus; In vitro
- **Desc. génériques :** Influenzavirus A; Orthomyxoviridae; Virus

**Descripteur(s) français**

- **Descripette(s) :** Synthèse chimique; Acide sialique; Influenzavirus aviaire; Copolymérisation radicale; Relation structure activité; Acrylamide dérivé copolymer; Thioglycoside; Hémagglutination; Inhibition; Antiviral; Virus grippal A; In vitro; Glycopolymère; 2-Thionon-2-ulparyanosidonique acide dérivé; Non-2-ulopyranaridosidonique acide dérivé
- **Desc. génériques :** Influenzavirus A; Orthomyxoviridae; Virus

**Localisation** : INIST-22446, 354000171844260480

**Origine de la notice** : INIST

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Pandemic (H1N1) 2009 influenza: experience from the critical care unit

Titre : Pandemic (H1N1) 2009 influenza: experience from the critical care unit

Auteur(s) : PATEL (M.); DENNIS (A.); FLUTTER (C.); THORNTON (S.); D'MELLO (O.); SHERWOOD (N.)
Affiliation(s) : City Hospital, Birmingham, GBR

Source : Anaesthesia; vol. 64; no. 11; pp. 1241-1245
ISSN : 0003-2409
CODEN : ANASAB
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 14 ref.

Résumé : This case series details experience of critical care admissions with pandemic (H1N1) 2009 influenza from an intensive care unit in the West Midlands. We present four critically ill patients admitted with severe hypoxia. Two of the patients failed a trial of continuous positive airway pressure and all underwent controlled ventilation within 24 h of admission. Bilevel and high frequency oscillatory ventilation were the most useful modes. Our patients generally had one organ failure and were ventilator dependent for relatively short periods of time. Three of the patients made a full recovery and one required ongoing dialysis. We also discuss service planning and our response to the pandemic. We were well prepared with stocks of personal protective equipment but had to modify plans as the outbreak progressed. Our cases and discussion provide useful information for other intensive care units preparing for the predicted autumn surge of H1N1 cases.

Code(s) de classement : 002B27A

Descripateur(s) anglais
Descriputeur(s) : Influenza; Anesthesia
Desc. génériques : Viral disease; Infection

Descriputeur(s) français
Descriputeur(s) : Grippe; Anesthésie
Desc. génériques : Virose; Infection

Localisation : INIST-7599, 354000170092760150
Origine de la notice : INIST
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Characterization of triple reassortant H1N1 influenza A viruses from swine in Ohio

Titre : Characterization of triple reassortant H1N1 influenza A viruses from swine in Ohio

Auteur(s) : YASSINE (H. M.); KHATRI (M.); ZHANG (Y. J.); LEE (C. W.); BYRUM (B. A.); O’QUIN (J.); SMITH (K. A.); SAIF (Y. M.)

Affiliation(s) : Food Animal Health Research Program, Ohio Agricultural Research and Development Center, The Ohio State University, 1680 Madison Avenue, Wooster, OH 44691, USA; Animal Disease Diagnostic Laboratory, Ohio Department of Agriculture, E. Main Street, Reynoldsburg, OH 43068, USA; Ohio Department of Health, E. Main Street, Reynoldsburg, OH, USA

Source : Veterinary microbiology : (Amsterdam); vol. 139; no. 1-2; pp. 132-139
ISSN : 0378-1135
CODEN : VMICDQ
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 3/4 p.

Résumé : An H1N1 influenza A virus, A/swine/Ohio/24366/07, was isolated from pigs in an Ohio county fair. Twenty-six people who came in contact with the infected pigs developed respiratory disease and two of these people were laboratory confirmed as H1N1 by the Centers for Disease Control and Prevention (CDC). The A/swine/Ohio/24366/07 virus we isolated from swine was shown at the CDC to have 100% identical genome sequence to the human virus associated with the county fair. This prompted us to characterize three swine and two human origin H1N1 influenza A viruses isolated at different time points in the State of Ohio. The three swine viruses were shown to be triple reassortant viruses harboring genes of human (PB1), swine (HA, NA, NP, M, and NS), and avian (PB2 and PA) lineage viruses. Although viruses evaluated in this study were isolated during a short time interval (3 years), genetic drift was observed within the HA and NA genes, including changes at the receptor binding and antigenic sites of HA1 protein. Nevertheless, all viruses exhibited antigenic similarity as evaluated with hemagglutination inhibition and virus neutralizing tests. Internal genes were similar to other reassortant viruses of various subtypes currently circulating in the United States. Interestingly, two of the swine viruses including the 2007 isolate replicated well in human airway epithelial cells, however, another virus isolated in 2006 showed very little replication.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Descripteur(s) : Influenza A virus; Swine; Ohio; Microbiology; Veterinary; Genetic reassortment
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; United States; North America; America

Descripteur(s) français

Descripteur(s) : Virus grippal A; Porcin; Ohio; Microbiologie; Vétérinaire; Réassortiment génétique
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Etats-Unis; Amérique du Nord; Amérique

Localisation : INIST-16884, 354000170065870160
Origine de la notice : INIST
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Four different sublineages of highly pathogenic avian influenza H5N1 introduced in Hungary in 2006-2007

Four different sublineages of highly pathogenic avian influenza H5N1 introduced in Hungary in 2006-2007

Auteur(s) : SZELECZKY (Zsófia); DAN (Adam); URSU (Krisztila); IVANICS (Eva); KISS (Istvan); ERDELYI (Karoly); BELAK (Sandor); MULLER (Claude P.); BROWN (Ian H.); BALINT (Adam)

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Source : Veterinary microbiology : (Amsterdam); vol. 139; no. 1-2; pp. 24-33

Résumé : Highly pathogenic avian influenza (HPAI) H5N1 viruses were introduced to Hungary during 2006-2007 in three separate waves. This study aimed at determining the full-length genomic coding regions of the index strains from these epizootics in order to: (i) understand the phylogenetic relationship to other European H5N1 isolates, (ii) elucidate the possible connection between the different outbreaks and (iii) determine the putative origin and way of introduction of the different virus variants. Molecular analysis of the HA gene of Hungarian HPAI isolates obtained from wild birds during the first introduction revealed two groups designated Hungarian1 (HUN1) and Hungarian2 (HUN2) within sublineage 2.2B and clade 2.2.1, respectively. Sequencing the whole coding region of the two index viruses A/mute swan/Hungary/3472/2006 and A/mute swan/4571/Hungary/2006 suggests the role of wild birds in the introduction of HUN1 and HUN2 viruses: the most similar isolates to HUN1 and HUN2 group were found in wild avian species in Croatia and Slovakia, respectively. The second introduction of HPAI H5N1 led to the largest epizootic in domestic waterfowl in Europe. The index strain of the epizootic A/goose/ Hungary/14756/2006 clustered to sublineage 2.2.A1 forming the Hungarian3 (HUN3) group. A common ancestry of HUN3 isolates with Bavarian strains is suggested as the most likely scenario of origin. Hungarian4 (HUN4) viruses isolated from the third introduction clustered with isolate A/turkey/United Kingdom/750/2007 forming a sublineage 2.2.A2. The origin and way of introduction of HUN4 viruses is still obscure, thus further genetic, phylogenetic, ecological and epidemiological data are required in order to elucidate it.

Code(s) de classement : 002A05C10
Evaluation of the efficacy and safety of a statin/caffeine combination against H5N1, H3N2 and H1N1 virus infection in BALB/c mice

**Titre** : Evaluation of the efficacy and safety of a statin/caffeine combination against H5N1, H3N2 and H1N1 virus infection in BALB/c mice

**Auteur(s)** : ZEYU LIU; ZHONGMIN GUO; GUOLING WANG; DINGMEI ZHANG; HONGXUAN HE; GUOWEI LI; YUGE LIU; HIGGINS (Denise); WALSH (Aoiffe); SHANAHAN-PRENDERGAST (Leo); JIAHAI LU

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**Source** : European journal of pharmaceutical sciences; vol. 38; no. 3; pp. 215-223

**ISSN** : 0928-0987

**Date de publication** : 2009

**Pays de publication** : IRL

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 3/4 p.

**Résumé** : The development of novel antiviral drugs is necessary for the prevention and treatment of a potential avian influenza pandemic. The aim of this study was to evaluate the efficacy and safety of a novel statin/caffeine combination against H5N1, H3N2 and H1 N1 virus infection in a murine model. In H5N1-, H3N2- and H1 N1-infected BALB/c mice, 50 μg statin/200 μg caffeine effectively ameliorated lung damage and inhibited viral replication and was at least as effective as oseltamivir and ribavirin. The statin/caffeine combination also appeared to be more effective when administered preventatively rather than as treatment. These findings provide justification for further research into this novel antiviral formulation.

**Code(s) de classement** : 002B02A03

**Descrip teur(s) anglais**

- **Descrip teur(s)** : Evaluation; Efficiency; Toxicity; Safety; Statin derivative; Caffeine; Viral disease; Animal; Mouse; Influenza; Oseltamivir; Ribavirin; Pharmaceutical technology; Antilipemic agent; Psychotropic; Respiratory analeptic; CNS stimulant; Antiviral

- **Desc. génériques** : Infection; Rodentia; Mammalia; Vertebrata; Xanthine derivatives; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor; Neuraminidase inhibitor; Nucleoside analog

**Descrip teur(s) français**

- **Descrip teur(s)** : Evaluation; Efficacité; Toxicité; Sécurité; Dérivé de la statine; Caféine; Virose; Animal; Souris; Grippé; Oséltamivir; Ribavirine; Technologie pharmaceutique; Hypolipémiante; Psychotrope; Analectique respiratoire; Stimulant SNC; Antiviral; Influenzavirus A(H3N2); Influenzavirus A(H1N1)

- **Desc. génériques** : Infection; Rodentia; Mammalia; Vertebrata; Dérivé de la xanthine; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme; Inhibiteur neuraminidase; Analogue de nucléoside

**Localisation** : INIST-26027, 354000170063630040

**Origine de la notice** : INIST

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Sequence diversity of the haemagglutinin open reading frame of recent highly pathogenic avian influenza H5N1 isolates from Egypt

**Titre** : Sequence diversity of the haemagglutinin open reading frame of recent highly pathogenic avian influenza H5N1 isolates from Egypt

**Auteur(s)** : ABDEL-MONEIM (Ahmed S.); SHANY (Salama A. S.); FEREIDOUNI (Sasan R.); EID (Bahaa T. M.); EL-KADY (Magdy F.); STARICK (Elke); HARDER (Timm); KEIL (Günther M.)

**Affiliation(s)** : Virology Department, Beni-Suef University, Beni-Suef 62511, EGY; Poultry Department, Faculty of Veterinary Medicine, Beni-Suef University, Beni-Suef 62511, EGY; Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Südufer 10, 17493 Greifswald-Insel Riems, DEU

**Source** : Archives of virology; vol. 154; no. 9; pp. 1559-1562

**ISSN** : 0304-8608

**Date de publication** : 2009

**Pays de publication** : AUT

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 15 ref.

**Résumé** : The sequences encoding the haemagglutinin (HA) of twelve H5N1 isolates obtained in 2006 and 2007 from different avian species in backyard holdings and poultry farms in Egypt revealed amino acid variations across the polypeptide and also in the polybasic cleavage motif of three of the isolates from backyard poultry with one, so far, unique mutation in an isolate from a chicken. The HAs of two isolates (A/goose/Egypt/R4/2007, A/chicken/Egypt/R3/2007) collected on the same day in the same village from two neighbouring houses were found to differ from each other. Five out of the seven nucleotide exchanges in these two isolates were translationally silent, and two resulted in amino acid substitutions: one in the polybasic cleavage motif and the other in the signal peptide. Circulation of different H5N1 strains possessing considerable variations in backyard poultry, particularly domestic waterfowl, draws attention to the evolution of H5N1 subtypes in Egypt.

**Code(s) de classement** : 002A05C10; 002A05C04

**Déscriputeur(s) anglais**

- **Desc. génériques** : Influenza A virus; Hemagglutinin; Open reading frame; Pathogenicity; Isolate; Egypt; Avian influenza
- **Desc. spécifique** : Influenza virus A; Orthomyxoviridae; Virus; Africa; Infection; Viral disease

**Déscriputeur(s) français**

- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Afrique; Infection; Virose
- **Desc. spécifique** : Virus grippal A; Hémagglutinine; Cadre lecture ouvert; Pouvoir pathogène; Isolat; Egypte; Grippe aviaire

**Localisation** : INIST-6355, 354000170011820250

**Origine de la notice** : INIST

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Novel H1N1 Pandemic: When Pigs Fly

**Titre**: Novel H1N1 Pandemic: When Pigs Fly

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**Source**: The Pediatric infectious disease journal; vol. 28; no. 10; pp. 911-914
**ISSN**: 0891-3668
**CODEN**: PIDJEV
**Date de publication**: 2009
**Pays de publication**: USA
**Langue(s)**: ENG
**Type de document**: P
**Nombre de références**: 12 ref.

**Code(s) de classement**: 002B05C02C

**Descripteur(s) anglais**
- **Descripteur(s)**: Influenza; Pig; Pediatrics; Animal
- **Desc. génériques**: Viral disease; Infection; Artiodactyla; Ungulata; Mammalia; Vertebrata

**Descripteur(s) français**
- **Descripteur(s)**: Grippe; Porc; Pédiatrie; Animal; Pandémie
- **Desc. génériques**: Virose; Infection; Artiodactyla; Ungulata; Mammalia; Vertebrata

**Localisation**: INIST-20356, 354000170045090110
**Origine de la notice**: INIST
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A Single-Amino-Acid Substitution in a Polymerase Protein of an H5N1 Influenza Virus Is Associated with Systemic Infection and Impaired T-Cell Activation in Mice

Titre : A Single-Amino-Acid Substitution in a Polymerase Protein of an H5N1 Influenza Virus Is Associated with Systemic Infection and Impaired T-Cell Activation in Mice

Auteur(s) : FORNEK (Jamie L.); GILLIM-ROSS (Laura); SANTOS (Celia); CARTER (Victoria); WARD (Jerrold M.); CHENG (Lily I.); PROLL (Sean); KATZE (Michael G.); SUBBARAO (Kanta)

Affiliation(s) : Department of Microbiology, University of Washington, Box 358070, Seattle, Washington 98195, USA; Laboratory of Infectious Diseases, NIAID, NIH, Bldg. 33, Room 3E13C_1, 33 North Dr., MSC 3203, Bethesda, Maryland 20892, USA; Comparative Medicine Branch, NIAID, NIH, Rockville, Maryland 20852, USA

Source : Journal of virology; vol. 83; no. 21; pp. 11102-11115

ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 30 ref.

Résumé : The transmission of H5N1 influenza viruses from birds to humans poses a significant public health threat. A substitution of glutamic acid for lysine at position 627 of the PB2 protein of H5N1 viruses has been identified as a virulence determinant. We utilized the BALB/c mouse model of H5N1 infection to examine how this substitution affects virus-host interactions and leads to systemic infection. Mice infected with H5N1 viruses containing lysine at amino acid 627 in the PB2 protein exhibited an increased severity of lesions in the lung parenchyma and the spleen, increased apoptosis in the lungs, and a decrease in oxygen saturation. Gene expression profiling revealed that T-cell receptor activation was impaired at 2 days postinfection (dpi) in the lungs of mice infected with these viruses. The inflammatory response was highly activated in the lungs of mice infected with these viruses and was sustained at 4 dpi. In the spleen, immune-related processes including NK cell cytotoxicity and antigen presentation were highly activated by 2 dpi. These differences are not attributable solely to differences in viral replication in the lungs but to an inefficient immune response early in infection as well. The timing and magnitude of the immune response to highly pathogenic influenza viruses is critical in determining the outcome of infection. The disruption of these factors by a single-amino-acid substitution in a polymerase protein of an influenza virus is associated with severe disease and correlates with the spread of the virus to extrapulmonary sites.

Code(s) de classement : 002A05C10

Descriputeur(s) anglais
Desc. associé: Avian influenza virus; Influenza A virus; Associated virus; Mouse; Protein; T-Lymphocyte; Animal; Viral disease
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Infection

Descriputeur(s) français
Desc. associé: Grippe aviaire; Virus grippe; Virus associé; Souris; Protéine T; Animal; Virose
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Infection

Localisation : INIST-13592, 354000170071970230
Origine de la notice : INIST
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Interdigitated array microelectrode based impedance immunosensor for detection of avian influenza virus H5N1

Titre : Interdigitated array microelectrode based impedance immunosensor for detection of avian influenza virus H5N1

Auteur(s) : RONGHUI WANG; YUN WANG; LASSITER (Kentu); YANBIN LI; HARGIS (Billy); TUNG (Steve); BERGHMAN (Luc); BOTTJE (Walter)

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Source : Talanta; vol. 79; no. 2; pp. 159-164
ISSN : 0039-9140
CODEN : TLNTA2
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 37 ref.

Résumé : Continuous outbreaks of avian influenza (AI) in recent years with increasing threat to animals and human health have warranted the urgent need for rapid detection of pathogenic AI viruses. In this study, an impedance immunosensor based on an interdigitated array (IDA) microelectrode was developed as a new application for sensitive, specific and rapid detection of avian influenza virus H5N1. Polyclonal antibodies against AI virus H5N1 surface antigen HA (Hemagglutinin) were oriented on the gold microelectrode surface through protein A. Target H5N1 viruses were then captured by the immobilized antibody, resulting in a change in the impedance of the IDA microelectrode surface. Red blood cells (RBCs) were used as biolabels for further amplification of the binding reaction of the antibody-antigen (virus). The binding of target AI H5N1 onto the antibody-modified IDA microelectrode surface was further confirmed by atomic force microscopy. The impedance immunosensor could detect the target AI H5N1 virus at a titer higher than 10^3 EID50/ml (EID50: 50% Egg Infective Dose) within 2 h. The response of the antibody-antigen (virus) interaction was shown to be virus titer-dependent, and a linear range for the titer of H5N1 virus was found between 10^3 and 10^7 EID50/ml. Equivalent circuit analysis indicated that the electron transfer resistance of the redox probe [Fe(CN)6]3-/4- and the double layer capacitance were responsible for the impedance change due to the protein A modification, antibody immobilization, BSA(bovine serum albumin) blocking, H5N1 viruses binding and RBCs amplification. No significant interference was observed from non-target RNA viruses such as Newcastle disease virus and Infectious Bronchitis disease virus. (The H5N1 used in the study was inactivated virus.).

Code(s) de classement : 001C04A

Descripteur(s) anglais

- Microelectrode; Impedance; Immunosensor; Gold; Immobilization; Atomic force microscopy; Equivalent circuit; Electron transfer; Double layers; Capacitance; Interference; Chemical sensor; Human; Antibody; Protein; Blood; Serum albumin

Descripteur(s) français

- Microélectrode; Impédance; Immunodétecteur; Or; Immobilisation; Microscopie force atomique; Schéma équivalent; Transfert électron; Couche double; Capacité électrique; Interférence; Capteur chimique; Homme; Anticorps; Protéine; Sang; Sérumalbumine

Localisation : INIST-9221, 354000187502660070
Humoral and Cellular Immune Responses after Influenza Vaccination in Kidney Transplant Recipients

Titre : Humoral and Cellular Immune Responses after Influenza Vaccination in Kidney Transplant Recipients

Auteur(s) : CANDON (S.); THERVET (E.); LEBON (P.); SUBERBIELLE (C.); ZUBER (J.); LIMAC (C.); CHARRON (D.); LEGENDRE (C.); CHATENOUD (L.)

Affiliation(s) : Université Paris Descartes, 75006 Paris, FRA; INSERM U580, Paris, FRA; Service d’Immunologie Biologique, Hôpital Necker-Enfants Malades, Paris, FRA; Service de Transplantation Rénale Adulte, Hôpital Necker-Enfants Malades, Paris, FRA; Service de Virologie, Hôpital Cochin, Saint-Vincent de Paul, Paris, FRA; Laboratoire d’Immunologie et Histocompatibilité, CIB-HOG, Hôpital Saint Louis, Paris, FRA

Source : American journal of transplantation : (Print); vol. 9; no. 10; pp. 2346-2354

ISSN : 1600-6135

Date de publication : 2009

Pays de publication : GBR

Langue(s) : ENG

Type de document : P

Nombre de références : 43 ref.

Résumé : It has been speculated that influenza vaccination of renal allograft recipients could be associated with de novo production and/or increased titers of anti-HLA antibodies (HLA-Ab). To directly address this issue, we recruited 66 stable renal transplant recipients and 19 healthy volunteers during the 2005-2006 vaccination campaign. At day 0 and day 30 following vaccination, HLA-Ab were screened and in parallel influenza-specific antibody and T-cell responses were assessed. Humoral postvaccinal responses to A/H1N1 and A/H3N2 strains, but not B strain, were less frequent in transplanted patients than in control subjects. Significant expansion of influenza-specific IFN- gamma -producing T cells was observed at similar frequencies in patients and controls. There was no correlation between cellular and humoral postvaccinal responses. No impact of sex, age or immunosuppressive regimen could be evidenced. Vaccination was not associated with any significant change in preexisting or de novo anti-HLA sensitization. No episode of allograft rejection was recorded in any of the patients. Our results suggest that flu vaccination is safe in stable renal transplanted patients. Larger studies are needed for definitive statistical proof of the safety and effectiveness, with regard to the quality of the immune response, of yearly influenza vaccination in immunosuppressed patients.

Code(s) de classement : 002B25H; 002B05C02C; 002B30A03

Descripteur(s) anglais

- Descripteur(s) : Immunoprophylaxis; Humoral immunity; Immune response; Kidney transplantation; Cellular immunity; Influenza; Homotransplantation; Vaccination; Prevention; Kidney; HLA-System; Major histocompatibility system; Class I histocompatibility antigen; Antibody; Treatment
- Desc. génériques : Surgery; Viral disease; Infection; Graft; Urinary system

Descripteur(s) français

- Descripteur(s) : Immunoprophylaxie; Immunité humorale; Réponse immune; Transplantation rénale; Immunité cellulaire; Grippé; Homotransplantation; Vaccination; Prévention; Rein; Système HLA; Système histocompatibilité majeur; Antigène histocompatibilité classe I; Anticorps; Traitement
- Desc. génériques : Chirurgie; Virose; Infection; Greffe; Appareil urinaire

Localisation : INIST-27587, 354000171204530160

Origine de la notice : INIST

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GrippeA/H1N1 mexicaine: peu de certitudes, beaucoup d'incertitudes : LA GRIPPE A/H1N1; Mexican flu: more doubts than prooven evidencies

Titre : GrippeA/H1N1 mexicaine: peu de certitudes, beaucoup d'incertitudes : LA GRIPPE A/H1N1; Mexican flu: more doubts than prooven evidencies

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Source : La Lettre du gynécologue; no. 345; pp. 25-27
ISSN : 0759-1594
Date de publication : 2009
Pays de publication : FRA
Langue(s) : FRE
Type de document : P
Nombre de références : 6 ref.

Code(s) de classement : 002B20; 002B05C02C

Descripteur(s) anglais
Descripteur(s) : Influenza; Uncertainty; Gynecology; Obstetrics
Desc. génériques : Viral disease; Infection

Descripteur(s) français
Descripteur(s) : Grippe; Incertitude; Gynécologie; Obstétrique
Desc. génériques : Virose; Infection

Localisation : INIST-22016B, 354000171192400070
Origine de la notice : INIST
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Recommandations pour la pratique clinique chez les femmes enceintes en cas d'épidémie de grippe A/H1 N1 : LA GRIPPE A/H1N1; Recommendation for pregnant women exposed A/H1N1 virus

Titre : Recommandations pour la pratique clinique chez les femmes enceintes en cas d'épidémie de grippe A/H1 N1 : LA GRIPPE A/H1N1; Recommendation for pregnant women exposed A/H1N1 virus

Collectivité(s) auteur : Société française d'anesthésie et de réanimation (SFAR), FRA
Source : La Lettre du gynécologue; no. 345; pp. 13-19
ISSN : 0759-1594
Date de publication : 2009
Pays de publication : FRA
Type de document : P
Langue(s) : FRE
Nombre de références : 6 ref.

Code(s) de classement : 002B20; 002B05C02C

Descripteur(s) anglais

- Descripteur(s) : Influenza A; Recommendation; Public health; Female; Human; Virus; Woman; Pregnancy; Epidemic; Gynecology; Obstetrics
- Desc. génériques : Viral disease; Infection

Descripteur(s) français

- Descripteur(s) : Grippe A; Recommandation; Santé publique; Femelle; Homme; Virus; Femme; Gestation; Epidémie; Gynécologie; Obstétrique
- Desc. génériques : Virose; Infection

Localisation : INIST-22016B, 354000171192400050
Origine de la notice : INIST
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Recommandations pour les femmes enceintes en cas d'épidémie de grippe A/H1 N1 : LA GRIPPE A/H1N1

Titre : Recommandations pour les femmes enceintes en cas d'épidémie de grippe A/H1 N1 : LA GRIPPE A/H1N1

Auteur(s) : LANSAC (J.); DARAÏ (E.); LUTON (D.)
Affiliation(s) : CNGOF; FRA

Source : La Lettre du gynécologue; no. 345; pp. 20-24
ISSN : 0759-1594
Date de publication : 2009
Pays de publication : FRA
Langue(s) : FRE
Type de document : P
Nombre de références : 4 ref.

Résumé : Les femmes enceintes doivent savoir qu'en cas de grippe par le virus A H1N1 l'affection peut être bénigne (comme en cas de grippe saisonnière habituelle), mais qu'elle peut aussi entraîner une complication pulmonaire grave pour la maman comme pour le bébé. Ces complications sont plus fréquentes chez les femmes enceintes que dans la population générale.

Code(s) de classement : 002B20; 002B05C02C

Descripteur(s) anglais
- Descripteur(s) : Influenza A; Recommendation; Public health; Female; Human; Woman; Pregnancy; Epidemic; Gynecology; Obstetrics
- Desc. génériques : Viral disease; Infection

Descripteur(s) français
- Descripteur(s) : Grippe A; Recommandation; Santé publique; Femelle; Homme; Femme; Gestation; Epidémie; Gynécologie; Obstétrique
- Desc. génériques : Virose; Infection

Localisation : INIST-22016B, 354000171192400060
Origine de la notice : INIST
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In Vitro Generation of Neuraminidase Inhibitor Resistance in A(H5N1) Influenza Viruses

Titre : In Vitro Generation of Neuraminidase Inhibitor Resistance in A(H5N1) Influenza Viruses

Auteur(s) : HURT (Aeron C.); HOLIEN (Jessica K.); BARR (Ian G.)
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Source : Antimicrobial agents and chemotherapy; vol. 53; no. 10; pp. 4433-4440
ISSN : 0066-4804
CODEN : AACHAX
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 35 ref.

Résumé : To identify mutations that can arise in highly pathogenic A(H5N1) viruses under neuraminidase inhibitor selective pressure, two antigenically different strains were serially passaged with increasing levels of either oseltamivir or zanamivir. Under oseltamivir pressure, both A(H5N1) viruses developed a H274Y neuraminidase mutation, although in one strain the mutation occurred in combination with an I222M neuraminidase mutation. The H274Y neuraminidase mutation reduced oseltamivir susceptibility significantly (900- to 2,500-fold compared to the wild type). However the dual H274Y/I222M neuraminidase mutation had an even greater impact on resistance, with oseltamivir susceptibility reduced significantly further (8,000-fold compared to the wild type). A similar affect on oseltamivir susceptibility was observed when the dual H274Y/I222M mutations were introduced, by reverse genetics, into a recombinant seasonal human A(H1N1) virus and also when an alternative I222 substitution (I222V) was generated in combination with H274Y in A(H5N1) and A(H1N1) viruses. These viruses remained fully susceptible to zanamivir but demonstrated reduced susceptibility to peramivir. Following passage of the A(H5N1) viruses in the presence of zanamivir, the strains developed a D198G neuraminidase mutation, which reduced susceptibility to both zanamivir and oseltamivir, and also an E119G neuraminidase mutation, which demonstrated significantly reduced zanamivir susceptibility (1,400-fold compared to the wild type). Mutations in hemagglutinin residues implicated in receptor binding were also detected in many of the resistant strains. This study identified the mutations that can arise in A(H5N1) under either oseltamivir or zanamivir selective pressure and the potential for dual neuraminidase mutations to result in dramatically reduced drug susceptibility.

Code(s) de classement : 002B02S

Descripteur(s) anglais
Descripteur(s) : In vitro; Neuraminidase inhibitor; Resistance; Influenza A virus; Influenzavirus A(H5N1)
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) français
Descripteur(s) : In vitro; Inhibiteur neuraminidase; Résistance; Virus grippal A; Influenzavirus A(H5N1)
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST-13334, 354000171121200530
Origine de la notice : INIST
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Triple Combination of Oseltamivir, Amantadine, and Ribavirin Displays Synergistic Activity against Multiple Influenza Virus Strains In Vitro

Titre : Triple Combination of Oseltamivir, Amantadine, and Ribavirin Displays Synergistic Activity against Multiple Influenza Virus Strains In Vitro

Auteur(s) : NGUYEN (Jack T.); HOOPES (Justin D.); SMEE (Donald F.); PRICHARD (Mark N.); DRIEBE (Elizabeth M.); ENGELTHALER (David M.); LE (Minh H.); KEIM (Paul S.); SPENCE (R. Paul); WENT (Gregory T.)

Affiliation(s) : Adams Pharmaceuticals, Inc., Emeryville, California, USA; Institute for Antiviral Research, Utah State University, Logan, Utah, USA; University of Alabama School of Medicine, Birmingham, Alabama, USA; Translational Genomics Research Institute, Flagstaff, Arizona, USA

Source : Antimicrobial agents and chemotherapy; vol. 53; no. 10; pp. 4115-4126
ISSN : 0066-4804
CODEN : AACHAX
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 51 ref.

Résumé : The recurring emergence of influenza virus strains that are resistant to available antiviral medications has become a global health concern, especially in light of the potential for a new influenza virus pandemic. Currently, virtually all circulating strains of influenza A virus in the United States are resistant to either of the two major classes of anti-influenza drugs (adamantanes and neuraminidase inhibitors). Thus, new therapeutic approaches that can be rapidly deployed and that will address the issue of recurring resistance should be developed. We have tested double and triple combinations of the approved anti-influenza drugs oseltamivir and amantadine together with ribavirin against three influenza virus strains using cytopathic effect inhibition assays in MDCK cells. We selected A/New Caledonia/20/99 (H1N1) and A/Sydney/05/97 (H3N2) as representatives of the wild-type versions of the predominant circulating seasonal influenza virus strains and A/Duck/ MN/1525/81 (H5N1) as a representative of avian influenza virus strains. Dose-response curves were generated for all drug combinations, and the degree of drug interaction was quantified using a model that calculates the synergy (or antagonism) between the drugs in double and triple combinations. This report demonstrates that a triple combination of antivirals was highly synergistic against influenza A virus. Importantly, the synergy of the triple combination was 2- to 13-fold greater than the synergy of any double combination depending on the influenza virus subtype. These data support the investigation of a novel combination of oseltamivir, amantadine, and ribavirin as an effective treatment for both seasonal and pandemic influenza virus, allowing the efficient use of the existing drug supplies.

Code(s) de classement : 002B02S

Descrip territoriales anglais
Descrip territoriales : Oseltamivir; Amantadine; Ribavirin; Display; Biological activity; Multiple; Influenzavirus; Strain; In vitro; Antiviral; Antiparkinson agent
Desc. génériques : Orthomyxoviridae; Virus; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor; Neuraminidase inhibitor; Agonist; Antagonist; Dopamine receptor; Glutamate receptor; NMDA receptor; Dopamine agonist; Amantadine derivatives; Nucleoside analog

Descrip territoriales français
Descrip territoriales : Osétamivir; Amantadine; Ribavirine; Affichage; Activité biologique; Multiple; Influenzavirus; Souche; In vitro; Antiviral; Antiparkinonien; Trithérapie
Desc. génériques : Orthomyxoviridae; Virus; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme; Inhibiteur neuraminidase; Agoniste; Antagoniste; Récepteur dopaminergique; Récepteur glutamate;
Récepteur NMDA; Stimulant dopaminergique; Dérivé de l'amantadine; Analogue de nucléoside

**Localisation** : INIST-13334, 354000171121200080

**Origine de la notice** : INIST

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Novel swine influenza virus subtype H3N1 in Italy

Titre : Novel swine influenza virus subtype H3N1 in Italy

Auteur(s) : MORENO (Ana); BARBIERI (Ilaria); SOZZI (Enrica); LUPPI (Andrea); LELLI (Davide); LOMBARDI (Guerino); GRAZIA ZANONI (Maria); CORDIOLI (Paolo)

Affiliation(s) : Department of Animal Health, Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna (IZSLER), Via Bianchi, 9, 25124 Brescia, ITA

Source : Veterinary microbiology : (Amsterdam); vol. 138; no. 3-4; pp. 361-367
ISSN : 0378-1135
CODEN : VMICDQ
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 3/4 p.

Résumé : To date, three subtypes of swine influenza viruses, H1N1, H1N2, and H3N2 have been isolated in Italy. In 2006, a novel swine influenza virus subtype (H3N1) was isolated from coughing pigs. RT-PCR performed on lung tissues, experimental infection in pigs with the novel isolate, and cloning the virus by plaque assay confirmed this unique H and N combination. The novel isolate was also antigenically and genetically characterized. Genetic and phylogenetic analysis showed that the complete HA gene of the H3N1 strain has the highest nucleotide identity to three Italian H3N2 strains, one isolated in 2001 and two in 2004, whereas the full length NA sequence is closely related to three H1N1 subtype viruses isolated in Italy in 2004. The remaining genes are also closely related to respective genes found in H1N1 and H3N2 SIVs currently circulating in Italy. This suggests that the novel SIV could be a reassortant between the H3N2 and H1N1 SIVs circulating in Italy.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Europe

Descripteur(s) français

Desc. génériques : Influenzavirus porcin; Porcin; Soustype; Italie; Génétique; Microbiologie; Vétérinaire

Localisation : INIST-16884, 354000170243170200

Origine de la notice : INIST
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Atypical clinical presentation of H1N1 influenza in a dialysis patient

Titre : Atypical clinical presentation of H1N1 influenza in a dialysis patient

Auteur(s) : WIEBE (Chris); RESLERova (Martina); KOMENDA (Paul); BUETI (Joe); RIGATTO (Claudio); SOOD (Manish M.)

Affiliation(s) : Department of Medicine, University of Manitoba, Winnipeg, Manitoba, CAN; Department of Medicine, St Boniface General Hospital, Winnipeg, Manitoba, CAN; Department of Medicine, Health Sciences Centre, Winnipeg, Manitoba, CAN

Source : Lancet : (British edition); vol. 374; no. 9697
ISSN : 0140-6736
CODEN : LANCAO
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 5 ref.

Code(s) de classement : 002B01; 002B05C02C

Descriptor(s) anglais
- Descripteur(s) : Dialysis; Atypical; Symptomatology; Influenza A; Patient; Human; Medicine
- Desc. génériques : Viral disease; Infection

Descriptor(s) français
- Descripteur(s) : Dialyse; Atypique; Symptomatologie; Grippe A; Malade; Homme; Médecine
- Desc. génériques : Virose; Infection

Localisation : INIST-5004, 354000170050190210
Origine de la notice : INIST
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A (H1N1) Journal de la pandémie

Titre : A (H1N1) Journal de la pandémie

Auteur(s) : FLAHAULT (Antoine); NAU (Jean-Yves)
Source : 319 p.
Éditeur : Plon, Paris
Date de publication : 2009
Pays de publication : FRA
Langue(s) : FRE
Type de document : L

Résumé : Fin avril 2009, un nouveau virus de la grippe émerge au Mexique : le A (H1NI). En quelques semaines, il se répand à l'échelon planétaire. Pourquoi ? En quoi est-il différent des virus responsables des épidémies saisonnières ? Pourquoi une telle mobilisation internationale face à une menace qui n'a pas (encore ?) fait la preuve de sa gravité ? Deux docteurs en médecine, l'un spécialiste d'épidémiologie, l'autre journaliste scientifique, ont tous deux tenu quotidiennement le journal de bord des quatre premiers mois de la pandémie ; quatre mois décisifs... De l'émergence du virus à la quête d'un vaccin et aux interrogations sur le Tamiflu, ce journal nous conduit aussi de l'ombre des cabinets présidentiels aux fermetures d'écoles, du pèlerinage à La Mecque à la réorganisation des salles d'attente chez les médecins français, des mouchoirs et des solutions hydro-alcooliques pour le lavage des mains. Sans oublier ceux qui ne voient là qu'une "grippette" et une opération politico-médiatique responsable d'une invraisemblable gabegie financière. Un feuilleton sans précédent, un polar médico-scientifique, qui nous concerne tous.

Code(s) de classement : 002B30A01

Descripteur(s) anglais
Desc. génériques : Influenza; Epidemic; Virus; Risk; History; Vaccine; Treatment; Vaccination; Prevention; Critical study; France

Descripteur(s) français
Desc. génériques : Grippe; Epidémie; Virus; Risque; Histoire; Vaccin; Traitement; Vaccination; Prévention; Etude critique; France

Localisation : BDSP/EHESP-174992
Origine de la notice : BDSP

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Le point sur ... Questions-réponses sur la pandémie grippale

Titre : Le point sur ... Questions-réponses sur la pandémie grippale

Source : LIAISONS SOCIALES QUOTIDIEN; vol. 02; no. 179; 4 p.
ISSN : 1955-5024
Date de publication : 2009-09-03
Pays de publication : FRA
Langue(s) : FRE
Type de document : P

Résumé : Les pouvoirs recommandent aux entreprises de se préparer dès aujourd'hui au risque de pandémie grippale de type A/H1N1. Dans les prochains mois, ce virus pourrait en effet avoir de lourdes conséquences sur l'activité des entreprises : taux d'absentéisme important (personnes malades ou retenues chez elles en raison de la fermeture des crèches et des écoles ou de perturbations dans les transports en commun, etc.), ralentissement ou paralysie de la production et des services aux clients, difficultés d'approvisionnement et défaillance des fournisseurs et sous-traitants. La pandémie pourrait également perturber les services de l'énergie et des télécommunications, et restreindre la circulation sur le territoire national et les échanges internationaux. Plusieurs circulaires de la Direction générale du travail listent les mesures de prévention et d'organisation du travail à mettre en œuvre en amont de la pandémie, ainsi que la conduite à tenir en cas de crise pandémique. Ce bulletin "questions-réponses" synthétise les différentes consignes ministérielles applicables aujourd'hui. Elles seront appelées à évoluer en fonction de la propagation du virus.

Code(s) de classement : 002B30A01

Descripteur(s) anglais
- Descripteur(s) : Epidemic; Influenza; Absenteeism; Firm; Instruction; Ministry; Prevention; Physician; Occupational medicine; Occupational role; Virus; Vaccine; France
- Desc. génériques : Viral disease; Infection; Europe

Descripteur(s) français
- Descripteur(s) : Épidémie; Grippe; Absentéisme; Entreprise; Instruction; Ministre; Prévention; Médecin; Médecine du travail; Rôle professionnel; Virus; Vaccin; France
- Desc. génériques : Virose; Infection; Europe

Localisation : BDSP/EHESP-174924
Origine de la notice : BDSP
Plan de continuité de l'activité en cas de pandémie grippale : mode d'emploi

Titre : Plan de continuité de l'activité en cas de pandémie grippale : mode d'emploi

Source : LIAISONS SOCIALES QUOTIDIEN; vol. 03; no. 180; 4 p.
ISSN : 1955-5024
Date de publication : 2009-09-03
Pays de publication : FRA
Langue(s) : FRE
Type de document : P
Nombre de références : dissem.

Résumé : Face au risque de pandémie grippale A/H1N1, qui pourrait occasionner un fort absentéisme des salariés et désorganiser l'activité économique, les pouvoirs publics recommandent aux entreprises, quels que soient leur taille ou leur secteur d'activité, de préparer un plan de continuité. Ce document vise à organiser le fonctionnement de l'entreprise en cas de pandémie. Rédigé sous la responsabilité du chef d'entreprise, il formalise les mesures permettant de protéger les salariés présents et de poursuivre l'activité de l'entreprise. Ce plan, préparé en amont de la pandémie, doit être régulièrement actualisé en fonction de l'évolution de la situation. Dans une circulaire du 18 décembre 2007, rectifiée en février 2008, la Direction générale du travail a détaillé le contenu de ce document. L'Anact (Agence nationale pour l'amélioration des conditions de travail) propose quant à elle une méthodologie pour élaborer le plan

Code(s) de classement : 002B30A01

Descripteur(s) anglais
  Descripteur(s) : Epidemic; Influenza; Absenteeism; Firm; Methodology; Plane; Circular; Regulation; Job engineering; Prevention; France
  Desc. génériques : Viral disease; Infection; Europe

Descripteur(s) français
  Descripteur(s) : Epidémie; Grippe; Absentéisme; Entreprise; Méthodologie; Plan; Circulaire; Réglementation; Organisation travail; Prévention; France
  Desc. génériques : Virose; Infection; Europe

Localisation : BDSP/EHESP-174236
Origine de la notice : BDSP
Genetic Evolution of H9 Subtype Influenza Viruses from Live Poultry Markets in Shanghai, China

Titre : Genetic Evolution of H9 Subtype Influenza Viruses from Live Poultry Markets in Shanghai, China

Auteur(s) : GE (Fei-Fei); ZHOU (Jin-Ping); JIAN LIU; JIAN WANG; ZHANG (Wei-Yi); SHENG (Li-Ping); FENG XU; JU (Hou-Bing); SUN (Quan-Yun); LIU (Pei-Hong)

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Source : Journal of clinical microbiology : (Print); vol. 47; no. 10; pp. 3294-3300
ISSN : 0095-1137
CODEN : JCMIDW
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 30 ref.

Résumé : H9N2 influenza viruses have become established and maintain long-term endemicity in poultry. The complete genomes of seven avian H9N2 influenza viruses were characterized. These seven influenza virus isolates were obtained from live poultry markets in Shanghai, China, in 2002 and from 2006 to 2008. Genetic analysis revealed that all seven isolates had an RSSR motif at the cleavage site of hemagglutinin (HA), indicating low pathogenicity in chickens. Phylogenetic analyses indicated that the seven avian H9N2 viruses belonged to the lineage represented by Duck/Hong Kong/Y280/97 (H9N2), a virus belonging to the Chicken/Beijing/1/94-like (H9N2) lineage, and that they are all quadruple reassortants consisting of genes from different lineages. The six internal genes of the isolates possessed H5N1-like sequences, indicating that they were reassortants of H9 and H5 viruses. All of the viruses had nonstructural (as well as HA and neuraminidase) genes derived from the Duck/Hong Kong/Y280/97-like virus lineage but also had other genes of mixed avian virus origin, including genes similar to those of H5N1 viruses (Gs/GD-like). The infected chickens showed no signs of disease. These results show the genetic and biological diversity of H9N2 viruses in Shanghai and support their potential role as pandemic influenza agents.

Code(s) de classement : 002A05

Describeur(s) anglais
Desc. génériques : Asia; Farming animal; Viral disease; Infection; Veterinary
Describeur(s) français
Desc. génériques : Asie; Animal élevage; Virose; Infection; Vétérinaire

Localisation : INIST-17088, 354000170037820330
Origine de la notice : INIST
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Two genotypes of H1N2 swine influenza viruses appeared among pigs in China

Titre : Two genotypes of H1N2 swine influenza viruses appeared among pigs in China

Auteur(s) : CHUANTIAN XU; QIYUN ZHU; HUANLIANG YANG; XIUMEI ZHANG; CHUANLING QIAO; YAN CHEN; XIAOGUANG XIN; HUALAN CHEN

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Source : Journal of clinical virology; vol. 46; no. 2; pp. 192-195

ISSN : 1386-6532

Date de publication : 2009

Pays de publication : NLD

Langue(s) : ENG

Type de document : P

Nombre de références : 12 ref.

Résumé : Background: H1N2 is one of the main subtypes of influenza, which circulates in swine all over the world. Objectives: To investigate the prevalence and genetic of H1N2 in swine of China. Study design: Two H1N2 swine influenza viruses were isolated from Tianjin and Guangdong province of China in 2004 and 2006, respectively. The molecular evolution of eight gene segments was analyzed. Result: A/Swine/Tianjin/1/2004 has low identity with A/Swine/Guangdong/1/2006; in the phylogenetic tree of PA gene, A/Swine/Guangdong/1/2006 and A/Swine/Guangxi/1/2006 along with the H1N2 swine isolates of North America formed a cluster; A/Swine/Tianjin/2004 and A/Swine/Zhejiang/2004, along with the classical H1N1 swine isolates formed another cluster; except that NA gene of A/Swine/Tianjin/1/2004 fell into the cluster of the H3N2 human influenza virus, indicating the reassortment between H3N2 human and H1N1 swine influenza viruses. Conclusion: Two different genotypes of H1N2 appeared among pigs in China. A/swine/Guangdong/1/06 was probably from H1N2 swine influenza viruses of North America; while A/swine/Tianjin/1/04 may come from reassortments of classical H1N1 swine and H3N2 human viruses prevalent in North America.

Code(s) de classement : 002A05C10; 002B05C02J

Descripteur(s) anglais

- Swine; Human; Genotype; Pig; China; Microbiology; Influenza
- Artiodactyla; Ungulata; Mammalia; Vertebrata; Asia; Veterinary; Viral disease; Infection; Farming animal

Descripteur(s) français

- Porcin; Homme; Génotype; Porc; Chine; Microbiologie; Grippe
- Artiodactyla; Ungulata; Mammalia; Vertebrata; Asie; Vétérinaire; Virose; Infection; Animal élevage

Localisation : INIST-26272, 354000170245720200

Origine de la notice : INIST

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Grippe A/H1N1 de 2009 : gravité clinique modérée; A/H1N1 2009 flu : moderate clinical severity

Titre : Grippe A/H1N1 de 2009 : gravité clinique modérée; A/H1N1 2009 flu : moderate clinical severity

Source : La Revue Prescrire; vol. 29; no. 312; pp. 770-771
ISSN : 0247-7750
Date de publication : 2009
Pays de publication : FRA
Langue(s) : FRE
Type de document : P
Nombre de références : 15 ref.

Résumé : L’analyse de l’épidémie hivernale (australe) en Nouvelle-Zélande a montré que les complications mortelles de la grippe due au virus A/H1N1 de 2009 (H1N1v) sont rares: environ 1 décès pour 20 000 personnes ayant une infection symptomatique. · Les facteurs de risque de complications apparaissent similaires à ceux des grippe saisonnières: grossesse au cours du 3e trimestre, diabète, maladie respiratoire ou cardiaque sévère, immunodépression. · Les décès chez des personnes jeunes en bonne santé ont été exceptionnels. · En pratique, la gravité clinique modérée de la grippe H1N1v ne justifie pas un recours à des actions préventives aux conséquences démesurées.

Code(s) de classement : 002B02W; 002B05C02C; 002B30A03B

Describeur(s) anglais
- Describeur(s) : Influenza A; Severity score; Symptomatology; Diagnosis; Epidemiology; Recommendation; Prevention; Risk factor; Human
- Desc. génériques : Viral disease; Infection

Describeur(s) français
- Describeur(s) : Grippe A; Indice gravité; Symptomatologie; Diagnostic; Epidémiologie; Recommandation; Prévention; Facteur risque; Homme; Influenzavirus A(H1N1)
- Desc. génériques : Virose; Infection

Localisation : INIST-21322, 354000171091590150
Origine de la notice : INIST
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H1N1 Influenza in Pregnancy: Cause for Concern

**Titre** : H1N1 Influenza in Pregnancy: Cause for Concern

**Auteur(s)** : SALEEBY (Erin); CHAPMAN (Jocelyn); MORSE (Jessica); BRYANT (Allison)

**Affiliation(s)** : Department of Obstetrics, Gynecology, and Reproductive Sciences, University of California, San Francisco, San Francisco, California, USA

**Source** : Obstetrics and gynecology : (New York. 1953); vol. 114; no. 4; pp. 885-891

**ISSN** : 0029-7844

**CODEN** : OBGNAS

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 13 ref.

**Code(s) de classement** : 002B20; 002B05C02C

**Descripteur(s) anglais**

- Descripteur(s) : Influenza; Pregnancy; Gynecology; Obstetrics
- Desc. génériques : Viral disease; Infection

**Descripteur(s) français**

- Descripteur(s) : Grippe; Gestation; Gynécologie; Obstétrique
- Desc. génériques : Virose; Infection

**Localisation** : INIST-7207, 354000170248040240

**Origine de la notice** : INIST

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Evaluation of Twenty Rapid Antigen Tests for the Detection of Human Influenza A H5N1, H3N2, H1N1, and B Viruses

Titre : Evaluation of Twenty Rapid Antigen Tests for the Detection of Human Influenza A H5N1, H3N2, H1N1, and B Viruses

Auteur(s) : TAYLOR (Janette); MCPHIE (Kenneth); DRUCE (Julian); BIRCH (Chris); DWYER (Dominic E.)
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Source : Journal of medical virology; vol. 81; no. 11; pp. 1918-1922
ISSN : 0146-6615
CODEN : JMVIDB
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 3/4 p.

Résumé : Twenty rapid antigen assays were compared for their ability to detect influenza using dilutions of virus culture supernatants from human isolates of influenza A H5N1 (clade 1 and 2 strains), H3N2 and H1N1 viruses, and influenza B. There was variation amongst the rapid antigen assays in their ability to detect different influenza viruses. Six of the 12 assays labeled as distinguishing between influenza A and B had comparable analytical sensitivities for detecting both influenza A H5N1 strains, although their ability to detect influenza A H3N2 and H1N1 strains varied. The two assays claiming H5 specificity did not detect either influenza A H5N1 strains, and the two avian influenza-specific assays detected influenza A H5N1, but missed some influenza A H3N2 virus supernatants. Clinical trials of rapid antigen tests for influenza A H5N1 are limited. For use in a pandemic where novel influenza strains are circulating (such as the current novel influenza A H1N1 09 virus), rapid antigen tests should ideally have comparable sensitivity and specificity for the new strains as for co-circulating seasonal influenza strains.

Code(s) de classement : 002A05C10; 002B05C02J

Descripteur(s) anglais : Human; Evaluation; Antigen; Detection; Influenza; Influenzavirus A(H5N1)
Desc. génériques : Viral disease; Infection

Descripteur(s) français : Homme; Evaluation; Antigène; Détect; Grippe; Influenzavirus A(H3N2); Influenzavirus A(H5N1)
Desc. génériques : Virose; Infection

Localisation : INIST-17422, 354000170266010100
Origine de la notice : INIST
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Development of a Consensus Microarray Method for Identification of Some Highly Pathogenic Viruses

Titre : Development of a Consensus Microarray Method for Identification of Some Highly Pathogenic Viruses

Auteur(s) : KANG (Xiao-Ping); LI (Yong-Qiang); SUN (Qing-Ge); LIU HONG; ZHU (Qing-Yu); YANG (Yin-Hui)

Affiliation(s) : State Key Laboratory of Pathogen and Biosecurity, Beijing Institute of Microbiology and Epidemiology, Beijing, CHN

Source : Journal of medical virology; vol. 81; no. 11; pp. 1945-1950
ISSN : 0146-6615
CODEN : JMVIDB
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 1/2 p.

Résumé : Some highly pathogenic viruses, such as Chikungunya virus, Japanese encephalitis virus, Yellow fever virus, Dengue virus, Hanta virus, SARS-CoV, and H5N1 avian influenza virus can cause severe infectious diseases. However, the consensus method for detecting these viruses has not been well established. A rapid and sensitive microarray approach for detection of these viruses and a panel of specific probes covering nine genera and 16 virus species were designed. 70-mer oligonucleotides were used at the genus level and 50-mer oligonucleotides were at the species level, respectively. To decrease the interference of the host genome in hybridization, the consensus genus primers were designed and used to reverse transcribe only virus genome. The synthesis of the second strand was carried out with a random primer sequence (5'-GTTTCCCAGTAGGTCTCNNNNN-3'). The amplified products were labeled and processed for microarray analyses. This microarray-based method used the highly conserved consensus primers to synthesize specifically the virus cDNA and could identify effectively Chikungunya virus, Japanese encephalitis virus, Yellow fever virus, Dengue virus, Tick borne encephalitis virus, and H5N1 avian influenza virus. Using this method, one unknown virus isolated from pig brain in Shanxi Province, China was identified. This method may have an important potential application for the diagnosis of virus infection.

Code(s) de classement : 002A05C10; 002B05C02J; 002A05C08; 002A05C04

Descriputeur(s) anglais

Descriputeur(s) : Method; Identification; Pathogenicity; Species; Detection

Descriputeur(s) français

Descriputeur(s) : Méthode; Identification; Pouvoir pathogène; Espèce; Détexion

Localisation : INIST-17422, 354000170266010140
Origine de la notice : INIST
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Rapid Antigen Tests for Diagnosis of Pandemic (Swine) Influenza A/H1N1

Title: Rapid Antigen Tests for Diagnosis of Pandemic (Swine) Influenza A/H1N1

Authors: VASOO (Shawn); STEVENS (Jane); SINGH (Kamaljit)
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Source: Clinical infectious diseases; vol. 49; no. 7; pp. 1090-1093
ISSN: 1058-4838
CODEN: CIDIEL
Date of publication: 2009
Pays de publication: USA
Langue(s): ENG
Type de document: P
Nombre de références: 13 ref.

Abstract: We found that the sensitivities of 3 rapid influenza antigen tests for pandemic influenza A/H1N1 virus were low to moderate: BD Directigen EZ Flu A+B test (Becton Dickinson), 46.7%; BinaxNOW Influenza A&B (Inverness Medical), 38.3%; and QuickVue Influenza A+B Test (Quidel), 53.3%. A patient with influenza-like illness who has a negative rapid antigen test result should undergo further testing using reverse-transcription polymerase chain reaction.

Code(s) de classement: 002B05C02C

Descriptor(s) anglais
Descriptor(s): Influenza A; Rapid technique; Antigen; Diagnosis
Desc. génériques: Viral disease; Infection

Descriptor(s) français
Descriptor(s): Grippe A; Technique rapide; Antigène; Diagnostic; Pandémie
Desc. génériques: Virose; Infection

Localisation: INIST-18407, 354000170024610170
Origine de la notice: INIST
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Virologically Confirmed Population-Based Burden of Hospitalization Caused by Influenza A and B among Children in Hong Kong

**Titre** : Virologically Confirmed Population-Based Burden of Hospitalization Caused by Influenza A and B among Children in Hong Kong

**Auteur(s)** : CHIU (Susan S.); CHAN (Kwok-Hung); HONG CHEN; YOUNG (Betty W.); LIM (Wilina); HING SANG WONG (Wilfred); YU LUNG LAU; PEIRIS (J. S. Malik)

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**Source** : Clinical infectious diseases; vol. 49; no. 7; pp. 1016-1021

**ISSN** : 1058-4838

**CODEN** : CIDIEL

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 30 ref.

**Résumé** : Background. We sought to determine the virologically confirmed hospitalization rates associated with influenza virus infection among Hong Kong children. Methods. Patients <18 years of age who lived on Hong Kong Island (a separate island within Hong Kong) and were admitted to either of the only 2 public hospitals on the island for a febrile acute respiratory infection on 1 fixed day of the week in each hospital from October 2003 through September 2006 were prospectively recruited. These 2 hospitals together accounted for 72.5% of all general pediatric admissions in Hong Kong Island with a known population denominator. Nasopharyngeal aspirates were obtained from all recruited patients and were tested for influenza A and influenza B viruses by direct antigen detection and culture. Results. All cases of influenza A during 2003-2004 were caused by H3N2 virus, whereas 85.7% of cases during 2004-2005 were due to H3N2 virus, and 93.5% during 2005-2006 were due to H1N1 virus. During 2004-2005, infants <1 year of age had the highest rate of hospitalization for influenza A (103.8 cases per 10,000 population), whereas children 1 year of age had the highest rate of hospitalization for influenza B (95.5 cases per 10,000 population), whereas children 1 year of age had the highest rate of hospitalization during the other 2 seasons (95.5 and 54.6 cases per 10,000 population during 2003-2004 and 2005-2006, respectively). A protection rate of 25%, presumably attributable to maternal antibodies, was seen in infants <1 year of age who were hospitalized during 2003-2004 with infection due to an H3N2 virus that had been in circulation. The hospitalization rates for influenza B were highest among children 2-4 years of age. Conclusions. This population-based study of hospitalizations due to virologically confirmed influenza demonstrated a very high burden of disease among young children in Hong Kong. The morbidity varied with virus type, subtype, and antigenic variants.

**Code(s) de classement** : 002B05C02C

**Descripteur(s) anglais**

* Descripteur(s) : Influenza A; Influenza B; Hospitalization; Hong Kong; Child

* Desc. génériques : Viral disease; Infection; China; Asia; Human

**Descripteur(s) français**

* Descripteur(s) : Grippe A; Grippe B; Hospitalisation; Hong Kong; Enfant

* Desc. génériques : Virose; Infection; Chine; Asie; Homme

**Localisation** : INIST-18407, 354000170024610050

**Origine de la notice** : INIST

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Host Genetic Variation Affects Resistance to Infection with a Highly Pathogenic H5N1 Influenza A Virus in Mice

Titre : Host Genetic Variation Affects Resistance to Infection with a Highly Pathogenic H5N1 Influenza A Virus in Mice

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Source : Journal of virology; vol. 83; no. 20; pp. 10417-10426
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 50 ref.

Résumé : Despite the prevalence of H5N1 influenza viruses in global avian populations, comparatively few cases have been diagnosed in humans. Although viral factors almost certainly play a role in limiting human infection and disease, host genetics most likely contribute substantially. To model host factors in the context of influenza virus infection, we determined the lethal dose of a highly pathogenic H5N1 virus (A/Hong Kong/213/03) in C57BL/6J and DBA/2J mice and identified genetic elements associated with survival after infection. The lethal dose in these hosts varied by 4 logs and was associated with differences in replication kinetics and increased production of proinflammatory cytokines CCL2 and tumor necrosis factor alpha in susceptible DBA/2J mice. Gene mapping with recombinant inbred BXD strains revealed five loci or Qivr (quantitative trait loci for influenza virus resistance) located on chromosomes 2, 7, 11, 15, and 17 associated with resistance to H5N1 virus. In conjunction with gene expression profiling, we identified a number of candidate susceptibility genes. One of the validated genes, the hemolytic complement gene, affected virus titer 7 days after infection. We conclude that H5N1 influenza virus-induced pathology is affected by a complex and multigenic host component.

Code(s) de classement : 002A05C10; 002A05C05; 002A05C04

Descripteur(s) anglais
- Desc. généraux : Rodentia; Mammalia; Vertebrata
- Descripteur(s) : Mouse; Genetics; Resistance; Infection; Pathogenicity; Animal; Influenzavirus A(H5N1)

Descripteur(s) français
- Desc. généraux : Rodentia; Mammalia; Vertebrata
- Descripteur(s) : Souris; Génétique; Résistance; Infection; Pouvoir pathogène; Animal; Influenzavirus A(H5N1)

Localisation : INIST-13592, 354000171123360100
Origine de la notice : INIST
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Zanamivir-Resistant Influenza Viruses with a Novel Neuraminidase Mutation

Titre : Zanamivir-Resistant Influenza Viruses with a Novel Neuraminidase Mutation

Auteur(s) : HURT (Aeron C.); HOLIEN (Jessica K.); PARKER (Michael); KELSO (Anne); BARR (Ian G.)
Affiliation(s) : WHO Collaborating Centre for Reference and Research on Influenza, 10 Wreckyn Street, North Melbourne, Victoria 3051, AUS; Monash University, School of Applied Sciences, Churchill, Victoria 3842, AUS; Structural Biology Laboratory, St. Vincent's Institute of Medical Research, Fitzroy, Victoria 3065, AUS; Department of Biochemistry and Molecular Biology, Bio21 Molecular Science and Biotechnology Institute, The University of Melbourne, Parkville, Victoria 3052, AUS

Source : Journal of virology; vol. 83; no. 20; pp. 10366-10373
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 30 ref.

Résumé : The neuraminidase inhibitors zanamivir and oseltamivir are marketed for the treatment and prophylaxis of influenza and have been stockpiled by many countries for use in a pandemic. Although recent surveillance has identified a striking increase in the frequency of oseltamivir-resistant seasonal influenza A (H1N1) viruses in Europe, the United States, Oceania, and South Africa, to date there have been no reports of significant zanamivir resistance among influenza A (H1N1) viruses or any other human influenza viruses. We investigated the frequency of oseltamivir and zanamivir resistance in circulating seasonal influenza A (H1N1) viruses in Australasia and Southeast Asia. Analysis of 391 influenza A (H1N1) viruses isolated between 2006 and early 2008 from Australasia and Southeast Asia revealed nine viruses (2.3%) that demonstrated markedly reduced zanamivir susceptibility and contained a previously undescribed Gln136Lys (Q136K) neuraminidase mutation. The mutation had no effect on oseltamivir susceptibility but caused approximately a 300-fold and a 70-fold reduction in zanamivir and peramivir susceptibility, respectively. The role of the Q136K mutation in conferring zanamivir resistance was confirmed using reverse genetics. Interestingly, the mutation was not detected in the primary clinical specimens from which these mutant isolates were grown, suggesting that the resistant viruses either occurred in very low proportions in the primary clinical specimens or arose during MDCK cell culture passage. Compared to susceptible influenza A (H1N1) viruses, the Q136K mutant strains displayed greater viral fitness than the wild-type virus in MDCK cells but equivalent infectivity and transmissibility in a ferret model.

Code(s) de classement : 002A05C10

Descriputeur(s) anglais
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Glycosidases; Glycosylases; Hydrolases; Enzyme

Descriputeur(s) français
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Glycosidases; Glycosylases; Hydrolases; Enzyme

Localisation : INIST-13592, 354000171123360050
Origine de la notice : INIST
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On June 11, 2009, Dr. Margaret Chan, Director-General of the World Health Organization (WHO), declared the first influenza pandemic of the 21st century. It was the first time in history that an influenza outbreak had been tracked in real-time from the emergence of a new strain of influenza A (H1N1) up to its spread to all continents over a period of 9 weeks. In recent years the international community has been working closely to prepare for such situations. A notable example of this cooperation occurred in response to the threat posed by the highly pathogenic avian influenza A virus (H5N1). Vaccine availability is a major challenge that will require increasing worldwide production and ensuring a widespread access. In this regard it is important to underline the fact that 70% of influenza vaccine is produced in Europe and the United States. In 2006 WHO implemented a global pandemic influenza action plan (GAP) aiming at increasing the world's production capacity for pandemic vaccine. The GAP contains three elements: 1) increased use of seasonal influenza vaccination in industrialized and developing countries (resolution WHA 56.19), 2) technology transfer, 3) development of new production technologies. Nevertheless numerous barriers still prevent people living in developing countries from rapid and fair access to pandemic influenza vaccine. Capacity for production of pandemic vaccine is limited and advanced purchase agreements between industrialized countries and vaccine manufacturers reduce potential access of developing countries to pandemic vaccine. Economic and logistic factors also limit global access to pandemic vaccine. Therefore, WHO is working with industrialized countries, pharmaceutical companies and the international community as a whole to promote global solidarity and cooperation and thus ensure distribution of pandemic vaccine in poor countries with no local production. The current pandemic situation highlights the increasing globalization of public health stakes with regard to influenza vaccination. The purpose of this presentation is to review the various challenges for production and distribution of vaccines and underline the progress that has been accomplished since 2005.
Poly( gamma -glutamic acid) nano-particles combined with mucosal influenza virus hemagglutinin vaccine protects against influenza virus infection in mice

Titre : Poly( gamma -glutamic acid) nano-particles combined with mucosal influenza virus hemagglutinin vaccine protects against influenza virus infection in mice

Auteur(s) : OKAMOTO (Shigefumi); MATSUURA (Masaaki); AKAGI (Takami); AKASHI (Mitsuru); TANIMOTO (Takeshi); ISHIKAWA (Toyokazu); TAKAHASHI (Michiaki); YAMANISHI (Koichi); MORI (Yasuko)
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Source : Vaccine; vol. 27; no. 42; pp. 5896-5905
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 31 ref.

Résumé : Adding poly( gamma -glutamic acid) nano-particles ( gamma -PGA-NPs), a safe, natural material, to subcutaneous immunization with influenza virus hemagglutinin (HA) vaccine increases the protective immune responses against influenza virus in mice. Here, we examined whether intranasal administration of the HA vaccine with gamma -PGA-NPs would induce protection from influenza virus challenge in mice. Intranasal immunization with the mixture of gamma -PGA-NPs and HA vaccine from an influenza virus strain A/PR/8/34 (H1N1) or A/New Caledonia/20/99 (H1N1) enhanced protection of mice from A/PR/8/34 infection. Intranasal immunization with A/New Caledonia/20/99 HA vaccine and gamma -PGA-NPs induced cell-mediated immune responses and neutralizing antibody production for both A/New Caledonia/20/99 and A/PR/8/34. These data suggest that gamma -PGA-NPs may have potential for clinical applications as a mucosal adjuvant.

Code(s) de classement : 002A05F04; 002A05C10

Descriptrue(s) anglais

Descriptrue(s) : Influenzavirus; Mouse; Mucosa; Hemagglutinin; Vaccine; Influenza; Immunization; Glutamic acid
Desc. génériques : Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Viral disease; Infection; Aminoacid

Descriptrue(s) français

Descriptrue(s) : Influenzavirus; Souris; Muqueuse; Hémagglutinine; Vaccin; Grippe; Immunisation; Acide glutamique
Desc. génériques : Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Virose; Infection; Aminoacide

Localisation : INIST-20289, 354000170244810260
Origine de la notice : INIST
Copyright de notice : © 2009 INIST-CNRS. All rights reserved.
Superior efficacy of a recombinant flagellin:H5N1 HA globular head vaccine is determined by the placement of the globular head within flagellin

Titre : Superior efficacy of a recombinant flagellin:H5N1 HA globular head vaccine is determined by the placement of the globular head within flagellin

Auteur(s) : LANGZHOU SONG; YI ZHANG; YUN (Nadezhda E.); POUSSARD (Allison L.); SMITH (Jeanon N.); SMITH (Jennifer K.); BORISEVICH (Viktoriya); LINDE (Jenna J.); ZACKS (Michele A.); HONG LI; KAVITA (Uma); REISEROVA (Lucia); XIANGYU LIU; DUMUREN (Kunmi); BALASUBRAMANIAN (Bhuvaneswari); WEAVER (Bruce); PARENT (Jason); UMLAUF (Scott); GE LIU; HULEATT (Jim); TUSSEY (Lynda); PAESSLER (Slobodan)

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Source : Vaccine; vol. 27; no. 42; pp. 5875-5884
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Type de document : P
Nombre de références : 45 ref.

Résumé : Transmission of highly pathogenic avian influenza (HPAI) between birds and humans is an ongoing threat that holds potential for the emergence of a pandemic influenza strain. A major barrier to an effective vaccine against avian influenza has been the generally poor immunopotency of many of the HPAI strains coupled with the manufacturing constraints employing conventional methodologies. Fusion of flagellin, a toll-like receptor-5 ligand, to vaccine antigens has been shown to enhance the immune response to the fused antigen in preclinical studies. Here, we have evaluated the immunogenicity and efficacy of a panel of flagellin-based hemagglutinin (HA) globular head fusion vaccines in inbred mice. The HA globular head of these vaccines is derived from the A/Vietnam/1203/04 (VN04; H5N1) HA molecule. We find that replacement of domain D3 of flagellin with the VN04 HA globular head creates a highly effective vaccine that elicits protective HAI titers which protect mice against disease and death in a lethal challenge model.

Code(s) de classement : 002A05F04; 002A05C10

Descriptor(s) anglais
Desc. généraux : Avian influenza virus; Efficiency; Flagellin; Vaccine; Avian influenza
Desc. spécifique : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen; Viral disease; Infection

Descriptor(s) français
Desc. généraux : Influenzavirus aviaire; Efficacité; Flagelline; Vaccin; Grippe aviaire
Desc. spécifique : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogène; Virose; Infection

Localisation : INIST-20289, 354000170244810240
Origine de la notice : INIST
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Elderberry flavonoids bind to and prevent H1N1 infection in vitro

**Titre** : Elderberry flavonoids bind to and prevent H1N1 infection in vitro

**Auteur(s)** : ROSCHEK (Bill JR); FINK (Ryan C.); MCMICHAEL (Matthew D.); DAN LI; ALBERTE (Randall S.)

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**Source** : Phytochemistry; vol. 70; no. 10; pp. 1255-1261

**ISSN** : 0031-9422

**Date de publication** : 2009

**Pays de publication** : NLD

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 1/2 p.

**Résumé** : A ionization technique in mass spectrometry called Direct Analysis in Real Time Mass Spectrometry (DART TOF-MS) coupled with a Direct Binding Assay was used to identify and characterize anti-viral components of an elderberry fruit (Sambucus nigra L.) extract without either derivatization or separation by standard chromatographic techniques. The elderberry extract inhibited Human Influenza A (H1N1) infection in vitro with an IC50 value of 252 ± 34 µg/mL. The Direct Binding Assay established that flavonoids from the elderberry extract bind to H1N1 virions and, when bound, block the ability of the viruses to infect host cells. Two compounds were identified, 5,7,3',4'-tetra-0-methylquercetin (1) and 5,7-dihydroxy-4-0xo-2-(3,4,5-trihydroxyphenyl)chroman-3-yl-3,4,5-trihydroxycyclohexanecarboxylate (2), as H1N1-bound chemical species. Compound 1 and dihydromyricetin (3), the corresponding 3-hydroxyflavonone of 2, were synthesized and shown to inhibit H1N1 infection in vitro by binding to H1N1 virions, blocking host cell entry and/or recognition. Compound 1 gave an IC50 of 0.13 µg/mL (0.36 µM) for H1N1 infection inhibition, while dihydromyricetin (3) achieved an IC50 of 2.8 µg/mL (8.7 µM). The H1N1 inhibition activities of the elderberry flavonoids compare favorably to the known anti-influenza activities of Oseltamivir (Tamiflu®; 0.32 µM) and Amantadine (27 µM).

**Code(s) de classement** : 002A10D; 002B02S05

**Descriputeur(s) anglais**

- **Desc. génériques** : Flavonoid; Infection; In vitro; Sambucus nigra; Antiviral; Time of flight spectrometer; Influenza; Plant origin; Chemical structure
- **Desc. spécifiques** : Caprifoliaceae; Dicotyledones; Angiospermae; Spermatophyta; Viral disease; Polyphenol; Hardwood forest tree; Phenols

**Descriputeur(s) français**

- **Desc. génériques** : Flavonoïde; Infection; In vitro; Sambucus nigra; Anti-viral; Spectromètre temps vol; Grippe; Origine végétale; Structure chimique; Influenzavirus A(H1N1)
- **Desc. spécifiques** : Caprifoliaceae; Dicotyledones; Angiospermae; Spermatophyta; Virole; Polyphénol; Arbre forestier feuillus; Phénols

**Localisation** : INIST-9408, 354000188112580070

**Origine de la notice** : INIST

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Immunoinformatic comparison of T-cell epitopes contained in novel swine-origin influenza A (H1N1) virus with epitopes in 2008-2009 conventional influenza vaccine

Titre : Immunoinformatic comparison of T-cell epitopes contained in novel swine-origin influenza A (H1N1) virus with epitopes in 2008-2009 conventional influenza vaccine

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Source : Vaccine; vol. 27; no. 42; pp. 5740-5747
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 74 ref.

Résumé : In March 2009 a novel swine-origin influenza A (H1N1) virus (S-OIV) emerged in Mexico and the Western United States. Vaccination with conventional influenza vaccine (CIV) does not result in cross-reactive antibodies, however, the disproportionate number of cases (37%) occurring among persons younger than 50 years old suggested that adaptive immune memory might be responsible for the relative lack of virulence in older, healthy adults. Using EpiMatrix, a T-cell epitope prediction and comparison tool, we compared the sequences of the three hemagglutinin (HA) and neuraminidase (NA) proteins contained in 2008-2009 CIV to their counterparts in A/California/04/2009 (H1N1) looking for cross-conserved T-cell epitope sequences. We found greater than 50% conservation of T helper and CTL epitopes between novel S-OIV and CIV HA for selected HLA. Conservation was lower among NA epitopes. Sixteen promiscuous helper T-cell epitopes are contained in the S-OIV H1N1 HA sequence, of which nine (56%) were 100% conserved in the 2008-2009 influenza vaccine strain; 81% were either identical or had one conservative amino acid substitution. Fifty percent of predicted CTL epitopes found in S-OIV H1N1 HA were also found in CIV HA sequences. Based on historical performance, we expect these epitope predictions to be 93-99% accurate. This in silico analysis supports the proposition that T-cell response to cross-reactive T-cell epitopes, due to vaccination or exposure, may have the capacity to attenuate the course of S-OIV H1N1 induced disease-in the absence of cross-reactive antibody response. The value of the CIV or live-attenuated influenza vaccine containing the 2008-2009 vaccine strains, as defense against H1N1, could be further tested by evaluating human immune responses to the conserved T-cell epitopes using PBMC from individuals infected with H1N1 and from CIV vaccinees.

Code(s) de classement : 002A05F04; 002A05C10

Descripteur(s) anglais

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Veterinary; Viral disease; Infection

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Veterinary; Viral disease; Infection

Localisation : INIST-20289, 354000170244810070
Does receipt of seasonal influenza vaccine predict intention to receive novel H1N1 vaccine: Evidence from a nationally representative survey of U.S. adults

Title: Does receipt of seasonal influenza vaccine predict intention to receive novel H1N1 vaccine: Evidence from a nationally representative survey of U.S. adults

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Source: Vaccine; vol. 27; no. 42; pp. 5732-5734
ISSN: 0264-410X
CODEN: VACCDE
Date de publication: 2009
Pays de publication: GBR
Langue(s): ENG
Type de document: P
Nombre de références: 8 ref.

Résumé: We analyze data on the intention of U.S. adults to receive novel H1N1 vaccine if available this fall, and studies the relationship between the intention to be vaccinated against novel H1N1 and the uptake of seasonal influenza vaccine last year. We surveyed a nationally representative sample of U.S. adults (n = 2067) via the Internet between May 26th and June 8th, 2009. Our results imply a vaccination rate for novel H1N1 of 49.6%, which corresponds to roughly 115 million adult vaccinations. Moreover, novel H1N1 vaccination intentions are strongly associated with seasonal influenza vaccinations, suggesting common attitudinal barriers to both vaccines.

Code(s) de classement: 002A05F04

Descripteur(s) anglais

Descripteur(s): Vaccine; Vaccination; Influenza A
Desc. génériques: Viral disease; Infection

Descripteur(s) français

Descripteur(s): Vaccin; Vaccination; Grippe A
Desc. génériques: Virose; Infection

Localisation: INIST-20289, 354000170244810050
Origine de la notice: INIST
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Clinical effectiveness of oseltamivir for influenza A(H1 N1) virus with H274Y neuraminidase mutation

Titre : Clinical effectiveness of oseltamivir for influenza A(H1 N1) virus with H274Y neuraminidase mutation

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Source : The Journal of infection; vol. 59; no. 3; pp. 207-212
ISSN : 0163-4453
CODEN : JINFD2
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 32 ref.

Résumé : Objective: To evaluate the clinical effectiveness of oseltamivir therapy started within 48 h of the onset for influenza A(H1N1) virus with H274Y neuraminidase (NA) mutation. Methods: Virus was isolated before and four to six days after starting oseltamivir treatment from 73 outpatients with influenza A(H1N1) virus in the 2007-2008 and 2008-2009 seasons. NA inhibition assays (IC50) and sequence analyses were done using influenza viruses isolated from these patients. Body temperature was evaluated before and on the second, third, and fourth days after starting treatment.

Results: H274Y mutation was not shown in the 2007-2008 season (44 patients) and shown in all 29 patients in the 2008-2009 season by NA sequence analyses. The mean IC50 before oseltamivir treatment was significantly higher in 2008-2009 (319.3 ± 185.4 nM) than in 2007-2008 (1.5 ± 0.8 nM; p < .001). Patients <= 15 years with oseltamivir-resistant virus infection had a higher ratio of patients persisted virus after oseltamivir treatment than patients > 15 years (50% and 11.8%, respectively, p = 0.038), and a significant higher body temperature during oseltamivir treatment, compared to patients <=15 years treated for oseltamivir-sensitive virus infection. Conclusion: The clinical effectiveness of oseltamivir for the A(H1N1) virus was reduced in the 2008-2009 season compared with the previous season, especially in children, probably due to the H274Y mutation. Oseltamivir seems to be not recommended for children and patients with high-risk underlying diseases infected with H274Y mutated A(H1N1) virus.

Code(s) de classement : 002B01; 002B05C02C; 002B02S05

Descriptor(s) anglais

Desc. génériques : Viral disease; Infection; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor; Neuraminidase inhibitor

Descriptor(s) français

Desc. génériques : Virose; Infection; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme; Inhibiteur neuraminidase

Localisation : INIST-18250, 354000188101280070
Origue de la notice : INIST
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H1N1 pneumonitis treated with intravenous zanamivir

**Titre** : H1N1 pneumonitis treated with intravenous zanamivir

**Auteur(s)** : KIDD (I. Michael); DOWN (Jim); NASTOULI (Eleni); SHULMAN (Rob); GRANT (Paul R.); HOWELL (David Cj); SINGER (Mervyn)

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**Source** : Lancet : (British edition); vol. 374; no. 9694

**ISSN** : 0140-6736

**CODEN** : LANCAO

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 4 ref.

**Code(s) de classement** : 002B01; 002B02S05

**Descripteur(s) anglais**

*Descripteur(s) :* Pneumonia; Treatment; Intravenous administration; Zanamivir; Medicine; Antiviral

*Desc. génériques :* Respiratory disease; Lung disease; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor; Neuraminidase inhibitor

**Descripteur(s) français**

*Descripteur(s) :* Pneumonie; Traitement; Voie intraveineuse; Zanamivir; Médecine; Antiviral

*Desc. génériques :* Pathologie de l'appareil respiratoire; Pathologie des poumons; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme; Inhibiteur neuraminidase

**Localisation** : INIST-5004, 354000171985740220

**Origine de la notice** : INIST

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Intracellular metabolism of favipiravir (T-705) in uninfected and influenza A (H5N1) virus-infected cells

Titre : Intracellular metabolism of favipiravir (T-705) in uninfected and influenza A (H5N1) virus-infected cells

Auteur(s) : SMEE (Donald E.); HURST (Brett L.); EGAWA (Hiroyuki); TAKAHASHI (Kazumi); KADOTA (Takumi); FURUTA (Yousuke)

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Source : Journal of antimicrobial chemotherapy : (Print); vol. 64; no. 4; pp. 741-746

ISSN : 0305-7453
CODEN : JACHDX
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 13 ref.

Résumé : Objectives: To determine the metabolism of favipiravir (T-705, 6-fluoro-3-hydroxy-2-pyrazinecarboxamide) to its ribosylated, triphosphorylated form (T-705 RTP) in uninfected and influenza A/Duck/MN/1525/81 (H5N1) virus-infected cells. Effects of treatment on intracellular guanosine triphosphate (GTP) pools and influenza virus-inhibitory activity were also assessed. Methods: A strong anion exchange HPLC separation method with UV detection was used to quantify T-705 RTP and GTP levels in Madin-Darby canine kidney cells. Antiviral activity was determined by virus yield reduction assay. Results: Accumulation of T-705 RTP in uninfected cells increased linearly from 3 to 320 pmol/10^6 cells in cells exposed to 1-1000 μM extracellular T-705 for 24 h, approaching maximum levels by 9 h. Virus infection did not result in greater T-705 RTP accumulation compared with uninfected cells. Catabolism of T-705 RTP occurred after removal of T-705 from the extracellular medium, with a half-life of decay of 5.6 ± 0.6 h. Based upon these results, short-term incubation of T-705 with H5N1 virus-infected cells was predicted to provide an antiviral benefit. Indeed, 4-8 h 10-100 μM T-705 treatment of cells resulted in virus yield reductions, but less than continuous exposure. A 100-fold higher extracellular concentration of T-705 was required to inhibit intracellular GTP levels compared with ribavirin, which helps explain ribavirin’s greater toxicity. Conclusions: The favourable intracellular metabolic properties of T-705 combined with its reduced cell-inhibitory properties make this compound an attractive candidate for treating human influenza virus infections.

Code(s) de classement : 002B02S

Description(s) anglais

Desc. (s) : Intracellular; Metabolism; Influenza A virus; Infected cell; Antiviral; Phosphorylation; Guanosine; DNA-directed RNA polymerase; Ribavirin; Favipiravir; Influenzavirus A(H5N1)

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Nucleotidyltransferases; Transferases; Enzyme; Pharmacokinetics; Purine derivatives; Purine nucleoside; Ribonucleoside; Nucleoside analog

Code(s) de classement français

Description(s) : Intracellulaire; Métabolisme; Virus grippal A; Cellule infectée; Antiviral; Phosphorylation; Guanosine; DNA-directed RNA polymerase; Ribavirine; Favipiravir; Influenzavirus A(H5N1)

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Nucleotidyltransferases; Transferases; Enzyme; Pharmacocinétique; Dérivé de la purine; Purine nucléoside; Ribonucléoside; Analog de nucléoside

Localisation : INIST-17084, 354000188120250120
Origine de la notice : INIST
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A Cell Culture (Vero)-Derived H5N1 Whole-Virus Vaccine Induces Cross-Reactive Memory Responses

Titre : A Cell Culture (Vero)-Derived H5N1 Whole-Virus Vaccine Induces Cross-Reactive Memory Responses

Auteur(s) : EHRLICH (Hartmut J.); MÜLLER (Markus); FRITSCH (Sandor); ZEITLINGER (Markus); BEREZUK (Greg); LÖW-BASELLI (Alexandra); VAN DER VELDEN (Maikel V. W.); PÖLLABAUER (Eva Maria); MARITSCH (Friedrich); PAVLOVA (Borislava G.); TAMBYAH (Paul A.); OH (Helen M. L.); MONTOMOLI (Emanuele); KISTNER (Otfried); NOEL BARRETT (P.)

Affiliation(s) : Global R&D, Baxter BioScience, Medical University Vienna, Vienna General Hospital, Vienna, AUT; Department of Clinical Pharmacology, Medical University Vienna, Vienna General Hospital, Vienna, AUT; National University of Singapore, SGP; Changi General Hospital, SGP; University of Siena, Siena, ITA

Source : The Journal of infectious diseases; vol. 200; no. 7; pp. 1113-1118
ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 15 ref.

Résumé : Novel strategies are required to provide rapid vaccine coverage in the event of an influenza pandemic. A phase I/II dose finding/ formulation study was performed with a whole-virus H5N1 clade 1 A/Vietnam vaccine (2-dose priming regimen) to evaluate safety and immunogenicity. Seventy-seven of 141 subjects in this study received a booster (12-17 months after priming) with a 7.5- μ g dose of a clade 2.1 A/Indonesia vaccine. The prime-boost regimen resulted in antibody responses against clade 1, 2.1, 2.2, and 2.3 viruses that were significantly higher than those after the priming regimen. These findings demonstrate that a prime-boost regimen may alleviate vaccine supply constraints in a pandemic. Clinical trials registration. NCT00530660.

Code(s) de classement : 002A05C10; 002B05; 002A05F04

Description anglais

Desc. génériques : Avian influenza virus; Influenza A virus; Cell culture; Vaccine; Microbiology; Infection

Description français

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen

Localisation : INIST-2052, 354000171956200140
Origine de la notice : INIST
Copyright de notice : © 2009 INIST-CNRS. All rights reserved.
Viral Genetic Determinants of H5N1 Influenza Viruses That Contribute to Cytokine Dysregulation

Titre : Viral Genetic Determinants of H5N1 Influenza Viruses That Contribute to Cytokine Dysregulation

Auteur(s) : KA PUN MOK; WONG (Charmaine H. K.); CHEUNG (Chung Y.); CHAN (Michael C.); LEE (Suki M. Y.); NICHOLLS (John M.); YI GUAN; PEIRIS (Joseph S. M.)

Affiliation(s) : Department of Microbiology, Li Ka Shing Faculty of Medicine, University of Hong Kong, HKG; Department of Pathology, Li Ka Shing Faculty of Medicine, University of Hong Kong, HKG; HKU-Pasteur Research Centre, Pok Fu Lam, Hong Kong Special Administrative Region, HKG

Source : The Journal of infectious diseases; vol. 200; no. 7; pp. 1104-1112
ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 23 ref.

Résumé : Human disease caused by highly pathogenic avian influenza (H5N1) is associated with fulminant viral pneumonia and mortality rates in excess of 60%. Cytokine dysregulation is thought to contribute to its pathogenesis. In comparison with human seasonal influenza (H1N1) viruses, clade 1, 2.1, and 2.2 H5N1 viruses induced higher levels of tumor necrosis factor- alpha in primary human macrophages. To understand viral genetic determinants responsible for this hyperinduction of cytokines, we constructed recombinant viruses containing different combinations of genes from high-cytokine (A/Vietnam/1203/04) and low-cytokine (A/WSN/33) phenotype H1N1 viruses and tested their cytokine-inducing phenotype in human macrophages. Our results suggest that the H5N1 polymerase gene segments, and to a lesser extent the NS gene segment, contribute to cytokine hyperinduction in human macrophages and that a putative H5 pandemic virus that may arise through genetic reassortment between H5N1 and one of the current seasonal influenza viruses may have a markedly altered cytokine phenotype.

Code(s) de classement : 002A05C10; 002B05

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus

Desc. génériques : Influenza A virus; Genetics; Cytokine; Microbiology; Infection

Desc. génériques : Virus grippal A; Génétiqute; Cytokine; Microbiologie; Infection

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST-2052, 354000171956200130
Origine de la notice : INIST
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Single-Reaction Genomic Amplification Accelerates Sequencing and Vaccine Production for Classical and Swine Origin Human Influenza A Viruses

Titre : Single-Reaction Genomic Amplification Accelerates Sequencing and Vaccine Production for Classical and Swine Origin Human Influenza A Viruses

Auteur(s) : BIN ZHOU; DONNELLY (Matthew E.); SCHOLDS (Derek T.); GEORGE (Kirsten St.); HATTA (Masato); KAWAOKA (Yoshihiro); WENTWORTH (David E.)

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Source : Journal of virology; vol. 83; no. 19; pp. 10309-10313
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 23 ref.

Résumé : Pandemic influenza A viruses that emerge from animal reservoirs are inevitable. Therefore, rapid genomic analysis and creation of vaccines are vital. We developed a multisegment reverse transcription-PCR (M-RTPCR) approach that simultaneously amplifies eight genomic RNA segments, irrespective of virus subtype. M-RTPCR amplicons can be used for high-throughput sequencing and/or cloned into modified reverse-genetics plasmids via regions of sequence identity. We used these procedures to rescue a contemporary H3N2 virus and a swine origin H1N1 virus directly from human swab specimens. Together, M-RTPCR and the modified reverse-genetics plasmids that we designed streamline the creation of vaccine seed stocks (9 to 12 days).

Code(s) de classement : 002A05C10; 002A05C07

Descripteur(s) anglais
- Descripteur(s) : Swine; Pig; Human; Influenza A virus; Genomics; Amplification; Vaccine; Origin
- Desc. génériques : Artiodactyla; Ungulata; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Veterinary

Descripteur(s) français
- Descripteur(s) : Porcin; Porc; Homme; Virus grippal A; Génomique; Amplification; Vaccin; Origine
- Desc. génériques : Artiodactyla; Ungulata; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Vétérinaire

Localisation : INIST-13592, 354000171986320660
Origine de la notice : INIST
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Elastase-Dependent Live Attenuated Swine Influenza A Viruses Are Immunogenic and Confer Protection against Swine Influenza A Virus Infection in Pigs

Titre : Elastase-Dependent Live Attenuated Swine Influenza A Viruses Are Immunogenic and Confer Protection against Swine Influenza A Virus Infection in Pigs

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Source : Journal of virology; vol. 83; no. 19; pp. 10198-10210
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 54 ref.

Résumé : Influenza A viruses cause significant morbidity in swine, resulting in a substantial economic burden. Swine influenza virus (SIV) infection also poses important human public health concerns. Vaccination is the primary method for the prevention of influenza virus infection. Previously, we generated two elastase-dependent mutant SIVs derived from A/Sw/Saskatchewan/18789/02(H1N1): A/Sw/Sk-R345V (R345V) and A/Sw/Sk-R345A (R345A). These two viruses are highly attenuated in pigs, making them good candidates for a live-virus vaccine. In this study, the immunogenicity and the ability of these candidates to protect against SIV infection were evaluated in pigs. We report that intratracheally administrated R345V and R345A induced antigen-specific humoral and cell-mediated immunity characterized by increased production of immunoglobulin G (IgG) and IgA antibodies in the serum and in bronchoalveolar lavage fluid, high hemagglutination inhibition titers in serum, an enhanced level of lymphocyte proliferation, and higher numbers of gamma interferon-secreting cells at the site of infection. Based on the immunogenicity results, the R345V virus was further tested in a protection trial in which pigs were vaccinated twice with R345V and then challenged with homologous A/Sw/Saskatchewan/ 18789/02, H1N1 antigenic variant A/Sw/Indiana/1726/88 or heterologous subtypic H3N2 A/Sw/Texas/4199-2/9/ 98. Our data showed that two vaccinations with R345V provided pigs with complete protection from homologous H1N1 SIV infection and partial protection from heterologous subtypic H3N2 SIV infection. This protection was characterized by significantly reduced macroscopic and microscopic lung lesions, lower virus titers from the respiratory tract, and lower levels of proinflammatory cytokines. Thus, elastase-dependent SIV mutants can be used as live-virus vaccines against swine influenza in pigs.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Desc. génériques : Artiodactyla; Ungulata; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Veterinary; Viral disease; Infection

Descripteur(s) français

Desc. génériques : Artiodactyla; Ungulata; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Vétérinaire; Virose; Infection

Localisation : INIST-13592, 354000171986320510

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Detection of Mammalian Virulence Determinants in Highly Pathogenic Avian Influenza H5N1 Viruses: Multivariate Analysis of Published Data

Titre : Detection of Mammalian Virulence Determinants in Highly Pathogenic Avian Influenza H5N1 Viruses: Multivariate Analysis of Published Data

Auteur(s) : LYCETT (S. J.); WARD (M. J.); LEWIS (F. I.); POON (A. F. Y.); KOSAKOVSKY POND (S. L.); LEIGH BROWN (A. J.)

Affiliation(s) : Institute of Evolutionary Biology, University of Edinburgh, West Mains Road, Edinburgh EH9 3JT, GBR; University of California at San Diego, 150 West Washington Street, Suite 100, San Diego, California 92103, USA

Source : Journal of virology; vol. 83; no. 19; pp. 9901-9910
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P

Résumé : Highly pathogenic avian influenza (HPAI) virus H5N1 infects water and land fowl and can infect and cause mortality in mammals, including humans. However, HPAI H5N1 strains are not equally virulent in mammals, and some strains have been shown to cause only mild symptoms in experimental infections. Since most experimental studies of the basis of virulence in mammals have been small in scale, we undertook a meta-analysis of available experimental studies and used Bayesian graphical models (BGM) to increase the power of inference. We applied text-mining techniques to identify 27 individual studies that experimentally determined pathogenicity in HPAI H5N1 strains comprising 69 complete genome sequences. Amino acid sequence data in all 11 genes were coded as binary data for the presence or absence of mutations related to virulence in mammals or nonconsensus residues. Sites previously implicated as virulence determinants were examined for association with virulence in mammals in this data set, and the sites with the most significant association were selected for further BGM analysis. The analyses show that virulence in mammals is a complex genetic trait directly influenced by mutations in polymerase basic 1 (PB1) and PB2, nonstructural 1 (NS1), and hemagglutinin (HA) genes. Several intra- and intersegment correlations were also found, and we postulate that there may be two separate virulence mechanisms involving particular combinations of polymerase and NS1 mutations or of NS1 and HA mutations.

Code(s) de classement : 002A05C10; 002A05C04

Descripteur(s) français

Descripteur(s) : Mammalia; Influenzavirus aviaire; Détective; Virulence; Pouvoir pathogène; Analyse donnée; Influenzavirus A(H5N1)
Desc. généraux : Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) anglais

Descripteur(s) : Mammalia; Avian influenza virus; Detection; Virulence; Pathogenicity; Data analysis; Influenzavirus A(H5N1)

Desc. généraux : Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST-13592, 354000171986320250
Origine de la notice : INIST
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Influenza-associated morbidity in subtropical Taiwan

**Titre** : Influenza-associated morbidity in subtropical Taiwan

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**Source** : International journal of infectious diseases; vol. 13; no. 5; pp. 589-599

**ISSN** : 1201-9712

**Date de publication** : 2009

**Pays de publication** : NLD

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 33 ref.

**Résumé** : Objectives: The purpose of this study was to assess the characteristics of influenza-associated morbidity in subtropical Taiwan, corresponding to the seasonal patterns, weather, and co-circulation of influenza (sub)types, and other respiratory viruses, where the burden of influenza is poorly quantified. Methods: This study applied the virus variation-guided Poisson seasonal regression models to evaluate the impact of epidemic influenza on morbidity in Taiwan for 1999-2006. The models allow for the adjusting of influenza-associated morbidity for factors such as annual trend, seasonality, temperature, relative humidity, influenza A (H1N1), A (H3N2), B, and respiratory syncytial virus. Results: Influenza-associated morbidity was associated more strongly with temperature than relative humidity. Influenza A (H3N2) was more coordinated with other virus (sub)types than A (H1N1). Type B dominated simultaneously with A (H3N2) at times, whereas A (H3N2) and A (H1N1) rarely dominated simultaneously with each other. Epidemiologically, A (H3N2) appeared to be the dominant subtype (51%), followed by type B (39%) and then A (H1N1) (10%) for influenza-associated morbidity. Conclusions: This study suggests that seasonality and influenza (sub)types contribute significantly to influenza morbidity in subtropical Taiwan. This is important for influenza control managers who are involved actively in using epidemic and climate information to achieve influenza-reduction targets in subtropical regions.

**Code(s) de classement** : 002B05C02C

**Descrip** **teur(s) anglais**

*Desc. génériques* : Viral disease; Infection; Asia; Epidemiology

**Descrip** **teur(s) français**

*Desc. génériques* : Virose; Infection; Asie; Epidémiologie

**Localisation** : INIST-26659, 354000171941850100

**Origine de la notice** : INIST

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Peut-on évaluer les risques ? Psychose de la grippe, miroir des sociétés

Titre : Peut-on évaluer les risques ? Psychose de la grippe, miroir des sociétés

Auteur(s) : DUCLOS (Denis)
Source : LE MONDE DIPLOMATIQUE; vol. 56; no. 666; pp. 18-19
ISSN : 0026-9395
Date de publication : 2009-09
Pays de publication : FRA
Langue(s) : FRE
Type de document : P
Nombre de références : dissem.

Résumé : D'après l'Organisation mondiale de la santé (OMS), les pays de l'hémisphère Nord ont commandé plus d'un milliard de doses de vaccin contre la grippe A (H1N1) aux laboratoires pharmaceutiques. Lesquels ne devraient pouvoir en fournir au début de l'automne, qu'une quantité limitée. Pendant que les nations industrialisées multiplient les mesures préventives susceptibles de limiter l'impact économique et sanitaire d'un virus certes très contagieux mais, pour le moment, peu létal, des voix s'élèvent pour dénoncer un emballement politico-médiatique. Il est possible de traiter du risque comme d'une réalité objective. Les grandes peurs - de la technologie, de l'étranger, du terroriste, de la maladie... - se multiplient, parfois attisées par qui y trouve son compte. Car, des services de sécurité à l'industrie pharmaceutique, l'anxiété est un marché. Au fond, la panique suscitée par la grippe tend un miroir aux sociétés. S'y reflètent les intérêts, les fantasmes et l'ombre d'une régexion obscurantiste qui prête aux scientifiques de noirs desseins. Tout tourne, dès lors, autour de cette question : comment réduire le risque en amont pour échapper à l'angoisse permanente ?

Code(s) de classement : 002B30A01

Descripteur(s) anglais
  Descripteur(s) : Epidemic; Influenza; Risk management; Information; Health; Mass media; Risk analysis; Critical study; World
  Desc. génériques : Viral disease; Infection

Descripteur(s) français
  Descripteur(s) : Epidémie; Grippe; Gestion risque; Information; Santé; Mass media; Analyse risque; Etude critique; Monde
  Desc. génériques : Virose; Infection

Localisation : BDSP/EHESP-174178
Origine de la notice : BDSP
Questions éthiques soulevées par une possible pandémie grippale

Titre : Questions éthiques soulevées par une possible pandémie grippale

Auteur(s) : DREIFUSS NETTER (F.); DICKELE (A.M.); GAUDRAY (P.); et al.; ALPEROVITCH (A.), rapp.

Source : LES CAHIERS DU COMITE CONSULTATIF NATIONAL D'ETHIQUE POUR LES SCIENCES DE LA VIE ET DE LA SANTE; no. 59; pp. 2-14

ISSN : 1260-8599

Date de publication : 2009-04/2009-06

Pays de publication : FRA

Langue(s) : FRE

Type de document : P

Nombre de références : dissem.

Résumé : Le Comité Consultatif National d'Ethique (CCNE) a été saisi de questions éthiques relatives à la possible pandémie due au virus H5N1 par l'Espace Ethique de l'AP-HP. La question qui paraît essentielle aux yeux du Comité est celle de savoir si l'état d'urgence induit par une pandémie grippale comporte l'éventualité d'une mise à l'arrière-plan de certains principes éthiques fondamentaux. Faut-il subordonner les libertés individuelles à d'autres valeurs plus ajustées à l'efficacité de la stratégie de lutte contre ce fléau sanitaire ? Jusqu'où une limitation aux allées et venues des personnes peut-elle être imposée ? A quelle condition notre société pourrait-elle accepter que certains de ses membres soient prioritairement vaccinés dans la phase de pénurie vaccinale ? (Adapté de l'intro)

Code(s) de classement : 002B30A11

Descripteur(s) anglais

- Description(s) : Ethics; Medicine; Epidemic; Influenza; Accessibility; Inequality; Care; Individual; Freedom; Vaccine; Choice; Priority; Hospital organization
- Desc. génériques : Viral disease; Infection

Descripteur(s) français

- Description(s) : Éthique; Médecine; Epidémie; Grippe; Accessibilité; Inégalité; Soin; Individu; Liberté; Vaccin; Choix; Priorité; Organisation hospitalière
- Desc. génériques : Soins; Infection

Localisation : BDSP/APHIDOC

Origine de la notice : BDSP
Since April 15 and 17, 2009, when the first two cases of novel influenza A (H1N1) infection were identified from two southern California counties, novel influenza A (H1N1) cases have been documented throughout the world, with most cases occurring in the United States and Mexico. In the United States, early reports of illnesses associated with novel influenza A (H1N1) infection indicated the disease might be similar in severity to seasonal influenza, with the majority of patients not requiring hospitalization and only rare deaths reported, generally in persons with underlying medical conditions. As of May 17, 2009, 553 novel influenza A (H1N1) cases, including 333 confirmed and 220 probable cases, had been reported in 32 of 61 local health jurisdictions in California. Of the 553 patients, 30 have been hospitalized. No fatal cases associated with novel influenza A (H1N1) infection had been reported in California. This report summarizes the 30 hospitalized cases as of May 17, including a detailed description of four cases that illustrate the spectrum of illness severity and underlying risk factors. This preliminary overview indicates that, although the majority of hospitalized persons infected with novel influenza A (H1N1) recovered without complications, certain patients had severe and prolonged disease. All hospitalized patients with novel influenza A (H1N1) infection should be monitored carefully and treated with antiviral therapy, including patients who seek care >48 hours after illness onset. (Résumé d'auteur)
A probiotic fermented dairy drink improves antibody response to influenza vaccination in the elderly in two randomised controlled trials

Titre : A probiotic fermented dairy drink improves antibody response to influenza vaccination in the elderly in two randomised controlled trials

Auteur(s) : BOGE (Thierry); REMIGY (Michel); VAUDAINE (Sarah); TANGUY (Jérôme); BOURDET-SICARD (Raphaëlle); VAN DER WERF (Sylvie)
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Source : Vaccine; vol. 27; no. 41; pp. 5677-5684
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 31 ref.

Résumé : Background: Influenza vaccination is recommended for the elderly in many countries, but immune responses are weaker compared to younger adults. Objective: To investigate the impact of daily consumption of a probiotic dairy drink on the immune response to influenza vaccination in an elderly population of healthy volunteers over 70 years of age. Design: Two randomised, multicentre, double-blind, controlled studies were conducted during two vaccination seasons in 2005-2006 (pilot) and 2006-2007 (confirmatory). Eighty-six and 222 elderly volunteers consumed either a fermented dairy drink, containing the probiotic strain Lactobacillus casei DN-114 001 and yoghurt ferments (Actimel®), or a non-fermented control dairy product twice daily for a period of 7 weeks (pilot) or 13 weeks (confirmatory). Vaccination occurred after 4 weeks of product consumption. Geometric mean antibody titres (GMT) against the 3 viral strains composing the vaccine (H1N1, H3N2, and B) were measured at several time intervals post-vaccination by haemagglutination inhibition test Results: In the pilot study, the influenza-specific antibody titres increased after vaccination, being consistently higher in the probiotic product group compared to the control group under product consumption. Similarly, in the confirmatory study, titres against the B strain increased significantly more in the probiotic group than in the control group at 3, 6 and 9 weeks post-vaccination under product consumption (p=0.020). Significant differences in seroconversion between the groups by intended to treat analysis were still found 5 months after vaccination. Similar GMT results were observed for the H3N2 strain and H1N1 strain, confirming the results of the pilot study. Conclusion: These studies demonstrate that daily consumption of this particular probiotic product increased relevant specific antibody responses to influenza vaccination in individuals of over 70 years of age and may therefore provide a health benefit in this population.

Code(s) de classement : 002A05F04; 002A05B15

Descripteur(s) anglais
Descripteur(s) : Lactobacillus; Probiotic; Humoral immunity; Immune response; Vaccination; Elderly; Influenza
Desc. génériques : Lactobacillaceae; Bacteria; Human; Lactic acid bacteria; Viral disease; Infection

Descripteur(s) français
Descripteur(s) : Lactobacillus; Probiotique; Immunité humorale; Réponse immune; Vaccination; Personne âgée; Grippé
Desc. génériques : Lactobacillaceae; Bactérie; Homme; Bactérie lactique; Virose; Infection
Proteomics-based characterization of hemagglutinins in different strains of influenza virus

Titre : Proteomics-based characterization of hemagglutinins in different strains of influenza virus

Auteur(s) : GETIE-KEBTIE (Melkamu); CHEN (David); EICHELBERGER (Maryna); ALTERMAN (Michail)

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Source : Proteomics. Clinical applications : (Print); vol. 3; no. 8; pp. 979-988
ISSN : 1862-8346
Date de publication : 2009
Pays de publication : DEU
Langue(s) : ENG
Type de document : P
Nombre de références : 23 ref.

Résumé : Infection with influenza A (subtypes H1N1 and H3N2) or B viruses results in over half a million deaths worldwide every year. Frequent antigenic changes (drift) in two major viral surface proteins hemagglutinin (HA) and neuraminidase lead to the constant emergence of antigenically distinct virus strains against which there is sub-optimal immunity in the population. Consequently the suitability of the viral strains included in the trivalent influenza vaccine (TIV) has to be re-evaluated annually. While virus seeds selected for vaccine manufacture are very well characterized, there is no assay in place to identify the source of HA in the formulated trivalent vaccine. Our study describes a proteomics-based method to identify the HA strain (not just subtype) and more fully characterize the final vaccine product. Unique and shared tryptic peptides of HAs were predicted by in silico tryptic digest of different influenza A and B virus strains. Recombinant HA and whole virus preparations of selected strains were then digested to identify the peptides detected by MS. Both subtype and strain-specific peptides were observed. The feasibility of this method to accurately identify HA strains in an inactivated TIV was tested using a 2006/2007 formulation. Each of the three HAs in the vaccine was identified in addition to a number of other viral and non-viral proteins. In summary, MS is a powerful method that is both specific and inclusive; in a single analysis, HAs of individual virus strains can be identified and the composition of the TIV fully characterized.

Code(s) de classement : 002A04B; 002B05C02C

Desc. génériques : Viral disease; Infection; Orthomyxoviridae; Virus

Descripteur(s) anglais
- Descripteur(s) : Proteomics; Characterization; Hemagglutinin; Strain; Peptides; Vaccine; Influenza; Influenzavirus
- Desc. génériques : Viral disease; Infection; Orthomyxoviridae; Virus

Descripteur(s) français
- Descripteur(s) : Protéomique; Caractérisation; Hémagglutinine; Souche; Peptide; Vaccin; Grippe; Influenzavirus
- Desc. génériques : Virose; Infection; Orthomyxoviridae; Virus

Localisation : INIST-27873, 354000171027580080
Origine de la notice : INIST
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Auteur(s) : JADHAO (Samadhan J.); NGUYEN (Doan C.); UYEKI (Timothy M.); SHAW (Michael); MAINES (Taronna); ROWE (Thomas); SMITH (Catherine); HUYNH (Lien P. T.); NGHIEM (Ha K.); NGUYEN (Hang K. L.); NGUYEN (Hanh H. T.); HOANG (Long T.); NGUYEN (Tung); PHUONG (Lien S.); KLIMOV (Alexander); TUMPEY (Terrence M.); COX (Nancy J.); DONIS (Ruben O.); MATSUOKA (Yumiko); KATZ (Jacqueline M.)

Affiliation(s) : Influenza Division, MS-G16, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, 1600 Clifton Road, NE, Atlanta, GA 30333, USA; National Institute of Hygiene and Epidemiology, Hanoi, VNM; National Center for Veterinary Diagnosis, Hanoi, VNM

Source : Archives of virology; vol. 154; no. 8; pp. 1249-1261
ISSN : 0304-8608
Date de publication : 2009
Pays de publication : AUT
Langue(s) : ENG
Type de document : P
Nombre de références : 45 ref.

Résumé : The first known cases of human infection with highly pathogenic avian influenza (HPAI) H5N1 viruses in Vietnam occurred in late 2003. However, HPAI H5N1 and low-pathogenic avian influenza (LPAI) H5N2 and H9N3 viruses were isolated from domestic waterfowl during live-bird market (LBM) surveillance in Vietnam in 2001 and 2003. To understand the possible role of these early viruses in the genesis of H5N1 strains infecting people, we performed sequencing and molecular characterization. Phylogenetic analysis revealed that the hemagglutinin (HA) genes of two geese HPAI H5N1 strains belonged to clade 3, and their surface glycoprotein and replication complex genes were most closely related (98.5-99.7% homologous) to A/duck/Guangxi/22/01 (H5N1) virus, detected contemporarily in southern China, whilst the M and NS genes were derived from an A/duck/Hong Kong/2986/00 (H5N1)-like virus. The H5 HA gene of the duck HPAI H5N1 strain belonged to clade 5 and acquired a gene constellation from A/quail/Shantou/3846/02 (H5N1), A/teal/China/2978.1/02 (H5N1) and A/partridge/Shantou/2286/03 (H5N1)-like viruses. The phylogenetic analysis further indicated that all eight gene segments of goose and duck HPAI H5N1 and LPAI H5N2 viruses were distinct from those of H5N1 clade-1 viruses known to have caused fatal human infections in Vietnam since late 2003. The duck H9N3 isolates derived genes from aquatic-bird influenza viruses, and their H9 HA belonged to the Korean lineage. The PB2 gene of A/duck/Vietnam/340/01 (H9N3) virus had lysine at position 627. Based on the molecular characterization of specific amino acid residues in the surface and relevant internal protein-coding genes, the Vietnamese H5N1 and H9N3 virus isolates indicated specificity to avian cell surface receptor and susceptibility for currently licensed antiinfluenza A virus chemotherapeutics. Our findings suggest that the H5N1 and H5N2 viruses that circulated among geese and ducks in LBMs in Hanoi, Vietnam, during 2001 and 2003 were not the immediate ancestors of the clade-1 viruses associated with fatal human infections in Vietnam. The clade-1 HPAI H5N1 viruses were independently introduced into Vietnam.

Code(s) de classement : 002A05C10; 002A05C05

Descripteur(s) anglais
Desc. généraux : Influenzavirus A; Orthomyxoviridae; Virus; Vertebrata; Asia; Zoopathogen

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Origin of the 2009 Mexico influenza virus: a comparative phylogenetic analysis of the principal external antigens and matrix protein

**Titre** : Origin of the 2009 Mexico influenza virus: a comparative phylogenetic analysis of the principal external antigens and matrix protein

**Auteur(s)** : BABAKIR-MINA (Muhammed); DIMONTE (Salvatore); FEDERICO PERNO (Carlo); CIOTTI (Marco)

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**Source** : Archives of virology; vol. 154; no. 8; pp. 1349-1352

**ISSN** : 0304-8608

**Date de publication** : 2009

**Pays de publication** : AUT

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 11 ref.

**Résumé** : Triple-reassortant swine influenza A (H1) viruses, containing genes from avian, human, and swine influenza viruses, emerged and became an outbreak among humans worldwide. Over a 1,000 cases were identified within the first month, chiefly in Mexico and the United States. Here, the phylogenetic analysis of haemagglutinin (HA), neuraminidase (NA), and matrix protein (MP) was carried out. The analysis showed that the H1 of this reassortant originated from American pigs, while NA and MP were more likely from European pigs. All of the 2009 isolates appear homogeneous and cluster together, although they are distinct from classical human A (H1N1) viruses.

**Code(s) de classement** : 002A05C10

**Descripteur(s) anglais**

*Descriptrue(s)*: Influenza A virus; Origin; Mexico; Phylogeny; Antigen; Protein

*Desc. génériques* : Influenzavirus A; Orthomyxoviridae; Virus; Central America; America

**Descripteur(s) français**

*Descriptrue(s)*: Virus grippal A; Origine; Mexique; Phylogènèse; Antigène; Protéine

*Desc. génériques* : Influenzavirus A; Orthomyxoviridae; Virus; Amérique Centrale; Amérique

**Localisation** : INIST-6355, 354000171909690180

**Origine de la notice** : INIST

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Replication and pathogenesis associated with H5N1, H5N2, and H5N3 low-pathogenic avian influenza virus infection in chickens and ducks

Titre : Replication and pathogenesis associated with H5N1, H5N2, and H5N3 low-pathogenic avian influenza virus infection in chickens and ducks

Auteur(s) : MUNDT (Egbert); GAY (Lauren); JONES (Les); SAAVEDRA (Geraldine); TOMPKINS (S. Mark); TRIPP (Ralph A.)

Affiliation(s) : Department of Population Health, Poultry Diagnostic and Research Center, College of Veterinary Medicine, University of Georgia, Athens 30602, GA, USA; Department of Infectious Diseases, College of Veterinary Medicine, University of Georgia, Athens 30602, GA, USA

Source : Archives of virology; vol. 154; no. 8; pp. 1241-1248

ISSN : 0304-8608

Date de publication : 2009

Pays de publication : AUT

Langue(s) : ENG

Type de document : P

Nombre de références : 28 ref.

Résumé : A comparative study examining replication and disease pathogenesis associated with low-pathogenic H5N1, H5N2, or H5N3 avian influenza virus (AIV) infection of chickens and ducks was performed. The replication and pathogenesis of highly pathogenic AIV (HPAIV) has received substantial attention; however, the behavior of low-pathogenic AIVs, which serve as precursors to HPAIVs, has received less attention. Thus, chickens or ducks were inoculated with an isolate from a wild bird [A/Mute Swan/MI/451072/06 (H5N1)] or isolates from chickens [A/Ck/PA/13609/93 (H5N2), A/Ck/TX/167280-4/02 (H5N3)], and virus replication, induction of a serological response, and disease pathogenesis were investigated, and the hemagglutinin and neuraminidase (NA) gene sequences of the isolates were determined. Virus isolated from tracheal and cloacal swabs showed that H5N1 replicated better in ducks, whereas H5N2 and H5N3 replicated better in chickens. Comparison of the NA gene sequences showed that chicken-adapted H5N2 and H5N3 isolates both have a deletion of 20 amino acids in the NA stalk region, which was absent in the H5N1 isolate. Histopathological examination of numerous organs showed that H5N2 and H5N3 isolates caused lesions in chickens in a variety of organs, but to a greater extent in the respiratory and intestinal tracts, whereas H5N1 lesions in ducks were observed mainly in the respiratory tract. This study suggests that the H5N1, H5N2, and H5N3 infections occurred at distinct sites in chicken and ducks, and that comparative studies in different model species are needed to better understand the factors influencing the evolution of these viruses.

Code(s) de classement : 002A05C10; 002A05C04

Descripteur(s) anglais
Desc. génériques : Avian influenzavirus; Chicken; Replication; Pathogenesis; Pathogenicity; Duck

Descripteur(s) français
Desc. génériques : Influenzavirus aviaire; Poulet; Réplication; Pathogénie; Pouvoir pathogène; Canard

Localisation : INIST-6355, 354000171909690070

Origine de la notice : INIST

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Rapid Multiplex Reverse Transcription-PCR Typing of Influenza A and B Virus, and Subtyping of Influenza A Virus into HI, 2, 3, 5, 7, 9, N1 (Human), N1 (Animal), N2, and N7, Including Typing of Novel Swine Origin Influenza A (H1N1) Virus, during the 2009 Outbreak in Milwaukee, Wisconsin

**Titre** : Rapid Multiplex Reverse Transcription-PCR Typing of Influenza A and B Virus, and Subtyping of Influenza A Virus into HI, 2, 3, 5, 7, 9, N1 (Human), N1 (Animal), N2, and N7, Including Typing of Novel Swine Origin Influenza A (H1N1) Virus, during the 2009 Outbreak in Milwaukee, Wisconsin

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**Source** : Journal of clinical microbiology : (Print); vol. 47; no. 9; pp. 2772-2778

**ISSN** : 0095-1137

**CODEN** : JCMIDW

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 26 ref.

**Résumé** : A large outbreak of novel influenza A (H1N1) virus (swine origin influenza virus [S-OIV]) infection in Milwaukee, WI, occurred in late April 2009. We had recently developed a rapid multiplex reverse transcription-PCR enzyme hybridization assay (FluPlex) to determine the type (A or B) and subtype (H1, H2, H3, H5, H7, H9, N1 [human], N1 [animal], N2, or N7) of influenza viruses, and this assay was used to confirm the diagnoses for the first infected patients in the state. The analytical sensitivity was excellent at 1.5 to 116 copies/reaction, or 10^-3 to 10^-1 50% tissue culture infective doses/ml. The testing of all existing hemagglutinin and neuraminidase subtypes of influenza A virus and influenza B virus (41 influenza virus strains) and 24 common respiratory pathogens showed only one low-level H3 cross-reaction with an H10N7 avian strain and only at 5.2 x 10^6 copies/reaction, not at lower concentrations. Comparisons of the FluPlex results with results from multiple validated in-house molecular assays, CDC-validated FDA-approved assays, and gene sequencing demonstrated 100% positive agreement for the typing of 179 influenza A viruses and 3 influenza B viruses, the subtyping of 110 H1N1 (S-OIV; N1 [animal], 62 H1N1 (human), and 6 H3N2 (human) viruses, and the identification of 24 negative clinical samples and 100% negative agreement for all viruses tested except H1N1 (human) (97.7%). The small number of false-positive H1N1 (human) samples most likely represent increased sensitivity over that of other in-house assays, with four of four results confirmed by the CDC’s influenza virus subtyping assay. The FluPlex is a rapid, inexpensive, sensitive, and specific method for the typing and subtyping of influenza viruses and demonstrated outstanding utility during the first 2 weeks of an S-OIV infection outbreak. Methods for rapid detection and broad subtyping of influenza viruses, including animal subtypes, are needed to address public concern over the emergence of pandemic strains. Attempts to automate this assay are ongoing.

**Code(s) de classement** : 002A05C10

**Descripteur(s) anglais**
Title: Rapid Semiautomated Subtyping of Influenza Virus Species during the 2009 Swine Origin Influenza A H1N1 Virus Epidemic in Milwaukee, Wisconsin

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Source: Journal of clinical microbiology: (Print); vol. 47; no. 9; pp. 2779-2786

ISSN: 0095-1137
CODEN: JCMIDW
Date of publication: 2009
Pays de publication: USA
Langue(s): ENG
Type de document: P
Nombre de références: 24 ref.

Résumé: In the spring of 2009, a novel influenza A (H1N1) virus (swine origin influenza virus [S-OIV]) emerged and began causing a large outbreak of illness in Milwaukee, WI. Our group at the Midwest Respiratory Virus Program laboratory developed a semiautomated real-time multiplex reverse transcription-PCR assay (Seasonal), employing the NucliSENS easyMAG system (bioMérieux, Durham, NC) and a Raider thermocycler (HandyLab Inc., Ann Arbor, MI), that typed influenza A virus, influenza B virus, and respiratory syncytial virus (RSV) and subtyped influenza A virus into the currently circulating H1 and H3 subtypes, as well as a similar assay that identified H1 of S-OIV. The Seasonal and H1 S-OIV assays demonstrated analytical limits of detection of <50 50% tissue culture infective doses/ml and 3 to 30 input copies, respectively. Testing of the analytical specificities revealed no cross-reactivity with 41 and 26 different common organisms and demonstrated outstanding reproducibility of results. Clinical testing showed 95% sensitivity for influenza A virus and influenza B virus and 95 and 97% specificity compared to tissue culture. Comparisons of results from other molecular tests showed levels of positive agreement with the Seasonal and H1 S-OIV assay results of 99 and 100% and levels of negative agreement of 98 and 100%. This study has demonstrated the use of a semiautomated system for sensitive, specific, and rapid detection of influenza A virus, influenza B virus, and RSV and subtyping of influenza A virus into human H1 and H3 and S-OIV strains. This assay/system performed well in clinical testing of regular seasonal influenza virus subtypes and was outstanding during the 2009 Milwaukee S-OIV infection outbreak. This recent outbreak of infection with a novel influenza A (H1N1) virus also demonstrates the importance of quickly distributing information on new agents and of having rapid influenza virus subtyping assays widely available for clinical and public health decisions.

Code(s) de classement: 002A05C10

Descriptor(s) anglais
Desc. génériques: Influenzavirus A; Orthomyxoviridae; Virus; United States; North America; America; Veterinary

Descriptor(s) français
Desc. génériques: Influenzavirus porcin; Virus grippal A; Origine; Epidémie; Wisconsin; Microbiologie

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Phosphoantigen-Expanded Human gamma delta T Cells Display Potent Cytotoxicity against Monocyte-Derived Macrophages Infected with Human and Avian Influenza Viruses

Titre : Phosphoantigen-Expanded Human gamma delta T Cells Display Potent Cytotoxicity against Monocyte-Derived Macrophages Infected with Human and Avian Influenza Viruses

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Source : The Journal of infectious diseases; vol. 200; no. 6; pp. 858-865

ISSN : 0022-1899
CODEN : JIDIAQ

Date de publication : 2009
Pays de publication : USA

Langue(s) : ENG

Type de document : P

Nombre de références : 48 ref.

Résumé : Background. Influenza virus is a cause of substantial annual morbidity and mortality worldwide. The potential emergence of a new pandemic strain (eg, avian influenza virus) is a major concern. Currently available vaccines and anti-influenza drugs have limited effectiveness for influenza virus infections, especially for new pandemic strains. Therefore, there is an acute need to develop alternative strategies for influenza therapy. gamma delta T cells have potent antiviral activities against different viruses, but no data are available concerning their antiviral activity against influenza viruses. Methods. In this study, we used virus-infected primary human monocyte-derived macrophages (MDMs) to examine the antiviral activity of phosphoantigen isopentenyl pyrophosphate (IPP)-expanded human V gamma 9V delta 2 T cells against influenza viruses. Results. V gamma 9V delta 2 T cells were selectively activated and expanded by IPP from peripheral blood mononuclear cells. IPP-expanded V gamma 9V delta 2 T cells efficiently killed MDMs infected with human (H1N1) or avian (H9N2 or H5N1) influenza virus and significantly inhibited viral replication. The cytotoxicity of V gamma 9V delta 2 T cells against influenza virus-infected MDMs was dependent on NKG2D activation and was mediated by Fas-Fas ligand and perforin-granzyme B pathways. Conclusion. Our findings suggest a potentially novel therapeutic approach to seasonal, zoonotic avian, and pandemic influenza-the use of phosphoantigens to activate gamma delta T cells against influenza virus infections.

Code(s) de classement : 002A05C10; 002B05

Descripteur(s) anglais
- Description(s) : Human; Avian influenzavirus; gamma / delta T cell receptor; Cytotoxicity; Monocyte; Macrophage; Microbiology; Infection
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen

Descripteur(s) français
- Description(s) : Homme; Influenzavirus aviaire; Récepteur cellule T gamma / delta ; Cytotoxicité; Monocyte; Macrophage; Microbiologie; Infection
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogène

Localisation : INIST-2052, 354000187654700050

Origine de la notice : INIST

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Dynamics of antiviral-resistant influenza viruses in the Netherlands, 2005-2008

Titre : Dynamics of antiviral-resistant influenza viruses in the Netherlands, 2005-2008

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Source : Antiviral research; vol. 83; no. 3; pp. 290-297

ISSN : 0166-3542
CODEN : ARSRDR
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 3-4 p.

Résumé : In the Netherlands, influenza specific antivirals are used for the therapy of influenza in nursing homes and hospitals, for prophylaxis in high risk groups and neuraminidase inhibitors are stockpiled as part of pandemic preparedness plans. To monitor the antiviral susceptibility profile, human influenza virus isolates derived from the Dutch influenza surveillance in 2005-2006 (n=87), 2006-2007 (n=58) and 2007-2008 (n=128) were analyzed with phenotypic assays and sequencing. For adamantanes, a high proportion (>74%) of A(H3N2) viruses had the S31 N mutation in M2 protein, while variation in the HA1 region of adamantane-sensitive viruses suggested that adamantane-sensitive variants were reseeded into the Dutch population and re-emerged as drug-sensitive due to M-segment reassortment. For neuraminidase inhibitors oseltamivir and zanamivir, 98% of types A and B influenza viruses prior to 2007-2008 were sensitive for both, whereas 24% of the A(H1N1) viruses obtained in 2007-2008 were oseltamivir-resistant while retaining sensitivity to zanamivir and adamantanes. Furthermore, oseltamivir-resistant A(H1N1) or adamantane-resistant A(H3N2) virus infections were not associated with differences in clinical symptoms compared to infections with sensitive variants. Our data show the dynamic nature of emergence of drug-resistant influenza viruses, stressing the need for surveillance of resistance trends as part of influenza monitoring programs.

Code(s) de classement : 002B02S05; 002B05C02C; 002B30A01A2

Descriputeur(s) anglais

Descriputeur(s) : Dynamics; Antiviral; Treatment resistance; Influenza; Netherlands; Surveillance; Oseltamivir; Zanamivir; Amantadine; Drug; Pharmacotherapy; Influenzavirus; Public health; Epidemiology; Antiparkinson agent

Desc. génériques : Viral disease; Infection; Europe; Treatment; Orthomyxoviridae; Virus; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor; Neuraminidase inhibitor; Agonist; Antagonist; Dopamine receptor; Glutamate receptor; NMDA receptor; Dopamine agonist; Amantadine derivatives

Descriputeur(s) français

Descriputeur(s) : Dynamique; Antiviral; Résistance traitement; Grippe; Pays-Bas; Surveillance; Oséltamivir; Zanamivir; Amantadine; Médicament; Pharmacothérapie; Influenzavirus; Santé publique; Epidémiologie; Antiparkinsonien

Desc. génériques : Virose; Infection; Europe; Traitement; Orthomyxoviridae; Virus; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme; Inhibiteur neuraminidase; Agoniste; Antagoniste; Récepteur dopaminergique; Récepteur glutamate; Récepteur NMDA; Stimulant dopaminergique; Dérivé de l'amantadine

Localisation : INIST-18839, 354000171894410110
Human monoclonal antibodies in single chain fragment variable format with potent neutralization activity against influenza virus H5N1

**Titre** : Human monoclonal antibodies in single chain fragment variable format with potent neutralization activity against influenza virus H5N1

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**Source** : Antiviral research; vol. 83; no. 3; pp. 238-244

**ISSN** : 0166-3542

**CODEN** : ARSRDR

**Date de publication** : 2009

**Pays de publication** : NLD

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 3/4 p.

**Résumé** : Effective diagnostic and therapeutic strategies are needed to control and combat the highly pathogenic avian influenza virus (AIV) subtype H5N1. To this end, we developed human monoclonal antibodies (mAbs) in single chain fragment variable (scFv) format towards the H5N1 avian influenza virus to gain new insights for the development of immunotherapy against human cases of H5N1. Using a biopanning based approach a large array of scFvs against H5N1 virus were isolated from the human semi-synthetic ETH-2 phage antibody library. H5N1 ELISA-positive scFvs with unique variable heavy (VH) and light (VL) chain gene sequences showed different biochemical properties and neutralization activity across H5N1 viral strains. In particular, the scFv clones AV.D1 and AV.C4 exerted a significant inhibition of the H5N1 A/Vietnam/1194/2004 virus infection in a pseudotype-based neutralization assay. Interestingly, these two scFvs displayed a cross-clade neutralizing activity versus A/whooping swan/Mongolia/244/2005 and A/Indonesia/5/2005 strains. These studies provide proof of the concept that human mAbs in scFv format with well-defined H5N1 recognition patterns and in vitro neutralizing activity can be easily and rapidly isolated by biopanning selection of an entirely artificial antibody repertoire using inactivated H5N1 virus as a bait.

**Code(s) de classement** : 002B02S05; 002B05C02C; 002B02A03

**Descripteurs anglais**

- **Description(s) :** Human; Monoclonal antibody; Neutralization; Avian influenza; Virus; Immunoprophylaxis; Single chain antibody; Immunotherapy; Performance evaluation; Technique; Influenzavirus A(H5N1)
- **Desc. génériques :** Viral disease; Infection

**Descripteurs français**

- **Description(s) :** Homme; Anticorps monoclonal; Neutralisation; Grippe aviaire; Virus; Immunoprophylaxie; Anticorps simple chaîne; Immunothérapie; Évaluation performance; Technique; Influenzavirus A(H5N1)
- **Desc. génériques :** Virose; Infection

**Localisation :** INIST-18839, 354000171894410040

**Origine de la notice :** INIST

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In vitro and in vivo characterization of new swine-origin H1N1 influenza viruses

**Titre** : In vitro and in vivo characterization of new swine-origin H1N1 influenza viruses

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**Source** : Nature : (London); vol. 460; no. 7258; pp. 1021-1025
**ISSN** : 0028-0836
**CODEN** : NATUAS
**Date de publication** : 2009
**Pays de publication** : GBR
**Langue(s)** : ENG
**Type de document** : P

**Résumé** : Influenza A viruses cause recurrent outbreaks at local or global scale with potentially severe consequences for human health and the global economy. Recently, a new strain of influenza A virus was detected that causes disease in and transmits among humans, probably owing to little or no pre-existing immunity to the new strain. On 11 June 2009 the World Health Organization declared that the infections caused by the new strain had reached pandemic proportion. Characterized as an influenza A virus of the H1N1 subtype, the genomic segments of the new strain were most closely related to swine viruses'. Most human infections with swine-origin H1N1 influenza viruses (S-OIVs) seem to be mild; however, a substantial number of hospitalized individuals do not have underlying health issues, attesting to the pathogenic potential of S-OIVs. To achieve a better assessment of the risk posed by the new virus, we characterized one of the first US S-OIV isolates, A/California/04/09 (H1N1; hereafter referred to as CA04), as well as several other S-OIV isolates, in vitro and in vivo. In mice and ferrets, CA04 and other S-OIV isolates replicated more efficiently than a currently circulating human H1N1 virus. In specific-pathogen-free miniature pigs, CA04 replicates without clinical symptoms. The assessment of human sera from different age groups suggests that infection with human
H1N1 viruses antigenically closely related to viruses circulating in 1918 confers neutralizing antibody activity to CA04. Finally, we show that CA04 is sensitive to approved and experimental antiviral drugs, suggesting that these compounds could function as a first line of defence against the recently declared S-OIV pandemic.

**Code(s) de classement** : 002B02S05; 002A05C04

**Descripseur(s) anglais**
- **Descripseur(s) :** In vivo; In vitro; Replication; Animal; Pathogenesis; Antiviral; Sensitivity resistance; Influenza A; Pandemic
- **Desc. génériques :** Viral disease; Infection

**Descripseur(s) français**
- **Descripseur(s) :** In vivo; In vitro; Réplication; Animal; Pathogénie; Antiviral; Sensibilité résistance; Grippe A; Influenzavirus A(H1N1); Influenzavirus A(H1N1) S-OIV; Grippe pandémique; Pandémie
- **Desc. génériques :** Virose; Infection

**Localisation** : INIST-142, 354000172577680190
**Origine de la notice** : INIST
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Antigenic and Genetic Characteristics of Swine-Origin 2009 A(H1N1) Influenza Viruses Circulating in Humans

Titre : Antigenic and Genetic Characteristics of Swine-Origin 2009 A(H1N1) Influenza Viruses Circulating in Humans

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Source : Science : (Washington, D.C.); vol. 325; no. 5937; pp. 197-201
ISSN : 0036-8075
CODEN : SCIEAS
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Notes : 1/2 ref. et notes

Résumé : Since its identification in April 2009, an A(H1N1) virus containing a unique combination of gene segments from both North American and Eurasian swine lineages has continued to circulate in humans. The lack of similarity between the 2009 A(H1N1) virus and its nearest relatives indicates that its gene segments have been circulating undetected for an extended period. Its low genetic diversity suggests that the introduction into humans was a single event or multiple events of similar viruses. Molecular markers predictive of adaptation to humans are not currently present in 2009 A(H1N1) viruses, suggesting that previously unrecognized molecular determinants could be responsible for the transmission among humans. Antigenically the viruses are homogeneous and similar to North American swine
A(H1N1) viruses but distinct from seasonal human A(H1N1).

Code(s) de classement : 002B05C02C; 002B23

Descripteur(s) anglais
- Descripteur(s) : Influenzavirus A; Characteristics; Genetics; Antigen; Human; Influenza A; Gene; Phylogenetic tree; Nucleotide sequence
- Desc. génériques : Orthomyxoviridae; Virus; Viral disease; Infection

Descripteur(s) français
- Descripteur(s) : Influenzavirus A; Caractéristiques; Génétique; Antigène; Homme; Grippe A; Gène; Arbre phylogénétique; Séquence nucléotide; Influenzavirus A(H1N1)
- Desc. génériques : Orthomyxoviridae; Virus; Virose; Infection

Localisation : INIST-6040, 354000172477510240
Origine de la notice : INIST
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A simple model for simulating immunity rate dynamics in a tropical free-range poultry population after avian influenza vaccination

Titre : A simple model for simulating immunity rate dynamics in a tropical free-range poultry population after avian influenza vaccination

Auteur(s) : LESNOFF (M.); PEYRE (M.); DUARTE (P. C.); RENARD (J.-F.); MARINER (J. C.)
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Source : Epidemiology and infection; vol. 137; no. 10; pp. 1405-1413
ISSN : 0950-2688
CODEN : EPINEU
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 40 ref.

Résumé : In developing countries, vaccination against highly pathogenic avian influenza subtype H5N1 (HPAI) in free-range poultry flocks is usually implemented as periodic campaigns and newborn chicks are generally not vaccinated by farmers between vaccination passes. The demographic population turnover leads to a continuous decrease in the population immunity rate (PIR) over time. We present a simple Leslie matrix model for estimating population turnover and PIR dynamics in a hypothetical small-size vaccinated free-range poultry population. Four different vaccination scenarios were identified assuming necessary procedures to achieve immunity. The results indicate that high levels of population immunity are difficult to sustain. Assuming an animal immunity response of 80 % after vaccination and a constant population size, PIR 4 months after vaccination was <= 30 % in all the scenarios. Predictions averaged over time showed mean PIR between 36 % and 48 %, which is below the population immunity thresholds for eradication approximated from Ro estimates.

Code(s) de classement : 002A05

Descripteur(s) anglais

Desc. généraux : Farming animal; Viral disease; Infection; Veterinary

Descripteur(s) français

Desc. généraux : Animal élevage; Virose; Infection; Vétérinaire

Localisation : INIST-6056, 354000187614460060
Origine de la notice : INIST
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Surveillance and Oseltamivir Resistance of Human Influenza A Virus in Turkey During the 2007-2008 Season

**Titre** : Surveillance and Oseltamivir Resistance of Human Influenza A Virus in Turkey During the 2007-2008 Season

**Auteur(s)** : CIBLAK (Meral Akcay); HASOKSUZ (Mustafa); ESCURET (Vanessa); VALETTE (Martine); GUL (Fadime); YILMAZ (Huseyin); TURAN (Nuri); BOZKAYA (Emel); BADUR (Selim)

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**Source** : Journal of medical virology; vol. 81; no. 9; pp. 1645-1651
**ISSN** : 0146-6615
**CODEN** : JMVIDB
**Date de publication** : 2009
**Pays de publication** : USA
**Langue(s)** : ENG
**Type de document** : P
**Nombre de références** : 1/4 p.

**Résumé** : Monitoring the activity of influenza viruses is important for establishing the circulating types and for detection of the emergence of novel subtypes and antiviral resistant strains. This is the first report from Turkey on the surveillance and oseltamivir resistance of influenza viruses in 2007-2008. Five hundred twenty-four nasal swabs were tested from different geographical regions in Turkey during November 2007-April 2008. One hundred sixty-three (31%) samples were positive for influenza viruses of which 111 (68%) were influenza A, 52 (31%) influenza B using an immuno-capture ELISA. Forty isolates were selected at random from influenza A positive samples and grown in MDCK cell cultures. The supernatant of the cell cultures was used for RNA extraction followed by RT-PCR to detect the sub-types. Sub-typing revealed all samples as A/H1N1. The N1 gene segment of 30 A/H1 N1 samples was sequenced in part, from the 201st to 365th residue, which included the critical region for oseltamivir resistance. Then resulting sequences were analyzed with oseltamivir sensitive and resistant strains obtained from National Center for Biotechnology Information (NCBI) GenBank by CLC Main Workbench Software. H275Y (H274Y according to N2 numbering) mutation, which is known to confer resistance to oseltamivir, was detected in 6 out of 30 (20%) H1N1 isolates from four cities (Istanbul, Bursa, Ankara, and Izmir). The D354G mutation was observed in all oseltamivir resistant H1N1 isolates but not in the oseltamivir sensitive isolates. Assay of neuraminidase activity revealed that these isolates were resistant to oseltamivir, but sensitive to zanamivir.

**Code(s) de classement** : 002A05C06

**Descripette(s) anglais**
- **Descripette(s)** : Human; Influenza A virus; Resistance; Turkey; Antiviral; Molecular epidemiology; Mutation; Oseltamivir; Influenza A
- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Asia; Neuraminidase inhibitor; Viral disease; Infection; Enzyme inhibitor; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme

**Descripette(s) français**
- **Descripette(s)** : Homme; Virus grippal A; Résistance; Turquie; Antiviral; Epidémiologie moléculaire; Mutation; Oséltamivir; Gripe A; Influenzavirus A(H1N1)
- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Asie; Inhibiteur neuraminidase; Virose; Infection; Inhibiteur enzyme; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme

**Localisation** : INIST-17422, 354000172524700190
**Origine de la notice** : INIST
DAS181 Inhibits H5N1 Influenza Virus Infection of Human Lung Tissues

**Titre :** DAS181 Inhibits H5N1 Influenza Virus Infection of Human Lung Tissues

**Auteur(s) :** CHAN (Renee W. Y.); CHAN (Michael C. W.); WONG (Adam C. N.); KARAMANSKA (Rositsa); DELL (Anne); HASLAM (Stuart M.); SIHOE (Alan D. L.); CHUI (W. H.); TRIANA-BALTZER (Gallen); QIXIANG LI; MALIK PEIRIS (J. S.); FANG FANG; NICOLLS (John M.)

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**Source :** Antimicrobial agents and chemotherapy; vol. 53; no. 9; pp. 3935-3941

**ISSN :** 0066-4804

**CODEN :** AACHAX

**Date de publication :** 2009

**Pays de publication :** USA

**Langue(s) :** ENG

**Type de document :** P

**Nombre de références :** 20 ref.

**Résumé :** DAS181 is a novel candidate therapeutic agent against influenza virus which functions via the mechanism of removing the virus receptor, sialic acid (Sia), from the adjacent glycan structures. DAS181 and its analogues have previously been shown to be potently active against multiple strains of seasonal and avian influenza virus strains in several experimental models, including cell lines, mice, and ferrets. Here we demonstrate that DAS181 treatment leads to desialylation of both alpha 2-6-linked and alpha 2-3-linked Sia in ex vivo human lung tissue culture and primary pneumocytes. DAS181 treatment also effectively protects human lung tissue and pneumocytes against the highly pathogenic avian influenza virus H5N1 (A/Vietnam/3046/2004). Two doses of DAS181 treatment given 12 h apart were sufficient to block H5N1 infection in the ex vivo lung tissue culture. These findings support the potential value of DAS181 as a broad-spectrum therapeutic agent against influenza viruses, especially H5N1.

**Code(s) de classement :** 002B02S; 002B05C

**Descripteur(s) anglais**
- Inhibitor; Viral disease; Human; Lung; Influenzavirus A(H5N1)
- Infection

**Descripteur(s) français**
- Inhibiteur; Virose; Homme; Poumon; Influenzavirus A(H5N1)
- Infection

**Localisation :** INIST-13334, 354000171827920430

**Origine de la notice :** INIST

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Widespread public misconception in the early phase of the H1N1 influenza epidemic

Titre : Widespread public misconception in the early phase of the H1N1 influenza epidemic

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Source : The Journal of infection; vol. 59; no. 2; pp. 122-127
ISSN : 0163-4453
CODEN : JINFD2
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 29 ref.

Résumé : Objectives: To investigate the community responses and preparedness for a possible epidemic of H1N1 influenza in Hong Kong shortly after an imported case was confirmed. Methods: A random sample of 550 Chinese adults in the Hong Kong general population was interviewed during May 7-9, 2009. Results: The public did not perceive a high likelihood of having a local H1N1 outbreak, nor did they regard H1N1 as a threatening disease. Frequent hand-washing (73.6%) and use of face-masks in case of flu symptoms (47.9%) were prevalent. The public approved of governmental policies including the quarantining of hotel guests, was not panicking and perceived a high self-efficacy of self-protection. However, misconceptions were prevalent and the public avoided visiting crowded places (9.3%), which many people wrongly believed was a government recommendation. Conclusion: Although the public response demonstrated vigilance and preparedness there were signs of complacency. Clear communication, updated scientific information and transparency on government decision making are warranted. Data of the study provide a baseline for an ongoing surveillance program to help shape policy and provide information to the international community.

Code(s) de classement : 002B01; 002B05C02C

Descripteur(s) anglais
  - Descripteur(s) : Influenza; Early phase; Epidemic
  - Desc. génériques : Viral disease; Infection

Descripteur(s) français
  - Descripteur(s) : Gripe; Phase initiale; Epidémie
  - Desc. génériques : Virose; Infection

Localisation : INIST-18250, 354000171825370070
Origine de la notice : INIST
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Long-lasting immunogenicity of a virosomal vaccine in older children and young adults with type I diabetes mellitus

Titre : Long-lasting immunogenicity of a virosomal vaccine in older children and young adults with type I diabetes mellitus

Auteur(s) : VINCENZO ZUCCOTTI (Gian); SCARAMUZZA (Andrea); RIBONI (Sara); MAMELI (Chiara); PARIANI (Elena); TANZI (Elisabetta); ZANETTI (Alessandro); RADAELLI (Giovanni)

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Source : Vaccine; vol. 27; no. 39; pp. 5357-5362

Résumé : To evaluate the long-lasting immunogenicity and reactogenicity of a virosomal influenza vaccine in subjects with type I diabetes, a trial was conducted during the 2007-2008 influenza season in Milan, Northern Italy. One hundred five subjects aged 9-30 years were randomized to receive by intramuscular injection vaccination by a single dose (0.5ml) of either a virosomal (Inflexal V®) (n=52) or a standard subunit (Influvac®) (n=53) vaccine. Serum hemagglutinin inhibition antibody titres were determined against the three recommended influenza-like strains, A/H1N1, A/H3N2 and B, at pre-vaccination, and 1 and 6 months post-vaccination. Geometric mean titres were increased in the two groups 1 and 6 months post-vaccination (P< 0.001). One month post-vaccination both vaccines met the CPMP requirement for immunogenicity with high seroprotection rates (>95%) for strains A/H1N1 and A/H3N2, and a seroprotection of 73% and 70% in the virosomal and subunit vaccine for strain B. Mean fold increase ranged 2.8 (A/H3N2)-6.2 (A/H1N1) in the virosomal group and 2.3 (A/H3N2)-4.8 (A/H1N1) in the subunit group. Immunogenicity declined 6 months post-vaccination in both groups, and the CPMP requirement for immunogenicity was satisfied only in the virosomal group. In subjects without pre-existing antibodies to strain B (titre <10), the virosomal vaccine showed higher immune response than the subunit vaccine 6 months post-vaccination, with a geometric mean titre (95% CI) of 40.2 (30.7-54.6) vs. 21.2 (14.6-30.8). Reactogenicity was similar in the two vaccines. All reactions were transient and not severe. The results indicate that in older children and young adults with type I diabetes influenza vaccination with a virosomal or a standard subunit vaccine is safe and adequately immunogenic against the three influenza vaccine strains. In addition, the virosomal vaccine may show better long-lasting immune response than the standard subunit vaccine, especially in subjects without pre-existing antibodies to influenza strains.

Code(s) de classement : 002A05F04

Description(s) : Immunogenicity; Vaccine; Elderly; Child; Toxicity; Type 1 diabetes; Influenza

Description(s) français : Immuogénicité; Vaccin; Personne âgée; Enfant; Toxicité; Diabète de type 1; Grippe

Localisation : INIST-20289, 354000187620890120

Origine de la notice : INIST

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Identification of HLA class II H5N1 hemagglutinin epitopes following subvirion influenza A (H5N1) vaccination

Titre : Identification of HLA class II H5N1 hemagglutinin epitopes following subvirion influenza A (H5N1) vaccination

Auteur(s) : ZINCKGRAF (John W.); SPOSATO (Margaret); ZIELINSKI (Veronica); POWELL (Doug); TREANOR (John J.); VON HOFE (Eric)

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Source : Vaccine; vol. 27; no. 39; pp. 5393-5401
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 42 ref.

Résumé : Prophylactic immunization against influenza infection requires CD4+ T-helper cell activity for optimal humoral and cellular immunity. Currently there is one FDA approved H5N1 subvirion vaccine available, although stockpiles of this vaccine are insufficient for broad population coverage and the vaccine has only demonstrated modest immunogenicity. Specific activation of CD4+ T-helper cells using class II H5N1 HA peptide vaccines may be a useful component in immunization strategy and design. Identification of HLA class II HA epitopes was undertaken in this report by obtaining PBMCs from volunteers previously immunized with an H5N1 inactivated subvirion vaccine, followed by direct ex vivo stimulation of CD4+ T cells against different sources of potential HA class 11 epitopes. In the 1st round of analysis, 35 donors were tested via IFN- gamma ELISPOT using pools of overlapping HA peptides derived from the H5N1 A/Thailand/4(SP-528)/2004 virus, recombinant H5N1 (rHA) and inactivated H5N1 subvirion vaccine. In addition, a series of algorithm-predicted epitopes coupled with the Ii-Key moiety of the MHC class II-associated invariant chain for enhanced MHC class II charging were also included. Specific responses were observed for all 20 peptide pools, with 6-26% of vaccinated individuals responding to any given pool (donor response frequency) and a magnitude of response ranging from 3- to >10-fold above background levels. Responses were similarly observed with the majority of algorithm-predicted epitopes, with a donor response frequency of up to 29% and a magnitude of response ranging from 3-10-fold (11/24 peptides) to >10-fold above background (7/24 peptides). PBMCs from vaccine recipients that had detectable responses to H5N1 rHA following 1st round analysis were used in a 2nd round of testing to confirm the identity of specific peptides based on the results of the 1st screening. Sixteen individual HA peptides identified from the library elicited CD4+ T cell responses between 3- and >10-fold above background, with two peptides being recognized in 21% of recipients tested. Eight of the putative MHC class II epitopes recognized were found in regions showing partial to significant sequence homology with New Caledonia H1N1 influenza HA, while eight were unique to H5N1 HA. This is the first study to identify H5N1 HA epitope-specific T cells in vaccine recipients and offers hope for the design of a synthetic peptide vaccine to prime CD4+ T-helper cells. Such a vaccine could be used to provide at least some minimal level of H5N1 protection on its own and/or prime for a subsequent dose of a more traditional but supply-limited vaccine.

Code(s) de classement : 002A05F04; 002A05C10

Descripteur(s) anglais

Descripteur(s) : Influenza A virus; Avian influenzavirus; Identification; HLA-System; Hemagglutinin; Antigenic determinant; Vaccination; T-Lymphocyte; Helper cell; Vaccine; Influenza A

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen; Viral disease; Infection

Descripteur(s) français

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Descripteur(s) : Virus grippal A; Influenzavirus aviaire; Identification; Système HLA; Hémagglutinine; Déterminant antigénique; Vaccination; Lymphocyte T; Cellule helper; Vaccin; Grippe A; Antigène CD4
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogène; Virose; Infection

Localisation : INIST-20289, 354000187620890170
Origine de la notice : INIST
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Studies of Cell-Mediated Immune Responses to Influenza Vaccination in Systemic Lupus Erythematosus

Titre : Studies of Cell-Mediated Immune Responses to Influenza Vaccination in Systemic Lupus Erythematosus

Auteur(s) : HOLVAST (Albert); VAN ASSEN (Sander); DE HAAN (Aalzen); HUCKRIEDE (Anke); BENNE (Cornelis A.); WESTRA (Johanna); PALACHE (Abraham); WILSCHUT (Jan); KALLENBERG (Cees G. M.); BIJL (Marc)

Affiliation(s) : University Medical Center Groningen, University of Groningen, Groningen, NLD; Laboratory for Infectious Diseases, Groningen, NLD; Solvay Pharmaceuticals, Weesp, NLD

Source : Arthritis and rheumatism; vol. 60; no. 8; pp. 2438-2447

Résumé : Objective. Both antibody and cell-mediated responses are involved in the defense against influenza. In patients with systemic lupus erythematosus (SLE), a decreased antibody response to subunit influenza vaccine has been demonstrated, but cell-mediated responses have not yet been assessed. This study was therefore undertaken to assess cell-mediated responses to influenza vaccination in patients with SLE. Methods. Fifty-four patients with SLE and 54 healthy control subjects received subunit influenza vaccine. Peripheral blood mononuclear cells and sera were obtained before and 1 month after vaccination. Cell-mediated responses to A/H1N1 and A/H3N2 vaccines were evaluated using an interferon- gamma (IFN gamma ) enzyme-linked immunospot assay and flow cytometry. Antibody responses were measured using a hemagglutination inhibition test. Results. Prior to vaccination, patients with SLE had fewer IFN gamma spot-forming cells against A/H1N1 compared with control subjects and a lower frequency of IFN gamma -positive CD8+ T cells. After vaccination, the number of IFN gamma spot-forming cells increased in both patients and control subjects, although the number remained lower in patients. In addition, the frequencies of CD4+ T cells producing tumor necrosis factor and interleukin-2 were lower in patients after vaccination compared with healthy control subjects. As expected for a subunit vaccine, vaccination did not induce a CD8+ T cell response. For A/H3N2-specific responses, results were comparable. Diminished cell-mediated responses to influenza vaccination were associated with the use of prednisone and/or azathioprine. The increase in A/H1N1-specific and A/H3N2-specific antibody titers after vaccination was lower in patients compared with control subjects. Conclusion. In addition to a decreased antibody response, cell-mediated responses to influenza vaccination are diminished in patients with SLE, which may reflect the effects of the concomitant use of immunosuppressive drugs. This may render these patients more susceptible to (complicated) influenza infections.
T-Cell Tolerance for Variability in an HLA Class I-Presented Influenza A Virus Epitope

**Titre** : T-Cell Tolerance for Variability in an HLA Class I-Presented Influenza A Virus Epitope

**Auteur(s)** : WAHL (Angela); MCCOY (William); SCHAFFER (Fredda); BARDET (Wilfried); BUCHLI (Rico); FREMONT (Daved H.); HILDEBRAND (William H.)

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**Source** : Journal of virology; vol. 83; no. 18; pp. 9206-9214

**ISSN** : 0022-538X

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 38 ref.

**Résumé** : To escape immune recognition, viruses acquire amino acid substitutions in class I human leukocyte antigen (HLA)-presented cytotoxic T-lymphocyte (CTL) epitopes. Such viral escape mutations may (i) prevent peptide processing, (ii) diminish class I HLA binding, or (iii) alter T-cell recognition. Because residues 418 to 426 of the hypervariable influenza A virus nucleoprotein (NP418-426) epitope are consistently bound by class I HLA and presented to CTL, we assessed the impact that intraepitope sequence variability has upon T-cell recognition. CTL elicited by intranasal influenza virus infection were tested for their cross-recognition of 20 natural NP418-426 epitope variants. Six of the variant epitopes, of both H1N1 and H3N2 origin, were cross-recognized by CTL while the remaining NP418-426 epitope variants escaped targeting. A pattern emerged whereby variability at position 5 (P5) within the epitope reduced T-cell recognition, changes at P4 or P6 enabled CTL escape, and a mutation at P8 enhanced T-cell recognition. These data demonstrate that substitutions at P4 and/or P6 facilitate influenza virus escape from T-cell recognition and provide a model for the number, nature, and location of viral mutations that influence T-cell cross-recognition.

**Code(s) de classement** : 002A05C10

**Descripteur(s) anglais**

- Influenza A virus; T-Lymphocyte; HLA-System; Antigenic determinant

**Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus

**Descripteur(s) français**

- Virus grippal A; Lymphocyte T; Système HLA; Déterminant antigénique

**Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus

**Localisation** : INIST-13592, 354000171848630180

**Origine de la notice** : INIST

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Identifying the species-origin of faecal droppings used for avian influenza virus surveillance in wild-birds

Titre : Identifying the species-origin of faecal droppings used for avian influenza virus surveillance in wild-birds

Auteur(s) : CHEUNG (Peter P.); CONNIE LEUNG (Y. H.); CHOW (Chun-Kin); NG (Chi-Fung); TSANG (Chun-Lok); WU (Yu-On); MA (Siu-Kit); SIA (Sin-Fun); YI GUAN; PEIRIS (J. S. M.)

Affiliation(s) : State Key Laboratory for Emerging Infectious Diseases and Department of Microbiology, Li Ka Shing Faculty of Medicine, The University of Hong Kong, HKG; HKU-Pasteur Research Centre, The University of Hong Kong, HKG

Source : Journal of clinical virology; vol. 46; no. 1; pp. 90-93
ISSN : 1386-6532
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG

Résumé : Background: Avian influenza virus (AIV) surveillance in birds is important for public health. Faecal droppings from wild-birds are more readily available for such studies, but the inability to identify the species-origin of faecal samples limits their value. Objectives: To develop, optimise, and field-test a method to simultaneously detect AIV and identify the species-origin from faecal samples. Study design: Analytical sensitivity of the species-identification RT-PCR was assessed on serial dilutions of faecal droppings. Overall sensitivity of the methods for species-identification and AIV detection was assessed on 92 faecal and cloacal samples collected from wildlife, poultry markets, and experimentally H5N1-infected birds. Results: All 92 samples were correctly identified to 24 different species, with a detection limit of 2.8 μg of faecal material. All 20 specimens previously shown by virus culture to be positive for influenza virus were correctly identified by RT-PCR for influenza A using the same nucleic-acid extracts used for species-identification. Conclusion: We have optimised and evaluated a method for identifying the species of origin and detecting AIV from bird faecal droppings that can be applied to routine surveillance of influenza viruses in wild-birds.

Code(s) de classement : 002A05C10; 002B05C02J

Descripteur(s) anglais
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Vertebrata; Zoopathogen; Viral disease; Infection

Descripteur(s) français
Desc. génériques : Influenzavirus aviaire; Aves; Homme; Origine; Fèces; Microbiologie; Virologie; Grippe

Localisation : INIST-26272, 354000171014790190
Origine de la notice : INIST
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Risk Parameters of Fulminant Acute Respiratory Distress Syndrome and Avian Influenza (H5N1) Infection in Vietnamese Children

Titre : Risk Parameters of Fulminant Acute Respiratory Distress Syndrome and Avian Influenza (H5N1) Infection in Vietnamese Children

Auteur(s) : KAWACHI (Shoji); SAN THI LUONG; SHIGEMATSU (Mika); FURUYA (Hiroyuki); PHUNG (Thuy Thi Bich); PHUC HUU PHAN; NUNOI (Hiroyuki); LIEM THANH NGUYEN; SUZUKI (Kazuo)

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Source : The Journal of infectious diseases; vol. 200; no. 4; pp. 510-515
ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 31 ref.

Résumé : A clinical picture of patients with acute respiratory distress syndrome (ARDS) induced by highly pathogenic avian influenza A (H5N1) has been reported. We reviewed 37 sets of clinical data for pediatric patients with ARDS at the National Hospital of Pediatrics (Hanoi, Vietnam); 12 patients with H5N1-positive and 25 with H5N1-negative ARDS were enrolled. The H5N1-negative patients had a clinical picture and mortality rate similar to that for the pediatric ARDS patients. However, the H5N1-positive patients had ARDS with normal ventilation capacity at the time of hospital admission, then rapidly proceeded to severe respiratory failure. The survival probability and days until final outcome in groups of H5N1-positive (n = 12) vs. H5N1-negative (n = 25) patients were 17% versus 52% and 12.3 ± 5.7 days (median, 11 days) versus 21.5 ± 13.8 days (median, 22 days), respectively. Our observations clarified the clinical picture of H5N1-induced fulminant ARDS and also confirmed that relatively older age (~6 years of age), high fever at onset, and leukopenia and/or thrombocytopenia at the time of hospital admission are risk parameters for H5N1-induced fulminant ARDS.

Code(s) de classement : 002A05C10; 002B05

Descriptrueur(s) anglais
Desc. génériques : Influenza A virus; Acute; Child; Microbiology; Infection; Respiratory distress; Avian influenza
Desc. génériques : Orthomyxoviridae; Virus; Human; Respiratory disease; Viral disease

Descriptrueur(s) français
Desc. génériques : Virus grippal A; Aigu; Enfant; Microbiologie; Infection; Détresse respiratoire; Grippe aviaire
Desc. génériques : Orthomyxoviridae; Virus; Homme; Pathologie de l'appareil respiratoire; Virose

Localisation : INIST-2052, 354000172551920050
Origine de la notice : INIST
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Safety and Immunogenicity of Multiple and Higher Doses of an Inactivated Influenza A/H5N1 Vaccine

Titre : Safety and Immunogenicity of Multiple and Higher Doses of an Inactivated Influenza A/H5N1 Vaccine

Auteur(s) : BEIGEL (John H.); VOELL (Jocelyn); HUANG (Chiung-Yu); BURBELO (Peter D.); CLIFFORD LANE (H.)

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Source : The Journal of Infectious Diseases; vol. 200; no. 4; pp. 501-509

ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 20 ref.

Résumé : Background. H5N1 avian influenza represents an episodic zoonotic disease with the potential to cause a pandemic, and antiviral resistance is of considerable concern. We sought to generate high-titer H5N1 antibodies in healthy volunteers for the purpose of developing hyperimmune intravenous immunoglobulin. Methods. We conducted a dose-escalating, unblinded clinical trial involving 75 subjects aged 18-59 years. Three cohorts of twenty-five subjects were enrolled sequentially and received 90, 120, or 180 μg of H5N1 A/Vietnam/1203/04 vaccine in 4 doses administered ~28 days apart. Results. No statistically significant dose-related increases in the geometric mean titers (GMTs) of serum hemagglutination inhibition antibody were observed when the 90-μg, 120-μg, and 180-μg cohorts were compared. When the cohorts were analyzed together to determine the effect of additional vaccinations, the GMTs of hemagglutination inhibition antibody after the first, second, third, and fourth vaccinations were 1:15.7, 1:22.2, and 1:36.0, respectively (first vaccination vs. baseline, P < .001; second vs. first vaccination, P = .02; and third vs. second vaccination, P < .001). The microneutralization GMTs after the first, second, third, and fourth vaccinations were 1:17.5, 1:33.1, 1:55.7, and 1:68.4, respectively (P < .001 for all comparisons). Conclusion. The results of our study suggest that a third and fourth dose of the H5N1 A/Vietnam/1203/04 vaccine may result in higher hemagglutination and microneutralization GMTs, compared with the GMTs resulting from fewer doses. There was no benefit to increasing the dose of the vaccine.
Novel swine-origin influenza A virus in humans: another pandemic knocking at the door

**Titre** : Novel swine-origin influenza A virus in humans: another pandemic knocking at the door

**Auteur(s)** : MICHAELIS (Martin); DOERR (Hans Wilhem); CINATL (Jindrich JR)

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**Source** : Medical microbiology and immunology; vol. 198; no. 3; pp. 175-183

**ISSN** : 0300-8584

**CODEN** : MMIYAO

**Date de publication** : 2009

**Pays de publication** : DEU

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 52 ref.

**Résumé** : Influenza A viruses represent a continuous pandemic threat. In April 2009, a novel influenza A virus, the so-called swine-origin influenza A (H1N1) virus (S-OIV), was identified in Mexico. Although S-OIV originates from triple-reassortant swine influenza A (H1) that has been circulating in North American pig herds since the end of the 1990s, S-OIV is readily transmitted between humans but is not epidemic in pigs. After its discovery, S-OIV rapidly spread throughout the world within few weeks. In this review, we sum up the current situation and put it into the context of the current state of knowledge of influenza and influenza pandemics. Some indications suggest that a pandemic may be mild but even "mild" pandemics can result in millions of deaths. However, no reasonable forecasts how this pandemic may develop can be made at this time. Despite stockpiling by many countries and WHO, antiviral drugs will be limited in case of pandemic and resistances may emerge. Effective vaccines are regarded to be crucial for the control of influenza pandemics. However, production capacities are restricted and development/production of a S-OIV vaccine will interfere with manufacturing of seasonal influenza vaccines. The authors are convinced that S-OIV should be taken seriously as pandemic threat and underestimation of the menace by S-OIV to be by far more dangerous than its overestimation.

**Code(s) de classement** : 002A05C10

**Descripteur(s) anglais**

- **Descriputeur(s)** : Porcine influenzavirus; influenza A virus; human; swine; origin; microbiology; immunology; influenza
- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; virus; artiodactyla; Ungulata; Mammalia; Vertebrata; Veterinary; viral disease; infection

**Descripteur(s) français**

- **Descriputeur(s)** : Influenzavirus porcin; Virus grippe A; homme; porc; origine; microbiologie; immunologie; grippe
- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; virus; artiodactyla; Ungulata; Mammalia; Vertebrata; vétérinaire; virose; infection

**Localisation** : INIST-3269, 354000172537910040

**Origine de la notice** : INIST

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Characterization of the H5N1 Highly Pathogenic Avian Influenza Virus Derived from Wild Pikas in China

Auteur(s) : JIYONG ZHOU; WENBO SUN; JUNHUA WANG; JUNQING GUO; WEI YIN; NANPING WU; LANJUAN LI; YAN YAN; MING LIAO; YU HUANG; KAIJIAN LUO; XUETAO JIANG; HUALAN CHEN
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Titre : Characterization of the H5N1 Highly Pathogenic Avian Influenza Virus Derived from Wild Pikas in China

Résumé : The highly pathogenic H5N1 avian influenza virus emerged from China in 1996 and has spread across Eurasia and Africa, with a continuous stream of new cases of human infection appearing since the first large-scale outbreak among migratory birds at Qinghai Lake. The role of wild birds, which are the natural reservoirs for the virus, in the epidemiology of the H5N1 virus has raised great public health concern, but their role in the spread of the virus within the natural ecosystem of free-ranging terrestrial wild mammals remains unclear. In this study, we investigated H5N1 virus infection in wild pikas in an attempt to trace the circulation of the virus. Seroepidemiological surveys confirmed a natural H5N1 virus infection of wild pikas in their native environment. The hemagglutination gene of the H5N1 virus isolated from pikas reveals two distinct evolutionary clades, a mixed/Vietnam H5N1 virus sublineage (MV-like pika virus) and a wild bird Qinghai (QH)-like H5N1 virus sublineage (QH-like pika virus). The amino acid residue (glutamic acid) at position 627 encoded by the PB2 gene of the MV-like pika virus was different from that of the QH-like pika virus; the residue of the MV-like pika virus was the same as that of the goose H5N1 virus (A/GS/Guangdong [GD]/1/96). Further, we discovered that in contrast to the MV-like pika virus, which is nonpathogenic to mice, the QH-like pika virus is highly pathogenic. To mimic the virus infection of pikas, we intranasally inoculated rabbits, a species closely related to pikas, with the H5N1 virus of pika origin. Our findings first demonstrate that wild pikas are mammalian hosts exposed to H5N1 subtype avian influenza viruses in the natural ecosystem and also imply a potential transmission of highly pathogenic avian influenza virus from wild mammals into domestic mammalian hosts and humans.

Code(s) de classement : 002A05C10; 002A05C04

Descripteur(s) anglais

Description(s) : Avian influenzavirus; Influenza A virus; Pathogenicity; China; Virology
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Asia

Descripteur(s) français

Description(s) : Influenzavirus aviaire; Virus grippal A; Pouvoir pathogène; Chine; Virologie
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Asie

Localisation : INIST-13592, 354000187579490620

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Mixed Infection and the Genesis of Influenza Virus Diversity

Titre : Mixed Infection and the Genesis of Influenza Virus Diversity

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Source : Journal of virology; vol. 83; no. 17; pp. 8832-8841
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 22 ref.

Résumé : The emergence of viral infections with potentially devastating consequences for human health is highly dependent on their underlying evolutionary dynamics. One likely scenario for an avian influenza virus, such as A/H5N1, to evolve to one capable of human-to-human transmission is through the acquisition of genetic material from the A/H1N1 or A/H3N2 subtypes already circulating in human populations. This would require that viruses of both subtypes coinfect the same cells, generating a mixed infection, and then reassort. Determining the nature and frequency of mixed infection with influenza virus is therefore central to understanding the emergence of pandemic, antigenic, and drug-resistant strains. To better understand the potential for such events, we explored patterns of intrahost genetic diversity in recently circulating strains of human influenza virus. By analyzing multiple viral genome sequences sampled from individual influenza patients we reveal a high level of mixed infection, including diverse lineages of the same influenza virus subtype, drug-resistant and -sensitive strains, those that are likely to differ in antigenicity, and even viruses of different influenza virus types (A and B). These results reveal that individuals can harbor influenza viruses that differ in major phenotypic properties, including those that are antigenically distinct and those that differ in their sensitivity to antiviral agents.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Descripteur(s) : Influenzavirus; Mixed infection; Virology
Desc. génériques : Orthomyxoviridae; Virus

Descripteur(s) français
Descripteur(s) : Influenzavirus; Infection mixte; Virologie
Desc. génériques : Orthomyxoviridae; Virus

Localisation : INIST-13592, 354000187579490500
Origine de la notice : INIST
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Palmitoylation of the Influenza A Virus M2 Protein Is Not Required for Virus Replication In Vitro but Contributes to Virus Virulence

**Titre** : Palmitoylation of the Influenza A Virus M2 Protein Is Not Required for Virus Replication In Vitro but Contributes to Virus Virulence

**Auteur(s)** : GRANTHAM (Michael L.); WU (Wai-Hong); LALIME (Erin N.); LORENZO (Maria E.); KLEIN (Sabra L.); PEKOSZ (Andrew)

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**Source** : Journal of virology; vol. 83; no. 17; pp. 8655-8661

**ISSN** : 0022-538X

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 38 ref.

**Résumé** : The influenza A virus M2 protein has important roles during virus entry and in the assembly of infectious virus particles. The cytoplasmic tail of the protein can be palmitoylated at a cysteine residue, but this residue is not conserved in a number of human influenza A virus isolates. Recombinant viruses encoding M2 proteins with a serine substituted for the cysteine at position 50 were generated in the A/WSN/33 (H1N1) and A/Udorn/72 (H3N2) genetic backgrounds. The recombinant viruses were not attenuated for replication in MDCK cells, Calu-3 cells, or in primary differentiated murine trachea epithelial cell cultures, indicating there was no significant contribution of M2 palmitoylation to virus replication in vitro. The A/WSN/33 M2C50S virus displayed a slightly reduced virulence after infection of mice, suggesting that there may be novel functions for M2 palmitoylation during in vivo infection.

**Code(s) de classement** : 002A05C10

**Descripteur(s) anglais**

- **Descripteur(s) :** Influenza A virus; Membrane protein; In vitro replication; Virulence; Virology
- **Desc. génériques :** Influenzavirus A; Orthomyxoviridae; Virus

**Descripteur(s) français**

- **Descripteur(s) :** Virus grippal A; Protéine membranaire; Réplication in vitro; Virulence; Virologie; Protéine M2
- **Desc. génériques :** Influenzavirus A; Orthomyxoviridae; Virus

**Localisation** : INIST-13592, 354000187579490330

**Origine de la notice** : INIST

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A Novel Genotype H9N2 Influenza Virus Possessing Human H5N1 Internal Genomes Has Been Circulating in Poultry in Eastern China since 1998

Titre : A Novel Genotype H9N2 Influenza Virus Possessing Human H5N1 Internal Genomes Has Been Circulating in Poultry in Eastern China since 1998

Auteur(s) : PINGHU ZHANG; YINGHUA TANG; XIAOWEN LIU; WENBO LIU; XIAORONG ZHANG; HONGQI LIU; DAXIN PENG; SONG GAO; YANTAO WU; LUYONG ZHANG; SHAN LU; XIUFAN LIU

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Source : Journal of virology; vol. 83; no. 17; pp. 8428-8438
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 36 ref.

Résumé : Many novel reassortant influenza viruses of the H9N2 genotype have emerged in aquatic birds in southern China since their initial isolation in this region in 1994. However, the genesis and evolution of H9N2 viruses in poultry in eastern China have not been investigated systematically. In the current study, H9N2 influenza viruses isolated from poultry in eastern China during the past 10 years were characterized genetically and antigenically. Phylogenetic analysis revealed that these H9N2 viruses have undergone extensive reassortment to generate multiple novel genotypes, including four genotypes (J, F, K, and L) that have never been recognized before. The major H9N2 influenza viruses represented by A/Chicken/Beijing/1/1994 (Ck/BJ/1/94)-like viruses circulating in poultry in eastern China before 1998 have been gradually replaced by A/Chicken/Shanghai/F/1998 (Ck/SH/F98)-like viruses, which have a genotype different from that of viruses isolated in southern China. The similarity of the internal genes of these H9N2 viruses to those of the H5N1 influenza viruses isolated from 2001 onwards suggests that the Ck/SH/F98-like virus may have been the donor of internal genes of human and poultry H5N1 influenza viruses circulating in Eurasia. Experimental studies showed that some of these H9N2 viruses could be efficiently transmitted by the respiratory tract in chicken flocks. Our study provides new insight into the genesis and evolution of H9N2 influenza viruses and supports the notion that some of these viruses may have been the donors of internal genes found in H5N1 viruses.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Desc. génériques : Influenza A virus; Human; Avian influenzavirus; Genotype; Genome; Poultry; China; Virology; Influenzavirus A(H5N1)

Descripteur(s) français
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Asia; Veterinary

Localisation : INIST-13592. 354000187579490110
Origine de la notice : INIST
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April 2009: an outbreak of swine-origin influenza A(H1N1) virus with evidence for human-to-human transmission

Titre : April 2009: an outbreak of swine-origin influenza A(H1N1) virus with evidence for human-to-human transmission

Auteur(s) : NAFFAKH (Nadia); VAN DER WERF (Sylvie)
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Source : Microbes and infection; vol. 11; no. 8-9; pp. 725-728
ISSN : 1286-4579
Date de publication : 2009
Pays de publication : FRA
Langue(s) : ENG
Type de document : P
Nombre de références : 24 ref.

Résumé : A swine-origin influenza A(H1N1) virus is currently responsible for an outbreak of infections in the human population, with laboratory-confirmed cases reported in several countries and clear evidence for human-to-human transmission. We provide a description of the outbreak at the end of April 2009, and a brief review of the zoonotic potential of swine influenza viruses.

Code(s) de classement : 002A05C10

Descriptor(s) anglais
  Description(s) : Porcine influenzavirus; Influenza A virus; Human; Swine; Origin; Transmission; Influenza
  Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Veterinary; Viral disease; Infection

Descriptor(s) français
  Description(s) : Influenzavirus porcin; Virus grippal A; Homme; Porcin; Origine; Transmission; Grippe
  Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Vétérinaire; Virose; Infection

Localisation : INIST-26816. 354000170905320010
Origine de la notice : INIST
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Modelling the impact of an influenza A/H1N1 pandemic on critical care demand from early pathogenicity data: the case for sentinel reporting

Titre : Modelling the impact of an influenza A/H1N1 pandemic on critical care demand from early pathogenicity data: the case for sentinel reporting

Auteur(s) : ERCOLE (A.); TAYLOR (B. L.); RHODES (A.); MENON (D. K.)
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Source : Anaesthesia; vol. 64; no. 9; pp. 937-941
ISSN : 0003-2409
CODEN : ANASAB
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 18 ref.

Résumé : Projected critical care demand for pandemic influenza H1N1 in England was estimated in this study. The effect of varying hospital admission rates under statistical uncertainty was examined. Early in a pandemic, uncertainty in epidemiological parameters leads to a wide range of credible scenarios, with projected demand ranging from insignificant to overwhelming. However, even small changes to input assumptions make the major incident scenario increasingly likely. Before any cases are admitted to hospital, 95% confidence limit on admission rates led to a range in predicted peak critical care bed occupancy of between 0% and 37% of total critical care bed capacity, half of these cases requiring ventilatory support. For hospital admission rates above 0.25%, critical care bed availability would be exceeded. Further, only 10% of critical care beds in England are in specialist paediatric units, but best estimates suggest that 30% of patients requiring critical care will be children. Paediatric intensive care facilities are likely to be quickly exhausted and suggest that older children should be managed in adult critical care units to allow resource optimisation. Crucially this study highlights the need for sentinel reporting and real-time modelling to guide rational decision making.

Code(s) de classement : 002B27A

Descripteur(s) anglais
Desc. généraux : Viral disease; Infection

Descripteur(s) français
Desc. généraux : Virose; Infection

Localisation : INIST-7599, 354000172579410030
Origine de la notice : INIST
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Impact parameters on hybridization process in detecting influenza virus (type A) using conductimetric-based DNA sensor

Titre : Impact parameters on hybridization process in detecting influenza virus (type A) using conductimetric-based DNA sensor

Auteur(s) : PHUONG DINH TAM; MAI ANH TUAN; NGUYEN VAN HIEU; NGUYEN DUC CHIEN
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Source : Physica. E, low-dimensional systems and nanostructures; vol. 41; no. 8; pp. 1567-1571
ISSN : 1386-9477
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 27 ref.

Résumé : This paper report various impact parameters on hybridization of probe/target DNA to detect the influenza virus (type A-H5N1) such as hybridization temperature, probe concentration, mismatch target and hybridization time. The DNA probe was attached to sensor surface by means of covalent bonding between amine of 3-aminopropyl-triethoxy-silance (APTS) and phosphate group of DNA sequence. The hybridization of probe/target DNA strands were detected by changing the surface conductance of sensors, which leads to the change in output signal of the system. The results reveal that the DNA sensor can detect as low as 0.5nM of target DNA in real samples. The response time of DNA sensor is approximately 4 min, and the sensitivity of DNA sensor is about 0.03 mV/nM.

Code(s) de classement : 002B05C02C

Descriputeur(s) anglais

Descriputeur(s) : Biosensor; DNA; Influenza A; Hybridization; Environmental factor; Sensitivity; Conductometry; Avian influenza
Desc. génériques : Viral disease; Infection; Nucleic acid

Descriputeur(s) français

Descriputeur(s) : Biodétecteur; DNA; Grippe A; Hybridation; Facteur milieu; Sensibilité; Conductimétrie; Grippe aviaire
Desc. génériques : Virose; Infection; Acide nucléique

Localisation : INIST-145E, 354000172443030380
Origine de la notice : INIST
Copyright de notice : © 2009 INIST-CNRS. All rights reserved.
Molecular Detection of a Novel Human Influenza (H1N1) of Pandemic Potential by Conventional and Real-Time Quantitative RT-PCR Assays

Titre : Molecular Detection of a Novel Human Influenza (H1N1) of Pandemic Potential by Conventional and Real-Time Quantitative RT-PCR Assays

Auteur(s) : POON (Leo L. M.); CHAN (K. H.); SMITH (G. J.); LEUNG (C. S. W.); GUAN (Y.); YUEN (K. Y.); PEIRIS (J. S. M.)

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Source : Clinical chemistry : (Baltimore, Md.); vol. 55; no. 8; pp. 1555-1558
ISSN : 0009-9147
CODEN : CLCHAU
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 11 ref.

Résumé : BACKGROUND: Influenza A viruses are medically important viral pathogens that cause significant mortality and morbidity throughout the world. The recent emergence of a novel human influenza A virus (H1N1) poses a serious health threat. Molecular tests for rapid detection of this virus are urgently needed. METHODS: We developed a conventional 1-step RT-PCR assay and a 1-step quantitative real-time RT-PCR assay to detect the novel H1N1 virus, but not the seasonal H1N1 viruses. We also developed an additional real-time RT-PCR that can discriminate the novel H1N1 from other swine and human H1 subtype viruses. RESULTS: All of the assays had detection limits for the positive control in the range of 1.0 × 10-4 to 2.0 × 10-3 of the median tissue culture infective dose. Assay specificities were high, and for the conventional and real-time assays, all negative control samples were negative, including 7 human seasonal H1N1 viruses, 1 human H2N2 virus, 2 human seasonal H3N2 viruses, 1 human H5N1 virus, 7 avian influenza viruses (HA subtypes 4, 5, 7, 8, 9, and 10), and 48 nasopharyngeal aspirates (NPAs) from patients with noninfluenza respiratory diseases; for the assay that discriminates the novel H1N1 from other swine and human H1 subtype viruses, all negative controls were also negative, including 20 control NPAs, 2 seasonal human H1N1 viruses, 2 seasonal human H3N2 viruses, and 2 human H5N1 viruses. CONCLUSIONS: These assays appear useful for the rapid diagnosis of cases with the novel H1N1 virus, thereby allowing better pandemic preparedness.

Code(s) de classement : 002B24; 002A02; 002A03

Descriptor(s) anglais
   Desc. génériques : Viral disease; Infection
   Descripteur(s) : Diagnosis; Detection; Human; Influenza; Quantitative analysis; Assay; Biochemistry; Clinical biology; Molecular biology; Pandemic; Real time polymerase chain reaction

Descriptor(s) français
   Desc. génériques : Virose; Infection
   Descripteur(s) : Diagnostic; Détectio; Homme; Grippe; Analyse quantitative; Dosage; Biochimie; Biologie clinique; Biologie moléculaire; Pandémie; Réaction chaîne polymérase en temps réel

Localisation : INIST-7603, 354000170938820160
Origine de la notice : INIST
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Emergence of European Avian Influenza Virus-Like H1N1 Swine Influenza A Viruses in China

Titre : Emergence of European Avian Influenza Virus-Like H1N1 Swine Influenza A Viruses in China

Auteur(s) : JINHUA LIU; YUHAI BI; KUN QIN; GUANGHUA FU; JUN YANG; JINSHAN PENG; GUANGPENG MA; QINFANG LIU; JUAN PU; FULIN TIAN

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Source : Journal of clinical microbiology : (Print); vol. 47; no. 8; pp. 2643-2646
ISSN : 0095-1137
CODEN : JCMIDW
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 14 ref.

Résumé : During swine influenza surveillance from 2007 to 2008, 10 H1N1 viruses were isolated and analyzed for their antigenic and phylogenetic properties. Our study revealed the emergence of avian-origin European H1N1 swine influenza virus in China, which highlights the necessity of swine influenza surveillance for potential pandemic preparedness.

Code(s) de classement : 002A05C10

Description(s) anglais
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Asia; Zoopathogen; Veterinary

Description(s) français
Desc. génériques : Influenzavirus aviaire; Influenzavirus porcin; Virus grippal A; Chine; Microbiologie; Syndrome pseudogrippal

Localisation : INIST-17088, 354000170967290500
Origine de la notice : INIST
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Detection of Novel (Swine Origin) H1N1 Influenza A Virus by Quantitative Real-Time Reverse Transcription-PCR

**Titre** : Detection of Novel (Swine Origin) H1N1 Influenza A Virus by Quantitative Real-Time Reverse Transcription-PCR

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**Source** : Journal of clinical microbiology : (Print); vol. 47; no. 8; pp. 2675-2677

**ISSN** : 0095-1137

**CODEN** : JCMIDW

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 8 ref.

**Code(s) de classement** : 002A05C10

**Descripteur(s) anglais**
- Descripteur(s) : Porcine influenzavirus; Influenza A virus; Detection; Origin; Quantitative analysis; Real time; Reverse transcription polymerase chain reaction; Microbiology
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Veterinary

**Descripteur(s) français**
- Descripteur(s) : Influenzavirus porcin; Virus grippal A; Détecton; Origine; Analyse quantitative; Temps réel; Réaction chaîne polymérase RT; Microbiologie
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Vétérinaire

**Localisation** : INIST-17088, 354000170967290590

**Origine de la notice** : INIST

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Pathogenesis and Transmission of Swine-Origin 2009 A(H1N1) Influenza Virus in Ferrets

Titre : Pathogenesis and Transmission of Swine-Origin 2009 A(H1N1) Influenza Virus in Ferrets

Auteur(s) : MUNSTER (Vincent J.); DE WIT (Emmie); VAN DEN BRAND (Judith M. A.); HERFST (Sander); SCHRAUWEN (Eefje J. A.); BESTEBROER (Theo M.); VAN DE VIJVER (David); BOUCHER (Charles A.); KOOPMANS (Marion); RIMMELZWAAN (Guus F.); KUIKEN (Thijs); OSTERHAUS (Albert D. M. E.); FOUCHIER (Ron A. M.)

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Source : Science : (Washington, D.C.); vol. 325; no. 5939; pp. 481-483

ISSN : 0036-8075

CODEN : SCIEAS

Date de publication : 2009

Pays de publication : USA

Langue(s) : ENG

Type de document : P

Notes : 1/4 ref. et notes

Résumé : The swine-origin A(H1N1) influenza virus that has emerged in humans in early 2009 has raised concerns about pandemic developments. In a ferret pathogenesis and transmission model, the 2009 A(H1N1) influenza virus was found to be more pathogenic than a seasonal A(H1N1) virus, with more extensive virus replication occurring in the respiratory tract. Replication of seasonal A(H1N1) virus was confined to the nasal cavity of ferrets, but the 2009 A(H1N1) influenza virus also replicated in the trachea, bronchi, and bronchioles. Virus shedding was more abundant from the upper respiratory tract for 2009 A(H1N1) influenza virus as compared with seasonal virus, and transmission via aerosol or respiratory droplets was equally efficient. These data suggest that the 2009 A(H1N1) influenza virus has the ability to persist in the human population, potentially with more severe clinical consequences.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais

- Description(s) : Influenza A; Transmission; Pathogenesis; Replication; Diffusion; Respiratory tract; Animal model; Influenzavirus A; Mustela furo
- Description(s) : Viral disease; Infection; Respiratory system; Orthomyxoviridae; Virus; Fissipedia; Carnivora; Mammalia; Vertebrata

Descripteur(s) français

- Description(s) : Grippe A; Transmission; Pathogénie; Récupération; Diffusion; Voie respiratoire; Modèle animal; Influenzavirus A; Mustela furo; Influenzavirus A(H1N1)
- Description(s) : Virose; Infection; Appareil respiratoire; Orthomyxoviridae; Virus; Fissipedia; Carnivora; Mammalia; Vertebrata; Mustelidae

Localisation : INIST-6040, 354000172535440330

Origine de la notice : INIST

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Transmission and Pathogenesis of Swine-Origin 2009 A(H1N1) Influenza Viruses in Ferrets and Mice

**Titre** : Transmission and Pathogenesis of Swine-Origin 2009 A(H1N1) Influenza Viruses in Ferrets and Mice

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**Source** : Science ; vol. 325; no. 5939; pp. 484-487

**ISSN** : 0036-8075

**CODEN** : SCIEAS

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Notes** : 1/4 ref. et notes

**Résumé** : Recent reports of mild to severe influenza-like illness in humans caused by a novel swine-origin 2009 A(H1N1) influenza virus underscore the need to better understand the pathogenesis and transmission of these viruses in mammals. In this study, selected 2009 A(H1N1) influenza isolates were assessed for their ability to cause disease in mice and ferrets and compared with a contemporary seasonal H1N1 virus for their ability to transmit to naïve ferrets through respiratory droplets. In contrast to seasonal influenza H1N1 virus, 2009 A(H1N1) influenza viruses caused increased morbidity, replicated to higher titers in lung tissue, and were recovered from the intestinal tract of intranasally inoculated ferrets. The 2009 A(H1N1) influenza viruses exhibited less efficient respiratory droplet transmission in ferrets in comparison with the highly transmissible phenotype of a seasonal H1N1 virus. Transmission of the 2009 A(H1N1) influenza viruses was further corroborated by characterizing the binding specificity of the viral hemagglutinin to the sialylated glycan receptors (in the human host) by use of dose-dependent direct receptor-binding and human lung tissue-binding assays.

**Code(s) de classement** : 002B05C02C

**Descripteur(s) anglais**

- **Desc. génériques** : Viral disease; Infection; Rodentia; Mammalia; Vertebrata; Respiratory system; Orthomyxoviridae; Virus; Fissipedia; Carnivora

**Descripteur(s) français**

- **Desc. génériques** : Grippose; Infection; Rodentia; Mammalia; Vertébrata; Appareil respiratoire; Orthomyxoviridae; Virus; Fissipéda; Carnivore; Mustélidae

**Localisation** : INIST-6040, 354000172535440340

**Origine de la notice** : INIST

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H1N1 2009 influenza virus infection during pregnancy in the USA

Titre : H1N1 2009 influenza virus infection during pregnancy in the USA

Auteur(s) : JAMIESON (Denise J.); HONEIN (Margaret A.); RASMUSSEN (Sonja A.); WILLIAM (Jennifer L.); SWERDLLOW (David L.); BIGGERSTAFF (Matthew S.); LINDSTROM (Stephen); LOUIE (Janice K.); CHRIST (Cara M.); BOHM (Susan R.); FONSECA (Vincent P.); RITGER (Kathleen A.); KUHLES (Daniel J.); EGGERS (Paula); BRUCE (Hollianne); DAVIDSON (Heidi A.); LUTTERLOH (Emily); HARRIS (Meghan L.); BURKE (Colleen); MACFARLANE (Kitty F.); SHU (Bo); OLSEN (Sonja J.)

Collectivité(s) auteur : Novel Influenza A (H1N1) Pregnancy Working Group, INC

Affiliation(s) : National Center for Chronic Disease Prevention and Health Promotion, Centers for Disease Control and Prevention, Atlanta, GA, USA; National Center on Birth Defects and Developmental Disabilities, Centers for Disease Control and Prevention, Atlanta, GA, USA; National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA; EIS Program, Office of Workforce and Career Development, Centers for Disease Control and Prevention, Atlanta, GA, USA; California Department of Public Health, Richmond, CA, USA; Arizona Department of Health Services, Phoenix, AZ, USA; Michigan Department of Community Health, Lansing, MI, USA; Texas Department of State Health Services, Austin, TX, USA; Chicago Department of Public Health, Chicago, IL, USA; Nassau County Department of Health, Uniondale, NY, USA; Delaware Division of Public Health, Dover, DE, USA; Snohomish Health District, Everett, WA, USA; DeKalb County Board of Health, Atlanta, GA, USA; Kentucky Department for Public Health, Frankfort, KY, USA; Iowa Department of Public Health, Des Moines, IA, USA; Philadelphia Department of Public Health, Philadelphia, PA, USA; Massachusetts Department of Public Health, Jamaica Plain, MA, USA

Source : Lancet : (British edition); vol. 374; no. 9688; pp. 451-458
ISSN : 0140-6736
CODEN : LANCAO
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 40 ref.

Résumé : Background Pandemic H1N1 2009 influenza virus has been identified as the cause of a widespread outbreak of febrile respiratory infection in the USA and worldwide. We summarised cases of infection with pandemic H1N1 virus in pregnant women identified in the USA during the first month of the present outbreak, and deaths associated with this virus during the first 2 months of the outbreak. Methods After initial reports of infection in pregnant women, the US Centers for Disease Control and Prevention (CDC) began systematically collecting additional information about cases and deaths in pregnant women in the USA with pandemic H1N1 virus infection as part of enhanced surveillance. A confirmed case was defined as an acute respiratory illness with laboratory-confirmed pandemic H1N1 virus infection by real-time reverse-transcriptase PCR or viral culture; a probable case was defined as a person with an acute febrile respiratory illness who was positive for influenza A, but negative for H1 and H3. We used population estimates derived from the 2007 census data to calculate rates of admission to hospital and death. Findings From April 15 to May 18, 2009, 34 confirmed or probable cases of pandemic H1N1 in pregnant women during the first month of the outbreak were reported to CDC from 13 states. 11 (32%) women were admitted to hospital. The estimated rate of admission for pandemic H1N1 influenza virus infection in pregnant women during the first month of the outbreak was higher than it was in the general population (0.32 per 100000 pregnant women, 95% CI 0.13-0.52 vs 0.076 per 100 000 population at risk, 95% CI 0.07-0.09). Between April 15 and June 16, 2009, six deaths in pregnant women were reported to the CDC; all were in women who had developed pneumonia and subsequent acute respiratory distress syndrome requiring mechanical ventilation. Interpretation Pregnant women might be at increased risk for complications from pandemic H1N1 virus infection. These data lend support to the present recommendation to promptly treat pregnant women with H1N1 influenza virus infection with anti-influenza drugs. Funding US CDC.
The general practice experience of the swine flu epidemic in Victoria - lessons from the front line : Pandemic (H1N1) 2009

**Titre** : The general practice experience of the swine flu epidemic in Victoria - lessons from the front line : Pandemic (H1N1) 2009

**Auteur(s)** : EIZENBERG (Peter)

**Affiliation(s)** : North East Valley Division of General Practice, Melbourne, VIC, AUS

**Source** : Medical journal of Australia; vol. 191; no. 3; pp. 151-153

**ISSN** : 0025-729X

**CODEN** : MJAUAG

**Date de publication** : 2009

**Pays de publication** : AUS

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 8 ref.

**Résumé** : The swine influenza (H1N1 09) outbreak in Victoria has provided an excellent opportunity to review the Australian Health Management Plan for Pandemic Influenza (AHMPPI) and to assess its performance in practice. General practitioners play a major role in seasonal flu management, and it was expected that the AHMPPI would enable GPs on the front line to maintain this central role during the swine flu pandemic. The role of front-line GPs has been made extremely difficult by deficiencies in implementation of the AHMPPI, including resource supply failures, time-consuming administrative burdens, delays in receiving laboratory test results and approval for provision of oseltamivir to patients, and a lack of clear communication about policy changes as the situation progressed. We must use this experience to ensure timely and appropriate review of the AHMPPI and the way it is implemented. Better consultation with front-line clinicians, particularly GPs, is crucial and must occur as a matter of urgent priority.

**Code(s) de classement** : 002B01; 002B05C02C; 002B30A01A

**Descripteur(s) anglais**

*General practice; Swine; Influenza; Epidemic; Epidemiology; Public health; Victoria*  
*Artiodactyla; Ungulata; Mammalia; Vertebrata; Viral disease; Infection; Australia; Oceania*

**Descripteur(s) français**

*Médecine générale; Porcin; Grippe; Epidémie; Epidémiologie; Santé publique; Victoria*  
*Artiodactyla; Ungulata; Mammalia; Vertebrata; Virose; Infection; Australie; Océanie*

**Localisation** : INIST-3557, 354000187547710090

**Origine de la notice** : INIST

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Australia's influenza containment plan and the swine flu epidemic in Victoria: Pandemic (H1N1) 2009

**Titre**: Australia's influenza containment plan and the swine flu epidemic in Victoria: Pandemic (H1N1) 2009

**Auteur(s)**: LINDSAY GRAYSON (M.); JOHNSON (Paul D. R.)

**Affiliation(s)**: Infectious Diseases Department, Austin Health, Melbourne, VIC, AUS

**Source**: Medical journal of Australia; vol. 191; no. 3

**ISSN**: 0025-729X

**CODEN**: MJUAUJ

**Date de publication**: 2009

**Pays de publication**: AUS

**Langue(s)**: ENG

**Nombre de références**: 4 ref.

**Résumé**: What lessons can be learnt from Australia's initial response to the outbreak?

**Code(s) de classement**: 002B01; 002B05C02C; 002B30A01A

**Descripteur(s) anglais**

- **Desc. génériques**: Oceania; Viral disease; Infection; Artiodactyla; Ungulata; Mammalia; Vertebrata

**Descripteur(s) français**

- **Desc. génériques**: Océanie; Virole; Infection; Artiodactyla; Ungulata; Mammalia; Vertebrata
Epidemiological characteristics of pandemic influenza H1N1 2009 and seasonal influenza infection: Pandemic (H1N1) 2009

Titre : Epidemiological characteristics of pandemic influenza H1N1 2009 and seasonal influenza infection: Pandemic (H1N1) 2009

Auteur(s) : KELLY (Heath A.); GRANT (Kristina A.); WILLIAMS (Simon); FIELDING (James); SMITH (David)

Affiliation(s) : Epidemiology Unit, Victorian Infectious Diseases Reference Laboratory, Melbourne, VIC, AUS; PathWest Laboratory Medicine, Perth, WA, AUS; Communicable Disease Prevention and Control Unit, Victorian Department of Human Services, Melbourne, VIC, AUS

Source : Medical journal of Australia; vol. 191; no. 3; pp. 146-149

ISSN : 0025-729X

CODEN : MJAUAJ

Date de publication : 2009

Pays de publication : AUS

Langue(s) : ENG

Type de document : P

Nombre de références : 16 ref.

Résumé : The median age of patients with pandemic influenza H1N1 2009 infection was reported as 20-25 years in initial case series from Europe and the United States. This has been lowered to 13 years in the US after testing of more patients, but this may reflect differential increased testing of school-aged children as part of the pandemic response. The median age of patients with seasonal influenza A(H1 N1) infection identified through sentinel surveillance in Western Australia and Victoria in 2007-2008 was 18 and 22 years, respectively. For pandemic influenza H1N1 2009 infection, the median age of the first 244 patients identified in WA was 22 years, and median age of the first 135 patients identified through sentinel surveillance in Victoria was 21 years. Other comparisons of the epidemiological features of pandemic and seasonal influenza are difficult because much less laboratory testing is done for seasonal than for pandemic influenza. While early surveillance data indicated co-circulation of both pandemic and seasonal strains in WA and Victoria, more recent data from both states indicate an increasing predominance of pandemic influenza. If the evolving pandemic allows, we should take advantage of the increased testing being conducted for pandemic influenza to learn more about the real impact of laboratory-confirmed seasonal influenza.

Code(s) de classement : 002B01; 002B30A01A; 002B30A11

Descripteur(s) anglais

Description(s) : Infection; Epidemiology; Public health; Characteristics; Influenza; 2009; Seasonal variation

Desc. génériques : Viral disease

Descripteur(s) français

Description(s) : Infection; Epidémiologie; Santé publique; Caractéristiques; Grippe; 2009; Variation saisonnière; Pandémie

Desc. génériques : Virose

Localisation : INIST-3557, 354000187547710070

Origine de la notice : INIST

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Summary of the Australasian Society for Infectious Diseases and the Thoracic Society of Australia and New Zealand guidelines: treatment and prevention of H1N1 influenza 09 (human swine influenza) with antiviral agents: Pandemic (H1N1) 2009

**Titre** : Summary of the Australasian Society for Infectious Diseases and the Thoracic Society of Australia and New Zealand guidelines: treatment and prevention of H1N1 influenza 09 (human swine influenza) with antiviral agents: Pandemic (H1N1) 2009

**Auteur(s)** : CHENG (Allen C.); DWYER (Dominic E.); KOTSIMBOS (Athomas C.); STARR (Mike); KORMAN (Tony M.); BUTTERY (Jim P.); JENKINS (Christine R.); KRAUSE (Vicki L.); JOHNSON (Paul D. R.)

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**Source** : Medical journal of Australia; vol. 191; no. 3; pp. 142-145

**ISSN** : 0025-729X

**CODEN** : MJAUAJ

**Date de publication** : 2009

**Pays de publication** : AUS

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 1 ref.

**Code(s) de classement** : 002B01; 002B30A03; 002B05C02C

**Descripteur(s) anglais**

- Description : Infection; Australasia; Society; Thorax; Australia; New Zealand; Recommendation; Treatment; Prevention; Influenza; Human; Swine; Antiviral
- Desc. généraux : Oceania; Viral disease; Artiodactyla; Ungulata; Mammalia; Vertebrata

**Descripteur(s) français**

- Description : Infection; Australasie; Société; Thorax; Australie; Nouvelle-Zélande; Recommandation; Traitement; Prévention; Grippe; Homme; Porcin; Antiviral
- Desc. généraux : Océanie; Virose; Artiodactyla; Ungulata; Mammalia; Vertebrata

**Localisation** : INIST-3557. 354000187547710060

**Origine de la notice** : INIST

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Swine flu update: bringing home the bacon : Pandemic (H1N1) 2009

Titre : Swine flu update: bringing home the bacon : Pandemic (H1N1) 2009

Auteur(s) : SENANAYAKE (Sanjaya N.)
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Source : Medical journal of Australia; vol. 191; no. 3; pp. 138-141
ISSN : 0025-729X
CODEN : MJAUAJ
Date de publication : 2009
Pays de publication : AUS
Langue(s) : ENG
Type de document : P
Nombre de références : 24 ref.

Résumé : In 6 weeks, swine influenza A(H1 N1) virus has spread from 10 to 74 countries. · Australia has the fifth highest number of cases and the third highest rate of infection among the top five affected nations. · People who are hospitalised with or die from this novel virus are more likely to have predisposing risk factors. · There is a predilection for younger age groups and sparing of older age groups. This may be a property of influenza A viruses in general rather than being specific to swine influenza A. · If unchecked, the sheer number of cases may lead to much higher numbers of deaths and hospitalised patients than would normally be attributed to a standard influenza season. · Paradoxically, the low case-fatality rate of the virus raises the question of how best to approach management of this outbreak. · It is uncertain how an expected vaccine against the novel virus will be used.

Code(s) de classement : 002B01; 002B05C02C

Descripteur(s) anglais
Descripteur(s) : Swine; Influenza
Desc. génériques : Artiodactyla; Ungulata; Mammalia; Vertebrata; Viral disease; Infection

Descripteur(s) français
Descripteur(s) : Porcin; Grippe
Desc. génériques : Artiodactyla; Ungulata; Mammalia; Vertebrata; Virose; Infection

Localisation : INIST-3557, 354000187547710050
Origine de la notice : INIST
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Understanding Australia's influenza pandemic policy on the strategic use of the antiviral drug stockpile: Pandemic (H1N1) 2009

**Titre** : Understanding Australia's influenza pandemic policy on the strategic use of the antiviral drug stockpile: Pandemic (H1N1) 2009

**Auteur(s)** : MCCAW (James M.); WOOD (James G.); MCBRYDE (Emma S.); NOLAN (Terry M.); WU (Joseph T.); LIPSITCH (Marc); MCVERNON (Jodie)

**Affiliation(s)** : Vaccine and Immunisation Research Group, Melbourne School of Population Health, University of Melbourne and Murdoch Childrens Research Institute, Melbourne, VIC, AUS; School of Public Health and Community Medicine, University of New South Wales, Sydney, NSW, AUS; Victorian Infectious Diseases Service, Royal Melbourne Hospital, Melbourne, VIC, AUS; Department of Medicine, University of Melbourne, Melbourne, VIC, AUS; Department of Community Medicine and School of Public Health, University of Hong Kong, HKG; Department of Epidemiology and Department of Immunology and Infectious Diseases, Harvard School of Public Health, Boston, Mass, USA

**Source** : Medical journal of Australia; vol. 191; no. 3; pp. 136-137

**ISSN** : 0025-729X

**CODEN** : MJAUAJ

**Date de publication** : 2009

**Pays de publication** : AUS

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 10 ref.

**Résumé** : Targeted post-exposure prophylaxis represents a more efficient use of the stockpile than treatment alone.

**Code(s) de classement** : 002B01; 002B30A11; 002B02S05

**Descripteur(s) anglais**
- **Descripteur(s) :** Knowledge; Comprehension; Australia; Health policy; Public health; Use; Antiviral; Drug
- **Desc. généraux :** Oceania

**Descripteur(s) français**
- **Descripteur(s) :** Connaissance; Compréhension; Australie; Politique sanitaire; Santé publique; Utilisation; Antiviral; Médicament; Grippe pandémique
- **Desc. généraux :** Océanie

**Localisation** : INIST-3557, 354000187547710040

**Origine de la notice** : INIST

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Life-threatening respiratory failure from H1N1 influenza 09 (human swine influenza) : Pandemic (H1N1) 2009

Titre : Life-threatening respiratory failure from H1N1 influenza 09 (human swine influenza) : Pandemic (H1N1) 2009

Auteur(s) : KAUFMAN (Melissa A.); DUKE (Graeme J.); MCGAIN (Forbes); FRENCH (Craig); ABOLTINS (Craig); LANE (Gary); GUTTERIDGE (Geoff A.)

Affiliation(s) : Northern Hospital, Melbourne, VIC, AUS; Western Hospital, Melbourne, VIC, AUS; Austin Hospital, Melbourne, VIC, AUS

Source : Medical journal of Australia; vol. 191; no. 3; pp. 154-156
ISSN : 0025-729X
CODEN : MJAUAJ
Date de publication : 2009
Pays de publication : AUS
Langue(s) : ENG
Type de document : P
Nombre de références : 14 ref.

Résumé : We present the first six cases of H1N1 influenza 09 (confirmed by a polymerase chain reaction test from nasopharyngeal swabs) in patients requiring admission to intensive care in Australia (in three hospitals in the north-western suburbs of Melbourne). These cases highlight the small but significant risk of life-threatening respiratory failure associated with H1N1 influenza 09 infection. (MJA 2009; 191: 154-156).

Code(s) de classement : 002B01; 002B11D; 002B05C02C

Descriptor(s) anglais
Descriptor(s) : Respiratory failure; Life-threatening; Critically ill; Influenza; Human; Swine
Desc. génériques : Viral disease; Infection; Artiodactyla; Ungulata; Mammalia; Vertebrata; Respiratory disease

Descriptor(s) français
Descriptor(s) : Insuffisance respiratoire; Menace vitale; Malade état grave; Grippe; Homme; Porcin
Desc. génériques : Virose; Infection; Artiodactyla; Ungulata; Mammalia; Vertebrata; Pathologie de l’appareil respiratoire

Localisation : INIST-3557, 354000187547710100
Origine de la notice : INIST
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Long lasting immunity in chickens induced by a single shot of influenza vaccine prepared from inactivated non-pathogenic H5N1 virus particles against challenge with a highly pathogenic avian influenza virus

**Titre** : Long lasting immunity in chickens induced by a single shot of influenza vaccine prepared from inactivated non-pathogenic H5N1 virus particles against challenge with a highly pathogenic avian influenza virus

**Auteur(s)** : SASAKI (Takashi); KOKUMAI (Norihide); OHGITANI (Toshiaki); SAKAMOTO (Ryuichi); TAKIKAWA (Noriyasu); ZHIFENG LIN; OKAMATSU (Masatoshi); SAKODA (Yoshihiro); KIDA (Hirosi)

**Affiliation(s)** : Avian Biologics Department, Kyoto Biken Laboratories, Inc., 24-16 Makishima-cho, Uji, Kyoto 611-0041, JPN; Division 2, Second Research Department, The Chemo-Sero-Therapeutic Research Institute, Kikuchi, Kumamoto 869-1298, JPN; Research Center for Biologicals, The Kitasato Institute, Kitamoto, Saitama 364-0026, JPN; Research Department, Nippon Institute for Biological Science, Ome, Tokyo 198-0024, JPN; Laboratory of Microbiology, Department of Disease Control, Graduate School of Veterinary Medicine, Hokkaido University, Sapporo, Hokkaido 060-0818, JPN; Research Center for Zoonosis Control, Hokkaido University, Sapporo, Hokkaido 060-0818, JPN

**Source** : Vaccine; vol. 27; no. 38; pp. 5174-5177

**ISSN** : 0264-410X

**CODEN** : VACCDE

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 23 ref.

**Résumé** : An influenza vaccine was prepared from inactivated whole particles of the non-pathogenic strain A/duck/Hokkaido/Vac-1/04 (H5N1) virus using an oil adjuvant containing anhydromannitol octadecenoate-ether (AMOE). The vaccine was injected intramuscularly into five 4-week-old chickens, and 138 weeks after vaccination, they were challenged intranasally with 100 times 50% chicken lethal dose of the highly pathogenic avian influenza (HPAI) virus A/chicken/Yamaguchi/7/04 (H5N1). All 5 chickens survived without exhibiting clinical signs of influenza, although 2 days post-challenge, 3 vaccinated chickens shed limited titres of viruses in laryngopharyngeal swabs.

**Code(s) de classement** : 002A05F04; 002A05C10

**Descriputeur(s) anglais**

- **Descriputeur(s) :** Chicken; Avian influenza virus; Influenza A virus; Inactivated strain; Pathogenicity; Vaccine; Immunoprotection; Influenza A; Avian influenza

  **Desc. génériques :** Aves; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Poultry; Viral disease; Infection; Veterinary; Zoopathogen; Farming animal

**Descriputeur(s) français**

- **Descriputeur(s) :** Poulet; Influenzavirus aviaire; Virus grippal A; Souche inactivée; Pouvoir pathogène; Vaccin; Immunoprotection; Grippe A; Grippe aviaire

  **Desc. génériques :** Aves; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Volaille; Virose; Infection; Vétérinaire; Zoopathogène; Animal élevage

**Localisation** : INIST-20289, 354000172567110020

**Origine de la notice** : INIST

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Vaccine production capacity for seasonal and pandemic (H1N1) 2009 influenza

Titre : Vaccine production capacity for seasonal and pandemic (H1N1) 2009 influenza

Auteur(s) : COLLIN (Nicolas); DE RADIGUES (Xavier)
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Source : Vaccine; vol. 27; no. 38; pp. 5184-5186
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 5 ref.

Résumé : The first influenza pandemic of the 21st century, due to a new strain of A(H1N1) virus, was declared on 11 June 2009 by the Director-General of the World Health Organization. Fortunately, the international community, including influenza vaccine manufacturers, has been increasing its preparedness for such an event, triggered by the need to stem the spread of the highly pathogenic avian influenza A(H5N1) virus over recent years. Today, the development of a pandemic influenza vaccine in the fastest possible time is a global priority. However, two major issues need to be taken into consideration: how long will it take to produce sufficient pandemic vaccine doses to immunize the global population at risk, including poor populations that have no resources to purchase the vaccine; and how will pandemic vaccine production affect availability of trivalent vaccine for the forthcoming 2009-2010 influenza season. To address these questions, WHO carried out a survey in May 2009 among influenza vaccine manufacturers on their planned seasonal and pandemic production with a view to developing recommendations on the distribution and use of pandemic influenza vaccine.

Code(s) de classement : 002A05F04; 002A05C10

Descripteur(s) anglais
Descripteur(s) : Influenza A virus; Vaccine; Influenza A
Desc. généraux : Influenzavirus A; Orthomyxoviridae; Virus; Viral disease; Infection

Descripteur(s) français
Descripteur(s) : Virus grippal A; Vaccin; Grippe A
Desc. généraux : Influenzavirus A; Orthomyxoviridae; Virus; Virose; Infection

Localisation : INIST-20289, 354000172567110040
Origine de la notice : INIST
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Safety and immunogenicity of a subvirion inactivated influenza A/H5N1 vaccine with or without aluminum hydroxide among healthy elderly adults

Titre : Safety and immunogenicity of a subvirion inactivated influenza A/H5N1 vaccine with or without aluminum hydroxide among healthy elderly adults

Auteur(s) : BRADY (Rebecca C.); TREANOR (John J.); ATMAR (Robert L.); KEITEL (Wendy A.); EDELMAN (Robert); CHEN (Wilbur H.); WINOKUR (Patricia); BELSHE (Robert); GRAHAM (Irene L.); LEE NOAH (Diana); KUO GUO; HILL (Heather)

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Source : Vaccine; vol. 27; no. 37; pp. 5091-5095
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 16 ref.

Résumé : A total of 600 healthy adults >=65 years were randomized to receive 2 vaccinations 1 month apart of a subvirion avian influenza A/H5N1 vaccine containing 3.75, 7.5, 15, or 45 μg of hemagglutinin (HA) with or without aluminum hydroxide (AlOH). All formulations were safe. Groups given the vaccine with AlOH had more injection site discomfort. Dose-related increases in antibody responses were noted after the second vaccination. Antibody responses to the vaccine were not enhanced by AlOH at any HA dose level. A microneutralization titer >=40 was observed in 36% and 40% of subjects who received 45 μg of HA with or without AlOH, respectively. © 2009 Elsevier Ltd. All rights reserved.

Code(s) de classement : 002A05F04; 002A05C10

Descripteur(s) anglais

Descripteur(s) : Influenza A virus; Immunogenicity; Inactivated strain; Elderly; Vaccine; Influenza A; Avian influenza
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Human; Infection; Viral disease

Descripteur(s) français

Descripteur(s) : Virus grippal A; Immunogénicité; Souche inactivée; Personne âgée; Vaccin; Grippe A; Grippe aviaire
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Homme; Infection; Virose

Localisation : INIST-20289, 354000172565960100
Origine de la notice : INIST
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Live vaccination with an H5-hemagglutinin-expressing infectious laryngotracheitis virus recombinant protects chickens against different highly pathogenic avian influenza viruses of the H5 subtype

**Titre** : Live vaccination with an H5-hemagglutinin-expressing infectious laryngotracheitis virus recombinant protects chickens against different highly pathogenic avian influenza viruses of the H5 subtype

**Auteur(s)** : PAVLOVA (Sophia P.); VEITS (Jutta); METTENLEITER (Thomas C.); FUCHS (Walter)

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**Source** : Vaccine; vol. 27; no. 37; pp. 5085-5090

**ISSN** : 0264-410X

**CODEN** : VACCDE

**Date de publication** : 2009

**Pays de publication** : GBR

**Language(s)** : ENG

**Type de document** : P

**Nombre de références** : 40 ref.

**Résumé** : Recently, we described an infectious laryngotracheitis virus (ILTV, gallid herpesvirus 1) recombinant, which had been attenuated by deletion of the viral dUTPase gene UL50, and abundantly expressed the hemagglutinin (HA) gene of a H5N1 type highly pathogenic avian influenza virus (HPAIV) of Vietnamese origin. In the present study, efficacy of this vectored vaccine (ILTV- DELTA UL501H5V) against different H5 HPAIV was evaluated in 6-week-old chickens. After a single ocular immunization all animals developed HA-specific antibodies, and were protected against lethal infection not only with the homologous HPAIV isolate A/duck/Vietnam/TG24-01/2005 (H5N1, clade 1, hemagglutinin amino acid sequence identity 100%), but also with heterologous HPAIV A/swan/Germany/R65/2006 (H5N1, clade 2.2, identity 96.1%) or HPAIV A/chicken/Italy/8/98 (H5N2, identity 93.8%). No symptoms of disease were observed after challenge with the H5N1 viruses, and only 20% of H5N2 challenged animals developed minimal clinical signs. Real-time RT-PCR analyses of oropharyngeal swabs revealed limited challenge virus replication, but the almost complete absence of HPAIV RNA from cloacal swabs indicated that no generalized infections occurred. Thus, unlike several previous vectors, ILTV- DELTA UL501H5V was able to protect chickens against different HPAIV isolates of the H5 subtype. Vaccination with HA-expressing ILTV also allowed differentiation of immunized from AIV-infected animals by serological tests for antibodies against influenza virus nucleoprotein.

**Code(s) de classement** : 002A05F04; 002A05C10

**Descriputeur(s) anglais**

- **Descriputeur(s)** : Chicken; Avian influenzavirus; Vaccination; Hemagglutinin; Recombinant virus; Pathogenicity; Subtype; Infection
- **Desc. génériques** : Aves; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Poultry; Veterinary; Zoopathogen; Farming animal

**Descriputeur(s) français**

- **Descriputeur(s)** : Poulet; Influenzavirus aviaire; Vaccination; Hémagglutinine; Virus recombinant; Pouvoir pathogène; Soustype; Infection
- **Desc. génériques** : Aves; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Volaille; Vétérinaire; Zoopathogène; Animal élevage

**Localisation** : INIST-20289, 354000172565960090

**Origine de la notice** : INIST

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Evaluation of Live Attenuated Influenza A Virus H6 Vaccines in Mice and Ferrets

Titre : Evaluation of Live Attenuated Influenza A Virus H6 Vaccines in Mice and Ferrets

Auteur(s) : ZHONGYING CHEN; SANTOS (Celia); ASPELUND (Amy); GILLIM-ROSS (Laura); HONG JIN; KEMBLE (George); SUBBARAO (Kanta)

Affiliation(s) : MedImmune, Mountain View, California 94043, USA; Laboratory of Infectious Diseases, NIAID, NIH, Bethesda, Maryland 20892, USA

Source : Journal of virology; vol. 83; no. 1; pp. 65-72
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 42 ref.

Résumé : Avian influenza A virus A/teal/HK/W312/97 (H6N1) possesses seven gene segments that are highly homologous to those of highly pathogenic human influenza H5N1 viruses, suggesting that a W312-like H6N1 virus might have been involved in the generation of the A/HK/97 H5N1 viruses. The continuous circulation and reassortment of influenza H6 subtype viruses in birds highlight the need to develop an H6 vaccine to prevent potential influenza pandemics caused by the H6 viruses. Based on the serum antibody cross-reactivity data obtained from 14 different H6 viruses from Eurasian and North American lineages, A/duck/HK/182/77, A/teal/HK/W312/97, and A/mallard/Alberta/89/85 were selected to produce live attenuated H6 candidate vaccines. Each of the H6 vaccine strains is a 6:2 reassortant ca virus containing HA and NA gene segments from an H6 virus and the six internal gene segments from cold-adapted A/Ann Arbor/6/60 (AA ca), the master donor virus that is used to make live attenuated influenza virus FluMist (intranasal) vaccine. All three H6 vaccine candidates exhibited phenotypic properties of temperature sensitivity (ts), ca, and attenuation (att) conferred by the internal gene segments from AA ca. Intranasal administration of a single dose of the three H6 ca vaccine viruses induced neutralizing antibodies in mice and ferrets and fully protected mice and ferrets from homologous wild-type (wt) virus challenge. Among the three H6 vaccine candidates, the A/teal/HK/W312/97 ca virus provided the broadest cross-protection against challenge with three antigenically distinct H6 wt viruses. These data support the rationale for further evaluating the A/teal/HK/W312/97 ca vaccine in humans.

Code(s) de classement : 002A05C10; 002A05C07

Descripteur(s) anglais
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Fissipedia; Carnivora

Descripteur(s) français
Desc. génériques : Virus grippal A; Souris; Evaluation; Souche atténuée; Vaccin; Animal; Furet; Virologie

Localisation : INIST-13592, 354000185429370060
Origine de la notice : INIST
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"Prepandemic" Immunization for Novel Influenza Viruses, "Swine Flu" Vaccine, Guillain-Barré Syndrome, and the Detection of Rare Severe Adverse Events

Titre : "Prepandemic" Immunization for Novel Influenza Viruses, "Swine Flu" Vaccine, Guillain-Barré Syndrome, and the Detection of Rare Severe Adverse Events

Auteur(s) : EVANS (David); CAUCHEMEZ (Simon); HAYDEN (Frederick G.)
Affiliation(s) : The Wellcome Trust, Imperial College London, London, GBR; MRC Centre for Outbreak Analysis and Modelling, Department of Infectious Diseases Epidemiology, Imperial College London, London, GBR; The Wellcome Trust, London, GBR; University of Virginia, Charlottesville, Virginia, USA

Source : The Journal of infectious diseases; vol. 200; no. 3; pp. 321-328
ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 32 ref.

Résumé : The availability of immunogenic, licensed H5N1 vaccines and the anticipated development of vaccines against "swine" influenza A(H1N1) have stimulated debate about the possible use of these vaccines for protection of those exposed to potential pandemic influenza viruses and for immunization or "priming" of populations in the so-called "prepandemic" (interpandemic) era. However, the safety of such vaccines is a critical issue in policy development for wide-scale application of vaccines in the interpandemic period. For example, wide-scale interpandemic use of H5N1 vaccines could lead to millions of persons receiving vaccines of uncertain efficacy potentially associated with rare severe adverse events and against a virus that may not cause a pandemic. Here, we first review aspects of the 1976 National Influenza Immunization Programme against "swine flu" and its well-documented association with Guillain-Barré syndrome as a case study illustration of a suspected vaccine-associated severe adverse event in a mass interpandemic immunization setting. This case study is especially timely, given the recent spread of a novel influenza A(H1N1) virus in humans in Mexico and beyond. Following this, we examine available safety data from clinical trials of H5N1 vaccines and briefly discuss how vaccine safety could be monitored in a postmarketing surveillance setting.

Code(s) de classement : 002A05F04; 002B05

Descripteur(s) anglais

Description(s) : Swine; Immunization; Vaccine; Detection; Toxicity; Microbiology; Infection; Influenza; Guillain-Barré syndrome
Desc. génériques : Artiodactyla; Ungulata; Mammalia; Vertebrata; Veterinary; Viral disease; Inflammatory disease; Peripheral nerve disease; Nervous system diseases

Descripteur(s) français

Description(s) : Porcin; Immunisation; Vaccin; Détectio; Toxicité; Microbiologie; Infection; Grippe; Polyradiculonévrite de Guillain-Barré
Desc. génériques : Artiodactyla; Ungulata; Mammalia; Vertebrata; Vétérinaire; Virose; Maladie inflammatoire; Pathologie du système nerveux périphérique; Pathologie du système nerveux

Localisation : INIST-2052, 354000170912740020
Origine de la notice : INIST
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Reassortment between Avian H5N1 and Human H3N2 Influenza Viruses in Ferrets: a Public Health Risk Assessment

**Titre** : Reassortment between Avian H5N1 and Human H3N2 Influenza Viruses in Ferrets: a Public Health Risk Assessment

**Auteur(s)** : JACKSON (Sara); VAN HOEVEN (Neal); CHEN (Li-Mei); MAINES (Taronna R.); COX (Nancy J.); KATZ (Jacqueline M.); DONIS (Ruben O.)

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**Source** : Journal of virology; vol. 83; no. 16; pp. 8131-8140

**ISSN** : 0022-538X

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 54 ref.

**Résumé** : This study investigated whether transmissible H5 subtype human-avian reassortant viruses could be generated in vivo. To this end, ferrets were coinfect ed with recent avian H5N1(A/Thailand/16/04) and human H3N2 (A/Wyoming/3/03) viruses. Genotype analyses of plaque-purified viruses from nasal secretions of coinfe cted ferrets revealed that approximately 9% of recovered viruses contained genes from both progenitor viruses. H5 and H3 subtype viruses, including reassortants, were found in airways extending toward and in the upper respiratory tract of ferrets. However, only parental H5N1 genotype viruses were found in lung tissue. Approximately 34% of the recovered reassortant viruses possessed the H5 hemagglutinin (HA) gene, with five unique H5 subtypes recovered. These H5 reassortants were selected for further studies to examine their growth and transmissibility characteristics. Five H5 viruses with representative reassortant genotypes showed reduced titers in nasal secretions of infected ferrets compared to the parental H5N1 virus. No transmission by direct contact between infected and naive ferrets was observed. These studies indicate that reassortment between H5N1 avian influenza and H3N2 human viruses occurred readily in vivo and furthermore that reassortment between these two viral subtypes is likely to occur in ferret upper airways. Given the relatively high incidence of reassortant viruses from tissues of the ferret upper airway, it is reasonable to conclude that continued exposure of humans and animals to H5N1 alongside seasonal influenza viruses increases the risk of generating H5 subtype reassortant viruses that may be shed from upper airway secretions.

**Code(s) de classement** : 002A05C10

**Descrip teur(s) anglais**

- **Descrip teur(s)** : Influenza A virus; Human; Ferret; Public health; Risk factor; Evaluation; Virology; Avian influenza; Genetic reassortment

- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Fissipedia; Carnivora; Mammalia; Vertebrata; Infection; Viral disease

**Descrip teur(s) français**

- **Descrip teur(s)** : Virus grippal A; Homme; Furet; Santé publique; Facteur risque; Evaluation; Virologie; Grippe aviaire; Influenzavirus A(H3N2); Réassortiment génétique

- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Fissipedia; Carnivora; Mammalia; Vertebrata; Infection; Virose

**Localisation** : INIST-13592, 354000170926780310

**Origine de la notice** : INIST

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Nuclear Factor 90 Negatively Regulates Influenza Virus Replication by Interacting with Viral Nucleoprotein

Titre : Nuclear Factor 90 Negatively Regulates Influenza Virus Replication by Interacting with Viral Nucleoprotein

Auteur(s) : PUI WANG; WENJUN SONG; MOK (Bobo Wing-Yee); PENGXI ZHAO; KUN QIN; LAI (Alexander); SMITH (Gavin J. D.); JINXIA ZHANG; TIANWEI LIN; YI GUAN; HONGLIN CHEN

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Source : Journal of virology; vol. 83; no. 16; pp. 7850-7861

ISSN : 0022-538X

Date de publication : 2009

Pays de publication : USA

Langue(s) : ENG

Type de document : P

Nombre de références : 66 ref.

Résumé : Interactions between host factors and the viral replication complex play important roles in host adaptation and regulation of influenza virus replication. A cellular protein, nuclear factor 90 (NF90), was copurified with H5N1 viral nucleoprotein (NP) from human cells in which NP was transiently expressed and identified by matrix-assisted laser desorption ionization-time of flight mass spectrometry analysis. In vitro coimmunoprecipitation of NF90 and NP coexpressed in HEK 293T cells or individually expressed in bacterial and HEK 293T cells, respectively, confirmed a direct interaction between NF90 and NP, independent of other subunits of the ribonucleoprotein complex. This interaction was prevented by a mutation, F412A, in the C-terminal region of the NP, indicating that the C-terminal of NP is required for NF90 binding. RNase V treatment did not prevent coprecipitation of NP and NF90, which demonstrates that the interaction is RNA binding independent. After small interfering RNA knockdown of NF90 expression in A549 and HeLa cells, viral polymerase complex activity and virus replication were significantly increased, suggesting that NF90 negatively affects viral replication. Both NP and NF90 colocalized in the nucleus of virus-infected cells during the early phase of infection, suggesting that the interaction between NF90 and NP is an early event in virus replication. Quantitative reverse transcription-PCR showed that NF90 downregulates both viral genome replication and mRNA transcription in infected cells. These results suggest that NF90 inhibits influenza virus replication during the early phase of infection through direct interaction with viral NP.

Code(s) de classement : 002A05C10

Descripeur(s) anglais
Desc. génériques : Orthomyxoviridae; Virus

Descripeur(s) français
Desc. génériques : Orthomyxoviridae; Virus

Localisation : INIST-13592, 354000170926780060

Origine de la notice : INIST

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Sulfated Membrane Adsorbers for Economic Pseudo-Affinity Capture of Influenza Virus Particles

**Titre** : Sulfated Membrane Adsorbers for Economic Pseudo-Affinity Capture of Influenza Virus Particles

**Auteur(s)** : OPITZ (Lars); LEHMANN (Sylvia); REIEHL (Udo); WOLFF (Michael W.)

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**Source** : Biotechnology and bioengineering; vol. 103; no. 6; pp. 1144-1154

**ISSN** : 0006-3592

**CODEN** : BIBIAU

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 1 p.1/4

**Résumé** : Strategies to control outbreaks of influenza, a contagious respiratory tract disease, are focused mainly on prophylactic vaccinations in conjunction with antiviral medications. Currently, several mammalian cell culture-based influenza vaccine production processes are being established, such as the technologies introduced by Novartis Behring (Optaflu®) or Baxter International Inc. (Celvapan). Downstream processing of influenza virus vaccines from cell culture supernatant can be performed by adsorbing virions onto sulfated column chromatography beads, such as Cellufine® sulfate. This study focused on the development of a sulfated cellulose membrane (SCM) chromatography unit operation to capture cell culture-derived influenza viruses. The advantages of the novel method were demonstrated for the Madin Darby canine kidney (MDCK) cell-derived influenza virus A/Puerto Rico/8/34 (H1N1). Furthermore, the SCM-adsorbers were compared directly to column-based Cellufine® sulfate and commercially available cation-exchange membrane adsorbers. Sulfated cellulose membrane adsorbers showed high viral product recoveries. In addition, the SCM-capture step resulted in a higher reduction of dsDNA compared to the tested cation-exchange membrane adsorbers. The productivity of the SCM-based unit operation could be significantly improved by a 30-fold increase in volumetric flow rate during adsorption compared to the bead-based capture method. The higher flow rate even further reduced the level of contaminating dsDNA by about twofold. The reproducibility and general applicability of the developed unit operation were demonstrated for two further MDCK cell-derived influenza virus strains: A/Wisconsin/67/2005 (H3N2) and B/Malaysia/2506/2004. Overall, SCM-adsorbers represent a powerful and economically favorable alternative for influenza virus capture over conventional methods using Cellufine® sulfate.

**Code(s) de classement** : 002A31; 215

**Descripteur(s) anglais**

- **Desc. généraux** : Viral disease; Infection

**Descripteur(s) français**

- **Desc. généraux** : Virose; Infection

**Localisation** : INIST-9164, 354000170853000100

**Origine de la notice** : INIST

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Oral administration of heat-killed Lactobacillus plantarum L-137 enhances protection against influenza virus infection by stimulation of type I interferon production in mice

Título : Oral administration of heat-killed Lactobacillus plantarum L-137 enhances protection against influenza virus infection by stimulation of type I interferon production in mice

Auteur(s) : MAEDA (Naoyoshi); NAKAMURA (Risa); HIROSE (Yoshitaka); MUROSAKI (Shinji); YAMAMOTO (Yoshihiro); KASE (Tetsuo); YOSHIKAI (Yasunobu)

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Source : International immunopharmacology : (Print); vol. 9; no. 9; pp. 1122-1125

Résumé : We have previously reported that heat-killed Lactobacillus plantarum L-137 (HK-LP) stimulates macrophage/ dendritic cells to produce T helper (Th) 1-related cytokines in vitro and in vivo in mice. We here examined the effect of oral administration of HK-LP on protection against influenza virus infection in mice. C57BL/6 mice were orally given HK-LP from day -7 to 7 and intranasally infected with influenza virus A/FM/1/47 (H1N1, a mouse-adapted strain) at 100 pfu on day 0. The survival time was significantly prolonged in mice treated with HK-LP than that in mice treated with PBS as controls. The viral titers in the lung were significantly lower in mice treated with HK-LP than controls at the early stage after influenza virus infection. An appreciable level of interferon (IFN)- beta was detected in the serum of mice treated with HK-LP, while no IFN- beta was detected in controls after influenza infection. Our results suggest that HK-LP, a potent IFN- beta inducer, is useful for prevention against influenza infection.

Code(s) de classement : 002B02

Descripteur(s) anglais
- Oral administration; Heat; Lactobacillus plantarum; Protection; Influenzavirus; Infection; Stimulation; Interferon; Cytokine; Production; Biosynthesis; Animal; Mouse
- Des. génériques : Lactobacillaceae; Bacteria; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Environmental factor; Temperature

Descripteur(s) français
- Voie orale; Chaleur; Lactobacillus plantarum; Protection; Influenzavirus; Infection; Stimulation; Interférone; Cytokine; Production; Biosynthèse; Animal; Souris
- Des. génériques : Lactobacillaceae; Bactérie; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Facteur milieu; Température

Localisation : INIST-27109, 354000172478430150

Origine de la notice : INIST

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Infection of mice with a human influenza A/H3N2 virus induces protective immunity against lethal infection with influenza A/H5N1 virus

**Titre** : Infection of mice with a human influenza A/H3N2 virus induces protective immunity against lethal infection with influenza A/H5N1 virus

**Auteur(s) :** KREIJTZ (J. H. C. M.); BODEWES (R.); VAN DEN BRAND (J. M. A.); DE MUTSERT (G.); BAAS (C.); VAN AMERONGEN (G.); FOUCHIER (R. A. M.); OSTERHAUS (A. D. M. E.); RIMMELZWAAN (G. F.)

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**Source :** Vaccine; vol. 27; no. 36; pp. 4983-4989

**ISSN :** 0264-410X

**CODEN :** VACCDE

**Date de publication :** 2009

**Pays de publication :** GBR

**Langue(s) :** ENG

**Type de document :** P

**Nombre de références :** 42 ref.

**Résumé :** The transmission of highly pathogenic avian influenza (HPAI) A viruses of the H5N1 subtype from poultry to man and the high case fatality rate fuels the fear for a pandemic outbreak caused by these viruses. However, prior infections with seasonal influenza A/H1N1 and A/H3N2 viruses induce heterosubtypic immunity that could afford a certain degree of protection against infection with the HPAI A/H5N1 viruses, which are distantly related to the human influenza A viruses. To assess the protective efficacy of such heterosubtypic immunity mice were infected with human influenza virus A/Hong Kong/2/68 (H3N2) 4 weeks prior to a lethal infection with HPAI virus A/Indonesia/5/05 (H5N1). Prior infection with influenza virus A/Hong Kong/2/68 prior to a lethal infection with HPAI virus A/Indonesia/5/05 (H5N1). Priming by infection with respiratory syncytial virus, a non-related virus did not have a beneficial effect on the outcome of A/H5N1 infections, indicating that adaptive immune responses were responsible for the protective effect. In mice primed by infection with influenza A/H3N2 virus cytotoxic T lymphocytes (CTL) specific for NP366-374 epitope ASNENMDAM and PA224-232 SCLENFRAYV were observed. A small proportion of these CTL was cross-reactive with the peptide variant derived from the influenza A/H5N1 virus (ASNENMEVM and SSLENFRAYV respectively) and upon challenge infection with the influenza A/H5N1 virus cross-reactive CTL were selectively expanded. These CTL, in addition to those directed to conserved epitopes, shared by the influenza A/H3N2 and A/H5N1 viruses, most likely contributed to accelerated clearance of the influenza A/H5N1 virus infection. Although also other arms of the adaptive immune response may contribute to heterosubtypic immunity, the induction of virus-specific CTL may be an attractive target for development of broad protective vaccines. Furthermore the existence of pre-existing heterosubtypic immunity may dampen the impact a future influenza pandemic may have.

**Code(s) de classement :** 002A05F04; 002A05C10

**Descripteur(s) anglais**

**Descrip teur(s) anglais**

**Descrip teur(s) :** Mouse; Influenza A virus; Human; Avian influenzavirus; Immunoprotection; Cytotoxicity; Cytotoxic T lymphocyte; T-Lymphocyte; Influenza A

**Desc. génériques :** Rodentia; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen; Viral disease; Infection

**Descripteur(s) français**

**Descrip teur(s) français**

**Descrip teur(s) :** Souris; Virus grippal A; Homme; Influenzavirus aviaire; Immunoprotection; Cytotoxicité; Lymphocyte T cytotoxique; Lymphocyte T; Grippe A

**Desc. génériques :** Rodentia; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogène; Virose; Infection

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Evaluation of two live attenuated cold-adapted H5N1 influenza virus vaccines in healthy adults

**Titre** : Evaluation of two live attenuated cold-adapted H5N1 influenza virus vaccines in healthy adults

**Auteur(s)** : KARRON (Ruth A.); TALAAT (Kawsar); LUKE (Catherine); CALLAHAN (Karen); THUMAR (Bhagvanji); DILORENZO (Susan); MCAULIFFE (Josephine); SCHAPPELL (Elizabeth); SUGUITAN (Amorsolo); MILLS (Kimberly); CHEN (Grace); LAMIRANDE (Elaine); COELINGH (Kathleen); HONG JIN; MURPHY (Brian R.); KEMBLE (George); SUBBARAO (Kanta)

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**Source** : Vaccine; vol. 27; no. 36; pp. 4953-4960
**ISSN** : 0264-410X
**CODEN** : VACCDE
**Date de publication** : 2009
**Pays de publication** : GBR
**Langue(s)** : ENG
**Type de document** : P
**Nombre de références** : 40 ref.

**Résumé** : Background: Development of live attenuated influenza vaccines (LAIV) against avian viruses with pandemic potential is an important public health strategy. Methods and findings: We performed open-label trials to evaluate the safety, infectivity, and immuno-genicity of H5N1 VN 2004 AA ca and H5N1 HK 2003 AA ca. Each of these vaccines contains a modified H5 hemagglutinin and unmodified N1 neuraminidase from the respective wild-type (wt) parent virus and the six internal protein gene segments of the A/Ann Arbor/6/60 cold-adapted (ca) master donor virus. The H5N1 VN 2004 AA ca vaccine virus was evaluated at dosages of 106.7 TCID50 and 107.5 TCID50, and the H5N1 HK 2003 AA ca vaccine was evaluated at a dosage of 107.5 TCID50. Two doses were administered intranasally to healthy adults in isolation at 4-8 week intervals. Vaccine safety was assessed through daily examinations and infectivity was assessed by viral culture and by realtime reverse transcription-polymerase chain reaction testing of nasal wash (NW) specimens. Immunogenicity was assessed by measuring hemagglutination-inhibition (HI) antibodies, neutralizing antibodies, and IgG or IgA antibodies to recombinant (r)H5 VN 2004 hemagglutinin (HA) in serum or NW. Fifty-nine participants were enrolled: 21 received 106.7 TCID50 and 21 received 107.5 TCID50 of H5N1 VN 2004 AA ca and 17 received H5N1 HK 2003 AA ca. Shedding of vaccine virus was minimal, as were HI and neutralizing antibody responses. Fifty-two percent of recipients of 107.5 TCID50 of H5N1 VN 2004 AA ca developed a serum IgA response to rH5 VN 2004 HA. Conclusions: The live attenuated H5N1 VN 2004 and HK 2003 AA ca vaccines bearing avian H5 HA antigens were very restricted in replication and were more attenuated than seasonal LAIV bearing human H1, H3 or B HA antigens. The H5N1 AA ca LAIV elicited serum ELISA antibody but not HI or neutralizing antibody responses in healthy adults. (ClinicalTrials.gov Identifiers: NCT00347672 and NCT00488046).

**Code(s) de classement** : 002A05F04; 002A05C10

**Descripteur(s) anglais**
*Descriptor(s) :* Avian influenza virus; Influenza A virus; Attenuated strain; Vaccine; Clinical trial; Influenza
*Desc. génériques :* Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen; Viral disease; Infection

**Descripteur(s) français**
*Descriptor(s) :* Influenzavirus aviaire; Virus grippal A; Souche atténuée; Vaccin; Essai clinique; Grippe
*Desc. génériques :* Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogène; Virose; Infection

**Localisation** : INIST-20289, 354000172528760130
**Origine de la notice** : INIST
A/H1N1 influenza virus THE BASICS

Titre : A/H1N1 influenza virus THE BASICS

Auteur(s) : WATTS (Geoff)
Source : BMJ. British medical journal : (International ed.); vol. 339; no. 7717; pp. 368-369
ISSN : 0959-8146
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 3 ref.

Résumé : Do you know your H1N1s from your H2N2s? Geoff Watts explains the basic science of the influenza virus.

Code(s) de classement : 002B01

Descripteur(s) anglais
    Descripteur(s) : Influenzavirus; Medicine
    Desc. génériques : Orthomyxoviridae; Virus

Descripteur(s) français
    Descripteur(s) : Influenzavirus; Médecine
    Desc. génériques : Orthomyxoviridae; Virus

Localisation : INIST-5002A, 354000172525460120
Origine de la notice : INIST
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Closure of schools during an influenza pandemic

Titre : Closure of schools during an influenza pandemic

Auteur(s) : CAUCHEMEZ (Simon); FERGUSON (Neil M.); WACHTEL (Claude); TEGNELL (Anders); SAOUR (Guillaume); DUNCAN (Ben); NICOLL (Angus)

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Source : Lancet. Infectious diseases : (print); vol. 9; no. 8; pp. 473-481

ISSN : 1473-3099

Date de publication : 2009

Pays de publication : GBR

Langue(s) : ENG

Type de document : P

Nombre de références : 42 ref.

Résumé : In response to WHO raising the influenza pandemic alert level from phase five to phase six, health officials around the world are carefully reviewing pandemic mitigation protocols. School closure (also called class dismissal in North America) is a non-pharmaceutical intervention that is commonly suggested for mitigating influenza pandemics. Health officials taking the decision to close schools must weigh the potential health benefits of reducing transmission and thus case numbers against high economic and social costs, difficult ethical issues, and the possible disruption of key services such as health care. Also, if schools are expected to close as a deliberate policy option, or just because of high levels of staff absenteeism, it is important to plan to mitigate the negative features of closure. In this context, there is still debate about if, when, and how school closure policy should be used. In this Review, we take a multidisciplinary and holistic perspective and review the multiple aspects of school closure as a public health policy. Implications for the mitigation of the swine-origin influenza A H1N1 pandemic are also discussed.

Code(s) de classement : 002B05C02C

Description(s) anglais

Descripteur(s) : Influenza; School environment
Desc. génériques : Viral disease; Infection

Description(s) français

Descripteur(s) : Grippe; Milieu scolaire; Pandémie
Desc. génériques : Virose; Infection

Localisation : INIST-27478, 354000170825540010

Origine de la notice : INIST

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Immunogenicity and adverse events of avian influenza A H5N1 vaccine in healthy adults: multiple-treatments meta-analysis

Titre : Immunogenicity and adverse events of avian influenza A H5N1 vaccine in healthy adults: multiple-treatments meta-analysis

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Source : Lancet. Infectious diseases : (print); vol. 9; no. 8; pp. 482-492
ISSN : 1473-3099
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 50 ref.

Résumé : Influenza H5N1 is thought to be a likely causative agent for a future human influenza pandemic. Several types of H5N1 vaccine have been tested, including different doses and adjuvants, and a meta-analysis is needed to identify the best formulation. We searched Medline, Embase, the Cochrane Library, and other online databases to February, 2009, in any language for randomised trials comparing different H5N1 vaccines with or without placebo in healthy adults. Primary outcomes were seroconversion, seroresponse, or both according to haemagglutination-inhibition and microneutralisation. Secondary outcomes were adverse events. Because of the large number of compared formulations, multiple-treatments meta-analysis was used for primary outcomes. Direct-comparison meta-analyses were also done. We included 13 trials, which assessed 58 groups. With non-aluminium adjuvant, sufficiently high immunogenicity (greater than 70%) was achieved even at 12 μg or less (given as two doses of 6 μg or less), and higher doses did not provide major improvements. Immunogenicity for non-adjuvanted and aluminium-adjuvanted formulations increased with increasing dose, but was not sufficiently high. No serious vaccine-related adverse events were reported across 9600 participants. Currently, H5N1 influenza vaccines with non-aluminium adjuvants might represent the best available option in a pandemic. Large-scale studies are needed to verify the high immunogenicity of non-aluminium-adjuvanted vaccines that use very low doses of antigen.
Randomized, Double-Blind Controlled Phase 3 Trial Comparing the Immunogenicity of High-Dose and Standard-Dose Influenza Vaccine in Adults 65 Years of Age and Older

**Titre** : Randomized, Double-Blind Controlled Phase 3 Trial Comparing the Immunogenicity of High-Dose and Standard-Dose Influenza Vaccine in Adults 65 Years of Age and Older

**Auteur(s)** : FALSEY (Ann R.); TREANOR (John J.); TORNEIPORTH (Nadia); CAPELLAN (Jose); GORSE (Geoffrey J.)

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**Source** : The Journal of infectious diseases; vol. 200; no. 2; pp. 172-180

**ISSN** : 0022-1899

**CODEN** : JIDIAQ

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 25 ref.

**Résumé** : Background. Influenza-associated morbidity and mortality has not decreased in the last decade, despite increased receipt of vaccine. To improve the immunogenicity of influenza vaccine, a high-dose (HD) trivalent, inactivated influenza vaccine was developed. Methods. A multicenter, randomized, double-blind controlled study was conducted to compare HD vaccine (which contains 60 μg of hemagglutinin per strain) with the licensed standard-dose (SD) vaccine (which contains 15 μg of hemagglutinin per strain) in adults ≥65 years of age. Results. HD vaccine was administered to 2575 subjects, and SD vaccine was administered to 1262 subjects. There was a statistically significant increase in the rates of seroconversion and mean hemagglutination inhibition titers at day 28 after vaccination among those who received HD vaccine, compared with those who received SD vaccine. Mean postvaccination titers for individuals who received HD vaccine were 116 for H1N1, 609 for H3N2, and 69 for B strain; for those who received SD vaccine, mean postvaccination titers were as 67 for H1N1, 333 for H3N2, and 52 for B strain. The HD vaccine met superiority criteria for both A strains, and the responses for B strain met noninferiority criteria. Seroprotection rates were also higher for those who received HD vaccine than for those who received SD vaccine, for all strains. Local reactions were more frequent in individuals who received HD vaccine, but the reactions were mild to moderate. Conclusions. There was a statistically significant increase in the level of antibody response induced by HD influenza vaccine, compared with that induced by SD vaccine, without an attendant increase in the rate or severity of clinically relevant adverse reactions. These results suggest that the high-dose vaccine may provide improved protective benefits for older adults.

**Code(s) de classement** : 002A05F04; 002B05

**Descripteur(s) anglais**

*Description(s) :* Immunogenicity; Standards; Vaccine; Age; Microbiology; Infection; Influenza

*Desc. génériques :* Viral disease

**Descripteur(s) français**

*Description(s) :* Immunogénicité; Norme; Vaccin; Age; Microbiologie; Infection; Grippe

*Desc. génériques :* Virose

**Localisation** : INIST-2052, 354000187517850040

**Origine de la notice** : INIST

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DNA Vaccination with a Single-Plasmid Construct Coding for Viruslike Particles Protects Mice against Infection with a Highly Pathogenic Avian Influenza A Virus

Titre : DNA Vaccination with a Single-Plasmid Construct Coding for Viruslike Particles Protects Mice against Infection with a Highly Pathogenic Avian Influenza A Virus

Auteur(s) : SZECSI (Judit); GABRIEL (Gülsah); EDFELDT (Gabriella); MICHELET (Maud); KLENK (Hans Dieter); COSSET (François-Loïc)

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Source : The Journal of infectious diseases; vol. 200; no. 2; pp. 181-190

ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 50 ref.

Résumé : Background. With seasonal outbreaks affecting millions of people each year and devastating pandemics, human influenza is a major health concern. The pandemic threat includes highly pathogenic avian influenza viruses (HPAIVs) that gained the ability to infect humans in Asia and quickly spread throughout the world. Major concerns have been raised regarding today’s vaccine production systems against influenza viruses, and new strategies to design efficient vaccines are under intensive investigation. Methods. We demonstrated elsewhere that viruslike particles (VLPs) incorporating HPAIV hemagglutinin induce strong humoral immune response when injected in mice. In the current study, we evaluated a novel strategy that combines the immunogenicity of influenza VLPs and the advantages of DNA vaccines. Results. We developed minimal expression vectors encoding all genetic information necessary to produce H7N1 influenza VLPs. We showed that mice vaccinated with small DNA amounts developed specific, high-titer neutralizing antibodies against homologous H7N1 strain and were protected against lethal doses of an antigenically distinct H7N7 HPAIV. Moreover, using some of these constructs, we were able to raise cross-neutralizing antibodies against an unrelated H5N1 HPAIV. Conclusions. DNA vaccination with constructs coding for influenza VLP production is a promising strategy to induce protection against different influenza viruses.

Code(s) de classement : 002A05C10; 002B05

Descripteur(s) anglais

Descripteur(s) : Mouse; Avian influenzavirus; Influenza A virus; Genetic vaccine; Plasmid; Pathogenicity; Microbiology; Infection

Desc. génériques : Rodentia; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen

Descripteur(s) français

Descripteur(s) : Souris; Influenzavirus aviaire; Virus grippal A; Vaccin génétique; Plasmide; Pouvoir pathogène; Microbiologie; Infection

Desc. génériques : Rodentia; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogène

Localisation : INIST-2052, 354000187517850050

Origine de la notice : INIST

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Historical Perspective Emergence of Influenza A (H1N1) Viruses

Titre : Historical Perspective Emergence of Influenza A (H1N1) Viruses

Auteur(s) : ZIMMER (Shanta M.); BURKE (Donald S.)
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Source : The New England journal of medicine; vol. 361; no. 3; pp. 279-285
ISSN : 0028-4793
CODEN : NEJMAG
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 48 ref.

Résumé : APRIL 17, 2009, OFFICIALS AT THE CENTERS FOR DISEASE CONTROL and Prevention (CDC) confirmed two cases of swine influenza in children living in neighboring counties in California.1 Here we take a perspective from systems biology to review the series of evolutionary and epidemiologic events, starting in 1918, that led to the emergence of the current swine-origin influenza A (H1N1) strain (S-OIV), which is widely known as swine flu. This article is one of two historical articles on influenza A (H1N1) viruses in this issue of the Journal.2 Our review focuses on the key steps that characterize this viral evolution (Fig. 1).

Code(s) de classement : 002B01; 002B30A01A; 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Case history; Emergence; Epidemiology; Influenza A; Medicine
Desc. génériques : Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Historique; Emergence; Epidémiologie; Grippe A; Médecine
Desc. génériques : Virose; Infection

Localisation : INIST-6013, 354000187518680090
Origine de la notice : INIST
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Differential RNA silencing suppression activity of NS1 proteins from different influenza A virus strains

**Titre** : Differential RNA silencing suppression activity of NS1 proteins from different influenza A virus strains

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**Affiliation(s)** : Laboratory of Experimental Virology, Department of Medical Microbiology, Center for Infection and Immunity Amsterdam (CINIMA), Academic Medical Center, University of Amsterdam, Meibergdreef 15, 1105 AZ Amsterdam, NLD; Department of Virology and National Influenza Center, Erasmus Medical Center, Dr Molewaterplein 50, 30015 GE Rotterdam, NLD; Phytovation B.V., Wassenaarseweg 72, 2333 AL Leiden, NLD

**Source** : Journal of general virology; vol. 90; no. p. 8; pp. 1916-1922

**ISSN** : 0022-1317

**CODEN** : JGVIAY

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 1 p.

**Résumé** : The NS1 gene of influenza A virus encodes a multi-functional protein that plays an important role in counteracting cellular antiviral mechanisms such as the interferon (IFN), protein kinase R and retinoic acid-inducible gene product I pathways. In addition, NS1 has recently been shown to have RNA interference (RNAi) or RNA silencing suppression (RSS) activity. This study analysed the IFN antagonistic activity of NS1 and the RSS activity for several influenza subtypes: H1N1, H3N2, H5N1 and H7N7. It was shown that the various NS1 proteins were capable of inhibiting the activation of an IFN-responsive promoter. However, differential RSS activity was measured among the NS1 variants. The NS1 protein of strain A/WSN/33 (H1N1) was most potent in suppressing short hairpin RNA-mediated gene silencing. In contrast, NS1 proteins of the highly pathogenic H5N1 strains A/VN/1194/04 and A/HK/156/97 were most potent in complementing the RSS function of the human immunodeficiency virus type 1 Tat protein. These results show that the ability of NS1 to suppress RNAi varies among influenza strains and is likely to contribute to differences in viral replication capacity and pathogenicity.

**Code(s) de classement** : 002A05C10

**Descripteur(s) anglais**

*Influenza A virus; Suppression; Protein; Strain; Microbiology*

**Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus

**Descripteur(s) français**

*Virus grippal A; Suppression; Protéine; Souche; Microbiologie*

**Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus

**Localisation** : INIST-13533, 354000172471080140

**Origine de la notice** : INIST

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Prävention und Kontrolle von pandemischen Infektionskrankheiten: Das EU-Projekt SARSControl; Prevention and Control of Infectious Diseases with Pandemic Potential: The EU-Project SARSControl

Titre : Prävention und Kontrolle von pandemischen Infektionskrankheiten: Das EU-Projekt SARSControl; Prevention and Control of Infectious Diseases with Pandemic Potential: The EU-Project SARSControl

Auteur(s) : AHMAD (A.); KRUMKAMP (R.); RICHARDUS (J. H.); REINTJES (R.)
Affiliation(s) : Hochschule für Angewandte Wissenschaften Hamburg, Department Gesundheitswissenschaften Deutschland, DEU; Erasmus MC, University Medical Center Rotterdam, Department of Public Health, NLD

Source : Das Gesundheitswesen : (Stuttgart. Thieme); vol. 71; no. 6; pp. 351-357
ISSN : 0941-3790
Date de publication : 2009
Pays de publication : DEU
Langue(s) : GER
Langue(s) du résumé : eng
Type de document : P
Nombre de références : 31 ref.

Résumé : Introduction: The influenza pandemics of the 20th century, the SARS epidemic in 2002/03 and the growing number of human cases infected with the H5N1 avian influenza virus clearly demonstrate that the threat of new pandemics is very real. These events have intensified pandemic prevention and control activities worldwide.

"SARSControl" is a three-year project funded by the European Commission with the objective to aid European member states in the public health management of new emerging infections. This article summarises the main research results and recommendations arising from this project. Method: The reports and papers published in the SARSControl project form the basis of this article. In addition, a literature search for SARS and pandemic influenza was conducted and information on pandemic planning and management guidelines obtained from the WHO and EU websites. The project results are discussed in this context. Results: A lack of knowledge and delayed international communication resulted in the rapid spread of SARS, highlighting the importance of a global system for rapid and transparent information transfer. Epidemiological and economic modelling studies have shown that, in comparison to travel restrictions, applying intervention measures to interrupt local transmission within a country and investing into vaccine research and anti-viral stockpiling, is a more cost-effective and efficient use of resources for the containment of pandemics. A study investigating the perceived threat associated with pandemics showed that the subjective risk perception of people varies among countries. This influences human behaviour and should hence be considered during risk communication and implementation of pandemic control measures. Discussion: The basic prerequisites of an efficient pandemic management are operationalisable pandemic plans, subjected to regular exercises, backed by adequate resources and a sound health-care infrastructure. At international level cross-border co-operation and information exchange on infection control is the key to pandemic mitigation and containment. Strengthening surveillance systems at the international level, to allow the timely monitoring of infectious agents and outbreaks is essential. Transferring such outbreak information in real time into mathematical models and the resulting essential epidemiological information to policy makers would facilitate a more efficient use of scarce resources. Involvement of the public in decisions regarding the implementation of restrictive control measures which often curtail individual liberty is necessary for the acceptance and ultimate success of pandemic control.

Code(s) de classement : 002B30A11; 002B30A03; 002B05C02C

Desc. génériques : Viral disease; Respiratory disease; Lung disease
Desc. ang: Infection; Prevention; Surveillance; Check; Public health; World; Influenza; Severe acute respiratory syndrome; Clinical management
Activation of toll-like receptor signaling pathway for protection against influenza virus infection; VACCINES, IMMUNISATION AND IMMUNOTHERAPY: Based on the Sixth World Congress on Vaccines, Immunisation and Immunotherapy, Milan, Italy, 23-25 September 2008

Titre : Activation of toll-like receptor signaling pathway for protection against influenza virus infection; VACCINES, IMMUNISATION AND IMMUNOTHERAPY: Based on the Sixth World Congress on Vaccines, Immunisation and Immunotherapy, Milan, Italy, 23-25 September 2008

Auteur(s) : WONG (J. P.); CHRISTOPHER (M. E.); VISWANATHAN (S.); KARPOFF (N.); DAI (X.); DAS (D.); SUN (L. Q.); WANG (M.); SALAZAR (A. M.); KURSTAK (Edouard), ed.

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Source : Vaccine; vol. 27; no. 25-26; pp. 3481-3483

ISSN : 0264-410X

CODEN : VACCDE

Date de publication : 2009

Pays de publication : GBR

Langue(s) : ENG

Type de document : P; C

Nombre de références : 9 ref.

Résumé : This study aims to evaluate the antiviral role of nucleic acid-based agonists for the activation of toll-like receptor (TLR) signaling pathways, and its protective role in respiratory influenza A virus infections. TLR-3 is expressed on myeloid dendritic cells, respiratory epithelium, and macrophages, and appears to play a central role in mediating both the antiviral and inflammatory responses of the innate immunity in combating viral infections. Influenza viruses can effectively inhibit the host's ability to produce interferons, and thereby suppress the immune system's antiviral defence mechanisms. Poly ICLC is a synthetic double stranded RNA comprising of polyriboinosinic-polyribocytidylic acid (Poly IC) stabilized with L-lysine (L) and carboxymethylcellulose (C). Poly ICLC and liposome-encapsulated Poly ICLC (LE Poly ICLC) are TLR-3 agonists and are potent inducer of interferons and natural killer cells. Intranasal pre-treatment of mice with Poly ICLC and LE Poly ICLC provided high level of protection against lethal challenge with a highly lethal avian H5N1 influenza (HPAI) strain (A/H5N1/chicken/Henan clade 2), and against lethal seasonal influenza A/PR/8/34 [H1 N1] and A/Aichi/2 [H3N2] virus strains. The duration of protective antiviral immunity to multiple lethal doses of influenza virus A/PR/8/34 virus had been previously found to persist for up to 3 weeks in mice for LE Poly ICLC and 2 weeks for Poly ICLC. Similarly, pre-treatment of mice with CpG oligonucleotides (TLR-9 agonist) was also found to provide complete protection against influenza A/PR/8/34 infection in mice. RT-PCR analysis of lung tissues of mice treated with Poly ICLC and LE Poly ICLC revealed upregulation of TLR-3 mRNAs gene expression. Taken together, these results do support the potential role of TLR-3 and TLR-9 agonists such as Poly ICLC and LE Poly ICLC in protection against lethal seasonal and HPAI virus infection.

Code(s) de classement : 002A05F04; 002A05C10

Descripteur(s) anglais

Descrip teur(s) : Influenzavirus; Toll like receptor; Liposome; Viral disease

Desc. génériques : Orthomyxoviridae; Virus; Infection

Descripteur(s) français

Descrip teur(s) : Influenzavirus; Récepteur TLR; Liposome; Virose

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Desc. génériques : Orthomyxoviridae; Virus; Infection

Localisation : INIST-20289, 354000188515100440
Origine de la notice : INIST
Copyright de notice : © 2009 INIST-CNRS. All rights reserved.
Immunogenicity of hemagglutinin from A/Bar-headed Goose/Qinghai/1A/05 and A/Anhui/1/05 strains of H5N1 influenza viruses produced in Nicotiana benthamiana plants; VACCINES, IMMUNISATION AND IMMUNOTHERAPY: Based on the Sixth World Congress on Vaccines, Immunisation and Immunotherapy, Milan, Italy, 23-25 September 2008

Titre : Immunogenicity of hemagglutinin from A/Bar-headed Goose/Qinghai/1A/05 and A/Anhui/1/05 strains of H5N1 influenza viruses produced in Nicotiana benthamiana plants; VACCINES, IMMUNISATION AND IMMUNOTHERAPY: Based on the Sixth World Congress on Vaccines, Immunisation and Immunotherapy, Milan, Italy, 23-25 September 2008

Auteur(s) : SHOJI (Yoko); FARRANCE (Christine E.); HONG BI; SHAMLOUL (Moneim); GREEN (Brian); MANCEVA (Slobodanka); RHEE (Amy); UGULAVA (Natalia); ROY (Gourgopal); MUSIYCHUK (Konstantin); CHICHESTER (Jessica A.); METT (Vadim); YUSIBOV (Vidadi); KURSTAK (Edouard), ed.

Collectivité(s) auteur : Infections Control World Organization (ICWO), Montreal, Québec, CAN, org-cong.

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Source : Vaccine; vol. 27; no. 25-26; pp. 3467-3470
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P; C
Nombre de références : 18 ref.

Résumé : Highly pathogenic avian influenza (HPAI) viruses of the H5N1 subtype have been identified as a potential pandemic threat by the World Health Organization (WHO). Since 1997, these viruses have been spreading from Asia to Europe and Africa with increasing genetic and antigenic diversities. Vaccination is the preferred strategy for the prevention and control of influenza infections and the availability of a system for the rapid engineering and production of vaccines is required in the event of an influenza pandemic. In this study, we engineered and produced recombinant hemagglutinin (HA) from A/Bar-headed Goose/Qinghai/1A/05 (clade 2.2) and A/Anhui/1/2005 (clade 2.3) in Nicotiana benthamiana plants. Immunization of mice with these plant-derived HA antigens elicited serum hemagglutination inhibition (HI) and virus neutralization (VN) antibodies. These results suggest the utility of our plant-expression system for recombinant influenza vaccine production.

Code(s) de classement : 002A05F04; 002A05C10

Descriptor(s) anglais

- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Solanaceae; Angiospermae; Spermatophyta; Experimental plant; Viral disease; Infection

Descriptor(s) français

- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Solanaceae; Angiospermae;
Influenza vaccination in patients with cirrhosis and in liver transplant recipients; VACCINES, IMMUNISATION AND IMMUNOTHERAPY: Based on the Sixth World Congress on Vaccines, Immunisation and Immunotherapy, Milan, Italy, 23-25 September 2008

Titre : Influenza vaccination in patients with cirrhosis and in liver transplant recipients; VACCINES, IMMUNISATION AND IMMUNOTHERAPY: Based on the Sixth World Congress on Vaccines, Immunisation and Immunotherapy, Milan, Italy, 23-25 September 2008

Auteur(s) : GAETA (Giovanni B.); PARIANI (Elena); AMENDOLA (Antonella); BRANCACCIO (Giuseppina); CUOMO (Gianluca); STORNAIUOLO (Gianfranca); ZAPPA (Alessandra); ZANETTI (Alessandro); KURSTAK (Edouard), ed.

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Source : Vaccine; vol. 27; no. 25-26; pp. 3373-3375

ISSN : 0264-410X
CODEN : VACCDE

Date de publication : 2009

Pays de publication : GBR

Type de document : P; C

Nombre de références : 12 ref.

Résumé : To assess the safety and immunogenicity of influenza vaccination, patients with cirrhosis undergoing treatment or not and liver transplant recipients under standard immunosuppression were vaccinated and followed up for 6 months. One month after vaccination, seroprotection rates and antibody GMTs against the three vaccine antigens were higher than baseline levels in all three patients groups. No differences in seroconversion and seroprotection rates were found within groups, but antibody GMTs against A/H1N1 and A/H3N2 strains were lower in liver transplant recipients than in patients with cirrhosis without treatment. No serious adverse events and no alteration of the liver function tests were observed. Patients with cirrhosis, including those under treatment, and liver transplant recipients benefit from influenza vaccination and can be safely immunized.

Code(s) de classement : 002A05F04

Descriptor(s) anglais

Descriptor(s) : Human; Vaccination; Liver; Recipient; Influenza; Cirrhosis

Desc. génériques : Digestive diseases; Viral disease; Infection; Hepatic disease; Digestive system

Descriptor(s) français

Descriptor(s) : Homme; Vaccination; Foie; Receveur; Grippe; Cirrhose

Desc. génériques : Pathologie de l'appareil digestif; Virose; Infection; Pathologie du foie; Appareil digestif

Localisation : INIST-20289, 354000188515100230

Origine de la notice : INIST

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Likelihood that an Unsubtypeable Influenza A Virus Result Obtained with the Luminex xTAG Respiratory Virus Panel Is Indicative of Infection with Novel A/H1N1 (Swine-Like) Influenza Virus

**Titre** : Likelihood that an Unsubtypeable Influenza A Virus Result Obtained with the Luminex xTAG Respiratory Virus Panel Is Indicative of Infection with Novel A/H1N1 (Swine-Like) Influenza Virus

**Auteur(s)** : GINOCCHIO (Christine C.); ST. GEORGE (Kirsten)

**Affiliation(s)** : North Shore-LIJ Health System Laboratories 10 Nevada Drive Lake Success, NY 11042, USA; Wadsworth Center New York State Department of Health Empire State Plaza P.O. Box 509 Albany, NY 12201-0509, USA

**Source** : Journal of clinical microbiology : (Print); vol. 47; no. 7; pp. 2347-2348

**ISSN** : 0095-1137

**CODEN** : JCMIDW

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 3 ref.

**Code(s) de classement** : 002A05C10

**Descripteur(s) anglais**

*Description(s) : Influenza A virus; Porcine influenza virus; Microbiology; Viral disease
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Veterinary; Infection

**Descripteur(s) français**

*Description(s) : Virus grippal A; Influenzavirus porcin; Microbiologie; Virose
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Vétérinaire; Infection

**Localisation** : INIST-17088, 354000187519260630

**Origine de la notice** : INIST

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Confirmation of the First Hong Kong Case of Human Infection by Novel Swine Origin Influenza A (H1N1) Virus Diagnosed Using Ultrarapid, Real-Time Reverse Transcriptase PCR

Titre : Confirmation of the First Hong Kong Case of Human Infection by Novel Swine Origin Influenza A (H1N1) Virus Diagnosed Using Ultrarapid, Real-Time Reverse Transcriptase PCR

Auteur(s) : LAU (Susanna K. P.); KWOK-HUNG CHAN ; YIP (Cyril C. Y.); TAK KEUNG NG; OWEN T. Y. TSANG; WOO (Patrick C. Y.); KWOK-YUNG YUEN

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Source : Journal of clinical microbiology : (Print); vol. 47; no. 7; pp. 2344-2346
ISSN : 0095-1137
CODEN : JCMDW
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 9 ref.

Code(s) de classement : 002A05C10

Descriptor(s) anglais
   Descriteur(s) : Human; Porcine influenzavirus; Influenza A virus; Hong Kong; Origin; Real time; RNA-directed DNA polymerase; Polymerase chain reaction; Microbiology
   Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; China; Asia; Nucleotidyltransferases; Transferases; Enzyme; Veterinary

Descriptor(s) français
   Descriteur(s) : Homme; Influenzavirus porcin; Virus grippal A; Hong Kong; Origine; Temps réel; RNA-directed DNA polymerase; Réaction chaîne polymérase; Microbiologie
   Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Chine; Asie; Nucleotidyltransferases; Transferases; Enzyme; Vétérinaire

Localisation : INIST-17088, 354000187519260620
Origine de la notice : INIST
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Decreased Antibody Response to Influenza Vaccination in Kidney Transplant Recipients: A Prospective Cohort Study

Titre : Decreased Antibody Response to Influenza Vaccination in Kidney Transplant Recipients: A Prospective Cohort Study

Auteur(s) : BIRDWELL (Kelly A.); IKIZLER (Mine R.); SANNELLA (Edith C.); LI WANG; BYRNE (Daniel W.); ALP IKIZLER (T.); WRIGHT (Peter F.)

Affiliation(s) : Division of Nephrology, Vanderbilt University Medical Center, Nashville, TN, USA; Division of Pediatric Infectious Diseases, Vanderbilt University Medical Center, Nashville, TN, USA; Department of Biostatistics, Vanderbilt University Medical Center, Nashville, TN, USA; Division of Infectious Disease and International Health, Dartmouth Medical School, Lebanon, NH, USA

Source : American journal of kidney diseases; vol. 54; no. 1; pp. 112-121
ISSN : 0272-6386
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 33 ref.

Résumé : Background: Antibody response to the inactivated influenza vaccine is not well described in kidney transplant recipient participants administered newer, but commonly used, immunosuppression medications. We hypothesized that kidney transplant recipient participants administered tacrolimus-based regimens would have decreased antibody response compared with healthy controls. Study Design: Prospective cohort study of 53 kidney transplant recipients and 106 healthy control participants during the 2006-2007 influenza season. All participants received standard inactivated influenza vaccine. Setting & Participants: Kidney transplant recipients administered tacrolimus-based regimens at a single academic medical center and healthy controls. Predictor: Presence of kidney transplant. Outcomes: Proportion of participants achieving seroresponse (4-fold increase in antibody titer) and seroprotection (antibody titer >= 1 :32) 1 month after vaccination. Measurements: Antibody titers before and 1 month after vaccination by means of hemagglutinin inhibition assays for influenza types A/H1N1, A/H3N2, and B. Results: A smaller proportion of the transplantation group compared with the healthy control group developed the primary outcomes of seroresponse or seroprotection for all 3 influenza types at 1 month after vaccination. The response to influenza type A/H3N2 was statistically different; the transplantation group had 69% decreased odds of developing seroresponse (95% confidence interval, 0.16 to 0.62; P = 0.001) and 78% decreased odds of developing seroprotection (95% confidence interval, 0.09 to 0.53; P = 0.001) compared with healthy controls. When participants less than 6 months from the time of transplantation were considered, this group had a significantly decreased response to the vaccine compared with healthy controls. Limitations: Decreased sample size, potential for confounders, outcome measure used is the standard but does not give information about vaccine efficacy. Conclusions: Kidney transplant recipients, especially within 6 months of transplantation, had diminished antibody response to the 2006-2007 inactivated influenza vaccine.

Code(s) de classement : 002B14; 002B05C02C

Descripteur(s) anglais

Desc. génériques : Viral disease; Infection; Urinary system; Surgery; Graft; Transplantation; Lactone; Macrolide; Calcineurin inhibitor; Protein synthesis inhibitor

Descripteur(s) français

Desc. génériques : Grippé; Réponse immune; Anticorps; Immunité humorale; Immunoprophylaxie; Vaccination; Prévention; Rein; Homotransplantation; Prospectif; Etude cohorte; Immunodépression; Immunodépresseur;
Tacrolimus; Néphrologie; Urologie; Immunomodulateur; Traitement; Antibactérien

Desc. génériques : Virose; Infection; Appareil urinaire; Chirurgie; Greffe; Transplantation; Lactone; Macrolide; Inhibiteur de la calcineurine; Inhibiteur synthèse protéique

Localisation : INIST-19098. 354000172451770170
Origine de la notice : INIST
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Identification of amino acid substitutions in mutated peptides of nucleoprotein from avian influenza virus

Titre : Identification of amino acid substitutions in mutated peptides of nucleoprotein from avian influenza virus

Auteur(s) : NING LIU; LEE (Kim-Chung); WENJUN SONG; PUI WANG; ZONGWEI CAI; HONGLIN CHEN

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Source : Talanta : (Oxford); vol. 78; no. 4-5; pp. 1492-1496
ISSN : 0039-9140
CODEN : TLNTA2
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 17 ref.

Résumé : Nucleoprotein (NP), the structural component of ribonucleoprotein complex of avian influenza virus, performs multiple essential functions in the regulation of viral RNA synthesis and in the control of nuclear traffic of viral proteins. Mutations have often been found in NP, some of which are relevant to viral survival strategies. In this study, we used nanospray-MS/MS to analyze tryptic digestion of nucleoprotein of avian influenza virus (H5N1) and to identify three mutated peptides. The MS/MS analyses allowed the confident determination of the three mutated amino acid residues F313Y, I194V and V4081/L in the mutated peptides of LLQNSQVYSIIRPNENPAHK, GVGMVMELVR and ASAGQI/LSVQPTFSVQR, respectively.

Code(s) de classement : 001C04C

Descripteur(s) anglais
Descripteur(s) : Regulation; Mass spectrometry MS/MS; Digestion; Residue; Aminoacid; Peptides; Protein

Descripteur(s) français
Descripteur(s) : Réglementation; Spectrométrie masse tandem; Digestion; Résidu; Aminoacide; Peptide; Protéine

Localisation : INIST-9221, 354000186123670440
Origine de la notice : INIST
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Enhancement of potent antibody and T-cell responses by a single-dose, novel nanoemulsion-formulated pandemic influenza vaccine

Titre : Enhancement of potent antibody and T-cell responses by a single-dose, novel nanoemulsion-formulated pandemic influenza vaccine

Auteur(s) : HUANG (Ming-Hsi); HUANG (Chiung-Yi); LIN (Su-Chen); CHEN (Jia-Huey); KU (Chien-Chun); CHOU (Ai-Hsiang); LIU (Shih-Jen); CHEN (Hsin-Wei); CHONG (Pele); LENG (Chih-Hsiang)

Affiliation(s) : Vaccine Research and Development Center, National Health Research Institutes, No. 35 Keyan Road, Zhunan Town, Miaoli County 35053, TWN

Source : Microbes and infection; vol. 11; no. 6-7; pp. 654-660

ISSN : 1286-4579

Date de publication : 2009

Pays de publication : FRA

Langue(s) : ENG

Type de document : P

Nombre de références : 24 ref.

Résumé : Vaccine shortages are a major obstacle to influenza pandemic preparedness. Increasing vaccine efficiency provides a potentially effective way to overcome this problem. Specifically, using single-dose immunization to induce protective immunity is an attractive approach to emergency/ massive vaccination. In this report, we propose a novel nanoemulsion comprised of the bioresorbable polymer, Span®85, and squalene forming a ready-to-use adjuvant, called PELC. After formulation with PELC, inactivated H5N1 virus was intramuscularly administered to mice via a single injection. The data demonstrate that inactivated virus containing 0.5 μg hemagglutinin (HA) and formulated with PELC induced more potent antigen-specific antibodies, hemagglutination inhibition, and virus neutralization than non-adjuvanted inactivated virus containing 5 μg HA. In addition, T-cell proliferative responses, as well as interferon- gamma (IFN- gamma ) and interleukin-4 (IL-4) secretion were significantly enhanced after immunization with PELC-adjuvanted inactivated virus. These results indicate that PELC can be used for effective single-dose immunization and could thus play an important role in influenza pandemic preparedness.

Code(s) de classement : 002A05F04; 002A05C10

Describeur(s) anglais

Descripteur(s) : Avian influenza virus; Humoral immunity; Immune response; Cellular immunity; Vaccine; Influenza

Desc. génériques : Influenza A; Orthomyxoviridae; Virus; Zoopathogen; Viral disease; Infection

Describeur(s) français

Descripteur(s) : Influenza virus aviaire; Immunité humorale; Réponse immune; Immunité cellulaire; Vaccin; Grippe

Desc. génériques : Influenza A; Orthomyxoviridae; Virus; Zoopathogène; Virose; Infection

Localisation : INIST-26816, 354000172412590040

Origine de la notice : INIST

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Susceptibility of Highly Pathogenic H5N1 Influenza Viruses to the Neuraminidase Inhibitor Oseltamivir Differs In Vitro and in a Mouse Model

Titre : Susceptibility of Highly Pathogenic H5N1 Influenza Viruses to the Neuraminidase Inhibitor Oseltamivir Differs In Vitro and in a Mouse Model

Auteur(s) : GOVORKOVA (Elena A.); ILYUSHINA (Natalia A.); MCCLAREN (Jennifer L.); NAIPOPOS (Tri S. P.); DOUANGNGEUN (Bounlom); WEBSTER (Robert G.)

Affiliation(s) : Department of Infectious Diseases, St. Jude Children's Research Hospital, Memphis, Tennessee 38105-2794, USA; The D. I. Ivanovsky Institute of Virology, Moscow 123098, RUS; Indonesia National Committee on Avian Influenza Control and Pandemic Influenza Preparedness, Jakarta, IDN; National Animal Health Centre, Vientiane, LAO; Department of Pathology, University of Tennessee, Memphis, Tennessee 38105, USA

Source : Antimicrobial agents and chemotherapy; vol. 53; no. 7; pp. 3088-3096
ISSN : 0066-4804
CODEN : AACHAX
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 39 ref.

Résumé : While the neuraminidase (NA) inhibitor oseltamivir is currently our first line of defense against a pandemic threat, there is little information about whether in vitro testing can predict the in vivo effectiveness of antiviral treatment. Using a panel of five H5N1 influenza viruses (H5 clades 1 and 2), we determined that four viruses were susceptible to the drug in vitro (mean 50% inhibitory concentration [IC50], 0.1 to 4.9 nM), and A/Turkey/65-1242/06 virus was slightly less susceptible (mean IC50, 10.8 nM). Two avian viruses showed significantly greater NA enzymatic activity (Vmax) than the human viruses, and the five viruses varied in their affinity for the NA substrate MUNANA (Km, 64 to 300 μM) and for oseltamivir carboxylate (Ki, 0.1 to 7.9 nM). The protection of mice provided by a standard oseltamivir regimen (20 mg/kg/day for 5 days) also varied among the viruses used. We observed (i) complete protection against the less virulent A/chicken/Jogjakarta/BBVET/IX/04 virus; (ii) moderate protection (60 to 80% survival) against three viruses, two of which are neurotropic; and (iii) no protection against A/Turkey/ 65-1242/06 virus, which induced high pulmonary expression of proinflammatory mediators (interleukin-1 alpha [IL-1 alpha ], IL-6, alpha interferon, and monocyte chemotactic protein 1) and contained a minor subpopulation of drug-resistant clones (I117V and E119A NA mutations). We found no correlation between in vitro susceptibility and in vivo protection (Spearman rank correlation coefficient p = -0.1; P > 0.05). Therefore, the in vivo efficacy of oseltamivir against highly pathogenic H5N1 influenza viruses cannot be reliably predicted by susceptibility testing, and more prognostic ways to evaluate anti-influenza compounds must be developed. Multiple viral and host factors modulate the effectiveness of NA inhibitor regimens against such viruses and new, more consistently effective treatment options, including combination therapies, are needed.

Code(s) de classement : 002B02S; 002B05C02C

Descriptor(s) anglais

Desc. génériques : Viral disease; Infection; Rodentia; Mammalia; Vertebrata; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor

Descriptor(s) français

Desc. génériques : Virus disease; Infection; Rodents; Mammals; Vertebrates; Exo- α-sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor

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Desc. génériques : Virose; Infection; Rodentia; Mammalia; Vertebrata; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme

Localisation : INIST-13334, 354000187991720550
Origine de la notice : INIST
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Evaluation of Vaccines for H5N1 Influenza Virus in Ferrets Reveals the Potential for Protective Single-Shot Immunization

Titre : Evaluation of Vaccines for H5N1 Influenza Virus in Ferrets Reveals the Potential for Protective Single-Shot Immunization

Auteur(s) : MIDDLETON (Deborah); ROCKMAN (Steven); PEARSE (Martin); BARR (Ian); LOWTHER (Sue); KLIPPEL (Jessica); RYAN (David); BROWN (Lorena)

Affiliation(s) : Australian Animal Health Laboratory, Geelong, Victoria, AUS; CSL Limited, Parkville, Victoria, AUS; WHO Collaborating Centre for Influenza Reference and Research, Parkville, Victoria, AUS; Department of Microbiology and Immunology, The University of Melbourne, Parkville, Victoria, AUS

Source : Journal of virology; vol. 83; no. 15; pp. 7770-7778

ISSN : 0022-538X

Date de publication : 2009

Pays de publication : USA

Langue(s) : ENG

Type de document : P

Nombre de références : 26 ref.

Résumé : As part of influenza pandemic preparedness, policy decisions need to be made about how best to utilize vaccines once they are manufactured. Since H5N1 avian influenza virus has the potential to initiate the next human pandemic, isolates of this subtype have been used for the production and testing of prepandemic vaccines. Clinical trials of such vaccines indicate that two injections of preparations containing adjuvant will be required to induce protective immunity. However, this is a working assumption based on classical serological measures only. Examined here are the dose of viral hemagglutinin (HA) and the number of inoculations required for two different H5N1 vaccines to achieve protection in ferrets after lethal H5N1 challenge. Ferrets inoculated twice with 30 µg of A/Vietnam/1194/2004 HA vaccine with AlPO4, or with doses as low as 3.8 µg of HA with Iscomatrix (ISCOMATRIX, referred to as Iscomatrix herein, is a registered trademark of CSL Limited) adjuvant, were completely protected against death and disease after H5N1 challenge, and the protection lasted at least 15 months. Cross-clade protection was also observed with both vaccines. Significantly, complete protection against death could be achieved with only a single inoculation of H5N1 vaccine containing as little as 15 µg of HA with AlPO4 or 3.8 µg of HA with Iscomatrix adjuvant. Ferrets vaccinated with the single-injection Iscomatrix vaccines showed fewer clinical manifestations of infection than those given AlPO4 vaccines and remained highly active. Our data provide the first indication that in the event of a future influenza pandemic, effective mass vaccination may be achievable with a low-dose "single-shot" vaccine and provide not only increased survival but also significant reduction in disease severity.

Code(s) de classement : 002A05C10; 002A05C07

Descripteur(s) anglais

Descripteur(s) : Avian influenza virus; Influenza A virus; Evaluation; Vaccine; Ferret; Prevention; Immunization; Virology

Desc. génériques : Influenza virus A; Orthomyxoviridae; Virus; Fissipedia; Carnivora; Mammalia; Vertebrata

Descripteur(s) français

Descripteur(s) : Influenza virus aviaire; Virus grippal A; Evaluation; Vaccin; Furet; Prévention; Immunisation; Virologie

Desc. génériques : Influenza virus A; Orthomyxoviridae; Virus; Fissipedia; Carnivora; Mammalia; Vertebrata

Localisation : INIST-13592, 354000172456640410

Origine de la notice : INIST

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Association of Increased Pathogenicity of Asian H5N1 Highly Pathogenic Avian Influenza Viruses in Chickens with Highly Efficient Viral Replication Accompanied by Early Destruction of Innate Immune Responses

Auteur(s) : SUZUKI (Koutaro); OKADA (Hironao); ITOH (Toshihiro); TADA (Tatsuya); MASE (Masaji); NAKAMURA (Kikuyasu); KUBO (Masanori); TSUKAMOTO (Kenji)
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Titre : Association of Increased Pathogenicity of Asian H5N1 Highly Pathogenic Avian Influenza Viruses in Chickens with Highly Efficient Viral Replication Accompanied by Early Destruction of Innate Immune Responses

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Résumé : The Asian H5N1 highly pathogenic avian influenza (HPAI) viruses have been increasing in pathogenicity in diverse avian species since 1996 and are now widespread in Asian, European, and African countries. To better understand the basis of the increased pathogenicity of recent Asian H5N1 HPAI viruses in chickens, we compared the fevers and mean death times (MDTs) of chickens infected with the Asian H5N1 A/chicken/Yamaguchi/7/04 (CkYM7) strain with those infected with the H5N1 Duck/Yokohama/aq10/03 (DkYK10) strain, using a wireless thermosensor. Asian H5N1 CkYM7 caused peracute death in chickens before fever could be induced, whereas DkYK10 virus induced high fevers and had a long MDT. Real-time PCR analyses of cytokine mRNA expressions showed that CkYM7 quickly induced antiviral and proinflammatory cytokine mRNA expressions at 24 h postinfection (hpi) that suddenly decreased at 32 hpi. In contrast, these cytokine mRNA expressions increased at 24 hpi in the DkYK10 group, but decreased from 48 hpi onward to levels similar to those resulting from infection with the low-pathogenicity H5N2 A/chicken/Ibaraki/1/2004 strain. Sequential titrations of viruses in lungs, spleens, and kidneys demonstrated that CkYM7 replicated rapidly and efficiently in infected chickens and that the viral titers were more than twofold higher than those of DkYK10. CkYM7 preferentially and efficiently replicated in macrophages and vascular endothelial cells, while DkYK10 grew moderately in macrophages. These results indicate that the increased pathogenicity in chickens of the recent Asian H5N1 HPAI viruses may be associated with extremely rapid and high replication of the virus in macrophages and vascular endothelial cells, which resulted in disruption of the thermoregulation system and innate immune responses.

Code(s) de classement : 002A05C10; 002A05C04

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Aves; Vertebrata; Veterinary
Enhanced Immunogenicity of Seasonal Influenza Vaccines in Young Children Using MF59 Adjuvant

Titre : Enhanced Immunogenicity of Seasonal Influenza Vaccines in Young Children Using MF59 Adjuvant

Auteur(s) : VESIKARI (Timo); PELLEGRINI (Michele); KARVONEN (Aino); GROTH (Nicola); BORKOWSKI (Astrid); O’HAGAN (Derek T.); PODDA (Audino)

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Source : The Pediatric infectious disease journal; vol. 28; no. 7; pp. 563-571
ISSN : 0891-3668
CODEN : PIDJEV
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 35 ref.

Résumé : Background: Children have high morbidity and hospitalization rates from seasonal influenza. Meta-analyses suggest that conventional inactivated influenza vaccines are of low efficacy in young children, making vaccines that induce greater and broader immune protection in this vulnerable population a medical priority. Adjuvanted influenza vaccines may offer a solution. Subjects and Methods: Unprimed healthy children (6 to <36 months) were enrolled in an observer-blinded study and randomly assigned to receive 2 doses of MF59-adjuvanted vaccine (Sub/MF59, n = 130) or nonadjuvanted split vaccine (split, n = 139); subgroups of these (n = 43 and 46, respectively) received a booster dose 1 year later. Safety and clinical tolerability were assessed after each dose. Hemagglutination inhibition antibody titers were measured against influenza A and B strains included in the formulation of the vaccines and against mismatched strains. Results: Clinical tolerability and safety were generally comparable between vaccine groups, though some transient, mild solicited reactions were more frequent in the Sub/MF59 group. Postvaccination hemagglutination inhibition antibody titers to all 3 vaccine strains were significantly higher with Sub/MF59 than with split vaccine (all comparisons \( P < 0.001 \)) after each of the 3 vaccine doses. In addition, Sub/MF59 induced significantly higher cross-reactivity against A/H3N2 and A/H1N1 mismatched strains. Conclusion: MF59-adjuvanted influenza vaccine was well tolerated in healthy young children after each of 3 doses and induced greater, longer-lasting, and broader immune responses than a nonadjuvanted split vaccine. The enhanced immunogenicity of the adjuvanted vaccine was most evident in very young children and for the B vaccine strain.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais
- Description(s) : Influenza; Immunoprophylaxis; Immunogenicity; Seasonal variation; Prevention; Child; Vaccine; Pediatrics
- Desc. génériques : Viral disease; Infection; Human; Epidemiology

Descripteur(s) français
- Description(s) : Gripppe; Immunophrophylaxie; Immunogénicité; Variation saisonnière; Prévention; Enfant; Vaccin; Pédiatrie
- Desc. génériques : Virose; Infection; Homme; Epidémiologie

Localisation : INIST-20356, 354000187469420010
Origine de la notice : INIST
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Survival of Avian H5N1 Influenza A Viruses in Calliphora nigribarbis (Diptera: Calliphoridae)

**Titre** : Survival of Avian H5N1 Influenza A Viruses in Calliphora nigribarbis (Diptera: Calliphoridae)

**Auteur(s)** : SAWABE (Kyoko); TANABAYASHI (Kiyoshi); HOTTA (Akiyoto); HOSHINO (Keita); ISAWA (Haruhiko); SASAKI (Toshinori); YAMADA (Akio); KURAHASHI (Hiromu); SHUDO (Chieko); KOBAYASHI (Mutsuo)

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**Source** : Journal of medical entomology; vol. 46; no. 4; pp. 852-855

**ISSN** : 0022-2585

**CODEN** : JIMENA6

**Date de publication** : 2009

**Pays de publication** : USA

**Type de document** : P

**Nombre de références** : 1/2 p.

**Résumé** : In a previous study, the highly pathogenic avian influenza (HPAI) H5N1 viruses were isolated from blow flies collected at the Tamba Town of Kyoto prefecture during the outbreak period in March 2004. In this study, we carried out virus exposure experiments to investigate whether the H5N1 virus would survive in a blow fly, Calliphora nigribarbis. The virus exposure experiments showed that the H5N1 influenza virus was isolated from the crop and intestine of C. nigribarbis for at least 24 h, and the viruses remained viable with titers ranging from 0.5 to 4.63 TCID50. This result suggests that C. nigribarbis could possibly transport the H5N1 virus over a distance of 2 km, which is the distance they can migrate within 24 h.

**Code(s) de classement** : 002A37A; 002A15D; 002A12J

**Descripteur(s) anglais**
- **Desc. génériques** : Vertebrata; Calliphoridae; Diptera; Insecta; Arthropoda; Invertebrata

**Descripteur(s) français**
- **Desc. génériques** : Vertebrata; Calliphoridae; Diptera; Insecta; Arthropoda; Invertebrata

**Localisation** : INIST-11536, 354000187469260160

**Origine de la notice** : INIST

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Nouvelle grippe A/H1N1 et antiviraux; New influenza A/H1N1 and antiviral drugs

Titre : Nouvelle grippe A/H1N1 et antiviraux; New influenza A/H1N1 and antiviral drugs

Source : La Revue Prescrire; vol. 29; no. 309
ISSN : 0247-7750
Date de publication : 2009
Pays de publication : FRA
Langue(s) : FRE
Type de document : P
Nombre de références : 7 ref.

Résumé : Début juin 2009, chez les malades ayant une grippe sévère due au nouveau virus A/H1 N1, l’efficacité clinique des antiviraux a été très peu évaluée, et reste incertaine.

Code(s) de classement : 002B02S05; 002B05C02C

Descripteur(s) anglais

- Influenza A; Antiviral; Oseltamivir; Zanamivir; Treatment efficiency; Human; Treatment; Pharmacotherapy; Drug
- Viral disease; Infection; Neuraminidase inhibitor; Enzyme inhibitor; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme

Descripteur(s) français

- Grippe A; Antiviral; Osélamivir; Zanamivir; Efficacité traitement; Homme; Traitement; Pharmacothérapie; Médicament; Influenzavirus A(H1N1)
- Virose; Infection; Inhibiteur neuraminidase; Inhibiteur enzyme; Exo- alpha -sialidase; Glycosidas; Glycosylases; Hydrolases; Enzyme

Localisation : INIST-21322, 354000188332600230
Origine de la notice : INIST
Copyright de notice : © 2009 INIST-CNRS. All rights reserved.
A Novel Small-Molecule Inhibitor of the Avian Influenza H5N1 Virus Determined through Computational Screening against the Neuraminidase

Titre : A Novel Small-Molecule Inhibitor of the Avian Influenza H5N1 Virus Determined through Computational Screening against the Neuraminidase

Auteur(s) : JIANGHONG AN; LEE (Davy C. W.); LAW (Anna H. Y.); YANG (Cindy L. H.); POON (Leo L. M.); LAU (Allan S. Y.); JONES (Steven J. M.)

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Source : Journal of medicinal chemistry : (Print); vol. 52; no. 9; pp. 2667-2672
ISSN : 0022-2623
CODEN : JMCMAR
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 31 ref.

Résumé : Computational molecular docking provides an efficient and innovative approach to examine small molecule and protein interactions. We have utilized this method to identify potential inhibitors of the H5N1 neuraminidase protein. Of the 20 compounds tested, 4-(4-((3-(2-amino-4-hydroxy-6-methyl-5-pyrimidinyl)-propyl)amino)phenyl)-1-chloro-3-buten-2-one (1) (NSC89853) demonstrated the ability to inhibit viral replication at a level comparable to the known neuraminidase inhibitor oseltamivir. Compound 1 demonstrated efficacy across a number of cell-lines assays and in both the H1N1 and H5N1 viruses. The predicted binding of 1 to the known H5N1 neuraminidase structure indicates a binding interface largely nonoverlapping with that of oseltamivir or another neuraminidase inhibitor zanamivir. These results indicate that 1 or similar molecules would remain effective in the presence of virus mutations conferring resistance to either oseltamivir or zanamivir and also vice versa.

Code(s) de classement : 002B02S05

Descripteur(s) anglais

Descripteur(s) : Small molecule; Inhibitor; Avian influenzavirus; Influenza A virus; Screening; Exo- alpha -sialidase; Molecular model; Transmission electron microscopy; Biological activity; In vitro; Cytotoxicity; Replication; Pyrimidine derivatives; Enone; Chlorine Organic compounds; Modeling; Cell line; Kidney; Dog; Morphology; Surface structure

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Glycosidases; Glycosylases; Hydrolases; Enzyme; Fissipedia; Carnivora; Mammalia; Vertebrata; Infection; Viral disease

Descripteur(s) français

Descripteur(s) : Molécule petite; Inhibiteur; Influenzavirus aviaire; Virus grippal A; Criblage; Exo- alpha -sialidase; Modèle moléculaire; Microscopie électronique transmission; Activité biologique; In vitro; Cytotoxicité; Réplication; Dérivé de la pyrimidine; Enone; Chloré Composé organique; Modélisation; Lignée cellulaire; Rein; Chien; Morphologie; Structure; surface; Lignée MDCK; But-3-én-2-one(4-[4-[3-[2-amino-4-hydroxy-6méthylpyrimidin-5-yl]propylamino]phényl]-1-chloro)

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Glycosidases; Glycosylases; Hydrolases; Enzyme; Fissipedia; Carnivora; Mammalia; Vertebrata; Infection; Virose

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Co-circulation of two genetically distinct sub-groups of A/H3N2 influenza strains during the 2006-2007 epidemic season in Corsica Island, France

Titre : Co-circulation of two genetically distinct sub-groups of A/H3N2 influenza strains during the 2006-2007 epidemic season in Corsica Island, France

Auteur(s) : FALCHI (Alessandra); VARESI (Laurent); ARENA (Christophe); LEVEQUE (Nicolas); RENOIS (Fanny); BLANCHON (Thierry); AMOROS (Jean Pierre); ANDREOLETTI (Laurent)

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Source : Journal of clinical virology; vol. 45; no. 3; pp. 265-268
ISSN : 1386-6532
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 27 ref.

Résumé : Background: Influenza virus is one of the major viral respiratory pathogens infecting human beings. Objectives: To determine the influenza A virus variants responsible for the 2006-2007 epidemic season in Corsica Island, France. Study design: Of 134 nasal samples of adult patients tested by culture and RT-PCR assays, 85 influenza A strains were identified; 81 (95%) were sub-typed as A/H3N2 and 4 (5%) were sub-typed as A/H1N1. Results: All of the HA sequences of the A/H3N2 viruses circulating in Corsica Island appeared to be closely related to the A/Wisconsin/67/2005 vaccine strain and segregated into two sub-groups that were genetically distinct from other viruses circulating in other countries during 2006/2007. One of these sub-groups was distinguished by the substitution H156Q whereas the second demonstrated at least one of the 3 other additional mutations (R142G, L157S and K173E) common to the HA1 sequence of A/Nepal/921/2006 reference strain. Among the 14 strains of this second sub-group, 10 viral strains had been isolated from vaccinated adult patients. Conclusion: These findings suggest that a prospective analysis of the HA sequences of influenza isolates may allow an early detection of newly evolved variants with potential epidemiological inference.

Code(s) de classement : 002A05C10; 002B05C02J; 002A05C06

Descriptor(s) anglais

Descriptor(s) : Influenza A virus; Strain; Epidemic; Corsica; Epidemiology; Microbiology; Virology; Influenza A

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; France; Europe; Viral disease; Infection

Descriptor(s) français

Descriptor(s) : Virus grippal A; Souche; Epidémie; Corse; Epidémiologie; Microbiologie; Virologie; Grippe A

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; France; Europe; Virose; Infection

Localisation : INIST-26272, 354000187987370230
Origine de la notice : INIST
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Emergence of a novel swine-origin influenza A virus (S-OIV) H1N1 virus in humans: Novel 2009 influenza AH1N1 (swine variant)

**Titre** : Emergence of a novel swine-origin influenza A virus (S-OIV) H1N1 virus in humans: Novel 2009 influenza AH1N1 (swine variant)

**Auteur(s)** : PEIRIS (J. S. Malik); POON (Leo L. M.); YI GUAN

**Affiliation(s)** : State Key Laboratory for Emerging Infectious Disease & Department of Microbiology, The University of Hong Kong, HKG; HKU-Pasteur Research Centre, HKG

**Source** : Journal of clinical virology; vol. 45; no. 3; pp. 169-173

**ISSN** : 1386-6532

**Date de publication** : 2009

**Pays de publication** : NLD

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 61 ref.

**Résumé** : A recently emerged novel influenza A H1N1 virus continues to spread globally. The virus contains a novel constellation of gene segments, the nearest known precursors being viruses found in swine and it likely arose through reassortment of two or more viruses of swine origin. H1N1, H1N2 and H3N2 subtype swine influenza viruses have occasionally infected humans before but such zoonotic transmission events did not lead to sustained human-to-human transmission in the manner this swine-origin influenza virus (S-OIV) has done. Its transmission among humans appears to be higher than that observed with seasonal influenza. Children and young adults appear to those most affected and also those who appear to maintain transmission. Clinical disease generally appears mild but complications leading to hospitalization can occur, especially in those with underlying lung or cardiac disease, diabetes or those on immunosuppressive therapies. There are concerns that the virus may reassort with existing human influenza virus giving rise to more transmissible or more pathogenic viruses. The virus appears to retain the potential to transmit back to swine and thus continued reassortment with swine viruses is a cause for concern.

**Code(s) de classement** : 002A05C10; 002B05C02J; 002A05C06

**Descripteur(s) anglais**

- Forcine influenzavirus; Influenza A virus; Human; Swine; Origin; Epidemiology; Microbiology; Virology; Influenza
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Veterinary; Viral disease; Infection

**Descripteur(s) français**

- Influenzavirus porcin; Virus grippal A; Homme; Porcin; Origine; Epidémiologie; Microbiologie; Virologie; Grippes
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Vétérinaire; Virose; Infection

**Localisation** : INIST-26272, 354000187987370020

**Origine de la notice** : INIST

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Development of a real-time RT-PCR for the detection of Swine-lineage Influenza A (H1N1) virus infections: Novel 2009 influenza AH1N1 (swine variant)

Titre : Development of a real-time RT-PCR for the detection of Swine-lineage Influenza A (H1N1) virus infections: Novel 2009 influenza AH1N1 (swine variant)

Auteur(s) : CARR (Michael J.); GUNSON (Rory); MACLEAN (Alasdair); COUGHLAN (Suzie); FITZGERALD (Margaret); SCULLY (Mary); O'HERLIHY (Brian); RYAN (John); O'FLANAGAN (Darina); CONNELL (Jeff); CARMAN (William F.); HALLD (William W.)

Affiliation(s) : National Virus Reference Laboratory, University College Dublin, Dublin, IRL; West of Scotland Specialist Virology Centre, Gartnave General Hospital, Glasgow, GBR; Department of public Health, Health Services Executive, Dr. Steeven's Hospital, Dublin, IRL; Emergency Department, St. Vincent's University Hospital, Dublin, IRL; Health Protection Surveillance Centre, 25-27 Middle Gardiner St, Dublin, IRL; Microbiology Department, St. Vincent's University Hospital, Dublin, IRL; Centre for Research in Infectious Diseases, University College Dublin, Dublin, IRL

Source : Journal of clinical virology; vol. 45; no. 3; pp. 196-199

Résumé : Background: A novel influenza A virus, subtype H1N1 of swine-lineage(H1N1 swl) has transmitted rapidly to many regions of the world with evidence of sustained transmission within some countries. Rapid detection and differentiation from seasonal influenza is essential to instigate appropriate patient and public health management and for disease surveillance. Objectives: To develop a rapid and sensitive real-time reverse transcriptase polymerase chain reaction (rtRT-PCR) for confirmation of H1N1 swl. Study design: A one-step rtRT-PCR approach was employed to target the matrix gene of the novel influenza A/H1N1 swl and validated against a panel of seasonal influenza A (H1N1 and H3N2), swine influenza A/H1N1 and avian influenza A/H5N1 viruses. The assay following validation was then used prospectively to detect H1N1 swl positive specimens from the recent outbreaks in the UK and the Republic of Ireland. Results: The one-step H1N1 swl matrix rtRT-PCR successfully detected H1N1 swl clinical specimens and did not cross-react with seasonal influenza A, subtypes H1N1 and H3N2 viruses and swine influenza A (H1N1). The H1N1 swl matrix assay did cross react with H5N1. The H1N1 swl matrix assay was then compared to two other assays using a dilution series and a panel of untyped influenza A positive clinical samples. These experiments found the assay to have a comparable sensitivity to the established universal influenza A rtRT-PCR and was more sensitive than the H1N1 swl specific assay that targeted the H1 region. Conclusions: The results demonstrate that the rtRT-PCR is sensitive and should be used alongside existing universal influenza A assays to rapidly detect the novel H1N1 swl virus.

Code(s) de classement : 002A05C10; 002B05C02J

Descripteur(s) anglais

Porcine influenzavirus; Influenza A virus; Real time; Reverse transcription polymerase chain reaction; Detection; Transcription; Gene; Microbiology; Virology; Influenza A

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Veterinary; Viral disease; Infection

Descripteur(s) français

Influenzavirus porcin; Virus grippal A; Temps réel; Réaction chaîne polymérase RT; Détectio; Transcription; Gène; Microbiologie; Virologie; Grippé A

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Vétérinaire; Virose; Infection
Evaluation of multiple test methods for the detection of the novel 2009 influenza A (H1 N1) during the New York City outbreak: Novel 2009 influenza AH1N1 (swine variant)

Titre : Evaluation of multiple test methods for the detection of the novel 2009 influenza A (H1 N1) during the New York City outbreak: Novel 2009 influenza AH1N1 (swine variant)

Auteur(s) : GINOCCHIO (Christine C.); ZHANG (Frank); MANJI (Ryhana); ARORA (Suman); BORNFREUND (Mark); FALK (Leon); LOTLIKAR (Madhavi); KOWERSKA (Margaret); BECKER (George); KOROLOGOS (Diamanto); DE GERONIMO (Marcella); CRAWFORD (James M.)

Affiliation(s) : Department of Pathology and Laboratory Medicine, North Shore-Long Island Jewish Health System, Lake Success, NY 11042, USA; Krasnoff Quality Management Institute, North Shore-Long Island Jewish Health System, Lake Success, NY 11042, USA

Source : Journal of clinical virology; vol. 45; no. 3; pp. 191-195

Résumé : Background: In response to the novel influenza A H1N1 outbreak in the NY City area, 6090 patient samples were submitted over a 5-week period for a total of 14,114 viral diagnostic tests, including rapid antigen, direct immunofluorescence (DFA), viral culture and PCR. Little was known about the performance of the assays for the detection of novel H1N1 in the background of seasonal H1N1, H3N2 and other circulating respiratory viruses. In addition, subtyping influenza A became critical for the identification of high risk and/or hospitalized patients with novel H1N1 infection and for monitoring the spread of the outbreak. Study design: This study analyzed the performances of the BinaxNOW Influenza A&B test (BinaxNOW), the 3M Rapid Detection Flu A+B test (3MA+B), direct immunofluorescence, R-Mix culture and the Luminex xTAG Respiratory Virus Panel (RVP) for the detection of seasonal influenza, novel H1N1 and other respiratory viruses. RVP was also evaluated for its ability to differentiate seasonal H1N1, H3N2 and novel H1N1. Results: The sensitivities, specificities, PPVs and NPVs for the detection of novel H1N1, determined by comparing all four-test methods, were: rapid antigen: 17.8%, 93.6%, 77.4%, 47.9%; DFA: 46.7%, 94.5%, 91.3%, 58.9%; R-Mix culture: 88.9%,100%,100%,87.9%; RVP: 97.8%,100%,100%, 97.3%. The individual sensitivities of BinaxNOW and 3MA + B as compared to R-Mix culture for the detection of novel H1N1 were 9.6% and 40%, respectively. All unsubtypeable influenza A specimens identified by RVP and tested with the CDC novel H1N1 specific RT-PCR assay were confirmed to be novel H1N1. Conclusions: Rapid antigen tests, DFA, R-Mix culture and the xTAG RVP test all detected the novel H1N1 strain, but with highly varied sensitivity. The RVP test provided the best diagnostic option as RVP demonstrated superior sensitivity for the detection of all influenza strains, including the novel H1N1, provided accurate influenza A subtyping and identified a significant number of additional respiratory pathogens.

Code(s) de classement : 002A05C10; 002B05C02J; 002A05C08

Descripteur(s) anglais

Descriptor(s) méthode : Influenza A virus; Method; Detection; New York; Microbiology; Virology; Influenza A

Descriptor(s) générique : Influenzavirus A; Orthomyxoviridae; Virus; United States; North America; America; Viral disease; Infection

Descripteur(s) français

Descriptor(s) technique : Virus grippal A; Méthode; Détection; New York; Microbiologie; Virologie; Grippe A

Descriptor(s) générique : Influenzavirus A; Orthomyxoviridae; Virus; Etats-Unis; Amérique du Nord; Amérique; Virose; Infection
Analytical sensitivity of rapid influenza antigen detection tests for swine-origin influenza virus (H1N1) : Novel 2009 influenza AH1N1 (swine variant)

Titre : Analytical sensitivity of rapid influenza antigen detection tests for swine-origin influenza virus (H1N1) : Novel 2009 influenza AH1N1 (swine variant)

Auteur(s) : CHAN (K. H.); LAI (S. T.); POON (L. L. M.); GUAN (Y.); YUEN (K. Y); PEIRIS (J. S. M.)

Affiliation(s) : Department of Microbiology, The University of Hong Kong, Hong Kong Special Administrative Region, CHN; Department of Medicine, Princess Margaret Hospital, Hong Kong Special Administrative Region, CHN; HKU-Pasteur Research Centre, Hong Kong Special Administrative Region, CHN

Source : Journal of clinical virology; vol. 45; no. 3; pp. 205-207

ISSN : 1386-6532

Date de publication : 2009

Pays de publication : NLD

Langue(s) : ENG

Type de document : P

Nombre de références : 10 ref.

Résumé : Background: A novel swine origin influenza virus (S-OIV) (H1N1) is spreading worldwide and threatens to become pandemic. Objectives: Determine analytical sensitivity of selected commercially available rapid influenza antigen detection tests in detecting S-OIV H1N1. Study design: Serial dilutions of two S-OIV isolates, one seasonal influenza A (H1N1) isolate and a nasopharyngeal aspirate from a patient with S-OIV disease were tested in five commercially available influenza antigen detection tests and by virus isolation in cell culture. Viral M gene copy number was determined by quantitative PCR methods. Results: The analytical sensitivity of the five influenza antigen detection tests for S-OIV (tissue culture infectious dose 50 (TCID50) log10 3.3-4.7 was comparable with that of seasonal influenza (TCID50 log10 4.0-4.5). Conclusion: The analytical sensitivity of the selected influenza A antigen detection tests for detection of S-IOV was comparable with that of seasonal influenza H1N1.

Code(s) de classement : 002A05C10; 002B05C02J

Descripteur(s) anglais
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Veterinary; Viral disease; Infection

Descripteur(s) français
Desc. génériques : Influenzavirus porcin; Sensibilité; Antigène; Détection; Origine; Microbiologie; Virologie; Grippe

Localisation : INIST-26272, 354000187987370100

Origine de la notice : INIST

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Preparing the outbreak assistance laboratory network in the Netherlands for the detection of the influenza virus A(H1N1) variant: Novel 2009 influenza AH1N1 (swine variant)

Titre : Preparing the outbreak assistance laboratory network in the Netherlands for the detection of the influenza virus A(H1N1) variant: Novel 2009 influenza AH1N1 (swine variant)

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Source : Journal of clinical virology; vol. 45; no. 3; pp. 179-184
ISSN : 1386-6532
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 15 ref.

Résumé : Background: Late April 2009, human infection with variant influenza virus A(H1N1)v emerged in the Northern Americas posing a threat that this virus may become the next pandemic influenza virus. Objectives: To prepare laboratories for surge capacity for molecular diagnosis of patients suspected for A(H1N1)v infection in the Netherlands. Study design: A panel of 10 blinded specimens containing seasonal A(H1N1) or A(H3N2), or A/Netherlands/602/2009(H1N1)v influenza virus, or negative control was distributed to the outbreak assistance laboratories (OAL) together with influenza virus A (M-gene), swine influenza virus A (NP-gene) and influenza virus A(H1N1)v (H1v-gene) specific primers and probes and protocol (CDC Atlanta, USA). Laboratories were asked to implement and test this protocol. Results: All OAL were able to detect A(H1N1)v using the CDC M-gene reagents, the majority with similar sensitivity as the in-house M-gene based assays. RT-PCRs used in routine diagnostic setting in the OAL specifically designed to detect H1, H3, or NS1 from seasonal influenza A viruses, did not or at very low level cross-react with A(H1N1)v. The CDC swine NP-gene and H1v-gene RT-PCRs showed somewhat reduced sensitivity compared to the CDC and in-house M-gene RT-PCRs. In contrast, in-house developed A(H1N1)v specific H1v-gene and N1v-gene RT-PCRs showed equal sensitivity to CDC and in-house M-gene RT-PCRs. Conclusions: The Dutch OAL are prepared for detection and specific identification of A(H1N1)v, although some level of cross-reactivity was observed with seasonal influenza viruses. Additionally, M-gene based generic influenza A virus detection is recommended to be able to detect emerging influenza A viruses in routine settings.

Code(s) de classement : 002A05C10; 002B05C02J

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Europe; Virose; Infection

Localisation : INIST-26272, 354000187987370040

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Detection of novel influenza A(H1N1) virus by real-time RT-PCR: Novel 2009 influenza A(H1N1) (swine variant)

**Titre**: Detection of novel influenza A(H1N1) virus by real-time RT-PCR: Novel 2009 influenza A(H1N1) (swine variant)

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**Source**: Journal of clinical virology; vol. 45; no. 3; pp. 203-204

**ISSN**: 1386-6532

**Date de publication**: 2009

**Pays de publication**: NLD

**Langue(s)**: ENG

**Type de document**: P

**Nombre de références**: 3 ref.

**Résumé**: Accurate and rapid diagnosis of novel influenza A(H1N1) infection is critical for minimising further spread through timely implementation of antiviral treatment and other public health based measures. In this study we developed two TaqMan-based reverse transcription PCR (RT-PCR) methods for the detection of novel influenza A(H1N1) virus targeting the haemagglutinin and neuraminidase genes. The assays were validated using 152 clinical respiratory samples, including 61 Influenza A positive samples, collected in Queensland, Australia during the years 2008 to 2009 and a further 12 seasonal H1N1 and H3N2 influenza A isolates collected from years 2000 to 2002. A wildtype swine H1N1 isolate was also tested. RNA from an influenza A (H1N1) virus isolate (Auckland, 2009) was used as a positive control. Overall, the results showed that the RT-PCR methods were suitable for sensitive and specific detection of novel influenza A(H1N1) RNA in human samples.

**Code(s) de classement**: 002A05C10; 002B05C02J

**Describeur(s) anglais**
- **Descripoteur(s)**: Influenza A virus; Detection; Real time; Reverse transcription polymerase chain reaction; Polymerase chain reaction; Microbiology; Virology; Influenza
- **Desc. génériques**: Influenzavirus A; Orthomyxoviridae; Virus; Viral disease; Infection

**Describeur(s) français**
- **Descripoteur(s)**: Virus grippal A; Détectio; Temps réel; Réaction chaîne polymérase RT; Réaction chaîne polymérase; Microbiologie; Virologie; Grippe
- **Desc. génériques**: Influenzavirus A; Orthomyxoviridae; Virus; Virose; Infection

**Localisation**: INIST-26272, 354000187987370090

**Origine de la notice**: INIST

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Multiplex PCR tests sentinel the appearance of pandemic influenza viruses including H1N1 swine influenza: Novel 2009 influenza AH1N1 (swine variant)

Titre: Multiplex PCR tests sentinel the appearance of pandemic influenza viruses including H1N1 swine influenza: Novel 2009 influenza AH1N1 (swine variant)

Auteur(s): MAHONY (James B.); HATCHETTE (Todd); OJKIC (Davor); DREWS (Steven J.); GUBBAY (Jonathan); LOW (Donald E.); PETRIC (Martin); TANG (Patrick); CHONG (Sylvia); LUINSTRA (Kathy); PETRICH (Astrid); SMIEJA (Marek)

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Source: Journal of clinical virology; vol. 45; no. 3; pp. 200-202

Résumé: Background: Since the turn of the century seven new respiratory viruses have infected man and two of these have resulted in worldwide epidemics. Both SARS Coronavirus which quickly spread to 29 countries in February 2003 and H1N1 swine influenza that recently spread from Mexico to 30 countries in three weeks represent major pandemic threats for mankind. Diagnostic assays are required to detect novel influenza strains with pandemic potential. Objective: In this report we evaluate the ability of a multiplex PCR test (xTAG<sup>TM</sup> RVP) to detect new, "non-seasonal" influenza viruses including the H1N1 swine influenza A/swine/California/04/2009. Study design: Laboratory based study using retrospective and prospective specimens. Results: This multiplex PCR test detected the present of non-seasonal (non-H1, non-H3) influenza in 20 of 20 patients infected with H1N1 swine flu virus. In addition to detecting the current swine flu the xTAG<sup>TM</sup> RVP test detected the H5N1 A/Vietnam/1203/2004 high pathogenicity avian influenza virus that circulated in South East Asia in 2003 as well as 17 out of 17 influenza A viruses representing 11 HA subtypes isolated from birds, swine and horses not yet seen in the human population. Conclusion: Based on these results we believe that this molecular test can perform an important role as a sentinel test to detect novel non-seasonal influenza A viruses in patients presenting with influenza-like illness (ILI) and therefore act as an early warning system for the detection of future pandemic influenza threats.

Code(s) de classement: 002A05C10; 002B05C02J

Desc. génériques: Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Veterinary; Viral disease; Infection

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The 2009 H1N1 influenza outbreak in its historical context: Novel 2009 influenza AH1N1 (swine variant)

Titre: The 2009 H1N1 influenza outbreak in its historical context: Novel 2009 influenza AH1N1 (swine variant)

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Source: Journal of clinical virology; vol. 45; no. 3; pp. 174-178
ISSN: 1386-6532
Date de publication: 2009
Pays de publication: NLD
Langue(s): ENG
Type de document: P
Nombre de références: 9 ref.

Résumé: Of the 16 known serotypes of influenza A haemagglutinin, 6 have been isolated from humans at the molecular level (H1, H2, H3, H5, H7, H9). 3 of these have been involved in past pandemics (H1, H2, H3). Traditional pandemic surveillance has focussed on monitoring antigenic shift, meaning the re-assortment of novel haemagglutinins into seasonal human influenza A viruses during rare events of double infection with seasonal and zoonotic strains. H5, from avian H5N1 influenza, has been the major cause for concern in recent years. However, the 2009 H1N1 zoonotic event demonstrates that even serotypes already encountered in past human pandemics may constitute new pandemic threats. The protein sequence divergence of the 2009 zoonotic H1 from human seasonal influenza H1 is around 20–24%. A similar level of divergence is found between the 2009 H1 and European swine flu. By contrast, its divergence from North American swine flu strains is around 1–9%. Given that the divergence between H1 and its nearest serotype neighbour H2 is around 40–46%, the 2009 H1 may be broadly considered as halfway towards a new serotype. The current situation is one of antigenic pseudo-shift.

Code(s) de classement: 002A05C10; 002B05C02J

Descripteur(s) anglais

- Descripteur(s) : Influenza A virus; Swine; Microbiology; Virology; Influenza A; Porcine influenza
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Veterinary; Viral disease; Infection

Descripteur(s) français

- Descripteur(s) : Virus grippal A; Porcin; Microbiologie; Virologie; Grippe A; Grippe porcine
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Vétérinaire; Virose; Infection

Localisation: INIST-26272, 354000187987370030
Origine de la notice: INIST
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Amplification of four genes of influenza A viruses using a degenerate primer set in a one step RT-PCR method

Title: Amplification of four genes of influenza A viruses using a degenerate primer set in a one step RT-PCR method

Authors: JINDAL (Naresh); CHANDER (Yogesh); DE ABIN (Martha); SREEVATSAN (Srinand); STALLKNECHT (David); HALVORSON (David A.); GOYAL (Sagar M.)

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Source: Journal of virological methods; vol. 160; no. 1-2; pp. 163-166

ISSN: 0166-0934
CODEN: JVMEDH
Date of publication: 2009
Pays de publication: NLD
Langue(s): ENG
Type de document: P
Nombre de références: 3/4 p.

Résumé: We designed a degenerate primer set that yielded full-length amplification of hemagglutinin (HA), neuraminidase (NA), matrix (M), and non-structural protein (NSP) genes of influenza A viruses in a single reaction mixture. These four genes were amplified from 15 HA (1-15) and 9 NA (1-9) subtypes of influenza A viruses of avian (n = 16) origin. In addition, 272 field isolates of avian origin were tested by this method. Full-length amplification of HA, NA, M, and NSP genes was obtained in 242 (88.9%), 254 (93.4%), 268 (98.5%), and 268 (98.5%) isolates, respectively. No gene was amplified in four isolates. Of these four isolates, two were subtyped as H4N6, one as H7N7, and one as H10N7. Amplification was successful for all 4 genes of H1N1, H2N3, and H3N2 isolates of swine influenza. Also, all four genes were amplified in one equine influenza (H3N8) isolate and seven isolates of human origin (H1N1 and H3N2). This appears to be the first study using degenerate primer set for full-length amplification of four genes of influenza A viruses in a single reaction. Further studies are needed to determine if this primer set can be used for subtyping of influenza virus isolates.

Code(s) de classement: 002A05C09

Descripteur(s) anglais
- Description(s): Influenza A virus; Gene amplification; Reverse transcription polymerase chain reaction; Method; Transcription; Microbiology; Virology
  - Description générales: Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) français
- Description(s): Virus grippe A; Amplification générique; Réaction chaîne polymérase RT; Méthode; Transcription; Microbiologie; Virologie
  - Description générales: Influenzavirus A; Orthomyxoviridae; Virus

Localisation: INIST-18295, 354000187985960230
Origine de la notice: INIST
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Rapid haemagglutinin subtyping and pathotyping of avian influenza viruses by a DNA microarray

Titre : Rapid haemagglutinin subtyping and pathotyping of avian influenza viruses by a DNA microarray

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Source : Journal of virological methods; vol. 160; no. 1-2; pp. 200-205
ISSN : 0166-0934
CODEN : JVMEDH
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 3/4 p.

Résumé : Rapid and reliable methods are fundamental for the comprehensive characterization of emerging and evolving avian influenza viruses. Although microarrays provide new possibilities with their parallel approach, their use in diagnostic laboratories is still limited due to economical and practical factors. An easy-to-use, low-cost microarray-based assay for haemagglutinin subtyping and pathotyping of avian influenza viruses and specific detection of highly pathogenic H5N1/Asia clade 2.2 is described as a novel diagnostic tool. The ArrayTube<TM> platform is user-friendly, inexpensive and allows processing of many samples. The sensitivity of the assay developed was comparable to real-time RT-PCR, and the simultaneous detection of different subtypes was possible. Validation with 90 influenza A virus isolates representing all 16 haemagglutinin subtypes and 44 field samples (cloacal swabs from wild and domestic birds) demonstrated the feasibility of the system for sensitive and specific characterization of AIV. Facilitating haemagglutinin subtyping and pathotyping for the majority of influenza A-positive cloacal swabs within 24 h, the new assay enables detailed AIV diagnosis even in less well-equipped laboratories.

Code(s) de classement : 002A05C09

Descripteur(s) anglais
- Description(s) : Avian influenza virus; Influenza A virus; Hemagglutinin; DNA chip; Subtype; Pathotype; Cleavage site; Microbiology; Method; Virology
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) français
- Description(s) : Influenzavirus aviaire; Virus grippe A; Hémagglutinine; Puce à DNA; Soustype; Pathotype; Site clivage; Microbiologie; Méthode; Virologie
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST-18295, 354000187985960310
Origine de la notice : INIST
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Single- and multiple-clade influenza A H5N1 vaccines induce cross protection in ferrets

Titre : Single- and multiple-clade influenza A H5N1 vaccines induce cross protection in ferrets

Auteur(s) : FORREST (Heather L.); KHALENKOV (Alexey M.); GOVORKOVA (Elena A.); KIM (Jeong-Ki); DEL GIUDICE (Giuseppe); WEBSTER (Robert G.)

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Source : Vaccine; vol. 27; no. 31; pp. 4187-4195
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 39 ref.

Résumé : The rapid evolution, genetic diversity, broad host range, and increasing human infection with avian influenza A (H5N1) viruses highlight the need for an efficacious cross-clade vaccine. Using the ferret model, we compared induction of cross-reactive immunity and protective efficacy of three single-clade H5N1 vaccines and a novel multiple-clade H5N1 vaccine, with and without MF59 adjuvant. Reverse genetics (rg) was used to generate vaccine viruses containing the hemagglutinin (HA) and neuraminidase genes of wild-type H5N1 viruses. Ferrets received two doses of inactivated whole-virus vaccine separated by 3 weeks. Single-clade vaccines (7.5 μg HA per dose) included rg-A/Vietnam/1203/04 (clade 1), rg-A/Hong Kong/213/03 (clade 1), and rg-A/Japanese White Eye/Hong Kong/1038/06 (clade 2.3). The multiple-clade vaccine contained 3.75 μg HA per dose of each single-clade vaccine and of rg-A/Whooper Swan/Mongolia/244/05 (clade 2.2). Two doses of vaccine were required to substantially increase anti-HA and virus neutralizing antibody titers to H5N1 viruses. MF59 adjuvant enhanced induction of clade-specific and cross-clade serum antibody responses, reduced frequency of infection (as determined by upper respiratory tract virus shedding and seroconversion data), and eliminated disease signs. The rg-A/Hong Kong/213/03 vaccine induced the highest antibody titers to homologous and heterologous H5N1 viruses, while rg-A/Japanese White Eye/Hong Kong/1038/06 vaccine induced the lowest. The multiple-clade vaccine was broadly immunogenic against clade 1 and 2 viruses. The rg-A/Vietnam/1203/04 vaccine (the currently stockpiled H5N1 vaccine) most effectively reduced upper respiratory tract virus shedding after challenge with clade 1 and 2 viruses. Importantly, all vaccines protected against lethal challenge with A/Vietnam/1203/04 virus and provided cross-clade protection.

Code(s) de classement : 002A05F04; 002A05C10

Descriptor(s) anglais

Desc. génériques : Influenza A virus; Vaccine; Cross protection; Immunological adjuvant; Influenza A

Descriptor(s) français

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Viral disease; Infection

Localisation : INIST-20289, 354000172430160130
Origine de la notice : INIST
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Cross-reactive antibodies in middle-aged and elderly volunteers after MF59-adjuvanted subunit trivalent influenza vaccine against B viruses of the B/Victoria or B/Yamagata lineages

**Titre** : Cross-reactive antibodies in middle-aged and elderly volunteers after MF59-adjuvanted subunit trivalent influenza vaccine against B viruses of the B/Victoria or B/Yamagata lineages

Auteur(s) : CAMILLONI (B.); NERI (M.); LEPRI (E.); IORIO (A. M.)

Affiliation(s) : Department of Medical and Surgical Specialties and Public Health, University of Perugia, Via del Giochetto, 06126 Perugia, ITA

Source : Vaccine; vol. 27; no. 31; pp. 4099-4103

ISSN : 0264-410X

CODEN : VACCDE

Date de publication : 2009

Pays de publication : GBR

Langue(s) : ENG

Type de document : P

Nombre de références : 22 ref.

**Résumé** : This study evaluated whether MF59-adjuvanted subunit trivalent influenza vaccine for the 2003/04 winter season (A/Moscow/10/99, H3N2; A/New Caledonia/20/99, H1N1; B/Hong Kong/330/01) would confer protection against mismatched and frequently co-circulating variants of influenza B/Victoria- and B/Yamagata-like virus strains. Haemagglutination inhibiting (HI) antibodies were measured in middle-aged and elderly volunteers against the homologous B/Victoria-like vaccine strain (B/Hong Kong/330/01) and against mismatched B/Victoria-like (B/Malaysia/2506/04) and B/Yamagata-like (B/Singapore/379/99 and B/Shanghai/361/02) strains. Immunization induced significant increases in the amounts of HI antibodies against all influenza B strains under investigation. However, the responses against the heterologous B/Shanghai/361/02 virus did not reach the desirable values of seroprotection. An age-dependent decline of the responses was found for B/Victoria-like antigens, but not for B/Yamagata-like strains. Although further studies are needed, our data support the recommendation of including influenza B viruses of the B/Victoria and B/Yamagata lineages in the future influenza vaccine preparations.

**Code(s) de classement** : 002A05F04

**Descriputeur(s) anglais**

_Antibody; Elderly; Immunological adjuvant; Subunit; Vaccine; Victoria; Immunogenicity; Influenza B_

_Desc. génériques : Human; Australia; Oceania; Viral disease; Infection_

**Descriputeur(s) français**

_Anticorps; Personne âgée; Adjuvant immunologique; Sousunité; Vaccin; Victoria; Immunogénicité; Grippe B_

_Desc. génériques : Homme; Australie; Océanie; Virose; Infection_

**Localisation** : INIST-20289, 354000172430160020

**Origine de la notice** : INIST

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Sialivac: An intranasal homologous inactivated split virus vaccine containing bacterial sialidase for the control of avian influenza in poultry

Titre : Sialivac: An intranasal homologous inactivated split virus vaccine containing bacterial sialidase for the control of avian influenza in poultry

Auteur(s) : WORRALL (E. E.); SUDARISMAN; PRIADI (A.)
Affiliation(s) : TyMawr, Trefilan, Lampeter, Ceredigion SA48 8RD, GBR; Local Disease Control Center (LDCC) Bogor, (2005-2007), IDN; Animal Health Services Unit, PT Peternakan Ayam Manggis, IDN

Source : Vaccine; vol. 27; no. 31; pp. 4161-4168
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 26 ref.

Résumé : A simple, effective inactivated avian flu vaccine composed of three homologous highly pathogenic (HP) H5N1 strains combined with Clostridium perfringens type A 107 sialidase/neuraminidase and chitosan as a trans epithelial carrier adjuvant applied intranasally to poultry is described. Poultry were vaccinated with an inactivated, solvent split, chitosan adjuvanted intranasal (IN) vaccine with and without C. perfringens sialidase and the resulting serum IgG antibody measured by haemagglutination inhibition (HI) and mucosal IgA by ELISA. The clinical effectiveness was demonstrated by disease intervention field trials, where the ability of an intranasal vaccine containing three homologous inactivated solvent split HP H5N1 strains, C. perfringens sialidase and chitosan was successful in controlling the disease in intensively reared commercial chickens. Evidence is presented by demonstrating effective intervention with IN vaccine during outbreaks in poultry previously vaccinated with commercial heterologous H5N2 intramuscular (IM) vaccine and reassorted H5N1 Re-1 vaccine which had failed to protect intensively reared birds. Intervention with the IN vaccine in such flocks completely halted the infection within 2-5 days. Survivors ceased to excrete live virus. Stimulation of the common mucosal immune system (CMIS) and the early production of secretory IgA and subsequently humoral IgG demonstrated by laboratory controlled experiments and field studies revealed the ability of intranasally vaccinated birds to resist lethal virus challenge. A strategy of mucosal immunisation is recommended to reduce the incidence of disease in intensively reared poultry and thus minimise the generation and transfer of mutated highly pathogenic subtypes to humans and other animals.

Code(s) de classement : 002A05F04; 002A05B15; 002A05C10

Description(s) anglais

- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Glycosidases; Glycosylases; Hydrolases; Enzyme; Infection; Viral disease; Farming animal; Veterinary; Polymer; Zoopathogen

Description(s) français

- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Glycosidases; Glycosylases; Hydrolases; Enzyme; Infection; Viral disease; Farming animal; Veterinary; Polymer; Zoopathogen

Localisation : INIST-20289, 354000172430160100
Origine de la notice : INIST

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Glycan analysis in cell culture-based influenza vaccine production: Influence of host cell line and virus strain on the glycosylation pattern of viral hemagglutinin

Titre : Glycan analysis in cell culture-based influenza vaccine production: Influence of host cell line and virus strain on the glycosylation pattern of viral hemagglutinin

Auteur(s) : SCHWARZER (Jana); RAPP (Erdmann); HENNIG (René); GENZEL (Yvonne); JORDAN (Ingo); SANDIG (Volker); REICHL (Udo)

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Source : Vaccine; vol. 27; no. 32; pp. 4325-4336
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 65 ref.

Résumé : Mammalian cell culture processes are commonly used for production of recombinant glycoproteins, antibodies and viral vaccines. Since several years there is an increasing interest in cell culture-based influenza vaccine production to overcome limitations of egg-based production systems, to improve vaccine supply and to increase flexibility in vaccine manufacturing. With the switch of the production system several key questions concerning the possible impact of host cell lines on antigen quality, passage-dependent selection of certain viral phenotypes or changes in hemagglutinin (HA) conformation have to be addressed to guarantee safety and efficiency of vaccines. In contrast to the production of recombinant glycoproteins, comparatively little is known regarding glycosylation of HA, derived from mammalian cell cultures. Within this study, a capillary DNA-sequencer (based on CGE-LIF technology), was utilized for N-glycan analysis of three different influenza virus strains, which were replicated in six different cell lines. Detailed results concerning the influence of the host cell line on complexity and composition of the HA N-glycosylation pattern, are presented. Strong host cell but also virus type and subtype dependence of HA N-glycosylation was found. Clear differences were already observed, by N-glycan fingerprint comparison. Further structural investigations of the N-glycan pools revealed that host cell dependence of HA N-glycosylation was mainly related to minor variations of the (monomeric) constitution of single N-glycans. To some extent, shifts in the N-glycan pool composition regarding the proportion of different N-glycan types were observed. In contrast to this, a principal switch of the N-glycan type attached to HA was observed when comparing different virus types (A and B) and subtypes (H1N1 and H3N2).

Code(s) de classement : 002A05F04; 002A05C10

Descriptor(s) anglais
Desc. génériques : Orthomyxoviridae; Virus; Viral disease; Infection

Descriptor(s) français
Desc. génériques : Orthomyxoviridae; Virus; Virose; Infection

Localisation : INIST-20289, 354000172425620130
Origine de la notice : INIST
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As the English government launches a dedicated telephone service and website that will prescribe antivirals to take the pressure off GPs, Adrian O'Dowd reports on the latest information on swine flu.
Assessing the severity of the novel influenza A/H1N1 pandemic

**Titre** : Assessing the severity of the novel influenza A/H1N1 pandemic

**Auteur(s)** : GARSKE (Tini); LEGRAND (Judith); DONNELLY (Christl A.); WARD (Helen); CAUCHEMEZ (Simon); FRASER (Christophe); FERGUSON (Neil M.); GHANI (Azra C.)

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**Source** : BMJ. British medical journal : (International ed.); vol. 339; no. 7714; pp. 220-224

**ISSN** : 0959-8146

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 26 ref.

**Résumé** : A major concern about the emergence of the novel strain of influenza A/H1N1 is the severity of illness it causes. Tini Garske and colleagues propose methods to obtain accurate estimates of the case fatality ratio as the pandemic unfolds.

**Code(s) de classement** : 002B01; 002B05C02C

**Descriptor(s) anglais**
- **Descriptor(s)** : Evaluation; Influenza A; Medicine
- **Desc. génériques** : Viral disease; Infection

**Descriptor(s) français**
- **Descriptor(s)** : Évaluation; Grippe A; Médecine; Grippe pandémique
- **Desc. génériques** : Virose; Infection

**Localisation** : INIST-5002A, 354000187480130200

**Origine de la notice** : INIST

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Triple-Reassortant Swine Influenza A (H1) in Humans in the United States, 2005-2009

**Titre** : Triple-Reassortant Swine Influenza A (H1) in Humans in the United States, 2005-2009

**Auteur(s) :** SHINDE (Vivek); BRIDGES (Carolyn B.); UYEKI (Timothy M.); BO SHU; BALISH (Amanda); XIYAN XU; LINDSTROM (Stephen); GUBAREVA (Larisa V.); DEYDE (Varough); GARTEN (Rebecca J.); HARRIS (Meghan); GERBER (Susan); VAGASKY (Susan); SMITH (Forrest); PASCOE (Neal); MARTIN (Karen); DUFFICY (Deborah); RITGER (Kathy); CONOVER (Craig); QUINLISK (Patricia); KLIMOV (Alexander); BRESEE (Joseph S.); FINELLI (Lyn)

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**Source :** The New England journal of medicine; vol. 360; no. 25; pp. 2616-2625

**ISSN :** 0028-4793

**CODEN :** NEJMAG

**Date de publication :** 2009

**Pays de publication :** USA

**Langue(s) :** ENG

**Type de document :** P

**Nombre de références :** 43 ref.

**Résumé :** BACKGROUND Triple-reassortant swine influenza A (H1) viruses - containing genes from avian, human, and swine influenza viruses - emerged and became enzootic among pig herds in North America during the late 1990s. METHODS We report the clinical features of the first 11 sporadic cases of infection of humans with triple-reassortant swine influenza A (H1) viruses reported to the Centers for Disease Control and Prevention, occurring from December 2005 through February 2009, until just before the current epidemic of swine-origin influenza A (H1N1) among humans. These data were obtained from routine national influenza surveillance reports and from joint case investigations by public and animal health agencies. RESULTS The median age of the 11 patients was 10 years (range, 16 months to 48 years), and 4 had underlying health conditions. Nine of the patients had had exposure to pigs, five through direct contact and four through visits to a location where pigs were present but without contact. In another patient, human-to-human transmission was suspected. The range of the incubation period, from the last known exposure to the onset of symptoms, was 3 to 9 days. Among the 10 patients with known clinical symptoms, symptoms included fever (in 90%), cough (in 100%), headache (in 60%), and diarrhea (in 30%). Complete blood counts were available for four patients, revealing leukopenia in two, lymphopenia in one, and thrombocytopenia in another. Four patients were hospitalized, two of whom underwent invasive mechanical ventilation. Four patients received oseltamivir, and all 11 recovered from their illness. CONCLUSIONS From December 2005 until just before the current human epidemic of swine-origin influenza viruses, there was sporadic infection with triple-reassortant swine influenza A (H1) viruses in persons with exposure to pigs in the United States. Although all the patients recovered, severe illness of the lower respiratory tract and unusual influenza signs such as diarrhea were observed in some patients, including those who had been previously healthy.

**Code(s) de classement :** 002B01; 002B05C02C

**Descriptor(s) anglais**

- Description(s) : Swine; Influenza A; Human; United States; 2005; Public health; 2009; Medicine
- Description génériques : Artiodactyla; Ungulata; Mammalia; Vertebrata; Viral disease; Infection; North America; America

**Descriptor(s) français**

- Description(s) : Porcin; Grippe A; Homme; Etats-Unis; 2005; Santé publique; 2009; Médecine
- Description génériques : Artiodactyla; Ungulata; Mammalia; Vertebrata; Virose; Infection; Amérique du Nord; Amérique
Emergence of a Novel Swine-Origin Influenza A (H1N1) Virus in Humans

**Titre** : Emergence of a Novel Swine-Origin Influenza A (H1N1) Virus in Humans

**Collectivité(s) auteur** : Novel Swine-Origin Influenza A (H1N1) Virus Investigation Team, USA

**Source** : The New England journal of medicine; vol. 360; no. 25; pp. 2605-2615

**ISSN** : 0028-4793

**CODEN** : NEJMAG

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 23 ref.

**Résumé** : BACKGROUND On April 15 and April 17, 2009, novel swine-origin influenza A (H1N1) virus (S-OIV) was identified in specimens obtained from two epidemiologically unlinked patients in the United States. The same strain of the virus was identified in Mexico, Canada, and elsewhere. We describe 642 confirmed cases of human S-OIV infection identified from the rapidly evolving U.S. outbreak. METHODS Enhanced surveillance was implemented in the United States for human infection with influenza A viruses that could not be subtyped. Specimens were sent to the Centers for Disease Control and Prevention for real-time reverse-transcriptase-polymerase-chain-reaction confirmatory testing for S-OIV. RESULTS From April 15 through May 5, a total of 642 confirmed cases of S-OIV infection were identified in 41 states. The ages of patients ranged from 3 months to 81 years; 60% of patients were 18 years of age or younger. Of patients with available data, 18% had recently traveled to Mexico, and 16% were identified from school outbreaks of S-OIV infection. The most common presenting symptoms were fever (94% of patients), cough (92%), and sore throat (66%); 25% of patients had diarrhea, and 25% had vomiting. Of the 399 patients for whom hospitalization status was known, 36 (9%) required hospitalization. Of 22 hospitalized patients with available data, 12 had characteristics that conferred an increased risk of severe seasonal influenza, 11 had pneumonia, 8 required admission to an intensive care unit, 4 had respiratory failure, and 2 died. The S-OIV was determined to have a unique genome composition that had not been identified previously. CONCLUSIONS A novel swine-origin influenza A virus was identified as the cause of outbreaks of febrile respiratory infection ranging from self-limited to severe illness. It is likely that the number of confirmed cases underestimates the number of cases that have occurred.

**Code(s) de classement** : 002B01; 002B30A01A

**Desc. génériques** : Artiodactyla; Ungulata; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus

**Desc. génériques** : Artiodactyla; Ungulata; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus

**Localisation** : INIST-6013, 354000187470800050

**Origine de la notice** : INIST

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Satellite-marked waterfowl reveal migratory connection between H5N1 outbreak areas in China and Mongolia

Titre : Satellite-marked waterfowl reveal migratory connection between H5N1 outbreak areas in China and Mongolia

Auteur(s) : PROSSER (Diann J.); TAKEKAWA (John Y.); NEWMAN (Scott H.); BAOPING YAN; DOUGLAS (David C.); YUANSHENG HOU; ZHI XING; DEHAI ZHANG; TIANXIAN LI; YONGDONG LI; DELONG ZHAO; PERRY (William M.); PALM (Eric C.)

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Source : Ibis : (London. 1859); vol. 151; no. 3; pp. 568-576
ISSN : 0019-1019
CODEN : IBISAL
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 2 p.1/4

Résumé : The role of wild birds in the spread of highly pathogenic avian influenza H5N1 has been greatly debated and remains an unresolved question. However, analyses to determine involvement of wild birds have been hindered by the lack of basic information on their movements in central Asia. Thus, we initiated a programme to document migrations of waterfowl in Asian flyways to inform hypotheses of H5N1 transmission. As part of this work, we studied migration of waterfowl from Qinghai Lake, China, site of the 2005 H5N1 outbreak in wild birds. We examined the null hypothesis that no direct migratory connection existed between Qinghai Lake and H5N1 outbreak areas in central Mongolia, as suggested by some H5N1 phylogeny studies. We captured individuals in 2007 from two of the species that died in the Qinghai Lake outbreaks and marked them with GPS satellite transmitters: Bar-headed Geese Anser indicus (n = 14) and Ruddy Shelduck Tadorna ferruginea (n = 11). Three of 25 marked birds (one Goose and two Shelducks) migrated to breeding grounds near H5N1 outbreak areas in Mongolia. Our results describe a previously unknown migratory link between the two regions and offer new critical information on migratory movements in the region.

Code(s) de classement : 002A14B02C2C; 002A15D

Descripteur(s) anglais

Desc. généraux : Vertebrata; Asia

Descripteur(s) français

Desc. généraux : Vertebrata; Asie

Localisation : INIST-3739, 354000187218200140
Origine de la notice : INIST
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Human Infection with Highly Pathogenic Avian Influenza A (H5N1) Virus: Review of Clinical Issues

Titre : Human Infection with Highly Pathogenic Avian Influenza A (H5N1) Virus: Review of Clinical Issues

Auteur(s) : UYEKI (Timothy M.)
Affiliation(s) : Epidemiology and Prevention Branch, Influenza Division, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, Georgia, USA

Source : Clinical infectious diseases; vol. 49; no. 2; pp. 279-290
ISSN : 1058-4838
CODEN : CIDIEL
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 132 ref.

Résumé : This article provides an updated review of the clinical issues related to human infection with highly pathogenic avian influenza A (H5N1) virus. The clinical data available to date are presented, as well as recent findings on the pathogenesis of and antiviral treatment and immunotherapy for H5N1 virus infection in humans and animal models.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais
- Descripteur(s) : Avian influenza; Bibliographic review; Human; Influenza A virus; Influenzavirus A(H5N1)
- Desc. génériques : Viral disease; Infection; Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) français
- Descripteur(s) : Grippe aviaire; Revue bibliographique; Homme; Virus grippal A; Influenzavirus A(H5N1)
- Desc. génériques : Virose; Infection; Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST-18407, 354000187996440200
Origine de la notice : INIST
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Lessons From Outbreaks of H1 N1 Influenza

Titre : Lessons From Outbreaks of H1 N1 Influenza

Auteur(s) : STEIN (Richard A.)
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Source : Annals of internal medicine; vol. 151; no. 1; pp. 59-62
ISSN : 0003-4819
CODEN : AIMEAS
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 25 ref.

Résumé : A new H1N1 triple-reassortant "swine" influenza virus was recently described in individuals from the United States and Mexico who presented with respiratory symptoms, and the same virus was subsequently confirmed in patients from several countries around the world. The circumstances surrounding the emergence of this pathogen, and the factors that facilitated the initial cross-species transmission, are still incompletely understood. It became apparent in the early days of the outbreak that the virus can be directly transmitted between humans. Pathogens that originate in animal reservoirs and subsequently acquire the potential for human-to-human transmission have caused outbreaks throughout human history. Although each outbreak is marked by its own particularities, it is important to remember the teachings that emerge from previous epidemics and pandemics. Integrating the important lessons of the past will provide the best opportunity to understand host-pathogen interaction and the most powerful approach to implementing effective prophylactic and therapeutic measures.

Code(s) de classement : 002B01; 002B30A11; 002B05C02C

Descripteur(s) anglais

Desc. principal(s) : Influenza; Epidemic; Public health; Medicine; Human
Desc. génériques : Viral disease; Infection

Descripteur(s) français

Desc. principal(s) : Grippe; Epidémie; Santé publique; Médecine; Homme
Desc. génériques : Virose; Infection

Localisation : INIST-2014, 354000187992480070
Origine de la notice : INIST
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Targeted N-Linked Glycosylation Analysis of H5N1 Influenza Hemagglutinin by Selective Sample Preparation and Liquid Chromatography/Tandem Mass Spectrometry

Titre : Targeted N-Linked Glycosylation Analysis of H5N1 Influenza Hemagglutinin by Selective Sample Preparation and Liquid Chromatography/Tandem Mass Spectrometry

Auteur(s) : BLAKE (Thomas A.); WILLIAMS (Tracie L.); PIRKLE (James L.); BARR (John R.)
Affiliation(s) : Biological Mass Spectrometry Laboratory, Division of Laboratory Sciences, National Center for Environmental Health, Centers for Disease Control and Prevention, 4770 Buford Highway, MS F-50, Atlanta, Georgia 30341, USA

Source : Analytical chemistry : (Washington); vol. 81; no. 8; pp. 3109-3118
ISSN : 0003-2700
CODEN : ANCHAM
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Notes : ref. et notes dissem.

Résumé : Using liquid chromatography/tandem mass spectrometry (LC/MS/MS) analysis of deglycosylated and intact glycopeptides from tryptic digest of whole influenza virus, we determined that the six predicted N-linked glycosylation sites within the N-terminal ectodomain of hemagglutinin (HA) from three selected H5N1 strains are occupied. The use of selective sample preparation strategies, including solid-phase extraction (SPE) of glycopeptides via hydrazide capture chemistry as well as hydrophilic interaction liquid chromatography (HIUC), sufficiently reduced sample complexity to allow determination of occupied glycosylation sites. The specific amino acid sequence of the tryptic glycopeptides for the identified sites varied slightly among strains, but the overall locations of the occupied glycosylation sites were conserved in the protein sequence. We used this knowledge of glycosylation site occupation to examine the glycans attached to these occupied sites on HA for a reassortant H5N1 strain grown in embryonated chicken eggs. By applying mass spectrometry-based methodologies for examining glycosylation to the study of influenza virus proteins, we can better understand the effect that this post-translational modification has upon the virulence and antigenicity of emerging strains.

Code(s) de classement : 001C04B02; 001C04C

Descriptor(s) anglais

Descriptor(s) : Sample preparation; Liquid chromatography; Mass spectrometry MS/MS; Glycopeptide; Solid phase extraction; Hydrazides; Aminoacid; Protein; Mass spectrometry; Glycosylation; Influenza; Hemagglutinin; Chemical enrichment
Desc. génériques : Viral disease; Infection

Descriptor(s) français

Descriptor(s) : Préparation échantillon; Chromatographie phase liquide; Spectrométrie masse tandem; Glycopeptide; Extraction SPE; Hydrazidure; Aminoacide; Protéine; Spectrométrie masse; Glycosylation; Grippe; Hémagglutinine; Enrichissement chimique
Desc. génériques : Virose; Infection

Localisation : INIST-120B, 354000186047030370
Origine de la notice : INIST
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Field assessment of an H5N1 inactivated vaccine in chickens and ducks in Lao PDR

**Titre** : Field assessment of an H5N1 inactivated vaccine in chickens and ducks in Lao PDR

**Auteur(s)** : BOLTZ (David A.); DOUANGNGEUN (Bounlom); SINTHASAK (Settha); PHOMMACHANH (Phouvong); MIDOUANGCHANH (Phetlamphone); WALKER (David); KEATING (Rachael); KHALENKOV (Alexey M.); KUMAR (Mahesh); WEBSTER (Robert G.)

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**Source** : Archives of virology; vol. 154; no. 6; pp. 939-944

**ISSN** : 0304-8608

**Date de publication** : 2009

**Pays de publication** : AUT

**Type de document** : P

**Nombre de références** : 34 ref.

**Résumé** : Despite the extensive use of poultry vaccines to control the spread of H5N1 influenza in poultry, H5N1 outbreaks continue to occur in domestic birds. Our objective was to determine the duration of the neutralizing antibody response under field conditions after vaccination with a laboratory-tested inactivated reverse genetics-derived H5N3 vaccine. H5N3 hemagglutination inhibition (HI) and virus neutralization (VN) antibodies were observed 40 weeks after vaccination of chickens with two doses and vaccination of ducks with one dose. Cross-clade antibodies to an H5N1 virus (A/chicken/Laos/A0464/07) antigenically distinct from the vaccine strain were detected in ducks after a single vaccination and were sustained for 28 weeks (for 40 weeks when a boost vaccination was given). Our results indicate that this inactivated H5N3 vaccine can produce long-lasting antibodies to homologous and heterologous viruses under field conditions.

**Code(s) de classement** : 002A05C10

**Descr ipteur(s) anglois**

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Aves; Vertebrata; Asia; Zoopathogen; Veterinary; Poultry; Farming animal

Desc. spécifiques : Avian influenzavirus; Chicken; Inactivated strain; Duck; Laos

**Descr ipteur(s) français**

Desc. génériques : Influenzavirus aviaire; Poulet; Souche inactivée; Canard; Laos

Desc. spécifiques : Influenzavirus A; Orthomyxoviridae; Virus; Aves; Vertebrata; Asie; Zoopathogène; Vétérinaire; Volaille; Animal élevage

**Localisation** : INIST-6355, 354000187206080040

**Origine de la notice** : INIST

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A single substitution in amino acid 184 of the NP protein alters the replication and pathogenicity of H5N1 avian influenza viruses in chickens

Titre : A single substitution in amino acid 184 of the NP protein alters the replication and pathogenicity of H5N1 avian influenza viruses in chickens

Auteur(s) : WASILENKO (Jamie L.); SARMENTO (Luciana); PANTIN-JACKWOOD (Mary J.)
Affiliation(s) : Southeast Poultry Research Laboratory, USDA-Agricultural Research Service, 934 College Station Road, Athens, GA 30605, USA

Source : Archives of virology; vol. 154; no. 6; pp. 969-979
ISSN : 0304-8608
Date de publication : 2009
Pays de publication : AUT
Langue(s) : ENG
Type de document : P
Nombre de références : 54 ref.

Résumé : Changes in the NP gene of H5N1 highly pathogenic avian influenza (HPAI) viruses have previously been shown to affect viral replication, alter host gene expression levels and affect mean death times in infected chickens. Five amino acids at positions 22, 184, 400, 406, and 423 were different between the two recombinant viruses studied. In this study, we individually mutated the five amino acids that differed and determined that the difference in virus pathogenicity after NP gene exchange was a result of an alanine to lysine change at position 184 of the NP protein. Infection with viruses containing a lysine at NP 184 induced earlier mortality in chickens, increased virus titers and nitric oxide levels in tissues, and resulted in up-regulated host immune genes, such as alpha -interferon (IFN- alpha ), gamma -interferon (IFN- gamma ), orthomyxovirus resistance gene 1 (Mx1), and inducible nitric oxide synthase (iNOS). This study underlines the importance of the NP in avian influenza virus replication and pathogenicity.

Code(s) de classement : 002A05C10; 002A05C04

Descripteur(s) anglais : Influenza A virus; Avian influenzavirus; Chicken; Protein; Replication; Pathogenicity
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Aves; Vertebrata; Zoopathogen; Veterinary; Poultry; Farming animal

Descripteur(s) français : Virus grippal A; Influenzavirus aviaire; Poulet; Protéine; Récupération; Pouvoir pathogène
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Aves; Vertebrata; Zoopathogène; Vétérinaire; Volaille; Animal élevage

Localisation : INIST-6355, 354000187206080070
Origine de la notice : INIST
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Functional significance of the hemadsorption activity of influenza virus neuraminidase and its alteration in pandemic viruses

**Titre** : Functional significance of the hemadsorption activity of influenza virus neuraminidase and its alteration in pandemic viruses

**Auteur(s)** : UHLENDORFF (Jennifer); MATROSOVICH (Tatyana); KLENK (Hans-Dieter); MATROSOVICH (Mikhail)

**Affiliation(s)** : Institute of Virology, Philipps University, Hans-Meerwein-Str.2, 35043 Marburg, DEU

**Source** : Archives of virology; vol. 154; no. 6; pp. 945-957

**ISSN** : 0304-8608

**Date de publication** : 2009

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 56 ref.

**Résumé** : Human influenza viruses derive their genes from avian viruses. The neuraminidase (NA) of the avian viruses has, in addition to the catalytic site, a separate sialic acid binding site (hemadsorption site) that is not present in human viruses. The biological significance of the NA hemadsorption activity in avian influenza viruses remained elusive. A sequence database analysis revealed that the NAs of the majority of human H2N2 viruses isolated during the influenza pandemic of 1957 differ from their putative avian precursor by amino acid substitutions in the hemadsorption site. We found that the NA of a representative pandemic virus A/Singapore/1/57 (H2N2) lacks hemadsorption activity and that a single reversion to the avian-virus-like sequence (N367S) restores hemadsorption. Using this hemadsorption-positive NA, we generated three NA variants with substitutions S370L, N400S and W403R that have been found in the hemadsorption site of human H2N2 viruses. Each substitution abolished hemadsorption activity. Although, there was no correlation between hemadsorption activity of the NA variants and their enzymatic activity with respect to monovalent substrates, all four hemadsorption-negative NAs desialylated macromolecular substrates significantly slower than did the hemadsorption-positive counterpart. The NA of the 1918 pandemic virus A/Brevig Mission/1/18 (H1N1) also differed from avian N1 NAs by reduced hemadsorption activity and less efficient hydrolysis of macromolecular substrates. Our data indicate that the hemadsorption site serves to enhance the catalytic efficiency of NA and they suggest that, in addition to changes in the receptor-binding specificity of the hemagglutinin, alterations of the NA are needed for the emergence of pandemic influenza viruses.

**Code(s) de classement** : 002A05C10

**Descripteur(s) anglais**

*Desc. génériques* : Orthomyxoviridae; Virus; Glycosidases; Glycosylases; Hydrolases; Enzyme

*Desc. topiques* : Influenzavirus; Exo- alpha -sialidase

**Descripteur(s) français**

*Desc. génériques* : Orthomyxoviridae; Virus; Glycosidases; Glycosylases; Hydrolases; Enzyme

*Desc. topiques* : Influenzavirus; Exo- alpha -sialidase

**Localisation** : INIST-6355, 354000187206080050

**Origine de la notice** : INIST

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Emergence and spread of oseltamivir-resistant A(H1N1) influenza viruses in Oceania, South East Asia and South Africa

Titre : Emergence and spread of oseltamivir-resistant A(H1N1) influenza viruses in Oceania, South East Asia and South Africa

Auteur(s) : HURT (Aeron C.); ERNEST (Joanne); DENG (Yi-Mo); IANNELLO (Pina); BESSELAAR (Terry G.); BIRCH (Chris); BUCHY (Philippe); CHITTAGANPITCH (Malinee); CHIU (Shu-Chun); DWYER (Dominic); GUIGON (Aurélie); HARROWER (Bruce); IP PENG KEI; KOK (Tuckweng); CUI LIN; MCPHIE (Ken); MOHD (Apandi); OLVEDA (Remigio); PANAYOTOU (Tony); RAWLINSON (William); SMITH (David); D'SOUZA (Holly); KOMADINA (Naomi); KELSO (Anne); BARR (Ian G.)

Affiliation(s) : WHO Collaborating Centre for Reference and Research on Influenza, North Melbourne, Victoria, AUS; Monash University, Churchill, Victoria, AUS; National Institute for Communicable Diseases of the National Health Laboratory Service, Sandringham, ZAF; Victorian Infectious Diseases Reference Laboratory, Victoria, AUS; Institut Pasteur, Phnom Penh, KHM; National Institute of Health, Nonthaburi, THA; Center for Research and Diagnostics, Centers for Disease Control, TWN; Centre for Infectious Diseases and Microbiology, ICPMR, Westmead Hospital, NSW, AUS; Pasteur Institute, NCL; Queensland Health Forensic and Scientific Services, QLD, AUS; Public Health Laboratory, Health Bureau, MAC; Institute of Medical and Veterinary Science, South Australia, AUS; National Public Health Laboratory, Ministry of Health, SGP; Institute Penyelidikan Perubatan, Kuala Lumpur, MYS; Research Institute of Tropical Medicine, Manila, PHL; Southern Health, Victoria, AUS; Prince of Wales Hospital, NSW, AUS; Centre for Disease Control, Darwin, AUS; PathWest Laboratories, Perth, WA, AUS; Auckland Hospital, Auckland, NZL

Source : Antiviral research; vol. 83; no. 1; pp. 90-93
ISSN : 0166-3542
CODEN : ARSRDR
Date de publication : 2009
Langue(s) : ENG
Type de document : P
Nombre de références : 1/4 p.

Résumé : The neuraminidase inhibitors (NAIs) are an effective class of antiviral drugs for the treatment of influenza A and B infections. Until recently, only a low prevalence of NAI resistance (<1%) had been detected in circulating viruses. However, surveillance in Europe in late 2007 revealed significant numbers of A(H1N1) influenza strains with a H274Y neuraminidase mutation that were highly resistant to the NAI oseltamivir. We examined 264 A(H1N1) viruses collected in 2008 from South Africa, Oceania and SE Asia for their susceptibility to NAIs oseltamivir, zanamivir and peramivir in a fluorescence-based neuraminidase inhibition assay. Viruses with reduced oseltamivir susceptibility were further analysed by pyrosequencing assay. The frequency of the oseltamivir-resistant H274Y mutant increased significantly after May 2008, resulting in an overall proportion of 64% (168/264) resistance among A(H1N1) strains, although this subtype represented only 11.6% of all isolates received during 2008. H274Y mutant viruses demonstrated on average a 1466-fold reduction in oseltamivir susceptibility and 527-fold reduction in peramivir sensitivity compared to wild-type A(H1N1) viruses. The mutation had no impact on zanamivir susceptibility. Ongoing surveillance is essential to monitor how these strains may spread or persist in the future and to evaluate the effectiveness of treatments against them.

Code(s) de classement : 002B02S05

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Asia; Africa; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor
Descripteur(s) français

Descripteur(s) : Epidémiologie; Oséltamivir; Résistance; Virus gripal A; Océanie; Asie du sud est; Afrique du Sud; Inhibiteur neuraminidase; Antiviral; Influenzavirus A(H1N1)

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Asie; Afrique; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme

Localisation : INIST-18839, 354000187095690120
Origine de la notice : INIST
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Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic

Titre : Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic

Auteur(s) : SMITH (Gavin J. D.); VIJAYKRISHNA (Dhanasekaran); BAHL (Justin); LYCETT (Samantha J.); WOROBAY (Michael); PYBUS (Oliver G.); SIU KIT MA; CHUNG LAM CHEUNG; RAGHWANI (Jayna); BHATT (Samir); PEIRIS (J. S. Malik); YI GUAN; RAMBAUT (Andrew)

Affiliation(s) : State Key Laboratory of Emerging Infectious Diseases & Department of Microbiology, Li Ka Shing Faculty of Medicine, The University of Hong Kong, 21 Sassoon Road, Pokfulam, HKG; Institute of Evolutionary Biology, University of Edinburgh, Ashvaorth Laboratories, King's Buildings, Edinburgh EH9 3JT, GBR; Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, Arizona 85705, USA; Department of Zoology, University of Oxford, South Parks Road, Oxford OX1 3PS, GBR

Source : Nature ; (London); vol. 459; no. 7250; pp. 1122-1125
ISSN : 0028-0836
CODEN : NATUAS
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 24 ref.

Résumé : In March and early April 2009, a new swine-origin influenza A (H1N1) virus (S-OIV) emerged in Mexico and the United States. During the first few weeks of surveillance, the virus spread worldwide to 30 countries (as of May 11) by human-to-human transmission, causing the World Health Organization to raise its pandemic alert to level 5 of 6. This virus has the potential to develop into the first influenza pandemic of the twenty-first century. Here we use evolutionary analysis to estimate the time-scale of the origins and the early development of the S-OIV epidemic. We show that it was derived from several viruses circulating in swine, and that the initial transmission to humans occurred several months before recognition of the outbreak. A phylogenetic estimate of the gaps in genetic surveillance indicates a long period of unsampled ancestry before the S-OIV outbreak, suggesting that the reassortment of swine lineages may have occurred years before emergence in humans, and that the multiple genetic ancestry of S-OIV is not indicative of an artificial origin. Furthermore, the unsampled history of the epidemic means that the nature and location of the genetically closest swine viruses reveal little about the immediate origin of the epidemic, despite the fact that we included a panel of closely related and previously unpublished swine influenza isolates. Our results highlight the need for systematic surveillance of influenza in swine, and provide evidence that the mixing of new genetic elements in swine can result in the emergence of viruses with pandemic potential in humans.

Code(s) de classement : 002A05C05; 002B05C02C

Description(s) anglois

Description(s) : Epidemic; Evolution; Phylogenetic tree; Phylogeny; Animal; Human; Influenza A; Genome; Genetic reassortment

Description(s) : Epidémie; Evolution; Arbre phylogénétique; Phylogénèse; Animal; Homme; Grippe A; Génome; Influenzavirus A(H1N1); Pandémie; Grippe pandémique; Réassortiment génétique

Localisation : INIST-142, 354000188571860220

Origine de la notice : INIST
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Applications of high-throughput genomics to antiviral research: Evasion of antiviral responses and activation of inflammation during fulminant RNA virus infection

Titre : Applications of high-throughput genomics to antiviral research: Evasion of antiviral responses and activation of inflammation during fulminant RNA virus infection

Auteur(s) : KASH (John C.)
Affiliation(s) : Viral Pathogenesis and Evolution Section, Laboratory of Infectious Diseases, National Institute of Allergy and Infectious Diseases (NIAID), National Institutes of Health (NIH), 33 North Drive, MSC 3203, Bethesda, MD 20892-3203, USA

Source : Antiviral research; vol. 83; no. 1; pp. 10-20
ISSN : 0166-3542
CODEN : ARSRDR
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 1 p.3/4

Résumé : Host responses can contribute to the severity of viral infection, through the failure of innate antiviral mechanisms to recognize and restrict the pathogen, the development of intense systemic inflammation leading to circulatory failure or through tissue injury resulting from overly exuberant cell-mediated immune responses. High-throughput genomics methods are now being used to identify the biochemical pathways underlying ineffective or damaging host responses in a number of acute and chronic viral infections. This article reviews recent gene expression studies of 1918 H1N1 influenza and Ebola hemorrhagic fever in cell culture and animal models, focusing on how genomics experiments can be used to increase our understanding of the mechanisms that permit those viruses to cause rapidly overwhelming infection. Particular attention is paid to how evasion of type I IFN responses in infected cells might contribute to over-activation of inflammatory responses. Reviewing recent research and describing how future studies might be tailored to understand the relationship between the infected cell and its environment, this article discusses how the rapidly growing field of high-throughput genomics can contribute to a more complete understanding of severe, acute viral infections and identify novel targets for therapeutic intervention.

Code(s) de classement : 002B02S05; 002B05C02C; 002B05C0214

Description(s) anglais
Description(s) : In vitro; High throughput screening; Genomics; Antiviral; Animal model; Inflammation; Target; RNA virus; Viral disease; Influenza; Ebola virus; Cytokine; Interferon; Research and development; Influenzavirus A(H5N1)
Desc. génériques : Infection; Filovirus; Filoviridae; Mononegavirales; Virus

Description(s) français
Description(s) : In vitro; Criblage haut débit; Génomique; Antiviral; Modèle animal; Inflammation; Cible; Virus à ARN; Virose; Grippe; Virus Ebola; Cytokine; Interféron; Recherche et développement; Analyse à haut débit; Influenzavirus A(H1N1); Influenzavirus A(H5N1)
Desc. génériques : Infection; Filovirus; Filoviridae; Mononegavirales; Virus

Localisation : INIST-18839, 354000187095690020
Origine de la notice : INIST
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Mechanism of the antiviral effect of hydroxytyrosol on influenza virus appears to involve morphological change of the virus

**Titre** : Mechanism of the antiviral effect of hydroxytyrosol on influenza virus appears to involve morphological change of the virus

**Auteur(s)** : YAMADA (Kentaro); OGAWA (Haruko); HARA (Ayako); YOSHIDA (Yukio); YONEZAWA (Yutaka); KARIJE (Kazuji); NGHIA (Vuong Bui); YOSHIMURA (Hiroyuki); YAMAMOTO (Yu); YAMADA (Manabu); NAKAMURA (Kuniyasu); IMAI (Kunitoshi)

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**Source** : Antiviral research; vol. 83; no. 1; pp. 35-44

**ISSN** : 0166-3542

**CODEN** : ARSRDR

**Date de publication** : 2009

**Pays de publication** : NLD

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 1/2 p.

**Résumé** : Hydroxytyrosol (HT), a small-molecule phenolic compound, inactivated influenza A viruses including H1N1, H3N2, H5N1, and H9N2 subtypes. HT also inactivated Newcastle disease virus but not bovine rotavirus, and fowl adenovirus, suggesting that the mechanism of the antiviral effect of HT might require the presence of a viral envelope. Pretreatment of MDCK cells with HT did not affect the propagation of H9N2 virus subsequently inoculated onto the cells, implying that HT targets the virus but not the host cell. H9N2 virus inactivated with HT retained unaltered hemagglutinating activity and bound to MDCK cells in a manner similar to untreated virus. Neuraminidase activity in the HT-treated virus also remained unchanged. However, in the cells inoculated with HT-inactivated H9N2 virus, neither viral mRNA nor viral protein was detected. Electron microscopic analysis revealed morphological abnormalities in the HT-treated H9N2 virus. Most structures found in the HT-treated virus were atypical of influenza virions, and localization of hemagglutinin was not necessarily confined on the virion surface. These observations suggest that the structure of H9N2 virus could be disrupted by HT.

**Code(s) de classement** : 002B02S05

**Descripteur(s) anglais**

- **Describeur(s)** : Mechanism of action; Antiviral; Influenzavirus; Influenza A virus; Envelope; Newcastle disease virus; Phenols; Bovine rotavirus; Aviadenovirus; Hydroxytyrosol

- **Desc. génériques** : Orthomyxoviridae; Virus; Influenzavirus A; Rubulavirus; Paramyxovirinae; Paramyxoviridae; Mononegavirales; Rotavirus; Reoviridae; Adenoviridae

**Descripteur(s) français**

- **Describeur(s)** : Mécanisme action; Antiviral; Influenzavirus; Virus grippal A; Enveloppe; Virus de la maladie de Newcastle; Phénols; Rotavirus bovin; Aviadenovirus; Hydroxytyrosol

- **Desc. génériques** : Orthomyxoviridae; Virus; Influenzavirus A; Rubulavirus; Paramyxovirinae; Paramyxoviridae; Mononegavirales; Rotavirus; Reoviridae; Adenoviridae

**Localisation** : INIST-18839, 354000187095690050

**Origine de la notice** : INIST

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Auteur(s) : TARANTOLA (A.); AIT BELGHITI (F.); BARBOZA (P.); BAUDON (C.); COHUET (S.); DEGAIL (M.A.); DEJOUR SALAMANCA (D.); GAUTHIER (V.); GUEGUEN (J.); LA RUCHE (G.); RACHAS (A.); VAILLANT (L.); GASTELLU ETCHEGORRY (M.)

Source : BEH WEB; no. 1; 1 p.
Date de publication : 2009-06-29
Pays de publication : FRA
Langue(s) : FRE
Type de document : P

Résumé : Au 5 juin 2009, un total de 21 915 cas (dont 128 décès) de grippe A (H1N1) v ont été déclarés par 72 pays. L'épidémie a diffusé à partir du Mexique et des Etats-Unis par le biais de voyageurs. La majorité des cas est d'évolution bénigne, mais des décès sont survenus dans cinq pays des Amériques. L'infection touche surtout les enfants et les sujets jeunes, en partie parce que de nombreux cas ont été décrits en milieu scolaire ou chez des voyageurs. Cependant, les jeunes adultes sont les plus représentés parmi les décès. Environ la moitié des décès ne présentaient pas de pathologie sous-jacente. Malgré les limites des dispositifs de surveillance et le caractère récent de cette pandémie, le profil épidémiologique se découvre peu à peu ; toutefois les incertitudes restent nombreuses. Le potentiel évolutif de la nouvelle souche de A (H1N1) v demeure incertain et notamment pendant la période de transmission saisonnière de la grippe (hiver austral dans l'hémisphère sud) et dans les pays en développement. (R.A.)

Code(s) de classement : 002B30A11

Descriptor(s) anglais
Descriptor(s) : Mexico; United States; School; Case history; Epidemiology; Sanitary surveillance; Death; Mortality; World
Desc. génériques : Central America; America; North America

Descriptor(s) français
Descriptor(s) : Mexique; Etats-Unis; Ecole; Historique; Epidémiologie; Surveillance sanitaire; Mort; Mortalité; Monde
Desc. génériques : Amérique Centrale; Amérique; Amérique du Nord

Localisation : BDSP/InVS
Origine de la notice : BDSP
Manifestations cliniques observées dans les premières séries de cas de grippe due au virus émergent de la grippe A (H1N1) v. Numéro spécial. Chronique d'un début de pandémie

**Titre** : Manifestations cliniques observées dans les premières séries de cas de grippe due au virus émergent de la grippe A (H1N1) v. Numéro spécial. Chronique d'un début de pandémie

**Auteur(s) :** HOEN (B.)

**Source :** BEH WEB; no. 1; 1 p.

**Date de publication :** 2009-06-29

**Pays de publication :** FRA

**Langue(s) :** FRE

**Type de document :** P

**Résumé :** Les manifestations cliniques observées sur les premiers groupes de patients touchés par le nouveau virus A (H1N1) commencent à être publiées. Cet article présente, à partir de 4 publications et avec les réserves liées aux biais inhérents à la nature des sources, une synthèse des données cliniques disponibles à ce jour. Les sujets touchés sont majoritairement des sujets jeunes. La majorité des patients présente un syndrome grippal comparable à celui observé lors de la grippe saisonnière. » ce jour, aucun décès n’a été observé chez les cas d’importation en Europe, au Japon ou en Australie. Les décès observés en Amérique du Nord sont survenus plutôt chez des sujets jeunes et présentant des comorbidités. (R.A.)

**Code(s) de classement :** 002B30A11

**Descripteur(s) anglais**
- Descripteur(s) : Sex; Symptomatology; Age

**Descripteur(s) français**
- Descripteur(s) : Sexe; Symptomatologie; Age

**Localisation :** BDSP/InVS

**Origine de la notice :** BDSP
Adaptation du dispositif de surveillance à la situation épidémiologique. Numéro spécial. Chronique d'un début de pandémie

Titre : Adaptation du dispositif de surveillance à la situation épidémiologique. Numéro spécial. Chronique d'un début de pandémie

Auteur(s) : BONMARIN (I.); VAUX (S.); LEVY BRUHL (D.)
Source : BEH WEB; no. 1; 1 p.
Date de publication : 2009-06-29
Pays de publication : FRA
Langue(s) : FRE
Type de document : P

Résumé : La surveillance de la grippe A (H1N1) va évoluer en fonction de la situation épidémiologique. Actuellement, elle est centrée sur la recherche exhaustive des cas afin d'éviter une diffusion du virus sur le territoire par la mise en place rapide des mesures de contrôle autour des cas. Cette surveillance individuelle comprend le signalement des cas importés et des cas groupés. Dès que les cas groupés dépasseront le cadre des contacts proches, une surveillance locale sera mise en place dans la zone touchée afin de repérer une diffusion débutante du virus dans la communauté et avant que les indicateurs des systèmes de surveillance sentinelles soient impactés. Quand les cas seront trop nombreux, la surveillance individuelle des cas sera relayée par la surveillance populationnelle et s'arrêtera. Au final, seule persistera la surveillance sentimentale auprès d'une partie de la population, surveillance utilisée chaque année pour suivre les épidémies de grippe saisonnière et comprenant le suivi des cas, des hospitalisations et des décès par différents réseaux. (R.A.)

Code(s) de classement : 002B30A11

Descripteur(s) anglais
Desc. génériques : Europe

Descripteur(s) français
Desc. génériques : Europe

Localisation : BDSP/InVS
Origine de la notice : BDSP
Le point sur les paramètres épidémiologiques dans l'épidémie due au nouveau virus de la grippe A (H1N1) v. Numéro spécial. Chronique d'un début de pandémie

Titre : Le point sur les paramètres épidémiologiques dans l'épidémie due au nouveau virus de la grippe A (H1N1) v. Numéro spécial. Chronique d'un début de pandémie

Auteur(s) : BERNILLON (P.); LEON (L.); BOELLE (P.Y.); DESENCLOS (J.C.)
Source : BEH WEB; no. 1; 1 p.
Date de publication : 2009-06-29
Pays de publication : FRA
Langue(s) : FRE
Type de document : P

Résumé : Depuis la reconnaissance de l'émergence du nouveau virus de la grippe A (H1N1) v, on dispose de premiers éléments quantifiés quant à sa transmissibilité. Cet article présente une synthèse des connaissances disponibles ainsi que des éléments d'interprétation des valeurs publiées. Concernant le potentiel de dissémination de l'infection, les premières estimations indiquent un taux de reproduction allant de 1,4 à 3,1, supérieur à la grippe saisonnière et proche de celui des pandémies passées ; les connaissances sur l'intervalle de génération (1,9 jours au Mexique, 3,5 jours en Espagne) restent limitées. Ces estimations préliminaires varient selon les populations dont la structure et la fréquence des contacts sociaux diffèrent ; elles vont donc continuer à évoluer avec la diffusion du virus. Les mesures d'impact sanitaire manquent aussi de précision à l'heure actuelle. Toutefois, les données disponibles suggèrent une transmissibilité et/ou une susceptibilité plus importante chez les enfants et adolescents. Les premières estimations de la létalité au Mexique évoquent une létalité supérieure à celle de la grippe saisonnière, mais ce phénomène n'a pas été observé ailleurs. Le suivi de ces paramètres au cours du temps est essentiel pour détecter tout changement susceptible d'orienter et adapter les mesures de gestion et de contrôle de la pandémie. (R.A.)

Code(s) de classement : 002B30A11

Descriptor(s) anglais
Descriptor(s) : Communicable disease; Prevention; Mortality

Descriptor(s) français
Descriptor(s) : Maladie contagieuse; Prévention; Mortalité

Localisation : BDSP/InVS
Origine de la notice : BDSP
VoozaFlu : un outil au service de la surveillance de la nouvelle grippe A (H1N1) v. Numéro spécial. Chronique d'un début de pandémie

Titre : VoozaFlu : un outil au service de la surveillance de la nouvelle grippe A (H1N1) v. Numéro spécial. Chronique d'un début de pandémie

Auteur(s) : DELMAS (G.); LAGREE (C.); BECQUEREL (S.); SEVIN (E.); DUBOIS (D.); BIELECKI (O.); VAUX (S.)
Source : BEH WEB; no. 1; 1 p.
Date de publication : 2009-06-29
Pays de publication : FRA
Langue(s) : FRE
Type de document : P

Résumé : Lors de survenue de l'alerte à la grippe à nouveau virus, le 25 avril 2009, l'Institut de veille sanitaire et la société EpiConcept ont développé un outil permettant la gestion et le suivi des signalements et des cas possibles, probables ou confirmés en temps réel par les multiples intervenants chargés de la surveillance. Cette application, baptisée VoozaFlu, a été opérationnelle dès le 29 avril, tout en continuant d'évoluer au gré des besoins de surveillance. (R.A.)

Code(s) de classement : 002B30A11

Descripteur(s) anglais
  Desc. génériques : Europe

Descripteur(s) français
  Desc. génériques : Europe

Localisation : BDSP/InVS
Origine de la notice : BDSP
Cas d'infection par le nouveau virus de la grippe A (H1N1) v en France, situation au 5 juin 2009. Numéro spécial. Chronique d'un début de pandémie

**Titre** : Cas d'infection par le nouveau virus de la grippe A (H1N1) v en France, situation au 5 juin 2009. Numéro spécial. Chronique d'un début de pandémie

**Auteur(s)** : VAUX (S.); BONMARIN (I.); ENOUF (V.); VALETTE (M.); VAN DER WERF (S.); LINA (B.); GASTELLU ETCHEGORRY (M.); LEVY BRUHL (D.); SAURA (C.)

**Source** : BEH WEB; no. 1; 1 p.

**Date de publication** : 2009-06-29

**Pays de publication** : FRA

**Langue(s)** : FRE

**Type de document** : P

**Résumé** : En raison de l'émergence d'un nouveau virus de la grippe A (H1N1) v en Amérique du Nord, une surveillance active des cas d'infections dues à ce virus a été mise en place en France. Son objectif est de permettre la mise en œuvre des mesures nécessaires pour retarder l'installation du virus sur le territoire national. Cet article décrit les caractéristiques cliniques et épidémiologiques des 57 premiers cas diagnostiqués et confirmés virologiquement en France au 5 juin 2009. (R.A.)

**Code(s) de classement** : 002B30A11

**Déscripteur(s) français**
- France; Epidémiologie; Surveillance sanitaire; Recommandation
- Desc. génériques : Europe

**Déscripteur(s) anglais**
- France; Epidemiology; Sanitary surveillance; Recommendation
- Desc. génériques : Europe

**Localisation** : BDSP/InVS

**Origine de la notice** : BDSP
Le point sur le virus de la nouvelle grippe A (H1N1) v. Numéro spécial. Chronique d'un début de pandémie

Titre : Le point sur le virus de la nouvelle grippe A (H1N1) v. Numéro spécial. Chronique d'un début de pandémie

Auteur(s) : ENOUF (V.); BOUSCAMBERT DUCHAMP (M.); VALETTE (M.); BURGIERE (A.); CARO (V); MANUGUERRA (J.C.); LINA (B.); VAN DER WERF (S.)

Source : BEH WEB; no. 1; 1 p.
Date de publication : 2009-06-29
Pays de publication : FRA
Type de document : P

Résumé : Les virus influenza A sont divisés en sous-types, en fonction de leurs glycoprotéines de surface, l'hémagglutinine (HA) et la neuraminidase (NA). Tous les sous-types de virus circulent parmi les oiseaux aquatiques. Certains sont détectés chez différents mammifères tels que les chevaux, les chats, les phoques et les porcs. Des cas de transmission de virus porcins H1N1 à l'homme ont été rapportés à de multiples reprises. Aux Etats-Unis, de 2005 à 2009, des virus porcins dits "triple réassortants" ont été responsables de cas humains sporadiques d'infection respiratoire. Le nouveau virus A (H1N1) v circulant aujourd'hui partage ses segments génomiques avec ces derniers et une autre souche porcine eurasiatique. En France, le virus A (H1N1) v est détecté à l'aide d'une méthode de RT-PCR spécifique du gène H1v, développée par les Centres nationaux de référence (CNR) du virus influenzae. L'analyse génétique et antigénique ne révèle pas de différences significatives entre les virus isolés en France et ailleurs dans le monde. D'aujourd'hui, tous les virus isolés sont sensibles aux inhibiteurs de la neuraminidase tels que l'oseltamivir et le zanamivir. Même si aujourd'hui la sévérité apparait modérée, l'acquisition d'une virulence accrue peut arriver à tout moment et nécessite une surveillance attentive de l'évolution de ce nouveau virus. (R.A.)

Code(s) de classement : 002B30A11

Descripteur(s) anglais
Descripteur(s) : Virus; Human; North America; Europe; Asia; Case history
Desc. génériques : America

Descripteur(s) français
Descripteur(s) : Virus; Homme; Amérique du Nord; Europe; Asie; Historique
Desc. génériques : Amérique

Localisation : BDSP/InVS
Origine de la notice : BDSP
Editorial. Grippe A (H1N1) v : L'Institut de veille sanitaire face à la pandémie. Numéro spécial. Chronique d'un début de pandémie

Titre : Editorial. Grippe A (H1N1) v : L'Institut de veille sanitaire face à la pandémie. Numéro spécial. Chronique d'un début de pandémie

Auteur(s) : WEBER (F.)
Source : BEH WEB; no. 1; 1 p.
Date de publication : 2009-06-29
Pays de publication : FRA
Langue(s) : FRE
Type de document : P

Code(s) de classement : 002B30A11

Descripteur(s) anglais
Desc. génériques : Europe

Descripteur(s) français
Desc. génériques : Europe

Localisation : BDSP/InVS
Origine de la notice : BDSP
Titre : Grippe A (virus H1N1). Une épidémie très médiatique

Auteur(s) : RESENDIZ (Francisco); SAMPEDRO (Javier); RAMIREZ (Pedro-J); ROSENTHAL (Elisabeth); JIMENEZ (David); ADAMS (Guy)

Source : COURRIER INTERNATIONAL; no. 966; pp. 36-41

ISSN : 1154-516X

Date de publication : 2009-05-07/2009-05-13

Pays de publication : FRA

Langue(s) : FRE

Type de document : P

Résumé : La pandémie de grippe A (H1N1) n'a pas eu lieu. La comparaison avec la grippe espagnole de 1918 est inepte et alarmiste. Comme pour le syndrome respiratoire aigu sévère (SRAS) en 2003 ou pour la grippe aviaire en 2004, la presse mondiale s'est fait l'écho de prédictions d'apocalypse avant de s'étonner d'une telle perte de sang-froid. L'organisation mondiale de la santé (OMS) a tenu son rôle de veille, là où la plupart des gouvernements sont tombés dans la démesure, surinformant à mauvais escient. Au final, l'épidémie est à ce jour moindre que la simple grippe saisonnière, qui tue chaque année entre 250 000 et 500 000 personnes dans le monde.

Code(s) de classement : 002B30A01

Descripteur(s) anglais
- Description : Epidemiology; Sanitary surveillance; Epidemic; Influenza; Risk management; Strategy; Virus; Definition; Contagion; Information; Health; Mass media; Internet; Biomedical information; Check; World
- Description génériques : Viral disease; Infection

Descripteur(s) français
- Description : Epidémiologie; Surveillance sanitaire; Epidémie; Grippe; Gestion risque; Stratégie; Virus; Définition; Contagion; Information; Santé; Mass media; Internet; Information biomédicale; Contrôle; Monde
- Description génériques : Virose; Infection

Localisation : BDSP/EHESP-172907

Origine de la notice : BDSP
Influenza A Virus in Taiwan, 1980-2006: Phylogenetic and Antigenic Characteristics of the Hemagglutinin Gene

**Titre** : Influenza A Virus in Taiwan, 1980-2006: Phylogenetic and Antigenic Characteristics of the Hemagglutinin Gene

**Auteur(s)** : WANG (Sheng-Fan); LEE (Yuan-Ming); CHAN (Yu-Jiun); LIU (Hsin-Fu); YEN (Yung-Fong); LIU (Wu-Tse); HUANG (Jason C.); CHEN (Yi-Ming Arthur)

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**Source** : Journal of medical virology; vol. 81; no. 8; pp. 1457-1470

**ISSN** : 0146-6615

**CODEN** : JMVIDB

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 1 p.1/4

**Résumé** : Limited amount of information is available in Taiwan on the genetic or antigenic characteristics of influenza A virus prior to the establishment of a Taiwan surveillance network in 2000. Isolates of H1N1 and H3N2 viruses in Taiwan between 1980 and 2006 were studied, and part of the hemagglutinin gene was analyzed due to its importance in terms of viral infection and antibody neutralization. Results from a phylogenetic analysis indicate continuous evolutionary topology in H3N2 isolates, and two distinct H1N1 lineages. Many genetic relationships between vaccine strains and epidemic isolates appearing in Taiwan before other global locations were also observed and recorded in addition to a gradual increase in the number of N-linked glycosylation sites on partial HA1 proteins since 1980. The results from pairwise comparisons of HA1 nucleotide and deduced amino acid sequences indicate shared identities within groups organized according to their bootstrap and P-values of approximately 95.5-100% and 95.7-100% in H1N1 and 94.5-100% and 93.2-100% in H3N2 viruses, respectively. Comparisons of amino acid substitutions in the five antigenic regions reveal highly non-synonymous changes occurring in the Sb region of H1N1 and in the B region of H3N2. The results of an antigenic analysis using a hemagglutinin inhibition (HI) test indicate the presence of some epidemic strains 1-2 years earlier in Taiwan than in other parts of the world, as well as higher vaccine mismatch rates. This information supports the need for continuous surveillance of emerging influenza viruses in Taiwan, which will be useful for making global vaccine decisions.

**Code(s) de classement** : 002A05C10; 002B05C02J

**Descriptor(s) anglais**

*Descriptor(s) anglais*

Influenza A virus; Taiwan; Phylogeny; Hemagglutinin; Gene; Influenza

*Desc. génériques* : Influenzavirus A; Orthomyxoviridae; Virus; Asie; Viral disease; Infection

**Descriptor(s) français**

*Descriptor(s) français*

Virus grippal A; Taiwan; Phylogénie; Hémagglutinine; Gêne; Grippe; Influenzavirus A(H1N1); Influenzavirus A(H3N2)

*Desc. génériques* : Influenzavirus A; Orthomyxoviridae; Virus; Asie; Virose; Infection

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Ocular Infection of Mice with Influenza A (H7) Viruses: a Site of Primary Replication and Spread to the Respiratory Tract

Titre : Ocular Infection of Mice with Influenza A (H7) Viruses: a Site of Primary Replication and Spread to the Respiratory Tract

Auteur(s) : BELSER (Jessica A.); WADFORD (Debra A.); JIANGUO XU; KATZ (Jacqueline M.); TUMPEY (Terrence M.)

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Source : Journal of virology; vol. 83; no. 14; pp. 7075-7084
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 53 ref.

Résumé : Avian H7 influenza viruses have been responsible for poultry outbreaks worldwide and have resulted in numerous cases of human infection in recent years. The high rate of conjunctivitis associated with avian H7 subtype virus infections may represent a portal of entry for avian influenza viruses and highlights the need to better understand the apparent ocular tropism observed in humans. To study this, mice were inoculated by the ocular route with viruses of multiple subtypes and degrees of virulence. We found that in contrast to human (H3N2 and H1N1) viruses, H7N7 viruses isolated from The Netherlands in 2003 and H7N3 viruses isolated from British Columbia, Canada, in 2004, two subtypes that were highly virulent for poultry, replicated to a significant titer in the mouse eye. Remarkably, an H7N7 virus, as well as some avian H5N1 viruses, spread systemically following ocular inoculation, including to the brain, resulting in morbidity and mortality of mice. This correlated with efficient replication of highly pathogenic H7 and H5 subtypes in murine corneal epithelial sheets (ex vivo) and primary human corneal epithelial cells (in vitro). Influenza viruses were labeled to identify the virus attachment site in the mouse cornea. Although we found abundant H7 virus attachment to corneal epithelial tissue, this did not account for the differences in virus replication as multiple subtypes were able to attach to these cells. These findings demonstrate that avian influenza viruses within H7 and H5 subtypes are capable of using the eye as a portal of entry.

Code(s) de classement : 002A05C10

Descriptor(s) anglais
Descriptor(s) : Mouse; Influenza A virus; Animal; Replication; Respiratory tract; Virology; Ocular infection
Desc. génériques : Rodentia; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus

Descriptor(s) français
Descriptor(s) : Souris; Virus grippal A; Animal; Réplication; Voie respiratoire; Virologie; Infection oculaire
Desc. génériques : Rodentia; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST-13592, 354000187213090100
Origine de la notice : INIST
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Emergence and pandemic potential of swine-origin H1N1 influenza virus

Titre : Emergence and pandemic potential of swine-origin H1N1 influenza virus

Auteur(s) : NEUMANN (Gabriele); NODA (Takeshi); KAWAOKA (Yoshihiro)
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Source : Nature ; (London); vol. 459; no. 7249; pp. 931-939
ISSN : 0028-0836
CODEN : NATUAS
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 100 ref.

Résumé : Influenza viruses cause annual epidemics and occasional pandemics that have claimed the lives of millions. The emergence of new strains will continue to pose challenges to public health and the scientific communities. A prime example is the recent emergence of swine-origin H1N1 viruses that have transmitted to and spread among humans, resulting in outbreaks internationally. Efforts to control these outbreaks and real-time monitoring of the evolution of this virus should provide us with invaluable information to direct infectious disease control programmes and to improve understanding of the factors that determine viral pathogenicity and/or transmissibility.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais
Descriptor(s) anglais : Influenza; Emerging disease; Epidemiology; Risk factor; Influenza A virus; Porcine influenza virus
Desc. génériques : Viral disease; Infection; Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) français
Descriptor(s) français : Grippe; Maladie émergente; Epidémiologie; Facteur risque; Virus grippal A; Influenzavirus porcin; Pandémie; Virus grippal A(H1N1)
Desc. génériques : Virose; Infection; Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST-142, 354000188524500120
Origine de la notice : INIST
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Characterization of an avian influenza virus H5N1 Egyptian isolate

**Titre** : Characterization of an avian influenza virus H5N1 Egyptian isolate

**Auteur(s)** : BAHGAT (M. M.); KUTKAT (M. A.); NASRAA (M. H.); MOSTAFA (A.); WEBBY (R.); BAHGAT (I. M.); ALI (M. A. A.)

**Affiliation(s)** : Virology Lab., Infectious Diseases and Immunology Group, the Center of Excellence for Advanced Sciences, the National Research Center, 12311 Dokki, Giza, EGY; Department of Poultry Diseases, Veterinary Research Division, National Research Center, 12311 Dokki, Giza, EGY; Department of Infectious Diseases, St. Jude Children's Research Hospital, 332 North Lauderdale, Memphis, TN 38105-2794, USA; Department of Biology, Faculty of Education, Seuss Canal University, Port Saied, EGY

**Source** : Journal of virological methods; vol. 159; no. 2; pp. 244-250

**ISSN** : 0166-0934

**CODEN** : JVMEDH

**Date de publication** : 2009

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 3/4 p.

**Résumé** : The highly pathogenic influenza virus H5N1 that infected chickens in Egypt in 2006 was characterized at immunologic and molecular levels. Cloacal swabs from chicken were analyzed by rapid antigen detection and RT-PCR using H5- and N1-specific primers, which confirmed the presence of an H5N1 influenza virus in infected chickens. Sequencing results revealed 100% homology of both genes with previously published sequences of H5N1 isolates from Egypt and the Middle East. The virus was isolated and propagated in MDBK cells in culture. Host cells showed a substantial cytopathic effect within 2 days of infection, which increased dramatically by the fourth day. Plaque infectivity titers of virus harvested from cell culture were initially 105 PFUs/ml and increased to 108 PFUs/ml after two additional passages and ultrafiltration. Formaldehyde treatment completely inactivated the virus, and MDBK cells inoculated with the killed virus showed no cytopathic effect. Two days after chickens were immunized with the killed virus, their sera showed that the killed Egyptian isolate was highly immunogenic. Western blot analysis showed that sera had antibodies reacting to four viral peptides: hemagglutinin (61.5 kDa), RNA-binding protein (56 kDa), neuraminidase (50 kDa), and 45-kDa protein. In a challenge infection, the vaccine protected immunized chickens from death and reduced viral shedding.
Avis du Haut conseil de la santé publique relatif à la menace de pandémie grippale, pertinence de l'utilisation d'un vaccin prépandémique dirigé contre le virus grippal A (H5N1)

Titre : Avis du Haut conseil de la santé publique relatif à la menace de pandémie grippale, pertinence de l'utilisation d'un vaccin prépandémique dirigé contre le virus grippal A (H5N1)

Collectivité(s) auteur : Haut Conseil de la Santé Publique. (H.C.S.P.). Paris., FRA
Source : BULLETIN EPIDEMIOLOGIQUE HEBDOMADAIRE; no. 16-17; pp. 164-167
ISSN : 0245-7466
Date de publication : 2009-04-20
Pays de publication : FRA
Langue(s) : FRE
Type de document : P

Code(s) de classement : 002B30A11

Descriptor(s) anglais
Desc. principal(s) : Epidemic; Influenza; Vaccine; France
Desc. génériques : Viral disease; Infection; Europe

Descriptor(s) français
Desc. principal(s) : Epidémie; Grippe; Vaccin; France
Desc. génériques : Virose; Infection; Europe

Localisation : BDSP/InVS
Origine de la notice : BDSP
SIMUGRIP-MG1 : soins primaires en cas de pandémie grippale H5N1 : évaluation d’un exercice de simulation dans un centre de consultation dédié

Titre : SIMUGRIP-MG1 : soins primaires en cas de pandémie grippale H5N1 : évaluation d’un exercice de simulation dans un centre de consultation dédié

Auteur(s) : MAUGIS BARTHE (Juliette)
Collectivité(s) auteur : Université Paris Descartes. Paris., FRA, tutelle
Source : 204 p.
Informations thèse : Université Paris Descartes. Paris., FRA, Th. Doct. Médecine
Date de publication : 2009 2009
Pays de publication : FRA
Langue(s) : FRE
Type de document : T

Code(s) de classement : 002B30A11

Descripteur(s) anglais
Descriptor(s) : Epidemic; Primary health care; Ambulatory; Care; Consultation; General practitioner; Simulation

Descripteur(s) français
Descriptor(s) : Epidémie; Soin santé primaire; Ambulatoire; Soin; Consultation; Médecin généraliste; Simulation

Localisation : BDSP/BIAM-PA5-2009-10
Origine de la notice : BDSP
Genetic microheterogeneity of emerging H275Y influenza virus A (H1N1) in Toronto, Ontario, Canada from the 2007-2008 respiratory season

Titre : Genetic microheterogeneity of emerging H275Y influenza virus A (H1N1) in Toronto, Ontario, Canada from the 2007-2008 respiratory season

Auteur(s) : ESHAGHI (A.); BOLOTIN (S.); BURTON (L.); LOW (D. E.); MAZZULLI (T.); DREWS (S. J.)

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Source : Journal of clinical virology; vol. 45; no. 2; pp. 142-145

Résumé : Background: The H275Y mutation (H274Y in N2 numbering) in the neuraminidase (NA) gene (segment 6) of the influenza virus A (H1N1) genome is linked to oseltamivir resistance. Objectives: To determine the percentage of influenza virus A (H1N1) isolates that carry the H275Y mutation in the NA gene in Toronto, Ontario, Canada and to characterize select oseltamivir resistant and susceptible isolates using sequence analysis. Study design: Sanger sequencing was used to determine strain type and H275Y mutations based on partial sequencing of the hemagglutinin (HA) (segment 4) and NA genes. Mutations in the NS1 gene (segment 8) were determined by Sanger sequencing and pyrosequencing. Statistical analysis of demographics and proportions of H275 and H275Y isolates with mutations was carried out using chi 2 analyses. Results: The HA gene of influenza virus A (H1N1) isolates collected during the 2007-2008 respiratory season was most like influenza A/Brisbane/59/2007, Clade 2, subclade B. Seventeen percent of these isolates possessed the H275Y mutation in the NA gene. H275Y isolates were more likely than H275 isolates to have the mutations A209T and R224G in NS1 ( chi 2 = 284.9, df = 2, p < 0.0001). Conclusions: During the 2007-2008 influenza season in Toronto, Ontario, Canada, 17% of influenza virus A (H1N1) isolates carried the H275Y mutation associated with oseltamivir resistance. These H275Y isolates were more likely than H275 isolates to exhibit unique microheterogeneity in the gene encoding the NS1 protein.

Code(s) de classement : 002A05C10; 002B05C02J; 002A05C05

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Canada; North America; America; Viral disease; Infection

Localisation : INIST-26272, 354000188606280130

Origine de la notice : INIST

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**H5N1 strain-specific Hemagglutinin CD4+ T cell epitopes restricted by HLA DR4**

**Titre** : H5N1 strain-specific Hemagglutinin CD4+ T cell epitopes restricted by HLA DR4

**Auteur(s)** : JUNBAO YANG; GEBE (John A.); HUSTON (Laurie); JAMES (Eddie); TAN (Venus); YUE (Betty B.); NEPOM (Gerald T.); KWOK (William W.)

**Affiliation(s)** : Benaroya Research Institute at Virginia Mason, 1201 Ninth Ave, Seattle, WA 98101-2795, USA

**Source** : Vaccine; vol. 27; no. 29; pp. 3862-3869

**ISSN** : 0264-410X

**CODEN** : VACCDE

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 30 ref.

**Résumé** : CD4+ T cells play a pivotal role in the viral immunity, and as such identification of unique strain-specific HLA class II restricted epitopes is essential for monitoring cellular strain-specific viral immunity. Using Tetramer-Guided Epitope Mapping technique, we identified HLA-DR0401 restricted HA epitopes that are strain-specific to H5N1 virion. Two immunodominant epitopes H5HA441-460 and H5HA57-76 were identified from in vitro stimulated human PBMC. Both epitopes elicit strong cellular immune responses when HLA-DR0401 transgenic mice are immunized with H5N1 subvirion indicating in vivo naturally processed immunodominant epitopes. The H5HA57-76 epitope is unique for the H5N1 strain but conserved among all H5N1 clades recommended for vaccine development by World Health Organization. The unique H5HA57-76 response was uncommon in unexposed individuals and only observed in the naïve T cell subset. Thus, H5N1 strain-specific H5HA57-76 immunogenic epitope represents a unique marker for monitoring the efficacy of vaccination or as a candidate vaccine peptide.

**Code(s) de classement** : 002A05F04; 002A05C10

**Descriputeur(s) anglais**

- **Descripiteur(s)** : Avian influenzavirus; Strain specificity; Hemagglutinin; T-Lymphocyte; Antigenic determinant; Histocompatibility restriction; Avian influenza
- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen; Viral disease; Infection

**Descriputeur(s) français**

- **Descripiteur(s)** : Influenzavirus aviaire; Spécificité souche; Hémagglutinine; Lymphocyte T; Déterminant antigénique; Restriction histocompatibilité; Grippe aviaire; Antigène CD4
- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogène; Virose; Infection

**Localisation** : INIST-20289, 354000188373290090

**Origine de la notice** : INIST

**Copyright de notice** : © 2009 INIST-CNRS. All rights reserved.
Cationic lipid/DNA complexes (JVRS-100) combined with influenza vaccine (Fluzone®) increases antibody response, cellular immunity, and antigenically drifted protection

**Titre** : Cationic lipid/DNA complexes (JVRS-100) combined with influenza vaccine (Fluzone®) increases antibody response, cellular immunity, and antigenically drifted protection

**Auteur(s)** : LAY (Marla); CALLEJO (Bernadette); CHANG (Stella); HONG (David K.); LEWIS (David B.); CARROLL (Timothy D.); MATZINGER (Shannon); FRITTS (Linda); MILLER (Christopher J.); WARNER (John F.); LIANG (Lily); FAIRMAN (Jeffery)

**Affiliation(s)** : Juvaris BioTherapeutics, Inc., Burlingame, CA 94010, USA; Department of Pediatrics and the Interdepartmental Program in Immunology, Stanford University, Stanford, CA, USA; California National Primate Research Center, University of California-Davis, Davis, CA, USA

**Source** : Vaccine; vol. 27; no. 29; pp. 3811-3820

**ISSN** : 0264-410X

**CODEN** : VACCDE

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 49 ref.

**Résumé** : Safe and effective adjuvants for influenza vaccines that could increase both the levels of neutralizing antibody, including against drifted viral subtypes, and T-cell immunity would be a major advance in vaccine design. The JVRS-100 adjuvant, consisting of DOTIM/cholesterol cationic liposome-DNA complexes, is particularly promising for vaccines that require induction of high levels of antibody and T-cell immunity, including CD8+ cytotoxic T lymphocytes (CTL). Inclusion of protein antigens with JVRS-100 results in the induction of enhanced humoral and cell-mediated (i.e., CD4+ and CD8+ T cells) immune responses. The JVRS-100 adjuvant combined with a split trivalent influenza vaccine (Fluzone®-sanofi pasteur) elicited increased antibody and T-cell responses in mice and non-human primates compared to vaccination with Fluzone® alone. Mice vaccinated with JVRS-100-Fluzone® and challenged with antigenically drifted strains of H1N1 (PR/8/34) and influenza B (B/Lee/40) viruses had higher grade protection, as measured by attenuation of weight loss and increased survival, compared to recipients of unadjuvanted vaccine. The results indicate that the JVRS-100 adjuvant substantially increases immunogenicity and protection from drifted-strain challenge using an existing influenza vaccine.

**Code(s) de classement** : 002A05F04

**Descripteur(s) anglais**

- Lipids; Mixed vaccine; Humoral immunity; Immune response; Cellular immunity; Immunological adjuvant; Influenza;
- Viral disease; Infection

**Descripteur(s) français**

- Lipide; Vaccin associé; Immunité humorale; Réponse immune; Immunité cellulaire; Adjuvant immunologique; Grippe;
- Virose; Infection

**Localisation** : INIST-20289, 354000188373290030

**Origine de la notice** : INIST

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Infection of HLA-DR1 Transgenic Mice with a Human Isolate of Influenza A Virus (H1N1) Primes a Diverse CD4 T-Cell Repertoire That Includes CD4 T Cells with Heterosubtypic Cross-Reactivity to Avian (H5N1) Influenza Virus

Titre : Infection of HLA-DR1 Transgenic Mice with a Human Isolate of Influenza A Virus (H1N1) Primes a Diverse CD4 T-Cell Repertoire That Includes CD4 T Cells with Heterosubtypic Cross-Reactivity to Avian (H5N1) Influenza Virus

Auteur(s) : RICHARDS (Katherine A.); CHAVES (Francisco A.); SANT (Andrea J.)
Affiliation(s) : David H. Smith Center for Vaccine Biology and Immunology, Aab Institute of Biomedical Sciences, Department of Microbiology and Immunology, University of Rochester, Rochester, New York 14642, USA

Source : Journal of virology; vol. 83; no. 13; pp. 6566-6577
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 88 ref.

Résumé : The specificity of the CD4 T-cell immune response to influenza virus is influenced by the genetic complexity of the virus and periodic encounters with variant subtypes and strains. In order to understand what controls CD4 T-cell reactivity to influenza virus proteins and how the influenza virus-specific memory compartment is shaped over time, it is first necessary to understand the diversity of the primary CD4 T-cell response. In the study reported here, we have used an unbiased approach to evaluate the peptide specificity of CD4 T cells elicited after live influenza virus infection. We have focused on four viral proteins that have distinct intracellular distributions in infected cells, hemagglutinin (HA), neuraminidase (NA), nucleoprotein, and the NS1 protein, which is expressed in infected cells but excluded from virion particles. Our studies revealed an extensive diversity of influenza virus-specific CD4 T cells that includes T cells for each viral protein and for the unexpected immunogenicity of the NS1 protein. Due to the recent concern about pandemic avian influenza virus and because CD4 T cells specific for HA and NA may be particularly useful for promoting the production of neutralizing antibody to influenza virus, we have also evaluated the ability of HA- and NA-specific CD4 T cells elicited by a circulating H1N1 strain to cross-react with related sequences found in an avian H5N1 virus and find substantial cross-reactivity, suggesting that seasonal vaccines may help promote protection against avian influenza virus.

Code(s) de classement : 002A05C10

Descriptor(s) anglais
- Descriputeur(s) : Transgenic animal; Mouse; Human; Avian influenzavirus; Infection; HLA-System; Isolate; T-Lymphocyte; Immunologic repertoire; Cross reaction; Virology; Influenzavirus A(H5N1)
- Desc. génériques : Rodentia; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus

Descriptor(s) français
- Descriputeur(s) : Animal transgénique; Souris; Homme; Influenzavirus aviaire; Infection; Système HLA; Isolat; Lymphocyte T; Répertoire immunologique; Réaction croisée; Virologie; Influenzavirus A(H1N1); Antigène CD4; Influenzavirus A(H5N1)
- Desc. génériques : Rodentia; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST-13592, 354000188584730240
Origine de la notice : INIST
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Human single chain monoclonal antibody that recognizes matrix protein of heterologous influenza A virus subtypes

**Titre** : Human single chain monoclonal antibody that recognizes matrix protein of heterologous influenza A virus subtypes

**Auteur(s)** : POUNGPAIR (Ornnuthchar); CHAICUMPA (Wanpen); KULKEAW (Kasem); MANEEWATCH (Santi); THUENG-IN (Kanyarat); SRIMANOTE (Potjanee); TONGTawe (Pongsri); SONgsERM (Thaweesak); LEKCHAROENSUK (Potntippa); TAPCHAISRI (Pramuan)

**Affiliation(s)** : Graduate Program, Faculty of Allied Health Science, Thammasat University, Pathumthani 12120, THA; Department of Parasitology, Faculty of Medicine Siriraj Hospital, Mahidol University, 2 Prannok Road, Bangkok-noi, Bangkok 10700, THA; Faculty of Veterinary Medicine, Kasetsart University, THA

**Source** : Journal of virological methods; vol. 159; no. 1; pp. 105-111

**ISSN** : 0166-0934

**CODEN** : JVMEDH

**Date de publication** : 2009

**Pays de publication** : NLD

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 1/4 p.

**Résumé** : Matrix protein (M1) is predominant and has pivotal role in the influenza A virus replication and assembly. It is therefore an attractive target for antiviral drugs, siRNA studies, and therapeutic antibodies. Nevertheless, therapeutic antibody that interferes with the M1 multiplex function has never been developed. In this study, human single monoclonal antibody fragments (HuScFvs) to M1 were generated. Full length recombinant M1 (rM1) was produced from cdNA prepared from genome of highly pathogenic avian influenza virus, A/H5N1. The rM1 was used as an antigen in phage bio-panning to select phage clones displaying HuScFv from a human antibody phage display library. Several phage clones displaying HuScFv bound to the rM1 and harboring the respective huscfv gene inserts were isolated. RFLP experiments revealed multiple DNA banding patterns which indicated epitope/affinity diversity of the HuScFv. The HuScFv were tested for their binding to native M1 of homologous and heterologous influenza A viruses using ELISA as well as incorporating immunostaining and immunofluorescence studies with infected MDCK cells. One such protein produced from a selected phage clone blocked binding of M1 to viral RNA. The HuScFv in their in vivo functional format, e.g. cell-penetrating molecules, should be developed and tested as a broad spectrum anti-A/influenza.

**Code(s) de classement** : 002A05C09

**Descripteur(s) anglais**

- **Descripteur(s) :** Human; Influenza A virus; Avian influenzavirus; Single chain antibody; Protein; Subtype; Phage display; Microbiology; Method; Virology; Influenza A
- **Desc. génériques :** Influenzavirus A; Orthomyxoviridae; Virus; Viral disease; Infection

**Descripteur(s) français**

- **Descripteur(s) :** Homme; Virus grippal A; Influenzavirus aviaire; Anticorps simple chaîne; Protéine; Soustype; Technique phage display; Microbiologie; Méthode; Virologie; Grippe A
- **Desc. génériques :** Influenzavirus A; Orthomyxoviridae; Virus; Virose; Infection

**Localisation** : INIST-18295, 354000188495480180

**Origine de la notice** : INIST

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Avian influenza: Global assessment of potential pandemic of the twenty first century

Titre : Avian influenza: Global assessment of potential pandemic of the twenty first century

Auteur(s) : ABUBAKAR (M. B.); AINI (I.); OMAR (A. R.); HAIR BEJO (M.)

Affiliation(s) : Biologics Laboratory, Faculty of Veterinary Medicine, University Putra Malaysia UPM, 43400 Serdang Selangor DE, MYS; Institute Bioscience, University Putra Malaysia UPM, 43400 Serdang Selangor DE, MYS

Source : International journal of food, agriculture and environment : (Print); vol. 7; no. 2; pp. 10-19

ISSN : 1459-0255

Date de publication : 2009

Pays de publication : FIN

Type de document : P

Nombre de références : 146 ref.

Résumé : The emergence of highly pathogenic avian influenza (HPAI) of Asian lineage and the subsequent spillover to other part of the globe and on going spread of Eurasian-Africa H5N1 epidemic into domestic, wild birds and human have generated unprecedented attention in recent times and threat of potential pandemic via the avian-human link. Historically, from 1878 through 1955, fowl plaque was described as a high mortality disease of poultry in many countries throughout Europe, Asia, North and South America and Africa and the etiology was proved to be a filterable virus. In the 1930s through the 1950s, fowl plaque disappeared as an endemic disease in most part of the world. In 1949, the first report of a low virulent disease in chickens caused by LPAI virus was reported. In 1955, the etiological of fowl plaque was determined to be influenza A virus, which subsequently was identified as the H7 subtype. In 1959, a "fowl plaque-like" outbreak was described in chickens, which was the first report of fowl plaque caused by a non-H7 AI virus, i.e. first fowl plaque outbreak from H5 subtype of AI virus. In 1961 the first wild birds infection and deaths were reported in common terns of South Africa. In 1966 and 1971, the first H5 and H7 LPAI viruses, respectively were identified; prior to this period, only HPAI viruses had H5 and H7 subtypes. In 1970, the AGID serological test was introduced, which allowed easy and rapid identification of AI virus-infected poultry flocks. In 1972, there was the first isolation of LPAI viruses in asymptomatic wild birds: ducks in the United State and shorebirds in Australia. In 1981, the term "highly pathogenic avian influenza" was accepted as standard nomenclature for fowl plaque and related synonyms. In 1983, LPAI virus was observed mutating to HPAI virus during LPAI field outbreak, and specific genomic changes were identified in the proteolytic cleavage site of the hemagglutinin responsible for the virulence change. In the late 1980s and early 1990s, molecular criteria were added to the definition for classifying an AI virus as HPAI. In 2002, there were the first reported infections and deaths in a wide variety of wild bird species from AI virus H5N1 HPAI virus. The primary goal of this review is to highlight the global situation of HPAI and provide baseline information to show the potential pandemic nature of the virus, so that control and prevention strategies can be improved.

Code(s) de classement : 002A

Descripteur(s) anglais

Descrip. génériques : Viral disease; Infection; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen

Descripteur(s) français

Descrip. génériques : Virose; Infection; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogène

Localisation : INIST-27691, 354000188479710010

Origine de la notice : INIST

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Risk Factors Associated with Subclinical Human Infection with Avian Influenza A (H5N1) Virus-Cambodia, 2006

Titre : Risk Factors Associated with Subclinical Human Infection with Avian Influenza A (H5N1) Virus-Cambodia, 2006

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Source : The Journal of infectious diseases; vol. 199; no. 12; pp. 1744-1752

ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 35 ref.

Résumé : Background. We conducted investigations in 2 villages in Cambodia where outbreaks of influenza H5N1 occurred among humans and poultry to determine the frequency of and risk factors for H5N1 virus transmission.

Methods. During May 2006, équivalent à 7 weeks after outbreaks of influenza H5N1 among poultry occurred, villagers living near households of 2 patients with influenza H5N1 were interviewed about potential H5N1 exposures and had blood samples obtained for H5N1 serological testing by microneutralization assay. A seropositive result was defined as an influenza H5N1 neutralizing antibody titer of >=1:80, with confirmation by Western blot assay. A case-control study was conducted to identify risk factors for influenza H5N1 virus infection. Control subjects, who had seronegative results of tests, were matched with H5N1 1-seropositive persons by village residence, households with an influenza H5N1-infected poultry flock, sex, and age. Results. Seven (1.0%) of 674 villagers tested seropositive for influenza H5N1 antibodies and did not report severe illness; 6 (85.7%) were male. The 7 H5N1-seropositive persons, all of whom were aged <=18 years, were younger than participants who tested seronegative for H5N1 antibodies (median age, 12.0 years vs. 27.4 years; P = .03) and were more likely than were the 24 control subjects to report bathing or swimming in household ponds (71.4% vs. 20.8%; matched odds ratio, 11.3; P = .03). Conclusions. Avian-to-human transmission of influenza H5N1 virus remains low, despite extensive poultry contact. Exposure to a potentially contaminated environment was a risk factor for human infection.

Code(s) de classement : 002A05C10; 002B05

Descripteur(s) anglais

Descripteur(s) : Human; Avian influenzavirus; Influenza A virus; Risk factor; Asymptomatic; Cambodia; Microbiology; Infection; Influenza A
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Asia; Zoopathogen; Viral disease

Descripteur(s) français

Descripteur(s) : Homme; Influenzavirus aviaire; Virus grippal A; Facteur risque; Asymptomatique; Cambodge; Microbiologie; Infection; Grippe A
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Asie; Zoopathogène; Virose

Localisation : INIST-2052, 354000187919970060
Origine de la notice : INIST
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Ecologic Risk Factor Investigation of Clusters of Avian Influenza A (H5N1) Virus Infection in Thailand

Titre : Ecologic Risk Factor Investigation of Clusters of Avian Influenza A (H5N1) Virus Infection in Thailand

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Source : The Journal of infectious diseases; vol. 199; no. 12; pp. 1735-1743
ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 37 ref.

Résumé : This study was conducted to investigate space and time clusters of highly pathogenic avian influenza A (H5N1) virus infection and to determine risk factors at the subdistrict level in Thailand. Highly pathogenic avian influenza A (H5N1) virus was diagnosed in 1890 poultry flocks located in 953 subdistricts during 2004-2007. The ecologic risk for H5N1 virus infection was assessed on the basis of a spatial-based case-control study involving 824 case subdistricts and 3296 control subdistricts from 6 study periods. Risk factors investigated in clustered areas of H5N1 included human and animal demographic characteristics, poultry production systems, and wild birds and their habitats. Six variables remained statistically significant in the final model: flock density of backyard chickens (odds ratio [OR], 0.98), flock density of fighting cocks (OR, 1.02), low and high human density (OR, 0.60), presence of quail flocks (OR, 1.21), free-grazing duck flocks (OR, 2.17), and a poultry slaughterhouse (OR, 1.33). We observed a strong association between subdistricts with H5N1 virus-infected poultry flocks and evidence of prior and concomitant H5N1 infection in wild birds in the same subdistrict.

Code(s) de classement : 002A05C10; 002B05

Descripteur(s) anglais
Descripteur(s) : Avian influenzavirus; Influenza A virus; Risk factor; Thailand; Microbiology; Infection; Influenza A
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Asia; Zoopathogen; Viral disease

Descripteur(s) français
Descripteur(s) : Influenzavirus aviaire; Virus grippal A; Facteur risque; Thaïlande; Microbiologie; Infection; Grippe A
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Asie; Zoopathogène; Virose

Localisation : INIST-2052, 354000187919970050
Origine de la notice : INIST
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Risk Factors for Human Illness with Avian Influenza A (H5N1) Virus Infection in China

Titre : Risk Factors for Human Illness with Avian Influenza A (H5N1) Virus Infection in China

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Source : The Journal of infectious diseases; vol. 199; no. 12; pp. 1726-1734

Résumé : Background. In China, 30 human cases of avian influenza A (H5N1) virus infection were identified through July 2008. We conducted a retrospective case-control study to identify risk factors for influenza H5N1 disease in China.

Methods. A questionnaire about potential influenza H5N1 exposures was administered to 28 patients with influenza H5N1 and to 134 randomly selected control subjects matched by age, sex, and location or to proxies. Conditional logistic regression analyses were performed. Results. Before their illness, patients living in urban areas had visited wet poultry markets, and patients living in rural areas had exposure to sick or dead backyard poultry. In multivariable analyses, independent risk factors for influenza H5N1 were direct contact with sick or dead poultry (odds ratio [OR], 506.6 [95% confidence interval [CI], 15.7-16319.6]; P < .001), indirect exposure to sick or dead poultry (OR, 56.9 [95% CI, 4.3-745.6]; P = .002), and visiting a wet poultry market (OR, 15.4 [95% CI, 3.0-80.2]; P = .001). Conclusions. To prevent human influenza H5N1 in China, the level of education about avoiding direct or close exposures to sick or dead poultry should be increased, and interventions to prevent the spread of influenza H5N1 at live poultry markets should be implemented.

Code(s) de classement : 002A05C10; 002B05

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Source : Clinical infectious diseases; vol. 48; no. 12; pp. 1639-1646
ISSN : 1058-4838
CODEN : CIDIEL
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 47 ref.

Résumé : Background. The first cases of avian influenza A (H5N1) in humans in Vietnam were detected in early 2004, and Vietnam has reported the second highest number of cases globally. Methods. We obtained retrospective clinical data through review of medical records for laboratory confirmed cases of influenza A (H5N1) infection diagnosed in Vietnam from January 2004 through December 2006. Standard data was abstracted regarding clinical and laboratory features, treatment, and outcome. Results. Data were obtained for 67 (72%) of 93 cases diagnosed in Vietnam over the study period. Patients presented to the hospital after a median duration of illness of 6 days with fever (75%), cough (89%), and dyspnea (81%). Diarrhea and mucosal bleeding at presentation were more common in fatal than in nonfatal cases. Common findings were bilateral pulmonary infiltrates on chest radiograph (72%), lymphopenia (73%), and increased serum transaminase levels (aspartate aminotransferase, 69%; alanine aminotransferase, 61%). Twenty-six patients died (case fatality rate, 39%; 95% confidence interval, 27%-51%) and the most reliable predictor of a fatal outcome was the presence of both neutropenia and raised alanine aminotransferase level at admission, which correctly predicted 91% of deaths and 82% of survivals. The risk of death was higher among persons aged <=16 years, compared with older persons (P<.001), and the risk of death was higher among patients who did not receive oseltamivir treatment (P = .048). The benefit of oseltamivir treatment remained after controlling for potential confounding by 1 measure of severity (odds ratio, 0.15; 95% confidence interval, 0.026-0.893; P = .034). Conclusion. In cases of infection with Influenza A (H5N1), the presence of both neutropenia and raised serum transaminase levels predicts a poor outcome. Oseltamivir treatment shows benefit, but treatment with corticosteroids is associated with an increased risk of death.

Code(s) de classement : 002B05C02C

Desc. génériques : Viral disease; Infection; Asia

Descripteur(s) anglais

Desc. génériques : Viral disease; Infection; Asia

Desc. : Influenza A; Symptomatology; Vietnam; Human; Influenzavirus A(H5N1)

Desc. : Grippe A; Symptomatologie; Vietnam; Homme; Influenzavirus A(H5N1)

Loc. génériques : Virose; Infection; Asie

Localisation : INIST-18407, 354000188286330010
Origine de la notice : INIST
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Crystal structure of an avian influenza polymerase PAN reveals an endonuclease active site

Titre : Crystal structure of an avian influenza polymerase PAN reveals an endonuclease active site

Auteur(s) : PUWEI YUAN; BARTLAM (Mark); ZHIYONG LOU; SHOUDENG CHEN; JIE ZHOU; XIAOJING HE; ZONGYANG LV; RUOWEN GE; XUEMEI LI; TAO DENG; FODOR (Ervin); ZIHE RAO; YINGFANG LIU

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Source : Nature : (London); vol. 458; no. 7240; pp. 909-913
ISSN : 0028-0836
CODEN : NATUAS
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 30 ref.

Résumé : The heterotrimeric influenza virus polymerase, containing the PA, PB1 and PB2 proteins, catalyses viral RNA replication and transcription in the nucleus of infected cells. PB1 holds the polymerase active site and reportedly harbours endonuclease activity2, whereas PB2 is responsible for cap binding2-4. The PA amino terminus is understood to be the major functional part of the PA protein and has been implicated in several roles, including endonuclease5 and protease activities6 as well as viral RNA/complementary RNA promoter binding7. Here we report the 2.2 ångström (Å) crystal structure of the N-terminal 197 residues of PA, termed PAN, from an avian influenza H5N1 virus. The PAN structure has an alpha / beta architecture and reveals a bound magnesium ion coordinated by a motif similar to the (P)DXN(D/E)XK motif characteristic of many endonucleases. Structural comparisons and mutagenesis analysis of the motif identified in PAN provide further evidence that PAN holds an endonuclease active site. Furthermore, functional analysis with in vivo ribonucleoprotein reconstitution and direct in vitro endonuclease assays strongly suggest that PAN holds the endonuclease active site and has critical roles in endonuclease activity of the influenza virus polymerase, rather than PB1. The high conservation of this endonuclease active site among influenza strains indicates that PAN is an important target for the design of new anti-influenza therapeutics.

Code(s) de classement : 002B02S05; 002A05C03

Descripțeur(s) anglais

Descripțeur(s) : Crystalline structure; Avian influenzavirus; RNA-directed RNA polymerase; Active site; Target; Antiviral; Design; Structure function relationship; Research and development; Influenzavirus A(H5N1)
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Nucleotidytransfersases; Transferases; Enzyme

Descripțeur(s) français

Descripțeur(s) : Structure cristalline; Influenzavirus aviaire; RNA-directed RNA polymerase; Site actif; Cible; Antiviral; Conception; Relation structure fonction; Recherche et développement; Endonuclease; Influenzavirus A(H5N1)
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Nucleotidytransfersases; Transferases; Enzyme

Localisation : INIST-142, 354000186276880230
Origine de la notice : INIST
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Magnetic bead-based DNA hybridization assay with chemiluminescence and chemiluminescent imaging detection

**Titre** : Magnetic bead-based DNA hybridization assay with chemiluminescence and chemiluminescent imaging detection

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**Source** : Analyst : (London. 1877. Print); vol. 134; no. 4; pp. 800-804

**ISSN** : 0003-2654

**CODEN** : ANALAO

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 28 ref.

**Résumé** : Simple and sensitive chemiluminescence (CL) and CL imaging methods have been developed for the magnetic bead-based DNA hybridization assay. The assay relies on the high sensitivity and long stable light signal of the CL system in which horseradish peroxidase (HRP) catalyzes the luminol H2O2 reaction with para-iodophenol (PIP) as the enhancer. In this protocol, a sandwich DNA hybridization is performed by mixing the target DNA with the magnetic bead-captured DNA and the biotinylated reporter DNA, followed through the biotin-streptavidin reaction with conjugated HRP, and then the conjugated HRP is determined by the CL system. The proposed CL protocol is suitable for for detection of sequence-specific DNA related to the avian influenza A H1N1 virus at levels as low as 10 amol, and the CL imaging detection has a similar sensitivity. The sensitivities of the proposed methods with the HRP label are better than most of the metal nanoparticle-based methods, and are comparable with that of utilizing amplified techniques for DNA hybridization detection. In addition, the perfectly complementary DNA sequences and the single-base mismatched DNA sequences can be better distinguished by a thermally-stringent hybridization and washing steps. So, the proposed CL method can offer great promise for single-nucleotide polymorphism (SNP) analysis. Moreover, the proposed method may have significant potential for the simultaneous detection of various DNA sequences when different capture DNA sequences and reporter DNA sequences are used in a microarray.

**Code(s) de classement** : 001C04F; 001C04A

**Desc. génériques** : Peroxidases; Oxidoreductases; Enzyme

**Desc. génériques** : Hybridation DNA; Analyse chimique; Chimiluminescence; Formation image; Sensibilité; Luminol; Métal; Nanoparticule; Polymorphisme mononucléotide; Mesure simultanée; Microanalyse; Capteur chimique; Réseau capteur; Peroxidase; DNA; Biotine

**Localisation** : INIST-1036, 354000186826670240

**Origine de la notice** : INIST

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An indirect sandwich ELISA for the detection of avian influenza H5 subtype viruses using anti-hemagglutinin protein monoclonal antibody

Titre : An indirect sandwich ELISA for the detection of avian influenza H5 subtype viruses using anti-hemagglutinin protein monoclonal antibody

Auteur(s) : QINGPING LUO; HONGLIANG HUANG; WEI ZOU; HANBING DAN; XUEBO GUO; ANDING ZHANG; ZHENJUN YU; HUANCHUN CHEN; MEILIN JIN

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Source : Veterinary microbiology : (Amsterdam); vol. 137; no. 1-2; pp. 24-30
ISSN : 0378-1135
CODEN : VMICDQ

Résumé : A sandwich ELISA test using AIV H5 subtype specific monoclonal antibody (clone 2H4) to an epitope of hemagglutinin protein has been developed. The monoclonal antibody was used to capture the antigen from clinical samples (swabs and tissues). Captured antigens from clinical samples were detected using polyclonal sera, purified AIV H5N1 particles were titrated in the sandwich ELISA and the limit of detection was determined to be approximately 1.0 ng of influenza viral protein in virus preparations. Fifteen AIV strains of H1-H15 subtypes and some other pathogens were tested by this system, and the test is specific to H5 subtype viruses as it failed to detect other AIV subtype viruses and other pathogens. Varieties of clinical samples originating from laboratory experiments (n = 382) and from fields (n = 288) were employed to test the efficacy of DAS-ELISA test. The test compared very well with the traditional method for detection of influenza virus: virus isolation (VI) in embryonated chicken eggs. In comparison to virus isolation the sensitivity and specificity of sandwich ELISA were found to be 98.6% and 97.6% respectively. In addition, the DAS-ELISA was used to test samples of experimentally infected birds and clinical samples obtained from central China in 2005. The assay proved to be sensitive and specific for the rapid detection of AIV H5 subtype virus from the tissues and swabs in infected animals.

Code(s) de classement : 002A05C10; 002A05F04

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Vertebrata; Zoopathogen

Desc. génériques : Influenzavirus aviaire; Aves; Technique ELISA; Détection; Soustype; Hémagglutinine; Protéine; Anticorps monoclonal; Microbiologie; Vétérinaire; Infection

Localisation : INIST-16884, 354000186306820040
Origine de la notice : INIST
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Population dynamics of swine influenza virus in farrow-to-finish and specialised finishing herds in the Netherlands

**Titre** : Population dynamics of swine influenza virus in farrow-to-finish and specialised finishing herds in the Netherlands

**Auteur(s)** : LOEFFEN (W. L. A.); HUNNEMAN (W. A.); QUAK (J.); VERHEIJDEN (J. H. M.); STEGEMAN (J. A.)  
**Affiliation(s)** : Department of Swine Health, Animal Health Service, P.O. Box 9, 7400AA Deventer, NLD; Central Veterinary Institute of Wageningen UR (CVI), P.O. Box 65, 8200AB Lelystad, NLD; Faculty of Veterinary Medicine, University of Utrecht, P.O. Box 80151, 3508 TD Utrecht, NLD

**Source** : Veterinary microbiology : (Amsterdam); vol. 137; no. 1-2; pp. 45-50  
**ISSN** : 0378-1135  
**CODEN** : VMICDQ  
**Date de publication** : 2009  
**Pays de publication** : NLD  
**Langue(s)** : ENG  
**Type de document** : P  
**Nombre de références** : 3/4 p.

**Résumé** : Influenza virus infections with subtypes H1N1, H3N2 and H1N2 are very common in domestic pigs in Europe. Data on possible differences of population dynamics in finishing pigs in farrow-to-finish herds and in specialised finishing herds are, however, scarce. The presence of sows and weaned piglets on the same premises may, however, affect the exposure of finishing pigs to influenza viruses. In a longitudinal study on 14 farrow-to-finish herds and 15 finishing herds, groups of pigs were followed by repeatedly testing the same animals for antibodies against all three influenza virus subtypes (H1N1, H3N2 and H1N2). At the end of the finishing period, the seroprevalences in farrow-to-finish and specialised finishing herds were 44.3% and 62.0%, respectively for H1N1, 6.6% and 19.3%, respectively for H3N2, and 57.2% and 25.6%, respectively for H1N2. For all three subtypes, the incidence of influenza virus infections was highest at the beginning of the finishing period in farrow-to-finish herds, while the incidence of influenza virus infections was highest at the end of the finishing period in finishing herds. Respiratory disease, probably related to the influenza infections, was observed in five of these herds only, but also occurred at the beginning of the finishing period in farrow-to-finish herds and at the end of the finishing period in finishing herds. The observed differences of population dynamics of influenza virus may affect choice and timing of intervention measures.

**Code(s) de classement** : 002A05C10

**Descriputeur(s) anglais**  
- **Descriputeur(s) :** Porcine influenzavirus; Swine; Population dynamics; Netherlands; Incidence; Epidemiology; Microbiology; Veterinary; Influenza  
- **Desc. génériques :** Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Europe; Viral disease; Infection

**Descriputeur(s) français**  
- **Descriputeur(s) :** Influenzavirus porcin; Porcin; Dynamique population; Pays-Bas; Incidence; Epidémiologie; Microbiologie; Vétérinaire; Grippe  
- **Desc. génériques :** Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Europe; Virose; Infection

**Localisation** : INIST-16884, 354000186306820070  
**Origine de la notice** : INIST  
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Characterization of an influenza A virus isolated from pigs during an outbreak of respiratory disease in swine and people during a county fair in the United States

Titre : Characterization of an influenza A virus isolated from pigs during an outbreak of respiratory disease in swine and people during a county fair in the United States

Auteur(s) : VINCENT (Amy L.); SWENSON (Sabrina L.); LAGER (Kelly M.); GAUGER (Phillip C.); LOIAcono (Christina); YAN ZHANG

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Source : Veterinary microbiology : (Amsterdam); vol. 137; no. 1-2; pp. 51-59
ISSN : 0378-1135
CODEN : VMICDQ
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 3/4 p.

Résumé : In August 2007, pigs and people became clinically affected by an influenza-like illness during attendance at an Ohio county fair. Influenza A virus was identified from pigs and people, and the virus isolates were characterized as swine H1N1 similar to swine viruses currently circulating in the U.S. pig population. The swine isolate, A/SW/OH/511445/2007 (OH07), was evaluated in an experimental challenge and transmission study reported here. Our results indicate that the OH07 virus was pathogenic in pigs, was transmissible among pigs, and failed to cross-react with many swine H1 anti-sera. Naturally exposed pigs shed virus as early as 3 days and as long as 7 days after contact with experimentally infected pigs. This suggests there was opportunity for exposure of people handling the pigs at the fair. The molecular analysis of the OH07 isolates demonstrated that the eight gene segments were similar to those of currently circulating triple reassortant swine influenza viruses. However, numerous nucleotide changes leading to amino acid changes were demonstrated in the HA gene and throughout the genome as compared to contemporary swine viruses in the same genetic cluster. It remains unknown if any of the amino acid changes were related to the ability of this virus to infect people. The characteristics of the OH07 virus in our pig experimental model as well as the documented human transmission warrant close monitoring of the spread of this virus in pig and human populations.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; North America; America; Infection

Descripteur(s) français
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Amérique du Nord; Amérique; Infection

Localisation : INIST-16884, 354000186306820080
Origine de la notice : INIST
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Antibody Recognition of a Highly Conserved Influenza Virus Epitope

Titre : Antibody Recognition of a Highly Conserved Influenza Virus Epitope

Auteur(s) : EKIERT (Damian C.); BHABHA (Gira); ELSLIGER (Marc-André); FRIESEN (Robert H. E.); JONGENEEL (Mandy); THROSBY (Mark); GOUDSMIT (Jaap); WILSON (Ian A.)

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Source : Science : (Washington, D.C.); vol. 324; no. 5924; pp. 246-251
ISSN : 0036-8075
CODEN : SCIEAS

Date de publication : 2009
Pays de publication : USA
Type de document : P
Notes : 1/4 p.ref. et notes

Résumé : Influenza virus presents an important and persistent threat to public health worldwide, and current vaccines provide immunity to viral isolates similar to the vaccine strain. High-affinity antibodies against a conserved epitope could provide immunity to the diverse influenza subtypes and protection against future pandemic viruses. Cocrystal structures were determined at 2.2 and 2.7 angstrom resolutions for broadly neutralizing human antibody CR6261 Fab in complexes with the major surface antigen (hemagglutinin, HA) from viruses responsible for the 1918 H1N1 influenza pandemic and a recent lethal case of H5N1 avian influenza. In contrast to other structurally characterized influenza antibodies, CR6261 recognizes a highly conserved helical region in the membrane-proximal stem of HA1 and HA2. The antibody neutralizes the virus by blocking conformational rearrangements associated with membrane fusion. The CR6261 epitope identified here should accelerate the design and implementation of improved vaccines that can elicit CR6261-like antibodies, as well as antibody-based therapies for the treatment of influenza.

Code(s) de classement : 002A05C04

Descripteur(s) anglais

Descripoteur(s) : Influenza A virus; Antigenic determinant; Recognition; Antibody; Fab-Fragment; Mechanism of action
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) français

Descripoteur(s) : Virus grippal A; Déterminant antigénique; Reconnaissance; Anticorps; Fragment peptidique Fab; Mécanisme action
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST-6040, 354000186016830260
Origine de la notice : INIST
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Investigation of the biological indicator for vaccine efficacy against highly pathogenic avian influenza (HPAI) H5N1 virus challenge in mice and ferrets

Titre : Investigation of the biological indicator for vaccine efficacy against highly pathogenic avian influenza (HPAI) H5N1 virus challenge in mice and ferrets

Auteur(s) : SONG (Min-Suk); OH (Taek-Kyu); PASCUA (Philippe Noriel Q.); MOON (Ho-Jin); JUN HAN LEE; YUN HEE BAEK; WOO (Kyu-Jin); YOON (Yeup); SUNG (Moon-Hee); POO (Haryoung); KIM (Chul-Joong); YOUNG KI CHOI

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Source : Vaccine; vol. 27; no. 24; pp. 3145-3152
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Nombre de références : 40 ref.

Résumé : To investigate the biological indicator for vaccine efficacy against HPAI H5N1 virus challenge of varying clades, two inactivated whole-virus H5N1 vaccines containing the hemagglutinin (HA) and neuraminidase (NA) genes of either clade 2.2 A/EM/Korea/W149/06 (RgKoreaW149/06xPR8) or clade 2.5 A/Ck/Korea/ES/03 (RgKoreaES223N/03XPR8) virus in the background of A/PR/8/34 (H1N1) were generated by reverse genetics. Administration of the vaccines (2-dose 1.77, 3.5, 7.5 or 15 μg of HA) elicited high HI titers in a dose-dependent manner. Mice immunized with RgKoreaW149/06xPR8 were completely protected from challenge against wild-type A/EM/Korea/W149/06 without clinical signs of infection. RgKoreaES223N/03XPR8 could not protect mice at 1.77 μg g while all immunized ferrets were completely protected. Two-dose (7.5 μg g) vaccinated mice (HI titer >=320) and triple dose (7.5 μg g) vaccinated ferrets with RgKoreaES223N/03XPR8 (HI titer >=640) protected vaccine recipients from mortality, inhibited nasal virus shedding and limited influenza virus tropism. Thus, these vaccines provided cross-protectivity in both models. More importantly, these results collectively suggested a positive correlation between vaccine-induced HI titers and inhibition of virus shedding including block of viral proliferation in major organs against a heterologous HPAI H5N1 virus. Although developing technologies or methods that will enable the reduction of administration dose/frequency remains to be resolved, our study demonstrated a considerable biological marker (>640 HI titer) for full protection of the vaccinated hosts that could provide a preliminary basis for the assessment of complete immunization.

Code(s) de classement : 002A05F04; 002A05C10

Descripteur(s) anglais

Avian influenzavirus; Mouse; Biological indicator; Vaccine; Efficiency; Pathogenicity; Biological marker; Cross protection

Descripteur(s) français

Avian influenzavirus; Souris; Indicateur biologique; Vaccin; Efficacité; Pouvoir pathogène; Marqueur biologique; Protection croisée

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Rapid subtyping of H9N2 influenza virus by a triple reverse transcription polymerase chain reaction

Titre : Rapid subtyping of H9N2 influenza virus by a triple reverse transcription polymerase chain reaction

Auteur(s) : CHEN (Hao-Tai); JIE ZHANG; MA (Li-Na); MA (Yan-Ping); DING (Yao-Zhong); MENG WANG; LIU (Xiang-Tao); ZHANG (Yong-Guang); LIU (Yong-Sheng)

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Source : Journal of virological methods; vol. 158; no. 1-2; pp. 58-62
ISSN : 0166-0934
CODEN : JVMEDH
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 1/4 p.

Résumé : The aim of this study was to develop a rapid, cost-saving triple reverse transcription polymerase chain reaction (triple RT-PCR) for subtyping H9N2 avian influenza viruses (AIVs). The three primer pairs for amplification of target sequences of nucleoprotein (NP), hemagglutinin (HA) and neuraminidase (NA) genes, respectively, were designed for subtyping the viruses in the triple RT-PCR. The sensitivity of triple RT-PCR was found to be 10^2 copies per reaction for each of NP, H9 and N2 gene. The specificity tests indicated that all of NP, HA and NA genes were positive for H9N2, only NP gene was positive for H5N1 and H1 N1 AIVs, and the results were negative for the other avian viruses including Newcastle disease virus, infectious bronchitis virus, infectious bursal disease virus, duck hepatitis virus and avian encephalomyelitis virus. A total of 112 clinical samples were evaluated by the assay and the results showed that the sensitivity and specificity of triple RT-PCR were in accordance with the virus isolation. In conclusion, this method is rapid and cost-effective making it feasible and attractive for large-scale epidemiological investigation of H9N2 influenza virus.

Code(s) de classement : 002A05C09

Descripteur(s) anglais
- Descripteur(s) : Influenza A virus; Influenzavirus; Reverse transcription polymerase chain reaction; Transcription; Microbiology; Method; Virology
- Desc. généraux : Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) français
- Descripteur(s) : Virus grippal A; Influenzavirus; Réaction chaîne polymérase RT; Transcription; Microbiologie; Méthode; Virologie
- Desc. généraux : Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST-18295, 354000188450900110
Origine de la notice : INIST
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Diagnosis and strain differentiation of avian influenza viruses by restriction fragment mass analysis

Titre : Diagnosis and strain differentiation of avian influenza viruses by restriction fragment mass analysis

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Source : Journal of virological methods; vol. 158; no. 1-2; pp. 63-69
ISSN : 0166-0934
CODEN : JVMEDH
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 3/4 p.

Résumé : Outbreaks of highly pathogenic avian influenza (HPAI) among poultry as well as wild birds are of continuing major public concern, not only because of high economical losses but also due to lethal infections in humans. Control of the infection relies on rapid detection and identification of the causative virus strain which is carried out currently primarily by real-time RT-PCR and DNA sequencing. In a pandemic, however, the analysis of very large numbers of samples may become necessary within a short period. A method is described for the characterisation of avian influenza virus (AIV) subtypes by restriction fragment mass fingerprint (RFMF) analysis. Amplified genomic fragments encoding the pathogenicity-determining region of the hemagglutinin gene were digested with a cocktail of restriction enzymes, and the restriction fragments were assayed by mass spectrometry. Characteristic spectra with sequence coverage ranging from 75 to 100% were obtained for a panel of 27 isolates representing 18 relevant serotypes. Three marker masses were identified that are highly specific for strains of the H5N1 virus. Within the H5N1 serotype, discrimination of individual strains was possible by detailed evaluation of the spectra. The procedure described is rapid, inexpensive and compatible with automation.

Code(s) de classement : 002A05C09

Descriputeur(s) anglais
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus

Descriputeur(s) français
Desc. génériques : Influenzavirus aviaire; Diagnostic; Souche; Méthode fingerprint; Microbiologie; Virologie

Localisation : INIST-18295, 354000188450900120
Origine de la notice : INIST
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Development of a novel real-time reverse-transcriptase PCR method for the detection of H275Y positive influenza A H1N1 isolates

Titre : Development of a novel real-time reverse-transcriptase PCR method for the detection of H275Y positive influenza A H1N1 isolates

Auteur(s) : BOLOTIN (S.); ROBERTSON (A. V.); ESHAGHI (A.); DE LIMA (C.); LOMBOS (E.); CHONG-KING (E.); BURTON (L.); MAZZULLI (T.); DREWS (S. J.)

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Source : Journal of virological methods; vol. 158; no. 1-2; pp. 190-194

ISSN : 0166-0934
CODEN : JVMEDH
Date de publication : 2009
Pays de publication : NLD

Langue(s) : ENG
Type de document : P
Nombre de références : 1/2 p.

Résumé : During the 2007-2008 influenza season global strain surveillance for antiviral resistance revealed the sudden emergence of oseltamivir resistance in influenza A H1N1 isolates. Although oseltamivir resistance rates vary from region to region, 16% of isolates tested globally were found to be oseltamivir resistant by a histidine to tyrosine mutation of residue 275 of the neuraminidase gene of influenza A. In order to implement effective resistance testing locally a novel real-time reverse-transcriptase PCR (RT-PCR) assay was developed for the detection of the H275Y mutation. To evaluate this method, 40 oseltamivir resistant and 61 oseltamivir sensitive H1N1 influenza isolates were tested using Sanger sequencing, which is the reference method for detection of resistance, pyrosequencing and the novel H275Y RT-PCR assay. In comparison to Sanger sequencing, the sensitivity and specificity of the H275Y RT-PCR assay were 100% (40/40) and 100% (61/61) respectively, while the sensitivity and specificity of pyrosequencing were 100% (40/40) and 97.5% (60/61) respectively. Although all three methods were effective in detecting the H275Y mutation associated with oseltamivir resistance, the H275Y RT-PCR assay was the most rapid and could easily be incorporated into an influenza subtyping protocol.

Code(s) de classement : 002A05C09

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Nucleotidyltransferases; Transferases; Enzyme; Viral disease; Infection

Desc. génériques français : Influenzavirus A; Orthomyxoviridae; Virus; Nucleotidyltransferases; Transferases; Enzyme; Viral disease; Infection

Localisation : INIST-18295, 354000188450900310
Origine de la notice : INIST
Copyright de notice : © 2009 INIST-CNRS. All rights reserved.
Protective Immunity Afforded by Inactivated H5N1 (NIBRG-14) Vaccine Requires Antibodies against Both Hemagglutinin and Neuraminidase in Mice

Titre : Protective Immunity Afforded by Inactivated H5N1 (NIBRG-14) Vaccine Requires Antibodies against Both Hemagglutinin and Neuraminidase in Mice

Auteur(s) : TAKAHASHI (Yoshimasa); HASEGAWA (Hideki); HARA (Yukari); ATO (Manabu); NINOMIYA (Ai); TAKAGI (Hirotaka); ODAGIRI (Takato); SATA (Tetsutaro); TASHIRO (Masato); KOBAYASHI (Kazuo)

Affiliation(s) : Department of Immunology, National Institute of Infectious Diseases, Tokyo, JPN; Department of Pathology, National Institute of Infectious Diseases, Tokyo, JPN; Department of Virology III, National Institute of Infectious Diseases, Tokyo, JPN; Division of Biosafety Control and Research, National Institute of Infectious Diseases, Tokyo, JPN

Source : The Journal of infectious diseases; vol. 199; no. 11; pp. 1629-1637

ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 21 ref.

Résumé : Background. Hemagglutination-inhibition (HI) antibody titers correlate with protective immunity to seasonal influenza viruses. However, inactivated H5N1 influenza vaccines from Vietnam 2004 strains afford protection without producing high or even detectable HI antibodies. Methods. BALB/c mice were immunized twice (at a 3-week interval) with inactivated whole-virus influenza vaccine produced using reverse genetics, with the internal genes of A/PR/8/34 (a high-yield strain) and the hemagglutinin (HA) and neuraminidase (NA) genes of A/Vietnam/1194/04 (H5N1) virus (NIBRG-14) adjuvanted with alum (5 µg of HA). Either HA- or NA-binding antibodies were absorbed from the immune serum. The protective efficacy of these antibodies was determined by injecting the absorbed serum into severe combined immunodeficiency mice, which were then challenged with highly pathogenic H5N1 virus (A/Vietnam/Jp1203/2004; Japanese isolate of A/Vietnam/1203/2004). Results. The NIBRG-14 vaccine elicited levels of anti-HA antibodies similar to levels elicited by the H1N1 vaccines, as well as levels of anti-NA antibodies higher than those elicited by the H1N1 vaccines. The absorption of either anti-HA or anti-NA antibody from immune serum samples obtained from NIBRG-14-vaccinated mice significantly reduced the protective efficacy of the serum. Conclusions. For NIBRG-14 vaccines to confer protection to vaccinated hosts, both anti-HA and anti-NA antibodies are required. This finding implies that the measurement of both antibody levels may be required for accurate evaluation of vaccine efficacy.

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A prime-boost vaccination of mice with heterologous H5N1 strains

Titre : A prime-boost vaccination of mice with heterologous H5N1 strains

Auteur(s) : IKENO (Daisuke); KIMACHI (Kazuhiko); KUDO (Yasuhiro); GOTO (Shuro); ITAMURA (Shigeyuki); ODAGIRI (Takato); TASHIRO (Masato); KINO (Yoichiro)

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Source : Vaccine; vol. 27; no. 23; pp. 3121-3125
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 23 ref.

Résumé : We evaluated the priming effect of an H5N1 pandemic vaccine in a mouse model to investigate strategies for influenza pandemic vaccination. For priming, an alum-adjuvanted inactivated whole H5N1 vaccine (NIBRG-14, clade 1) was used. As booster vaccines, several formulations of Indo05/05/2005(H5N1)PR8-IBCDC-RG2 vaccines (clades 2-1) were evaluated, including split, whole, alum-adjuvanted split, and alum-adjuvanted whole vaccines. Any type of booster vaccination elicited a significant HI antibody response despite the difference in antigenicity between the priming and booster vaccines. The split vaccine elicited a much stronger booster response than the alum-adjuvanted whole vaccine. When the mice were primed with the H1N1 or H3N2 vaccines, this did not affect the booster response to the H5N1 vaccine. These results indicated that an alum-adjuvanted whole vaccine is able to confer immunological memory to haemagglutinin even if the primed and boosted vaccine strains are in different clades and, once vaccinated, a split vaccine is preferred to evoke recall responses.

Code(s) de classement : 002A05F04; 002A05C10

Desc. génériques : Rodentia; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen; Viral disease; Infection

Localisation : INIST-20289, 354000188471610140
Origine de la notice : INIST
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Evaluation of conserved and variable influenza antigens for immunization against different isolates of H5N1 viruses

Titre : Evaluation of conserved and variable influenza antigens for immunization against different isolates of H5N1 viruses

Auteur(s) : PATEL (Ami); TRAN (Kaylie); GRAY (Michael); YAN LI; ZHUJUN AO; XIAOJIAN YAO; KOBASA (Darwyn); KOBINGER (Gary P.)

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Source : Vaccine; vol. 27; no. 23; pp. 3083-3089
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 34 ref.

Résumé : The combination of rapid evolution and high mortality in human cases of infections has raised concerns that the H5N1 avian influenza virus may become a new, possibly severe, pandemic virus. Vaccination is likely to be the most efficient strategy to mitigate the impact of the next influenza pandemic. The present study evaluates B and T cell immune responses generated by the H5N1 viral antigens, hemagglutinin (HA), neuraminidase (NA), nucleoprotein (NP), or the M2 ion channel in parallel, expressed from a DNA vaccine vehicle. Protection studies of immunized mice challenged with 100 LD50 of homologous or heterologous H5N1 viruses indicate that HA afforded better protection than the NA, NP or M2 DNA vaccines. The antibody response was also higher in HA-vaccinated mice as determined by hemagglutination inhibition (HI) and neutralizing antibodies (NAB) assays. Interestingly, the T cell response was higher against HA than against NA, NP or M2 and was detectable at low doses of the DNA-HA vaccine capable of inducing complete protection, despite the absence of a detectable B cell response. This study emphasizes the need to evaluate the relationship between both arms of the adaptive immune responses in regards to protective efficacy against influenza virus.

Code(s) de classement : 002A05F04; 002A05C10

Descripteur(s) anglais
- Descripteur(s) : Avian influenzavirus; Antigen; Immunization; Genetic vaccine; Isolate; Cellular immunity; Avian influenza
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Infection; Viral disease; Zoopathogen

Descripteur(s) français
- Descripteur(s) : Influenzavirus aviaire; Antigène; Immunisation; Vaccin génétique; Isolat; Immunité cellulaire; Grippe aviaire
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Infection; Virose; Zoopathogène

Localisation : INIST-20289, 354000188471610100
Origine de la notice : INIST
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Wegener's granulomatosis patients show an adequate antibody response to influenza vaccination

**Titre** : Wegener's granulomatosis patients show an adequate antibody response to influenza vaccination

**Auteur(s)** : HOLVAST (A.); STEGEMAN (C. A.); BENNE (C. A.); HUCKRIEDE (A.); WILSCHUT (J. C.); PALACHE (A. M.); KALLENBERG (C. G. M.); BIJL (M.)

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**Source** : Annals of the rheumatic diseases; vol. 68; no. 6; pp. 873-878

**ISSN** : 0003-4967

**CODEN** : ARDIAO

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 36 ref.

**Résumé** : Objectives: Wegener's granulomatosis (WG) is a systemic vasculitis characterised by relapsing and remitting disease activity. Immunosuppressive drugs are used to control disease, but increase susceptibility to infection. Therefore, influenza vaccination should be considered in WG patients. This study was performed to assess the immunogenicity of influenza vaccination in WG patients. Methods: A randomised, controlled trial was performed in WG patients with quiescent disease, defined as a Birmingham vasculitis activity score (BVAS) less than 2. Patients were randomly assigned to receive influenza vaccination (n = 49) or to participate as controls (n = 23). In addition, healthy controls (n = 49) were vaccinated. At entry and at 1 and 3-4 months after entry, antibody responses to vaccination were determined. Furthermore, disease activity was measured (BVAS), adverse effects were recorded and antineutrophil cytoplasmic autoantibody (ANCA) titres were determined. Results: WG patients achieved high seroprotection rates to all three influenza strains, comparable with healthy controls. Only the A/H1N1 strain patients had a lower seroconversion rate (p = 0.002) and geometric mean titre (p = 0.037) than controls. After 1 month, one control and one vaccinated WG patient had developed active disease. At 3-4 months, two additional control patients had developed active disease compared with none of the vaccinated patients (p = 0.099). Vaccination did not influence ANCA titres. Adverse effects did not differ between patients and healthy controls. Conclusions: Influenza vaccination in WG patients with quiescent disease induced a sufficient antibody response.

**Code(s) de classement** : 002B15; 002B05C02C; 002B07

**Descripteur(s) anglais**
- **Desc. génériques** : Viral disease; Infection; Cardiovascular disease; Systemic disease; Vascular disease; Vasculitis; Prevention

**Descripteur(s) français**
- **Desc. génériques** : Virose; Infection; Pathologie de l'appareil circulatoire; Maladie de système; Pathologie des vaisseaux sanguins; Vasculaire; Prévention

**Localisation** : INIST-6381, 354000186230910190

**Origine de la notice** : INIST
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An inactivated H5N2 vaccine reduces transmission of highly pathogenic H5N1 avian influenza virus among native chickens

Titre : An inactivated H5N2 vaccine reduces transmission of highly pathogenic H5N1 avian influenza virus among native chickens

Auteur(s) : POETRI (O. N.); BOUMA (A.); MURTINI (Sri); CLAASSEN (I.); KOCH (G.); SOEJOEDONO (Retno D.); STEGEMAN (J. A.); VAN BOVEN (M.)

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Source : Vaccine; vol. 27; no. 21; pp. 2864-2869

ISSN : 0264-410X

CODEN : VACCDE

Date de publication : 2009

Pays de publication : GBR

Langue(s) : ENG

Type de document : P

Nombre de références : 36 ref.

Résumé : Vaccination against H5N1 highly pathogenic avian influenza in endemically affected areas is a potentially attractive option for local prevention and control. In Indonesia the majority of local outbreaks have occurred in back yard flocks with native chickens, and it is therefore of interest to determine whether these birds can be protected against infection by vaccination. To this end two transmission experiments were carried out with H5N1 virus (A/chicken/Legok/2003) in vaccinated and unvaccinated native chickens. The vaccine contained an inactivated heterologous H5N2 strain (A/turkey/England/N28/73 H5N2). Birds were vaccinated at 4 and 7 weeks of age and challenged at 10 weeks of age. During 10 days post-challenge tracheal and cloacal swabs were taken for virus isolation, and serum blood was collected regularly to measure haemaglutinin inhibiting (HI) antibody responses. The results show that transmission of H5N1 virus was rapid and efficient in unvaccinated birds, that infection and transmission were completely prevented in vaccinated birds, and that vaccinated birds that were exposed to unvaccinated inoculated birds were still protected from infection. These findings indicate that vaccination with a heterologous H5N2 vaccine is able to prevent virus transmission in flocks of native chickens.

Code(s) de classement : 002A05F04; 002A05C10

Description(s) anglais

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Aves; Vertebrata; Zoopathogen; Viral disease; Infection; Poultry; Veterinary; Farming animal

Description(s) français

Desc. génériques : Influenzavirus aviaire; Virus grippal A; Poulet; Souche inactivée; Transmission; Pouvoir pathogène; Vaccination; Grippé aviaire

Localisation : INIST-20289, 354000186258720210

Origine de la notice : INIST

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Acquisition of a Polybasic Hemagglutinin Cleavage Site by a Low-Pathogenic Avian Influenza Virus Is Not Sufficient for Immediate Transformation into a Highly Pathogenic Strain

**Titre** : Acquisition of a Polybasic Hemagglutinin Cleavage Site by a Low-Pathogenic Avian Influenza Virus Is Not Sufficient for Immediate Transformation into a Highly Pathogenic Strain

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**Source** : Journal of virology; vol. 83; no. 11; pp. 5864-5868
**ISSN** : 0022-538X
**Date de publication** : 2009
**Pays de publication** : USA
**Langue(s)** : ENG
**Type de document** : P
**Nombre de références** : 34 ref.

**Résumé** : Highly pathogenic avian influenza viruses (HPAIV) differ from all other strains by a polybasic cleavage site in their hemagglutinin. All these HPAIV share the H5 or H7 subtype. In order to investigate whether the acquisition of a polybasic cleavage site by an avirulent avian influenza virus strain with a hemagglutinin other than H5 or H7 is sufficient for immediate transformation into an HPAIV, we adapted the hemagglutinin cleavage site of A/Duck/Ukraine/1/1963 (H3N8) to that of the HPAIV A/Chicken/Italy/8/98 (H5N2), A/Chicken/ HongKong/220/97 (H5N1), or A/Chicken/Germany/R28/03 (H7N7) and generated the recombinant wild-type and cleavage site mutants. In contrast to the wild type, multicycle replication of these mutants in tissue culture was demonstrated by positive plaque assays and viral multiplication in the absence of exogenous trypsin. Therefore, in vitro all cleavage site mutants resemble an HPAIV. However, in chicken they did not exhibit high pathogenicity, although they could be reisolated from cloacal swabs to some extent, indicating enhanced replication in vivo. These results demonstrate that beyond the polybasic hemagglutinin cleavage site, the virulence of HPAIV in chicken is based on additional pathogenicity determinants within the hemagglutinin itself or in the other viral proteins. Taken together, these observations support the notion that acquisition of a polybasic hemagglutinin cleavage site by an avirulent strain with a non-H5/H7 subtype is only one among several alterations necessary for evolution into an HPAIV.

**Code(s) de classement** : 002A05C10; 002A05C04

**Descrip teur(s) anglais**

Desc. **genre** : Influenza A virus; Avian influenzavirus; Hemagglutinin; Cleavage site; Pathogenicity; Strain; Virology

**Desc. généraux** : Influenzavirus A; Orthomyxoviridae; Virus

**Descrip teur(s) français**

Desc. **genre** : Virus grippal A; Influenzavirus aviaire; Hémagglutinine; Site clavage; Pouvoir pathogène; Souche; Virologie

**Desc. généraux** : Influenzavirus A; Orthomyxoviridae; Virus

**Localisation** : INIST-13592, 354000188443330550

**Origine de la notice** : INIST

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Intranasal Vaccination with 1918 Influenza Virus-Like Particles Protects Mice and Ferrets from Lethal 1918 and H5N1 Influenza Virus Challenge

Titre : Intranasal Vaccination with 1918 Influenza Virus-Like Particles Protects Mice and Ferrets from Lethal 1918 and H5N1 Influenza Virus Challenge

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Source : Journal of virology; vol. 83; no. 11; pp. 5726-5734
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 82 ref.

Résumé : Influenza vaccines capable of inducing cross-reactive or heterotypic immunity could be an important first line of prevention against a novel subtype virus. Influenza virus-like particles (VLPs) displaying functional viral proteins are effective vaccines against replication-competent homologous virus, but their ability to induce heterotypic immunity has not been adequately tested. To measure VLP vaccine efficacy against a known influenza pandemic virus, recombinant VLPs were generated from structural proteins of the 1918 H1N1 virus. Mucosal and traditional parenteral administrations of H1N1 VLPs were compared for the ability to protect against the reconstructed 1918 virus and a highly pathogenic avian H5N1 virus isolated from a fatal human case. Mice that received two intranasal immunizations of H1N1 VLPs were largely protected against a lethal challenge with both the 1918 virus and the H5N1 virus. In contrast, mice that received two intramuscular immunizations of 1918 VLPs were largely protected against a lethal challenge with both the 1918 virus and the H5N1 virus. In contrast, mice that received two intramuscular immunizations of 1918 VLPs were only protected against a homologous virus challenge. Mucosal vaccination of mice with 1918 VLPs induced higher levels of cross-reactive immunoglobulin G (IgG) and IgA antibodies than did parenteral vaccination. Similarly, ferrets mucosally vaccinated with 1918 VLPs completely survived a lethal challenge with the H5N1 virus, while only a 50% survival rate was observed in parenterally vaccinated animals. These results suggest a strategy of VLP vaccination against a pandemic virus and one that stimulates heterotypic immunity against an influenza virus strain with threatening pandemic potential.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Descripteur(s) : Avian influenzavirus; Mouse; Influenza A virus; Intranasal administration; Vaccination; Virus like particle; Prevention; Animal; Ferret; Virology; Flulike syndrome

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Fissipedia; Carnivora

Descripteur(s) français

Descripteur(s) : Influenzavirus aviaire; Souris; Virus grippal A; Voie intranasale; Vaccination; Particule type viral; Prévention; Animal; Furet; Virologie; Syndrome pseudogrippal

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Fissipedia; Carnivora

Localisation : INIST-13592. 354000188443330410
Origine de la notice : INIST
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Different Evolutionary Trajectories of European Avian-Like and Classical Swine H1N1 Influenza A Viruses

Titre : Different Evolutionary Trajectories of European Avian-Like and Classical Swine H1N1 Influenza A Viruses

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Source : Journal of virology; vol. 83; no. 11; pp. 5485-5494
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 64 ref.

Résumé : In 1979, a lineage of avian-like H1N1 influenza A viruses emerged in European swine populations independently from the classical swine H1N1 virus lineage that had circulated in pigs since the Spanish influenza pandemic of 1918. To determine whether these two distinct lineages of swine-adapted A/H1N1 viruses evolved from avian-like A/H1N1 ancestors in similar ways, as might be expected given their common host species and origin, we compared patterns of nucleotide and amino acid change in whole genome sequences of both groups. An analysis of nucleotide compositional bias across all eight genomic segments for the two swine lineages showed a clear lineage-specific bias, although a segment-specific effect was also apparent. As such, there appears to be only a relatively weak host-specific selection pressure. Strikingly, despite each lineage evolving in the same species of host for decades, amino acid analysis revealed little evidence of either parallel or convergent changes. These findings suggest that although adaptation due to evolutionary lineages can be distinguished, there are functional and structural constraints on all gene segments and that the evolutionary trajectory of each lineage of swine A/H1N1 virus has a strong historical contingency. Thus, in the context of emergence of an influenza A virus strain via a host switch event, it is difficult to predict what specific polygenic changes are needed for mammalian adaptation.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Desc. génériques : Vertebrata; Artiodactyla; Ungulata; Mammalia; Influenzavirus A; Orthomyxoviridae; Virus; Veterinary

Descripteur(s) français
Desc. génériques : Vertebrata; Artiodactyla; Ungulata; Mammalia; Influenzavirus A; Orthomyxoviridae; Virus; Vétérinaire

Localisation : INIST-13592, 354000188443330180
Origine de la notice : INIST
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Early Control of H5N1 Influenza Virus Replication by the Type I Interferon Response in Mice

Titre : Early Control of H5N1 Influenza Virus Replication by the Type I Interferon Response in Mice

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Source : Journal of virology; vol. 83; no. 11; pp. 5825-5834
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 72 ref.

Résumé : Widespread distribution of highly pathogenic avian H5N1 influenza viruses in domesticated and wild birds continues to pose a threat to public health, as interspecies transmission of virus has resulted in increasing numbers of human disease cases. Although the pathogenic mechanism(s) of H5N1 influenza viruses has not been fully elucidated, it has been suggested that the ability to evade host innate responses, such as the type I interferon response, may contribute to the virulence of these viruses in mammals. We investigated the role that type I interferons (alpha/beta interferon [IFN- alpha / beta ]) might play in H5N1 pathogenicity in vivo, by comparing the kinetics and outcomes of H5N1 virus infection in IFN- alpha / beta receptor (IFN- alpha / beta R)-deficient and SvEv129 wild-type mice using two avian influenza A viruses isolated from humans, A/Hong Kong/483/97 (HK/483) and A/Hong Kong/486/97 (HK/486), which exhibit high and low lethality in mice, respectively. IFN- alpha / beta R-deficient mice experienced significantly more weight loss and more rapid time to death than did wild-type mice. HK/486 virus caused a systemic infection similar to that with HK/483 virus in IFN- alpha / beta R-deficient mice, suggesting a role for IFN- alpha / beta in controlling the systemic spread of this H5N1 virus. HK/483 virus replicated more efficiently than HK/486 virus both in vivo and in vitro. However, replication of both viruses was significantly reduced following pretreatment with IFN- alpha / beta . These results suggest a role for the IFN- alpha / beta response in the control of H5N1 virus replication both in vivo and in vitro, and as such it may provide some degree of protection to the host in the early stages of infection.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata

Descripteur(s) français
Desc. génériques : Influenzavirus aviaire; Virus grippal A; Souris; Réplication; Interféron; Cytokine; Animal; Virologie

Localisation : INIST-13592, 354000188443330510
Origine de la notice : INIST
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Suitability of PER.C6® cells to generate epidemic and pandemic influenza vaccine strains by reverse genetics

Titre : Suitability of PER.C6® cells to generate epidemic and pandemic influenza vaccine strains by reverse genetics

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Source : Vaccine; vol. 27; no. 19; pp. 2588-2593
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 30 ref.

Résumé : Reverse genetics, the generation of influenza viruses from cDNA, presents a rapid method for creating vaccine strains. The technique necessitates the use of cultured cells. Due to technical and regulatory requirements, the choice of cell lines for production of human influenza vaccines is limited. PER.C6® cells, among the most extensively characterized and documented cells, support growth of all influenza viruses tested to date, and can be grown to high densities in large bioreactors in the absence of serum or micro carriers. Here, the suitability of these cells for the generation of influenza viruses by reverse genetics was investigated. A range of viruses reflective of vaccine strains was rescued exclusively using PER.C6 cells by various transfection methods, including an animal component-free procedure. Furthermore, a whole inactivated vaccine carrying the HA and NA segments of A/HK/156/97 (H5N1) that was both rescued from and propagated on PER.C6 cells, conferred protection in a mouse model. Thus PERC6 cells provide an attractive platform for generation of influenza vaccine strains via reverse genetics.

Code(s) de classement : 002A05F04

Descriptor(s) anglais
- Descripteur(s) : Epidemic; Vaccine strain; Genetic vaccine; Genetics; Influenza
- Desc. génériques : Viral disease; Infection

Descriptor(s) français
- Descripteur(s) : Epidémie; Souche vaccinale; Vaccin génétique; Génétique; Grippe
- Desc. génériques : Virosé; Infection

Localisation : INIST-20289, 354000187881750120
Origine de la notice : INIST
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Epidemiology of H5N1 avian influenza; Avian Influenza

Titre : Epidemiology of H5N1 avian influenza; Avian Influenza

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Source : Comparative immunology, microbiology and infectious diseases; vol. 32; no. 4; pp. 325-340
ISSN : 0147-9571
CODEN : CIMIDV
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Langue(s) du résumé : fre
Type de document : P
Nombre de références : 88 ref.

Résumé : Depuis 1996, des cas de grippe aviaire H5N1 hautement pathogène (HP) ont pu être observés chez les volailles domestiques, les oiseaux sauvages et les humains. Le risque de transmission est associé au contact direct avec des oiseaux infectés. La manière dont le virus H5N1 s'est propagé de l'Asie à l'Europe, l'Afrique et l'Extrême-Orient n'est pas claire; des facteurs de risque tels que le commerce illégal d'oiseaux exotiques et de volaille domestique, et la migration des oiseaux ont été attestés. Les mesures mises en place pour contrôler le virus, notamment l'abattage, le nettoyage, la désinfection et la vaccination, se sont révélées insuffisantes pour éradiquer le virus H5N1 en Asie, mais ont porté leurs fruits en Europe.

Code(s) de classement : 002A05C10

Description(s) anglais

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Infection; Viral disease; Farming animal; Veterinary

Description(s) français

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Infection; Virose; Animal élevage; Vétérinaire

Localisation : INIST-16817, 354000186881770060
Origine de la notice : INIST
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Highly pathogenic H5N1 avian influenza virus: Cause of the next pandemic?; Avian Influenza

**Titre** : Highly pathogenic H5N1 avian influenza virus: Cause of the next pandemic?; Avian Influenza

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**Source** : Comparative immunology, microbiology and infectious diseases; vol. 32; no. 4; pp. 287-300

**ISSN** : 0147-9571

**CODEN** : CIMIDV

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Langue(s) du résumé** : fre

**Type de document** : P

**Nombre de références** : 111 ref.

**Résumé** : Since 1997, when human infections with a highly pathogenic (HP) avian influenza A virus (AIV) subtype H5N1 - previously infecting only birds - were identified in a Hong Kong outbreak, global attention has focused on the potential for this virus to cause the next pandemic. From December 2003, an unprecedented H5N1 epizootic in poultry and migrating wild birds has spread across Asia and into Europe, the Middle East, and Africa. Humans in close contact with sick poultry and on rare occasion with other infected humans, have become infected. As of early March 2007, 12 countries have reported 167 deaths among 277 laboratory-confirmed human infections to WHO. WHO has declared the world to be in Phase 3 of a Pandemic Alert Period. This paper reviews the evolution of HP AIV H5N1, molecular changes that enable AIVs to infect and replicate in human cells and spread efficiently from person-to-person, and strategies to prevent the emergence of a pandemic virus.

**Code(s) de classement** : 002A05C10

**Descripateur(s) anglais**

- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen

**Descriputeur(s) français**

- **Desc. génériques** : Influenzavirus aviaire; Virus grippal A; Pouvoir pathogène; Microbiologie; Immunologie

**Localisation** : INIST-16817, 354000186881770030

**Origine de la notice** : INIST

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Avian influenza virus; Avian Influenza

Titre : Avian influenza virus; Avian Influenza

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Source : Comparative immunology, microbiology and infectious diseases; vol. 32; no. 4; pp. 301-310
ISSN : 0147-9571
CODEN : CIMIDV
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Langue(s) du résumé : fre
Type de document : P
Nombre de références : 63 ref.

Résumé : Habituellement, les virus de la grippe aviaire ne se reproduisent pas efficacement chez les humains, une transmission directe d'oiseau à homme étant dès lors peu probable. Cependant, depuis 1997, plusieurs cas d'infection humaine de différents sous-types (H5N1, H7N7 et H9N2) de grippes aviaires ont été identifiés et ont entraîné la crainte d'une éventuelle pandémie de grippe aviaire chez les humains. Bien qu'il existe des présomptions de transmission d'humain à humain, les virus influenza d'origine aviaire originaux, une fois isolés des humains, ne parviennent pas à se transmettre efficacement d'homme à homme. Néanmoins, l'inoculation du virus H5N1 d'origine aviaire par les humains augmente la probabilité de l'apparition d'un virus de la grippe aviaire adapté aux humains qui pourrait entraîner une pandémie. Dès lors, une meilleure compréhension des propriétés génétiques et biologiques de la restriction d'hôte des virus influenza permettra de déterminer si l'introduction d'un virus influenza original chez l'homme peut aboutir à une pandémie. Dans cet article, nous aborderons les connaissances actuelles sur le virus influenza de type A auquel s'apparentent toutes les souches du virus de la grippe aviaire.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen

Descripteur(s) français

Desc. génériques : Influenzavirus aviaire; Transmission; Microbiologie; Immunologie

Localisation : INIST-16817, 354000186881770040
Origine de la notice : INIST
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Avian influenza in birds and mammals; Avian Influenza

Titre : Avian influenza in birds and mammals; Avian Influenza

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Source : Comparative immunology, microbiology and infectious diseases; vol. 32; no. 4; pp. 255-273
ISSN : 0147-9571
CODEN : C1MIDV
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Langue(s) du résumé : fre
Type de document : P
Nombre de références : 98 ref.

Résumé : Les symptômes engendrés par les variantes du virus de la grippe aviaire changent en fonction de l'espèce infectée, de sa susceptibilité et de sa réaction à l'infection, ainsi que de la virulence de la variante en question. Bien que les variantes de la grippe aviaire puissent toucher un grand nombre d'animaux, il est rare qu'une variante ou un sous-type infecte plus d'une espèce. La variante H5N1 hautement pathogène du virus de la grippe aviaire (HPAIV) provient du virus A/goose/Guangdong/96 (H5N1 HPAIV) et a infecté diverses espèces dans le monde entier. Bien que les espèces affectées par le H5N1 HPAI sur le terrain diffèrent de celles qui ont été étudiées à des fins expérimentales, les symptômes qu'elles présentent sont similaires. Certaines espèces connaissent une défaillance des organes suivie d'une mort rapide sans aucun signe visible de la maladie. Cette catégorie couvre notamment les poulets et autres volailles de l'ordre des galliformes. Les autres espèces développent des signes neurologiques entraînant la mort de l'hôte. C'est ce que les études ont démontré pour les chats (Carnivora), les oies (Anseriformes), les rats (Struthioniformes), les pigeons inoculés à fortes doses (Columbiformes) et les canards infectés par le H5N1 HPAIV isolé depuis 2002 (Anseriformes). Dans le cas de certaines espèces, la maladie dure plus longtemps avec des signes plus présents et plus nombreux, et se termine inévitablement par une défaillance des organes internes entraînant la mort. Ceci a été vérifié pour les humains (Primates) ainsi que les représentants en laboratoire des maladies humaines, le furet (Carnivora), la souris (Rodentia) et les macaques (Primates). De plus, certaines espèces résistent plus au virus H5N1 HPAIV et développent peu ou pas de signes de la maladie. Ces espèces comprennent notamment les pigeons dans certaines études (Columbiformes), les canards inoculés avec une variante pré-2002 (Anseriformes) et les cochons (Artiodactyla).

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Desc. génériques : Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Infection; Viral disease; Zoopathogen

Descripteur(s) français
Desc. génériques : Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Infection; Virose; Zoopathogène

Localisation : INIST-16817, 354000186881770010
Origine de la notice : INIST

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Conventional and future diagnostics for avian influenza; Avian Influenza

Titre : Conventional and future diagnostics for avian influenza; Avian Influenza

Auteur(s) : CHARLTON (Bruce); CROSSLEY (Beate); HIETALA (Sharon); SANDROCK (Christian), ed.
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Source : Comparative immunology, microbiology and infectious diseases; vol. 32; no. 4; pp. 341-350
ISSN : 0147-9571
CODEN : CIMIDV
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Langue(s) du résumé : fre
Type de document : P
Nombre de références : 53 ref.

Résumé : La propagation significative et continue de la souche asiatique de la grippe aviaire H5N1 par delà les frontières depuis 2003, combinée à la transmission avérée des oiseaux aux humains et autres mammifères, a focalisé l'attention générale sur les stratégies de diagnostic et de détection du virus de la grippe aviaire. À côté des méthodes conventionnelles et historiques utilisées par les laboratoires pour isoler et identifier les virus, ainsi que détecter des anticorps spécifiques, de nouvelles technologies sont rapidement adaptées au contrôle et au diagnostic de la grippe aviaire dans le monde entier. Les outils moléculaires, en particulier, permettent d'améliorer les technologies de laboratoire sur puce parfaitement intégrées permettant la détection, la détermination du pathotype et la caractérisation phylogénétique de virus influenza de type A issus de spécimens cliniques. Plutôt que d'opter pour une approche unique, la tendance en matière de diagnostic de la grippe aviaire est plutôt à l'adoption d'une stratégie qui exploite les différentes technologies conventionnelles et avancées afin de réaliser des tests « sur mesure ».

Code(s) de classement : 002A05

Descripteur(s) anglais : Detection; Diagnosis; Microbiology; Immunology; Avian influenza
Desc. génériques : Infection; Viral disease

Descripteur(s) français : Détectio; Diagnostic; Microbiologie; Immunologie; Grippe aviaire
Desc. génériques : Infection; Virose

Localisation : INIST-16817, 354000186881770070
Origine de la notice : INIST
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Oseltamivir-Resistant Influenza A Viruses Circulating in Japan

**Titre :** Oseltamivir-Resistant Influenza A Viruses Circulating in Japan

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**Source :** Journal of clinical microbiology : (Print); vol. 47; no. 5; pp. 1424-1427

**ISSN :** 0095-1137

**CODEN :** JCMIDW

**Date de publication :** 2009

**Pays de publication :** USA

**Langue(s) :** ENG

**Type de document :** P

**Nombre de références :** 17 ref.

**Résumé :** Surveillance studies of the influenza viruses circulating in Europe and other countries in 2007 and 2008 have revealed rates of resistance to oseltamivir of up to 67% among H1N1 viruses. In the present study, we examined 202 clinical samples obtained from patients infected with H1N1 virus in Japan in 2007 and 2008 for oseltamivir resistance and found that three were oseltamivir resistant (1.5%). The 50% inhibitory concentrations (IC50s), as measured by a sialidase inhibition assay with these drug-resistant viruses, were > 100-fold higher than those of the nonresistant viruses (median IC50, 12.6 nmol/liter). The His274Tyr (strain N2 numbering) mutation of the neuraminidase protein, which is known to confer oseltamivir resistance, was detected in these three isolates. Phylogenetic analysis showed that one virus belonged to a lineage that is composed of drug-resistant viruses isolated in Europe and North America and that the other two viruses independently emerged in Japan. Continued surveillance studies are necessary to observe whether these viruses will persist.

**Code(s) de classement :** 002A05C10

**Descripteur(s) anglais**

**Description(s) :** Influenza A virus; Resistance; Japan; Microbiology; Oseltamivir; Antiviral

**Desc. génériques :** Influenzavirus A; Orthomyxoviridae; Virus; Asia; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor; Neuraminidase inhibitor

**Descripteur(s) français**

**Description(s) :** Virus grippal A; Résistance; Japon; Microbiologie; Oséltamivir; Antiviral

**Desc. génériques :** Influenzavirus A; Orthomyxoviridae; Virus; Asie; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme; Inhibiteur neuraminidase

**Localisation :** INIST-17088, 354000186129460210

**Origine de la notice :** INIST

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Influenza Antiviral Resistance Testing in New York and Wisconsin, 2006 to 2008: Methodology and Surveillance Data

Titre : Influenza Antiviral Resistance Testing in New York and Wisconsin, 2006 to 2008: Methodology and Surveillance Data

Auteur(s) : LAPLANTE (Jennifer M.); MARSHALL (Steven A.); SHUDT (Matthew); VAN (Tam T.); REISDORF (Erik S.); MINGLE (Lisa A.); SHULT (Peter A.); GEORGE (Kirsten St.)

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Source : Journal of clinical microbiology : (Print); vol. 47; no. 5; pp. 1372-1378

ISSN : 0095-1137
CODEN : ICMIDW
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 29 ref.

Résumé : The need for effective influenza antiviral susceptibility surveillance methods has increased due to the emergence of near-universal adamantane resistance in influenza A/H3N2 viruses during the 2005-2006 season and the appearance of oseltamivir resistance in the influenza A/H1N1 virus subtype during the 2007-2008 season. The two classes of influenza antivirals, the neuraminidase inhibitors (NAIs) and the adamantanes, are well characterized, as are many mutations that can confer resistance to these drugs. Adamantane resistance is imparted mainly by a S31N mutation in the matrix gene, while NAI resistance can result from a number of mutations in the neuraminidase gene. During the 2007-2008 season, a neuraminidase mutation (H274Y) conferring resistance to the NAI oseltamivir emerged worldwide in the A/H1N1 virus subtype. Surveillance methodology and data from New York (NY) and Wisconsin (WI) for the 2006-2007 and 2007-2008 influenza seasons are presented. We used an existing pyrosequencing method (R. A. Bright et al., Lancet 366:1175-1181, 2005) and a modified version of this method for detection of adamantane resistance mutations. For NAI resistance mutation detection, we used a mutation-specific pyrosequencing technique and developed a neuraminidase gene dideoxy sequencing method. Adamantane resistance in the A/H3N2 virus samples was 100% for 2007-2008, similar to the 99.8% resistance nationwide as reported by the CDC. Adamantane resistance was found in only 1.2% of NY and WI A/H1N1 virus samples, compared to that found in 10.8% of samples tested nationwide as reported by the CDC. Influenza A/H1N1 virus H274Y mutants were found in 11.1% of NY samples for 2007-2008, a level comparable to the 10.9% nationwide level reported by the CDC; in contrast, mutants were found in 17.4% of WI samples. These results indicate the need for regional influenza antiviral surveillance.
Emerging and re-emerging viruses in Malaysia, 1997-2007

Titre : Emerging and re-emerging viruses in Malaysia, 1997-2007

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Source : International journal of infectious diseases; vol. 13; no. 3; pp. 307-318
ISSN : 1201-9712
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 128 ref.

Résumé : Over the past decade, a number of unique zoonotic and non-zoonotic viruses have emerged in Malaysia. Several of these viruses have resulted in significant morbidity and mortality to those affected and they have imposed a tremendous public health and economic burden on the state. Amongst the most devastating was the outbreak of Nipah virus encephalitis in 1998, which resulted in 109 deaths. The culling of more than a million pigs, identified as the amplifying host, ultimately brought the outbreak under control. A year prior to this, and subsequently again in 2000 and 2003, large outbreaks of hand-foot-and-mouth disease due to enterovirus 71, with rare cases of fatal neurological complications, were reported in young children. Three other new viruses - Tioman virus (1999), Pulau virus (1999), and Melaka virus (2006) - whose origins have all been linked to bats, have been added to the growing list of novel viruses being discovered in Malaysia. The highly pathogenic H5N1 avian influenza has also been detected in Malaysia with outbreaks in poultry in 2004, 2006, and 2007. Fortunately, no human infections were reported. Finally, the HIV/AIDS epidemic has seen the emergence of an HIV-1 recombinant form (CRF33_01B) in HIV-infected individuals from various risk groups, with evidence of ongoing and rapid expansion.

Code(s) de classement : 002B05C02D; 002B05C02C; 002B06D01

Descripteur(s) anglais
Descripteur(s) : AIDS; Avian influenza; Malaysia; Enterovirus 71; HIV-1 virus; Influenzavirus A(H5N1)
Desc. génériques : Viral disease; Infection; Asia; Enterovirus; Picornaviridae; Virus; Human immunodeficiency virus; Lentivirus; Retroviridae; Immune deficiency; Immunopathology

Descripteur(s) français
Descripteur(s) : SIDAA; Grippe aviaire; Malaisie; Entérovirus 71; Virus HIV1; Influenzavirus A(H5N1)
Desc. génériques : Virose; Infection; Asie; Enterovirus; Picornaviridae; Virus; Virus immunodéficience humaine; Lentivirus; Retroviridae; Immunodéficit; Immunopathologie

Localisation : INIST-26659, 354000186108820030
Origine de la notice : INIST
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Antiviral Role of Toll-Like Receptor-3 Agonists Against Seasonal and Avian Influenza Viruses; New Developments in Drug and Vaccine Discoveries

Titre : Antiviral Role of Toll-Like Receptor-3 Agonists Against Seasonal and Avian Influenza Viruses; New Developments in Drug and Vaccine Discoveries

Auteur(s) : WONG (J. P.); CHRISTOPHER (M. E.); VISWANATHAN (S.); DAI (X.); SALAZAR (A. M.); SUN (L.-Q.); WANG (M.); BOURINBAIAR (Aldar S.), ed.
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Source : Current pharmaceutical design; vol. 15; no. 11; pp. 1269-1274
ISSN : 1381-6128
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 21 ref.

Résumé : The divergence and antigenic shifts in influenza viruses represent significant challenges for the development of effective vaccines and antiviral drugs against influenza viruses. In view of current challenges and/or deficiencies in the influenza pandemic influenza preparedness, novel antiviral strategies which are robust and can respond to constant viral mutations, are particularly needed to combat future pandemic threats. Toll-like receptor-3 (TLR-3) is an integral part of the host's innate immune system and serves as an important signaling pathway for the recognition of dsRNA for the triggering of antiviral and inflammatory responses to combat viral infections. This review examines dsRNA including Poly ICLC and liposome-encapsulated Poly ICLC (LE Poly ICLC) as TLR-3 agonists for their antiviral activity against seasonal and highly pathogenic avian influenza (HPAI) viruses. Furthermore, their roles in attenuating the antiviral and inflammatory cytokines in the host will also be explored. Preclinical studies in experimental animals suggest Poly ICLC and liposome-encapsulated Poly ICLC are safe and offer broad-spectrum protection against both seasonal and HPAI viruses, as well as other respiratory viruses including respiratory syncytial virus and SARS. Preliminary results from recent studies suggest these drugs up-regulate the production of interferons (-a, -p, and -y), and tumor necrosis factor (TNF-a) but downregulate some proinflammatory cytokines including IL-2 and IL-4. Taken together, these results suggest these TLR-3 agonists have a promising role to play as safe, effective and broad-spectrum anti-influenza drugs that could complement other antiviral drugs to combat seasonal, zoonotic and pandemic influenza viruses. The clinical safety of these drugs and their efficacy in pre-clinical studies may provide sufficient justification for regulatory agencies to consider their fast track development for use in future outbreaks of pandemic influenza or of other emerging respiratory pathogens.

Code(s) de classement : 002B05C02C; 002B02S05

Description(s) anglais

Description(s) : Antiviral; Toll like receptor 3; Agonist; Avian influenza; Review; Influenza; Pharmaceutical technology; Influenzavirus A(H5N1)
Desc. généraux : Viral disease; Infection

Description(s) français

Description(s) : Antiviral; Récepteur TLR3; Agoniste; Grippe aviaire; Article synthèse; Grippe; Technologie pharmaceutique; Grippe saisonnière; Influenzavirus A(H5N1)
Desc. généraux : Virose; Infection

Localisation : INIST-26320, 354000184910770100
Effects of Double Combinations of Amantadine, Oseltamivir, and Ribavirin on Influenza A (H5N1) Virus Infections in Cell Culture and in Mice

Titre : Effects of Double Combinations of Amantadine, Oseltamivir, and Ribavirin on Influenza A (H5N1) Virus Infections in Cell Culture and in Mice

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Source : Antimicrobial agents and chemotherapy; vol. 53; no. 5; pp. 2120-2128
ISSN : 0066-4804
CODEN : AACHAX
Date de publication : 2009
Pays de publication : USA
Type de document : P
Nombre de références : 29 ref.

Résumé : An amantadine-resistant influenza A/Duck/MN/1525/81 (H5N1) virus was developed from the low-pathogenic North American wild-type (amantadine-sensitive) virus for studying treatment of infections in cell culture and in mice. Double combinations of amantadine, oseltamivir (or the cell culture-active form, oseltamivir carboxylate), and ribavirin were used. Amantadine-oseltamivir carboxylate and amantadine-ribavirin combinations showed synergistic interactions over a range of doses against wild-type virus in Madin-Darby canine kidney (MDCK) cell culture, but oseltamivir carboxylate-ribavirin combinations did not. Primarily additive interactions were seen with oseltamivir carboxylate-ribavirin combinations against amantadine-resistant virus. The presence of amantadine in drug combinations against the resistant virus did not improve activity. The wild-type and amantadine-resistant viruses were lethal to mice by intranasal instillation. The resistant virus infection could not be treated with amantadine up to 100 mg/kg body weight/day, whereas the wild-type virus infection was treatable with oral doses of 10 (weakly effective) to 100 mg/kg/day administered twice a day for 5 days starting 4 h prior to virus exposure. Drug combination studies showed that treatment of the amantadine-resistant virus infection with amantadine-oseltamivir or amantadine-ribavirin combinations was not significantly better than using oseltamivir or ribavirin alone. In contrast, the oseltamivir-ribavirin (25- and 75-mg/kg/day combination) treatments produced significant reductions in mortality. The wild-type virus infection was markedly reduced in severity by all three combinations (amantadine, 10 mg/kg/ day combined with the other compounds at 20 or 40 mg/kg/day) compared to monotherapy with the three compounds. Results indicate a lack of benefit of amantadine in combinations against amantadine-resistant virus, but positive benefits in combinations against amantadine-sensitive virus.
Antagoniste; Récepteur dopaminergique; Récepteur glutamate; Récepteur NMDA; Stimulant dopaminergique; Dérivé de l'amantadine; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme; Inhibiteur neuraminidase; analogue de nucléoside

Localisation : INIST-13334, 354000184988660530
Origine de la notice : INIST
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Neutralizing monoclonal antibodies to different clades of Influenza A H5N1 viruses

Titre : Neutralizing monoclonal antibodies to different clades of Influenza A H5N1 viruses

Auteur(s) : OH (Sawyin); SELLECK (Paul); TEMPERTON (Nigel J.); CHAN (Paul K. S.); CAPECCHI (Barbara); MANAVIS (Jim); HIGGINS (Geoff); BURRELL (Christopher J.); KOK (Tuckweng)

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Source : Journal of virological methods; vol. 157; no. 2; pp. 161-167

ISSN : 0166-0934
CODEN : JVMEDH
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 3/4 p.

Résumé : Four IgG1k monoclonal antibodies (mAbs) against Influenza A/Chicken/Vietnam/8/2004 (H5N1) virus are described. Three of these showed neutralizing activities against H5N1 strains from clades 1, 2 and 3 using a retroviral pseudotype or live virus microneutralization assay. In the pseudotype assay, the IC90 neutralizing titre range was >1600-51,200, and with the microneutralization was 80 >= 10,240. MAb 1C1 showed strong neutralizing activities in both assays. All four mAbs reacted specifically to the immunogen by immunohistochemical staining and to A/Hong Kong/483/1997 (H5N1) and A/Thailand/1 (KAN-1 )/2004 (H5N1)-infected MDCK cells by immunofluorescence. ELISA titrations of the mAbs showed specificity for H5N1 haemagglutinin (HA) and no cross-reactivity to 15 other Influenza A subtypes. Only mAbs 1C1 and the non-neutralizing 1F7 reacted with HA1, the cleaved subunit of HA, by Western blot. These results suggest that the mAbs recognize distinct or overlapping epitopes and will be useful reagents for construction of specific rapid point-of-care assays or for therapeutic use.

Code(s) de classement : 002A05C09

Descriputeur(s) anglais
- Description(s) : Influenza A virus; Avian influenzavirus; Neutralizing antibody; Monoclonal antibody; Hemagglutinin; Neutralization; Microbiology; Method; Virology; Influenza
- Description(s) génériques : Influenzavirus A; Orthomyxoviridae; Virus; Viral disease; Infection

Descriputeur(s) français
- Description(s) : Virus grippal A; Influenzavirus aviaire; Anticorps neutralisant; Anticorps monoclonal; Hémagglutinine; Neutralisation; Microbiologie; Méthode; Virologie; Grippe
- Description(s) génériques : Influenzavirus A; Orthomyxoviridae; Virus; Virose; Infection

Localisation : INIST-18295, 354000186143140070
Origine de la notice : INIST
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Selection of H5N1 Influenza Virus PB2 during Replication in Humans

**Titre** : Selection of H5N1 Influenza Virus PB2 during Replication in Humans

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**Source** : Journal of virology; vol. 83; no. 10; pp. 5278-5281

**ISSN** : 0022-538X

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 19 ref.

**Résumé** : Highly pathogenic H5N1 influenza viruses continue to cause concern, even though currently circulating strains are not efficiently transmitted among humans. For efficient transmission, amino acid changes in viral proteins may be required. Here, we examined the amino acids at positions 627 and 701 of the PB2 protein. A direct analysis of the viral RNAs of H5N1 viruses in patients revealed that these amino acids contribute to efficient virus propagation in the human upper respiratory tract. Viruses grown in culture or eggs did not always reflect those in patients. These results emphasize the importance of the direct analysis of original specimens.

**Code(s) de classement** : 002A05C10

**Descripteur(s) anglais**
- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus
- **Descriputeur(s) :** Avian influenzavirus; Influenza A virus; Human; Replication; Virology

**Descripteur(s) français**
- **Desc. génériques** : Influenzavirus aviaire; Virus grippal A; Homme; Réplication; Virologie
- **Descriputeur(s) :** Influenzavirus aviaire; Virus grippal A; Homme; Réplication; Virologie

**Localisation** : INIST-13592, 354000186082170520

**Origine de la notice** : INIST

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Nonreplicating Vaccinia Virus Vectors Expressing the H5 Influenza Virus Hemagglutinin Produced in Modified Vero Cells Induce Robust Protection

**Titre** : Nonreplicating Vaccinia Virus Vectors Expressing the H5 Influenza Virus Hemagglutinin Produced in Modified Vero Cells Induce Robust Protection

**Auteur(s)** : MAYRHOFER (Josef); COULIBALY (Sogue); HESSEL (Annett); HOLZER (Georg W.); SCHWENDEINGER (Michael); BRÜHI (Peter); GERENCER (Marijan); CROWE (Brian A.); SHEN SHUO; WANJING HONG; YEE JOO TAN; DIETRICH (Barbara); SABARTH (Nicolas); SAVIDIS-DACHO (Helga); KISTNER (Otfried); BARRETT (P. Noel); FALKNER (Falko G.)

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**Source** : Journal of virology; vol. 83; no. 10; pp. 5192-5203

**ISSN** : 0022-538X

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 51 ref.

**Résumé** : The timely development of safe and effective vaccines against avian influenza virus of the H5N1 subtype will be of the utmost importance in the event of a pandemic. Our aim was first to develop a safe live vaccine which induces both humoral and cell-mediated immune responses against human H5N1 influenza viruses and second, since the supply of embryonated eggs for traditional influenza vaccine production may be endangered in a pandemic, an egg-independent production procedure based on a permanent cell line. In the present article, the generation of a complementing Vero cell line suitable for the production of safe poxviral vaccines is described. This cell line was used to produce a replication-deficient vaccinia virus vector H5N1 live vaccine, dW-HA5, expressing the hemagglutinin of a virulent clade 1 H5N1 strain. This experimental vaccine was compared with a formalin-inactivated whole-virus vaccine based on the same clade and with different replicating poxvirus-vectored vaccines. Mice were immunized to assess protective immunity after high-dose challenge with the highly virulent A/Vietnam/1203/2004(H5N1) strain. A single dose of the defective live vaccine induced complete protection from lethal homologous virus challenge and also full cross-protection against clade 0 and 2 challenge viruses. Neutralizing antibody levels were comparable to those induced by the inactivated vaccine. Unlike the whole-virus vaccine, the dW-HA5 vaccine induced substantial amounts of gamma interferon-secreting CD8 T cells. Thus, the nonreplicating recombinant vaccinia virus vectors are promising vaccine candidates that induce a broad immune response and can be produced in an egg-independent and adjuvant-independent manner in a proven vector system.

**Code(s) de classement** : 002A05C10

**Descripteur(s) anglais**

*Descriptor(s) : Vaccinia virus; Influenzavirus; Vector; Hemagglutinin; In vitro; Virology*

*Desc. génériques : Orthopoxvirus; Chordopoxvirinae; Poxviridae; Virus; Orthomyxoviridae*

**Descripteur(s) français**

*Descriptor(s) : Virus vaccine; Influenzavirus; Vecteur; Hémagglutinine; In vitro; Virologie*

*Desc. génériques : Orthopoxvirus; Chordopoxvirinae; Poxviridae; Virus; Orthomyxoviridae*

**Localisation** : INIST-13592. 354000186082170450

**Origine de la notice** : INIST

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Human single-chain antibodies that neutralize homologous and heterologous strains and clades of influenza A virus subtype H5N1

Titre : Human single-chain antibodies that neutralize homologous and heterologous strains and clades of influenza A virus subtype H5N1

Auteur(s) : MANEEWATCH (Santi); THANONGSAKSRIKUL (Jeeraphong); SONGSERM (Thaweasak); THUENG-IN (Kanyarat); KULKEAW (Kasem); THATHAISONG (Umapom); SRIMANOTE (Potjanee); TONGTAWE (Pongsri); TAPCHAISRI (Pramuan); CHAICUMPA (Wanpen)

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Source : Antiviral therapy : (London); vol. 14; no. 2; pp. 221-230
ISSN : 1359-6535
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 18 ref.

Résumé : Background: Human antibodies that interfere with the biological activity of haemagglutinins (HAs) of influenza viruses have high potential as an antiviral agent. Methods: Human single-chain antibody fragments (HuScFv) to recombinant and native HAs of the influenza virus H5N1 subtype were produced using a human antibody phage display library with the intention to increase the therapeutic arsenal against this highly pathogenic virus. Results: The HuScFv inhibited HA activity and neutralized infectivity of both homologous and heterologous strains and clades of the H5N1 subtype in Madin-Darby canine kidney cell cultures. Intraperitoneally injected HuScFv also mediated immunotherapeutic protection in mice that were intranasally challenged with highly pathogenic H5N1 viruses belonging to different strains and clades. Conclusions: Our data indicate that it might be worth pursuing these HuScFv further for future consideration as candidates for influenza intervention and treatment.
Animal models for the study of influenza pathogenesis and therapy

Titre : Animal models for the study of influenza pathogenesis and therapy

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Source : Antiviral research; vol. 82; no. 2
ISSN : 0166-3542
CODEN : ARSRDR
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 2 p.1/2

Résumé : Influenza A viruses causes a variety of illnesses in humans. The most common infection, seasonal influenza, is usually a mild, self-limited febrile syndrome, but it can be more severe in infants, the elderly, and immunodeficient persons, in whom it can progress to severe viral pneumonitis or be complicated by bacterial superinfection, leading to pneumonia and sepsis. Seasonal influenza also occasionally results in neurologic complications. Rarely, viruses that have spread from wild birds to domestic poultry can infect humans; such "avian influenza" can range in severity from mild conjunctivitis through the rapidly lethal disease seen in persons infected with the H5N1 virus that first emerged in Hong Kong in 1997. To develop effective therapies for this wide range of diseases, it is essential to have laboratory animal models that replicate the major features of illness in humans. This review describes models currently in use for elucidating influenza pathogenesis and evaluating new therapeutic agents.

Code(s) de classement : 002B02S05; 002B05C02C

Description(s) anglais

Description(s) : Animal model; Avian influenza; Etiopathogenesis; Treatment; Ferret; Antiviral; Performance evaluation; Technique; Influenzavirus A(H5N1)
Desc. génériques : Viral disease; Infection; Fissipedia; Carnivora; Mammalia; Vertebrata

Description(s) français

Description(s) : Modèle animal; Grippe aviaire; Etiopathogénie; Traitement; Furet; Antiviral; Evaluation performance; Technique; Influenzavirus A(H5N1)
Desc. génériques : Virose; Infection; Fissipedia; Carnivora; Mammalia; Vertebrata

Localisation : INIST-18839, 354000184973060030
Origine de la notice : INIST
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Systemic infection of avian influenza A virus H5N1 subtype in humans

Titre : Systemic infection of avian influenza A virus H5N1 subtype in humans

Auteur(s) : ZENGFENG ZHANG; JINXIA ZHANG; KAI HUANG; LI (Kang-Sheng); YUEN (Kwok-Yung); YI GUAN; HONGLIN CHEN; WAI FU NG

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Source : Human pathology; vol. 40; no. 5; pp. 735-739
ISSN : 0046-8177
CODEN : HPCQA4
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 8 ref.

Résumé : The viral dissemination in a patient with avian influenza A subtype H5N1 infection was retrospectively studied by the immunohistochemical localization of viral nucleoprotein antigen. The pathology was marked by diffuse alveolar damage, lymphoid depletion, and reactive hemophagocytic syndrome. Besides the lung and the upper respiratory tract, viral antigen was detected in the small and large intestinal epithelial cells, hematopoietic cells in the bone marrow, glial cells and neurons of the brain, and lymphocytes. The results confirmed that H5N1 virus disseminated to multiple organs beyond the respiratory system. However, specific pathological changes were noted in the respiratory system only, and productive viral replication confirmed by culture was noted only in the lung. More postmortem studies are needed to elucidate the pathogenesis of this highly fatal zoonotic disease.

Code(s) de classement : 002B24O; 002B05C02C

Descripteur(s) anglais : Infection; Systemic; Disseminated; Avian influenza; Influenza A virus; Subtype; Human; Tissue; Tropism; Immunohistochemistry; Anatomic pathology
Desc. génériques : Viral disease; Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) français : Infection; Systémique; Disséminé; Grippe aviaire; Virus grippal A; Soustype; Homme; Tissu; Tropisme; Immunohistochimie; Anatomopathologie
Desc. génériques : Virose; Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST-16045, 354000184970410160
Origine de la notice : INIST
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Design of oseltamivir analogs inhibiting neuraminidase of avian influenza virus H5N-1

**Titre** : Design of oseltamivir analogs inhibiting neuraminidase of avian influenza virus H5N-1

**Auteur(s)** : RUNGROTMONGKOL (Thanyada); FRECER (Vladimir); DE-EKNAMKUL (Wanchai); HANNONGBUA (Supot); MIERTUS (Stanislav)

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**Source** : Antiviral research; vol. 82; no. 1; pp. 51-58

**ISSN** : 0166-3542

**CODEN** : ARSRDR

**Date de publication** : 2009

**Pays de publication** : NLD

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 3/4 p.

**Résumé** : Neuraminidase is an important target for design of antiviral agents in the prophylaxis and treatment of avian influenza virus infections. We have shown the applicability of computer-assisted combinatorial techniques in the design, focusing and in silico screening of a virtual library of analogs of oseltamivir (Tamiflu) with the goal to find potent inhibitors of influenza A neuraminidase N1 that fill the cavity found adjacent to the active site. Crystal structure of oseltamivir-N1 complex was used in the structure-based focusing and virtual screening of the designed library. A target-specific Piecewise Linear Potential type 1 scoring function fitted for a training set of 14 carbocyclic inhibitors and validated for three other inhibitors was used to select virtual hits with predicted inhibitory activities in the subnanomolar range. The results of this computational study are useful as a rational guide for synthetic and medicinal chemists who are developing new drugs against the avian influenza virus H5N1.

**Code(s) de classement** : 002B02S05

**Description(s) anglais**

- **Descriputeur(s) anglais**
  - **Descriputeur(s)** : Design; Oseltamivir; Analog; Exo- alpha -sialidase; Avian influenzavirus; Subtype; Typing; Neuraminidase inhibitor; Computer aid; Chemical compound library; Combinatorial chemistry; In silico; Screening; Chemical structure; Structure activity relation; Antiviral; Influenzavirus A(H5N1)
  - **Desc. génériques** : Glycosidases; Glycosylases; Hydrolases; Enzyme; Influenzavirus A; Orthomyxoviridae; Virus; Enzyme inhibitor

**Description(s) français**

- **Descriputeur(s) français**
  - **Descriputeur(s)** : Conception; Oséltamivir; Analogue; Exo- alpha -sialidase; Influenzavirus aviaire; Soustype; Typage; Inhibiteur neuraminidase; Assistance ordinateur; Chimiothèque; Chimie combinatoire; In silico; Criblage; Structure chimique; Relation structure activité; Antiviral; Influenzavirus A(H5N1)
  - **Desc. génériques** : Glycosidases; Glycosylases; Hydrolases; Enzyme; Influenzavirus A; Orthomyxoviridae; Virus; Inhibiteur enzyme

**Localisation** : INIST-18839, 354000184929350070

**Origine de la notice** : INIST

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Anti-influenza virus activity and structure-activity relationship of aglycoristocetin derivatives with cyclobutenedione carrying hydrophobic chains

Titre : Anti-influenza virus activity and structure-activity relationship of aglycoristocetin derivatives with cyclobutenedione carrying hydrophobic chains

Auteur(s) : NAESENS (Lieve); VANDERLINDEN (Evelien); ROTH (Erzsébet); ANDREI (Graciela); SNOECK (Robert); PANNECOUQUE (Christophe); ILLYES (Eszter); BATTA ( Gyula); HERCZEGH (Pal); SZTARICSKAI (Ferenc)

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Source : Antiviral research; vol. 82; no. 1; pp. 89-94
ISSN : 0166-3542
CODEN : ARSRDR
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 1/2 p.

Résumé : Previous studies have demonstrated that glycopeptide compounds carrying hydrophobic substituents can have favorable pharmacological (i.e. antibacterial and antiviral) properties. We here report on the in vitro anti-influenza virus activity of aglycoristocetin derivatives containing hydrophobic side chain-substituted cyclobutenedione. The lead compound 8e displayed an antivirally effective concentration of 0.4 μM, which was consistent amongst influenza A/H1N1, A/H3N2 and B viruses, and a selectivity index >50. Structural analogues derived from aglycovancmycin were found to be inactive. The hydrophobic side chain was shown to be an important determinant of activity. The narrow structure-activity relationship and broad activity against several human influenza viruses suggest a highly conserved interaction site, which is presumably related to the influenza virus entry process. Compound 8e proved to be inactive against several unrelated RNA and DNA viruses, except for varicella-zoster virus, against which a favorable activity was noted.

Code(s) de classement : 002B02S05; 002B05C02C

Descripateur(s) anglais

Descripateur(s) : Influenzavirus; Structure activity relation; Glycopeptide; Antibiotic; Antibacterial agent; Ristocetin; Influenza; Antiviral; Biological activity; Hydrophobic site; Antiinfectious

Desc. génériques : Orthomyxoviridae; Virus; Viral disease; Infection; Peptides; Polypeptide

Descriputeur(s) français

Descriputeur(s) : Influenzavirus; Relation structure activité; Glycopeptide; Antibiotique; Antibactérien; Ristocétine; Grippé; Antiviral; Activité biologique; Site hydrophobe; Antiinfectieux

Desc. génériques : Orthomyxoviridae; Virus; Virose; Infection; Peptide; Polypeptide

Localisation : INIST-18839, 354000184929350120
Origine de la notice : INIST
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Different neuraminidase inhibitor susceptibilities of human H1N1, H1N2, and H3N2 influenza A viruses isolated in Germany from 2001 to 2005/2006

Titre : Different neuraminidase inhibitor susceptibilities of human H1N1, H1N2, and H3N2 influenza A viruses isolated in Germany from 2001 to 2005/2006

Auteur(s) : BAUER (Katja); RICHTER (Martina); WUTZLER (Peter); SCHMIDTKE (Michaela)

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Source : Antiviral research; vol. 82; no. 1; pp. 34-41

ISSN : 0166-3542
CODEN : ARSRDR

Date de publication : 2009
Pays de publication : NLD

Langue(s) : ENG

Type de document : P
Nombre de références : 1 p.

Résumé : In the flu season 2005/2006 amantadine-resistant human influenza A viruses (FLUAV) of subtype H3N2 circulated in Germany. This raises questions on the neuraminidase inhibitor (NAI) susceptibility of FLUAV. To get an answer, chemiluminescence-based neuraminidase inhibition assays were performed with 51 H1N1, H1N2, and H3N2 FLUAV isolated in Germany from 2001 to 2005/2006. According to the mean IC50 values (0.38-0.91 nM for oseltamivir and 0.76-1.13 nM for zanamivir) most H1N1 and H3N2 FLUAV were NAI-susceptible. But, about four times higher zanamivir concentrations were necessary to inhibit neuraminidase activity of H1N2 viruses. Two H1N1 isolates were less susceptible to both drugs in NA inhibition as well as virus yield reduction assays. Results from sequence analysis of viral hemagglutinin and neuraminidase genes and evolutionary analysis of N2 gene revealed (i) different subclades for N2 in H1N2 and H3N2 FLUAV that could explain the differences in zanamivir susceptibility among these viruses and (ii) specific amino acid substitutions in the neuraminidase segment of the two less NAI-susceptible H1N1 isolates. One H3N2 was isolate proved to be a mixture of a NA deletion mutant and full-length NA viruses.

Code(s) de classement : 002B02S05

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Europe; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Europe; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme

Localisation : INIST-18839, 354000184929350050

Origine de la notice : INIST
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Rapid identification of oseltamivir-resistant influenza A(H1N1) viruses with H274Y mutation by RT-PCR/restriction fragment length polymorphism assay

Titre : Rapid identification of oseltamivir-resistant influenza A(H1N1) viruses with H274Y mutation by RT-PCR/restriction fragment length polymorphism assay

Auteur(s) : LIZHENG GUO; GARTEN (Rebecca J.); FOUST (Angie S.); SESSIONS (Wendy M.); OKOMO-ADHIAMBO (Margaret); GUBAREVA (Larisa V.); KLIMOV (Alexander I.); XIYAN XU

Affiliation(s) : Virus Surveillance and Diagnosis Branch, Influenza Division, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, 1600 Clifton Rd, MS:G-16, Atlanta, GA 30333, USA

Source : Antiviral research; vol. 82; no. 1; pp. 29-33

ISSN : 0166-3542
CODEN : ARSRDR
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 3/4 p.

Résumé : In the beginning of 2007-2008 Northern Hemisphere influenza season, the frequency of influenza A(H1N1) viruses bearing a previously defined oseltamivir resistance conferring amino acid change of Histidine to Tyrosine at position 274 (H274Y) of the neuraminidase (NA) increased dramatically. In order to rapidly detect such resistant viruses, an RT-PCR/restriction fragment length polymorphism (RT-PCR/RFLP) assay targeting amino acid 274 of the N1 NA molecule was developed to investigate the presence or absence of the H274Y mutation. The reverse primer was engineered to produce a BspHI site in the amplicon for oseltamivir-sensitive viruses with Histidine at position 274 (274H). A total of 50 influenza A(H1N1) specimens including 30 oseltamivir-sensitive and 20 oseltamivir-resistant ones submitted to the Centers for Disease Control and Prevention (CDC) during the 2007-2008 influenza season were successfully characterized by this assay. The assay was specific for grown A(H1N1) viruses and original clinical specimens, with a lower limit of detection of approximately 10 RNA transcript copies per reaction. Our RT-PCR/RFLP assay provides a simple, rapid and sensitive tool to monitor the emergence and spread of H274Y oseltamivir-resistant influenza A(H1N1) viruses.

Code(s) de classement : 002B02S05; 002B05C02C

Descriputeur(s) anglais
Descripteur(s) : Identification; Oseltamivir; Sensitivity resistance; Influenza A virus; Mutation; Reverse transcription polymerase chain reaction; Restriction fragment length polymorphism; Genotype; Influenza A; Antiviral
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Viral disease; Infection; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor; Neuraminidase inhibitor

Descriputeur(s) français
Descripteur(s) : Identification; Oséltamivir; Sensibilité résistance; Virus grippal A; Mutation; Réaction chaîne polymérase RT; Polymorphisme longueur fragment restriction; Génotype; Grippe A; Antiviral; Influenzavirus A(H1N1)
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Virose; Infection; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme; Inhibiteur neuraminidase

Localisation : INIST-18839, 354000184929350040
Origine de la notice : INIST
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A comparison of the pathogenicity of avian and swine H5N1 influenza viruses in Indonesia

Title: A comparison of the pathogenicity of avian and swine H5N1 influenza viruses in Indonesia

Authors: TAKANO (Ryo); NIDOM (Chairul A.); KISO (Maki); MURAMOTO (Yukiko); YAMADA (Shinya); SHINYA (Kyoko); SAKAI-TAGAWA (Yuko); KAWAOKA (Yoshihiro)

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Source: Archives of virology; vol. 154; no. 4; pp. 677-681

ISSN: 0304-8608

Date de publication: 2009

Pays de publication: AUT

Langue(s): ENG

Type de document: P

Nombre de références: 24 ref.

Résumé: Highly pathogenic avian influenza H5N1 viruses are circulating in many countries. We recently discovered that these viruses have been transmitted to pigs on multiple occasions in Indonesia. To investigate whether avian H5N1 influenza viruses adapted to mammals through their introduction into pigs, we examined the growth of avian and swine isolates in cell culture and compared their pathogenicity in mice. We found that swine isolates were less virulent to mice than avian isolates, suggesting that the viruses became attenuated during their replication in pigs. Continuous surveillance of H5N1 viruses among pigs is clearly warranted.
INFLUENZA A/H1N1 : Questions and answers

Titre : INFLUENZA A/H1N1 : Questions and answers

Auteur(s) : COOMBES (Rebecca)
Affiliation(s) : World Health Organization, BMA, Health Protection Agency, Royal College of General Practitioners, Department of Health, European Centre for Disease Prevention and Control, INC

Source : BMJ. British medical journal : (International ed.); vol. 338; no. 7703; pp. 1104-1105
ISSN : 0959-8146
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P

Résumé : The pandemic alert level has been raised to phase 5-just one level short of a full pandemic-by the World Health Organization. As influenza A/H1N1 spreads quickly from its origins in Mexico, Rebecca Coombes assesses the threat and our levels of protection

Code(s) de classement : 002B01; 002B05C02C

Descriputeur(s) anglais
Descriputeur(s) : Influenza A; Medicine
Desc. génériques : Viral disease; Infection

Descriputeur(s) français
Descriputeur(s) : Grippe A; Médecine
Desc. génériques : Virose; Infection

Localisation : INIST-5002A, 354000184943600140
Origine de la notice : INIST
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Neuraminidase Stalk Length and Additional Glycosylation of the Hemagglutinin Influence the Virulence of Influenza H5N1 Viruses for Mice

Titre : Neuraminidase Stalk Length and Additional Glycosylation of the Hemagglutinin Influence the Virulence of Influenza H5N1 Viruses for Mice

Auteur(s) : MATSUOKA (Yumiko); SWAYNE (David E.); THOMAS (Colleen); RAMEIX-WELTI (Marie-Anne); NAFFAKH (Nadia); WARNES (Christine); ALTHOLTZ (Melanie); DONIS (Ruben); SUBBARAO (Kanta)

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Source : Journal of virology; vol. 83; no. 9; pp. 4704-4708

ISSN : 0022-538X

Date de publication : 2009

Pays de publication : USA

Langue(s) : ENG

Type de document : P

Nombre de références : 24 ref.

Résumé : Following circulation of avian influenza H5 and H7 viruses in poultry, the hemagglutinin (HA) can acquire additional glycosylation sites, and the neuraminidase (NA) stalk becomes shorter. We investigated whether these features play a role in the pathogenesis of infection in mammalian hosts. From 1996 to 2007, H5N1 viruses with a short NA stalk have become widespread in several avian species. Compared to viruses with a long-stalk NA, viruses with a short-stalk NA showed a decreased capacity to elute from red blood cells and an increased virulence in mice, but not in chickens. The presence of additional HA glycosylation sites had less of an effect on virulence than did NA stalk length. The short-stalk NA of H5N1 viruses circulating in Asia may contribute to virulence in humans.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Glycosidases; Glycosylases; Hydrolases; Enzyme

Descripteur(s) français

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Glycosidases; Glycosylases; Hydrolases; Enzyme

Localisation : INIST-13592, 354000184924550700

Origine de la notice : INIST

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Experimental Infection of Pigs with the Human 1918 Pandemic Influenza Virus

Titre : Experimental Infection of Pigs with the Human 1918 Pandemic Influenza Virus

Auteur(s) : WEINGARTL (Hana M.); ALBRECHT (Randy A.); LAGER (Kelly M.); BABIUK (Shawn); MARSZAL (Peter); NEUFELD (James); EMBURY-HYATT (Carissa); LEKCHAROENSUK (Porntippa); TUMPEY (Terrence M.); GARCIA-SASTRE (Adolfo); RICHT (Jürgen A.)

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Source : Journal of virology; vol. 83; no. 9; pp. 4287-4296
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 43 ref.

Résumé : Swine influenza was first recognized as a disease entity during the 1918 "Spanish flu" pandemic. The aim of this work was to determine the virulence of a plasmid-derived human 1918 pandemic H1N1 influenza virus (reconstructed 1918, or 1918/rec, virus) in swine using a plasmid-derived A/swine/Iowa/15/1930 H1N1 virus (1930/rec virus), representing the first isolated influenza virus, as a reference. Four-week-old piglets were inoculated intratracheally with either the 1930/rec or the 1918/rec virus or intranasally with the 1918/rec virus. A transient increase in temperature and mild respiratory signs developed postinoculation in all virus-inoculated groups. In contrast to other mammalian hosts (mice, ferrets, and macaques) where infection with the 1918/rec virus was lethal, the pigs did not develop severe respiratory distress or become moribund. Virus titers in the lower respiratory tract as well as macro- and microscopic lesions at 3 and 5 days postinfection (dpi) were comparable between the 1930/rec and 1918/rec virus-inoculated animals. In contrast to the 1930/rec virus-infected animals, at 7 dpi prominent lung lesions were present in only the 1918/rec virus-infected animals, and all the piglets developed antibodies at 7 dpi. Presented data support the hypothesis that the 1918 pandemic influenza virus was able to infect and replicate in swine, causing a respiratory disease, and that the virus was likely introduced into the pig population during the 1918 pandemic, resulting in the current lineage of the classical H1N1 swine influenza viruses.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Descripteur(s) : Swine; Pig; Human; Influenzavirus; Experimental disease; Animal; Virology
Desc. généraux : Artiodactyla; Ungulata; Mammalia; Vertebrata; Orthomyxoviridae; Virus; Veterinary

Descripteur(s) français
Descripteur(s) : Porcin; Porc; Homme; Influenzavirus; Pathologie expérimentale; Animal; Virologie
Desc. généraux : Artiodactyla; Ungulata; Mammalia; Vertebrata; Orthomyxoviridae; Virus; Vétérinaire

Localisation : INIST-13592, 354000184924550280
Origine de la notice : INIST

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Isolation and Genetic Characterization of H5N2 Influenza Viruses from Pigs in Korea

**Titre** : Isolation and Genetic Characterization of H5N2 Influenza Viruses from Pigs in Korea

**Auteur(s)** : JUN HAN LEE; PASCUA (Philippe Noriel Q.); SONG (Min-Suk); YUN HEE BAEK; KIM (Chul-Joong); CHOI (Hwan-Woon); SUNG (Moon-Hee); WEBBY (Richard J.); WEBSTER (Robert G.); POO (Haryoung); YOUNG KI CHOI

**Affiliation(s)** : College of Medicine and Medical Research Institute, Chungbuk National University, 12 Gaeshin-Dong, Heungduk-Ku, Cheongju 361-763, KOR; College of Veterinary Medicine, Chungnam National University, 220 Gung-Dong, Yuseoung-Gu, Daejeon 305-764, KOR; Choongang Vaccine Laboratory, Daejeon 305-348, KOR; Bioleaders Corporation, Daejeon, KOR; Division of Virology, Department of Infectious Diseases, St. Jude Children's Research Hospital, 262 Danny Thomas Place, Memphis, Tennessee 38105, USA; Korean Research Institute of Bioscience and Biotechnology, Daejeon, KOR

**Source** : Journal of virology; vol. 83; no. 9; pp. 4205-4215
**ISSN** : 0022-538X
**Date de publication** : 2009
**Pays de publication** : USA
**Langue(s)** : ENG
**Type de document** : P
**Nombre de références** : 57 ref.

**Résumé** : Due to dual susceptibility to both human and avian influenza A viruses, pigs are believed to be effective intermediate hosts for the spread and production of new viruses with pandemic potential. In early 2008, two swine H5N2 viruses were isolated from our routine swine surveillance in Korea. The sequencing and phylogenetic analysis of surface proteins revealed that the Sw/Korea/C12/08 and Sw/Korea/C13/08 viruses were derived from avian influenza viruses of the Eurasian lineage. However, although the Sw/Korea/C12/08 isolate is an entirely avian-like virus, the Sw/Korea/C13/08 isolate is an avian-swine-like reassortant with the PB2, PA, NP, and M genes coming from a 2006 Korean swine H3N1-like virus. The molecular characterization of the two viruses indicated an absence of significant mutations that could be associated with virulence or binding affinity. However, animal experiments showed that the reassortant Sw/Korea/C13/08 virus was more adapted and was more readily transmitted than the purely avian-like virus in a swine experimental model but not in ferrets. Furthermore, seroprevalence in swine sera from 2006 to 2008 suggested that avian H5 viruses have been infecting swine since 2006. Although there are no known potential clinical implications of the avian-swine reassortant virus for pathogenicity in pigs or other species, including humans, at present, the efficient transmissibility of the swine-adapted H5N2 virus could facilitate virus spread and could be a potential model for pandemic, highly pathogenic avian influenza (e.g., H5N1 and H7N7) virus outbreaks or a pandemic strain itself.

**Code(s) de classement** : 002A05C10; 002A05C05

**Descripteur(s) anglais**

*Descrip**t**eur(s)* : Swine; Pig; Isolation; Genetics; Influenza; Animal; Korea; Virology  
*Desc. génériques* : Artiodactyla; Ungulata; Mammalia; Vertebrata; Viral disease; Infection; Asia; Veterinary

**Descripteur(s) français**

*Descrip**t**eur(s)* : Porcin; Porc; Isolement; Génétique; Grippe; Animal; Corée; Virologie  
*Desc. génériques* : Artiodactyla; Ungulata; Mammalia; Vertebrata; Virose; Infection; Asie; Vétérinaire

**Localisation** : INIST-13592, 354000184924550210
**Origine de la notice** : INIST
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Optimizing Viral Protein Yield of Influenza Virus Strain A/Vietnam/1203/2004 by Modification of the Neuraminidase Gene

Titre : Optimizing Viral Protein Yield of Influenza Virus Strain A/Vietnam/1203/2004 by Modification of the Neuraminidase Gene

Auteur(s) : ADAMO (Joan E.); LIU (Teresa); SCHMEISSER (Falko); ZHIPING YE

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Source : Journal of virology; vol. 83; no. 9; pp. 4023-4029

ISSN : 0022-538X

Date de publication : 2009

Pays de publication : USA

Langue(s) : ENG

Type de document : P

Nombre de références : 28 ref.

Résumé : The preparation of high-yield prepandemic influenza virus H5N1 strains has presented a challenge to both researchers and vaccine manufacturers. The reasons for the relatively low yield of the H5N1 strains are not fully understood, but it might be partially dependent on the interactions between the hemagglutinin (HA) or neuraminidase (NA) surface glycoprotein and other influenza virus proteins. In this study, we have constructed chimeras between the A/Puerto Rico/8/34 (PR8) NA gene and the A/Vietnam/1203/2004 (VN1203) NA gene that have resulted in an increase in the virus yield of the reassortant viruses without a significant loss of NA activity. By combining the amino terminus of NA from the PR8 strain with the carboxy terminus of NA from VN1203, the surface epitopes unique to the H5N1 VN1203 NA glycoprotein are maintained. This reassortant virus had a higher titer and total protein yield in eggs, grew to a higher titer, produced large plaques on MDCK cells, and retained NA activity. This work describes a novel recombinant technique designed to increase the yields of vaccine candidates for the production of pandemic influenza virus vaccines. The relationship between the infectivity and protein yield of the reassortants also is discussed.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

- Descripteur(s) : Influenza A virus; Protein; Yield; Strain; Vietnam; Exo- alpha -sialidase; Gene; Virology
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Asia; Glycosidases; Glycosylases; Hydrolases; Enzyme

Descripteur(s) français

- Descripteur(s) : Virus grippal A; Protéine; Rendement; Souche; Vietnam; Exo- alpha -sialidase; Gène; Virologie
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Asie; Glycosidases; Glycosylases; Hydrolases; Enzyme

Localisation : INIST-13592, 354000184924550030

Origine de la notice : INIST

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Identifying spatio-temporal patterns of transboundary disease spread: examples using avian influenza H5N1 outbreaks

Titre : Identifying spatio-temporal patterns of transboundary disease spread: examples using avian influenza H5N1 outbreaks

Auteur(s) : FARNSWORTH (Matthew L.); WARD (Michael P.)
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Source : Veterinary research: (Print); vol. 40; no. 3
ISSN : 0928-4249
Date de publication : 2009
Langue(s) : ENG
Type de document : P
Nombre de références : 35 ref.

Résumé : Characterizing spatio-temporal patterns among epidemics in which the mechanism of spread is uncertain is important for generating disease spread hypotheses, which may in turn inform disease control and prevention strategies. Using a dataset representing three phases of highly pathogenic avian influenza H5N1 outbreaks in village poultry in Romania, 2005-2006, spatio-temporal patterns were characterized. We first fit a set of hierarchical Bayesian models that quantified changes in the spatio-temporal relative risk for each of the 23 affected counties. We then modeled spatial synchrony in each of the three epidemic phases using non-parametric covariance functions and Thin Plate Spline regression models. We found clear differences in the spatio-temporal patterns among the epidemic phases (local versus regional correlated processes), which may indicate differing spread mechanisms (for example wild bird versus human-mediated). Elucidating these patterns allowed us to postulate that a shift in the primary mechanism of disease spread may have taken place between the second and third phases of this epidemic. Information generated by such analyses could assist affected countries in determining the most appropriate control programs to implement, and to allocate appropriate resources to preventing contact between domestic poultry and wild birds versus enforcing bans on poultry movements and quarantine. The methods used in this study could be applied in many different situations to analyze transboundary disease data in which only location and time of occurrence data are reported.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
- Descripteur(s) : Influenza A virus; Epidemic; Poultry; Microbiology; Veterinary; Avian influenza
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Infection; Viral disease; Farming animal

Descripteur(s) français
- Descripteur(s) : Virus grippal A; Epidémie; Volaille; Microbiologie; Vétérinaire; Grippe aviaire
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Infection; Virose; Animal élevage

Localisation : INIST-14119, 354000186829800070
Origine de la notice : INIST
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Risk factors and characteristics of H5N1 Highly Pathogenic Avian Influenza (HPAI) post-vaccination outbreaks

Titre : Risk factors and characteristics of H5N1 Highly Pathogenic Avian Influenza (HPAI) post-vaccination outbreaks

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Source : Veterinary research : (Print); vol. 40; no. 3
ISSN : 0928-4249
Date de publication : 2009
Pays de publication : FRA
Langue(s) : ENG
Type de document : P
Nombre de références : 15 ref.

Résumé : Highly pathogenic avian influenza (HPAI) virus H5N1 is now endemic in South-East Asia but HPAI control methods differ between countries. A widespread HPAI vaccination campaign that started at the end of 2005 in Viet Nam resulted in the cessation of poultry and human cases, but in 2006/2007 severe HPAI outbreaks re-emerged. In this study we investigated the pattern of this first post-vaccination epidemic in southern Viet Nam identifying a spatio-temporal cluster of outbreak occurrence and estimating spatially smoothed incidence rates of HPAI. Spatial risk factors associated with HPAI occurrence were identified. Medium-level poultry density resulted in an increased outbreak risk (Odds ratio (OR) = 5.4, 95% confidence interval (CI): 1.6-18.9) but also climate-vegetation factors played an important role: medium-level normalised difference vegetation indices during the rainy season from May to October were associated with higher risk of HPAI outbreaks (OR = 3.7, 95% CI: 1.7-8.1), probably because temporal flooding might have provided suitable conditions for the re-emergence of HPAI by expanding the virus distribution in the environment and by enlarging areas of possible contacts between domestic waterfowl and wild birds. On the other hand, several agricultural production factors, such as sweet potatoes yield, increased buffalo density, as well as increased electricity supply were associated with decreased risk of HPAI outbreaks. This illustrates that preventive control measures for HPAI should include a promotion of low-risk agricultural management practices as well as improvement of the infrastructure in village households. Improved HPAI vaccination efforts and coverage should focus on medium poultry density areas and on the pre-monsoon time period.

Code(s) de classement : 002A05C10

Descriptor(s) anglais

Descriptor(s) : Influenza A virus; Avian influenzavirus; Risk factor; Pathogenicity; Vaccination; Poultry; Microbiology; Veterinary; Avian influenza
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Infection; Viral disease; Zoopathogen; Farming animal

Descriptor(s) français

Descriptor(s) : Virus grippal A; Influenzavirus aviaire; Facteur risque; Pouvoir pathogène; Vaccination; Volaille; Microbiologie; Vétérinaire; Grippe aviaire
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Infection; Virose; Zoopathogène; Animal élevage

Localisation : INIST-14119, 354000186829800030
Origine de la notice : INIST
Copyright de notice : © 2009 INIST-CNRS. All rights reserved.
Safety, immunogenicity and efficacy of poxvirus-based vector vaccines expressing the haemagglutinin gene of a highly pathogenic H5N1 avian influenza virus in pigs

**Titre** : Safety, immunogenicity and efficacy of poxvirus-based vector vaccines expressing the haemagglutinin gene of a highly pathogenic H5N1 avian influenza virus in pigs

**Auteur(s) :** KYRIAKIS (Constantinos S.); DE VLEESCHAUWER (Annebel); BARBE (Filip); BUBLOT (Michel); VAN REETH (Kristien)

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**Source** : Vaccine; vol. 27; no. 16; pp. 2258-2264

**ISSN** : 0264-410X

**CODEN** : VACCDE

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 43 ref.

**Résumé** : This study investigates the safety, immunogenicity and efficacy of different pox-vector vaccines expressing the haemagglutinin of a highly pathogenic (HP) H5N1 avian influenza virus (AIV) (A/chicken/Indonesia/7/03) in pigs. Pigs were vaccinated twice, with a 4-week interval, with a fowlpox (TROVAC®), a canarypox (ALVAC®), or a vaccinia (NYVAC) vector vaccine combined with an oil-in-water adjuvant, with the unadjuvanted NYVAC, or left unvaccinated. Six weeks after the second vaccination, all pigs were challenged intra-tracheally with low pathogenic (LP) H5N2 AIVA/chicken/Belgium/150199. Sera were examined in haemagglutination inhibition (HI) tests against the H5N1 AIV from which the vaccine haemagglutinin derived, the challenge virus and the human A/Vietnam/1194/04 HPAIV. After challenge pigs were compared for H5N2 virus replication in the trachea and 4 lung lobes at 24 or 72 h post-challenge. Vaccination was well tolerated by all animals. Antibody titres peaked 2 weeks after the second vaccination and were 2- to 4-fold higher against the vaccine virus than heterologous H5 viruses. The NYVAC and ALVAC adjuvanted vaccines consistently induced higher antibody titres than TROVAC or NYVAC without adjuvant. Following challenge, the H5N2 challenge virus was isolated from all unvaccinated pigs, while 19 out of 21 vaccinates showed complete virological protection. Pox-vector vaccines were safe, immunogenic and efficacious against challenge with a heterologous H5 AIV, offering an alternative to classical inactivated vaccines. It remains to be seen whether they would protect against a swine-adapted H5 virus, which may replicate 100-1000 times better than our challenge virus.

**Code(s) de classement** : 002A05F04; 002A05C10

**Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Zoopathogen; Veterinary

**Description(s) français**

- **Description(s)** : Influenzavirus aviaire; Virus grippal A; Porcin; Immunogénicité; Efficacité; Vecteur; Vaccin; Hémagglutinine; Gêne; Pouvoir pathogène
- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Zoopathogène; Vétérinaire

**Localisation** : INIST-20289, 354000185984590070

**Origine de la notice** : INIST
Immunogenicity, Safety, and Cross-Reactivity of an Inactivated, Adjuvanted, Prototype Pandemic Influenza (H5N1) Vaccine: A Phase II, Double-Blind, Randomized Trial

Titre : Immunogenicity, Safety, and Cross-Reactivity of an Inactivated, Adjuvanted, Prototype Pandemic Influenza (H5N1) Vaccine: A Phase II, Double-Blind, Randomized Trial

Auteur(s) : JIANG WU; FANG (Han-Hua); CHEN (Jiang-Ting); ZHOU (Ji-Chen); FENG (Zi-Jian); LI (Chang-Gui); QIU (Yuan-Zheng); YAN LIU; MIN LU; LIU (Li-Ying); DONG (Shan-Shan); QIANG GAO; ZHANG (Xiao-Mei); NAN WANG; YIN (Wei-Dong); DONG (Xiao-Ping)

Affiliation(s) : Beijing Centers for Diseases Control and Prevention, National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, CHN; National Institute for the Control of Pharmaceuticals and Biological Products, National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, CHN; Sinovac Biotech, National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, CHN; Huairou Center for Disease Control and Prevention, National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, CHN; State Key Laboratory for Infectious Disease Prevention and Control, National Institute for Viral Disease Control and Prevention, Beijing, CHN

Source : Clinical infectious diseases; vol. 48; no. 8; pp. 1087-1095
ISSN : 1058-4838
CODEN : CIDIEL
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 26 ref.

Résumé : Background. Avian influenza A virus H5N1 has the potential to cause a pandemic. Adjuvants and whole-virion vaccines are regarded as antigen sparing for pandemic vaccines. Methods. A double-blind, randomized trial was performed from 28 August to 22 December 2007 in 402 adults; 301 adults were randomly assigned to receive 2 doses of an inactivated, aluminum-adjuvanted, whole-virion H5N1 vaccine containing 5, 10, or 15 μg of hemagglutinin per dose 28 days apart, and 101 of them received 2 doses of 10 μg of vaccine 14 days apart. The vaccine was manufactured from the recombinant A/Vietman/1194/2004 (NIBRG14) strain. Blood samples were collected for hemagglutination inhibition and microneutralization assays. Results. All formulations were well tolerated, with no serious adverse events. Most local and systemic reactions were mild or moderate. Immune responses were induced after 1 dose in all vaccination groups. The highest immune response was seen after 2 doses of 15 μg of vaccine, with 90% and 100% seroconversion rates and 90% and 100% of participants having a titer of ≥1:40 for hemagglutination inhibition and microneutralization assays, respectively. Both the 10- and 15-μg doses met or exceeded European Union licensure criteria. Generally, higher immune responses were elicited in participants vaccinated 28 days apart than those vaccinated 14 days apart. Cross-reaction assays showed that after 2 doses of 10 μg of vaccine, 98% and 87% of participants had a microneutralization titer of ≥1:40 against heterologous Indonesia and Anhui strains, respectively. Conclusions. The inactivated, aluminum-adjuvanted, whole-virion H5N1 vaccine not only showed good immunogenicity and safety but also elicited significant cross-reactivity against heterologous H5N1 strains in clade 2.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Influenza A; Immunoprophylaxis; Immunogenicity; Cross reaction; Vaccine; Prevention; Phase II
Desc. génériques : Viral disease; Infection

Descripteur(s) français

Desc. génériques : Influenzavirus A(H5N1)

Desc. génériques : Virose; Infection

Localisation : INIST-18407, 354000186780790090

Origine de la notice : INIST

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Adherence with oseltamivir chemoprophylaxis among workers exposed to poultry during avian influenza outbreaks in southern Israel

Titre : Adherence with oseltamivir chemoprophylaxis among workers exposed to poultry during avian influenza outbreaks in southern Israel

Auteur(s) : BELMAKER (Ilana); LYANDRES (Michael); BILENKO (Natalya); DUKHAN (Larissa); MENDELSON (Ella); MANDELBOIM (Michal); SHAHAR-ROTBERG (Liora); BITRAN (Einat); YOSSEF (Yochi); GROTTO (Itamar)

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Source : International journal of infectious diseases; vol. 13; no. 2; pp. 261-265

ISSN : 1201-9712
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 17 ref.

Résumé : Objectives: To determine adherence with recommended pre- and post-exposure oseltamivir prophylaxis (OP) among workers exposed to poultry during five simultaneous avian influenza (AI) H5N1 outbreaks in poultry farms in southern Israel in March 2006, as well as the efficiency of the distribution system of oseltamivir in the community. Design: Epidemiological investigation identified 201 workers exposed to poultry during AI outbreaks. They were interviewed by a public health nurse regarding adherence with recommended OP, symptoms, and possible side effects. Data were collected on type of exposure, age, sex, rate of adherence with OP, and reasons for non-adherence. For eight workers, paired sera were drawn for the determination of antibodies to H5. Data were collected on the efficiency of the distribution of oseltamivir tablets to workers in the community. Results: High adherence with OP (87.6%) was found among poultry workers during outbreaks of AI, with no difference by type of exposure, age, or sex. There was a low rate of side effects of OP (1.5%). No exposed workers developed AI and none of the eight who had paired sera drawn showed seroconversion. The distribution of OP in the community was inefficient, with 27.7% of the tablets 'lost' or returned unusable. Conclusions: These data emphasize the importance of developing efficient targeted distribution systems in the community for OP, in order to prevent human infection during AI outbreaks.

Code(s) de classement : 002B05C02C; 002B02S05

Descripteur(s) anglais

Desc. génériques : Avian influenza; Oseltamivir; Adhesion; Prevention; Chemoprophylaxis; Poultry; Epidemic; Israel; Secondary effect; Toxicity; Antiviral; Farming animal; Meat animals

Desc. génériques : Viral disease; Infection; Asia; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor; Neuraminidase inhibitor

Descripteur(s) français

Desc. génériques : Grippe aviaire; Oséltamivir; Adhérence; Prévention; Chimio prophylaxie; Volaille; Epidémie; Israël; Effet secondaire; Toxicité; Antiviral; Animal élevage; Animal à viande

Desc. génériques : Virose; Infection; Asie; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme; Inhibiteur neuraminidase

Localisation : INIST-26659, 354000187448710230

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Low-dose supplementation with active hexose correlated compound improves the immune response to acute influenza infection in C57BL/6 mice

Titre : Low-dose supplementation with active hexose correlated compound improves the immune response to acute influenza infection in C57BL/6 mice

Auteur(s) : NOGUSA (Shoko); GERBINO (Jeffrey); RITZ (Barry W.)
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Source : Nutrition research : (New York, NY); vol. 29; no. 2; pp. 139-143
ISSN : 0271-5317
CODEN : NTRSDC
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 17 ref.

Résumé : Supplementation with mushroom-derived active hexose correlated compound (AHCC) modulates immunity and increases survival in response to a broad spectrum of acute infections, including influenza virus infection. However, dose-response data are nonexistent. Therefore, the aims of this study were to evaluate AHCC supplementation at various doses and determine the effects of low-dose supplementation on the immune response in a mouse model of influenza virus infection. We hypothesized that AHCC supplementation would influence the immune response to influenza infection in a dose-dependent manner. Male C57BL/6 mice were supplemented with AHCC at daily doses of 0.05, 0.1, 0.5, and 1 g/kg and infected intranasally with influenza A virus (H1N1, PR8). Supplemented mice demonstrated a dose-dependent increase in survival and reduction in the loss of body weight. To further evaluate the effects of low-dose AHCC supplementation on the immune response to influenza infection, mice were supplemented with 0.1 g/kg per day and infected with a sublethal dose of influenza virus. Supplemented mice exhibited enhanced virus clearance and decreased weight loss compared to controls. Low-dose supplementation did not influence total natural killer (NK) cell cytotoxicity, although lytic efficiency was increased in the spleens of AHCC-supplemented mice, indicating enhanced NK cell function per cell. In conclusion, these data suggest that the effects of AHCC on the immune response to influenza infection are dose dependent and that low-dose AHCC supplementation improves the response to influenza infection despite no effect on total NK cell cytotoxicity.

Code(s) de classement : 002A16E

Descriptor(s) anglais

Descriptor(s) : Low dose; Supplementation; Hexose; Immune response; Acute; Infection; Animal; Fungi; Influenza; Survival; Lung; Natural killer cell; Mammalia; Mouse; Virus
Desc. généraux : Viral disease; Vertebrata; Respiratory system; Rodentia

Descriptor(s) français

Descriptor(s) : Dose faible; Supplémentation; Hexose; Réponse immune; Aigu; Infection; Animal; Fungi; Grippe; Survie; Poumon; Cellule NK; Mammalia; Souris; Virus
Desc. généraux : Virose; Vertebrata; Appareil respiratoire; Rodentia

Localisation : INIST-18812, 354000187460660100
Origine de la notice : INIST
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Long-Distance Dispersal and Accelerating Waves of Disease: Empirical Relationships

**Titre** : Long-Distance Dispersal and Accelerating Waves of Disease: Empirical Relationships

**Auteur(s) :** MUNDT (Christopher C.); SACKETT (Kathryn E.); WALLACE (Larae D.); COWGER (Christina); DUDLEY (Joseph P.)

**Affiliation(s) :** Department of Botany and Plant Pathology, Oregon State University, Corvallis, Oregon 97331, USA; U.S. Department of Agriculture, Agricultural Research Service, Department of Plant Pathology, North Carolina State University, Raleigh, North Carolina 27695, USA; Science Applications International Corporation, Rockville, Maryland 20852, USA; Institute of Arctic Biology-University of Alaska Fairbanks, Department of Earth Science, University of Alaska Museum, Fairbanks, Alaska 99775, USA

**Source :** The American naturalist; vol. 173; no. 4; pp. 456-466

**ISSN :** 0003-0147

**CODEN :** AMNTA4

**Date de publication :** 2009

**Pays de publication :** USA

**Langue(s) :** ENG

**Type de document :** P

**Nombre de références :** 1 p.1/2

**Résumé :** Classic approaches to modeling biological invasions predict a “traveling wave” of constant velocity determined by the invading organism’s reproductive capacity, generation time, and dispersal ability. Traveling wave models may not apply, however, for organisms that exhibit long-distance dispersal. Here we use simple empirical relationships for accelerating waves, based on inverse power law dispersal, and apply them to diseases caused by pathogens that are wind dispersed or vectored by birds: the within-season spread of a plant disease at spatial scales of <100 m in experimental plots, historical plant disease epidemics at the continental scale, the unexpectedly rapid spread of West Nile virus across North America, and the transcontinental spread of avian influenza strain H5N1 in Eurasia and Africa. In all cases, the position of the epidemic front advanced exponentially with time, and epidemic velocity increased linearly with distance; regression slopes varied over a relatively narrow range among data sets. Estimates of the inverse power law exponent for dispersal that would be required to attain the rates of disease spread observed in the field also varied relatively little (1.74-2.36), despite more than a fivefold range of spatial scale among the data sets.

**Code(s) de classement :** 002A14B01; 002A15D

**Descripteur(s) anglais**

*Desc. génériques :* Vertebrata

**Descripteur(s) français**

*Desc. génériques :* Vertebrata

**Localisation :** INIST-2099, 354000187435920040

**Origine de la notice :** INIST

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Anionic polymer, poly(methyl vinyl ether-maleic anhydride)-coated beads-based capture of human influenza A and B virus

Titre : Anionic polymer, poly(methyl vinyl ether-maleic anhydride)-coated beads-based capture of human influenza A and B virus

Auteur(s) : SAKUDO (Akikazu); BABA (Koichi); TSUKAMOTO (Megumi); SUGIMOTO (Atsuko); OKADA (Takashi); KOBAYASHI (Takanori); KAWASHITA (Norihito); TAKAGI (Tatsuya); IKUTA (Kazuyoshi)

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Source : Bioorganic & medicinal chemistry; vol. 17; no. 2; pp. 752-757
ISSN : 0968-0896
Date de publication : 2009
Pays de publications : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 34 ref.

Résumé : An anionic magnetic beads-based method was developed for the capture of human influenza A and B viruses from nasal aspirates, allantoic fluid and culture medium. A polymer, poly(methyl vinyl ether-maleic anhydride) [poly(MVE-MA)], was used to endow magnetic beads with a negative charge and bioadhesive properties. After incubation with samples containing human influenza virus, the beads were separated from supernatants by applying a magnetic field. The absorption of the virus by the beads was confirmed by hemagglutinin assay, immunochromatography, Western blotting, egg infection, and cell infection. Successful capture was proved using 5 H1N1 influenza A viruses, 10 H3N2 influenza A viruses, and 6 influenza B viruses. Furthermore, the infectivity in chicken embryonated eggs and Madin-Darby canine kidney (MDCK) cells of the captured human influenza virus was similar to that of the total viral quantity of starting materials. Therefore, this method of capture using magnetic beads coated with poly(MVE-MA) can be broadly used for the recovery of infectious human influenza viruses.

Code(s) de classement : 002A05C09

Descriputeur(s) anglais
Descriteur(s) : Polyelectrolyte; Vinyl ether copolymer; Maleic anhydride copolymer; Human; Influenza B virus; Detection; Magnetic particles; Influenza A virus
Desc. génériques : Influenzavirus B; Orthomyxoviridae; Virus; Influenzavirus A

Descriputeur(s) français
Descriteur(s) : Polyelectrolyte; Vinyle richard copolymère; Maléique anhydride copolymère; Homme; Virus grippal B; Détention; Particule magnétique; Virus grippal A; Ether(méthyle vinyl) copolymère
Desc. génériques : Influenzavirus B; Orthomyxoviridae; Virus; Influenzavirus A

Localisation : INIST-26564, 354000185397430380
Origine de la notice : INIST
Copyright de notice : © 2009 INIST-CNRS. All rights reserved.
Amino Acid Residues in the Fusion Peptide Pocket Regulate the pH of Activation of the H5N1 Influenza Virus Hemagglutinin Protein

**Titre** : Amino Acid Residues in the Fusion Peptide Pocket Regulate the pH of Activation of the H5N1 Influenza Virus Hemagglutinin Protein

**Auteur(s)** : REED (Mark L.); YEN (Hui-Ling); DUBOIS (Rebecca M.); BRIDGES (Olga A.); SALOMON (Rachelle); WEBSTER (Robert G.); RUSSELL (Charles J.)

**Affiliation(s)** : Division of Virology, Department of Infectious Diseases, St. Jude Children's Research Hospital, 262 Danny Thomas Place, Memphis, Tennessee 38105-3678, USA; Department of Molecular Sciences, University of Tennessee, Memphis, Tennessee 38163, USA

**Source** : Journal of virology; vol. 83; no. 8; pp. 3568-3580

**ISSN** : 0022-538X

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 53 ref.

**Résumé** : The receptor specificity and cleavability of the hemagglutinin (HA) protein have been shown to regulate influenza A virus transmissibility and pathogenicity, but little is known about how its pH of activation contributes to these important biological properties. To identify amino acid residues that regulate the acid stability of the HA protein of H5N1 influenza viruses, we performed a mutational analysis of the HA protein of the moderately pathogenic A/chicken/Vietnam/C58/04 (H5N1) virus. Nineteen HA proteins containing point mutations in the HA2 coiled-coil domain or in an HA1 histidine or basic patch were generated. Wild-type and mutant HA plasmids were transiently transfected in cell culture and analyzed for total protein expression, surface expression, cleavage efficiency, pH of fusion, and pH of conformational change. Four mutations to residues in the fusion peptide pocket, Y23H and H24Q in the HA1 subunit and E105K and N114K in the HA2 subunit, and a K58I mutation in the HA2 coiled-coil domain significantly altered the pH of activation of the H5 HA protein. In some cases, the magnitude and direction of changes of individual mutations in the H5 HA protein differed considerably from similar mutations in other influenza A virus subtypes. Introduction of Y23H, H24Q, K58I, and N114K mutations into recombinant viruses resulted in virus-expressed HA proteins with similar shifts in the pH of fusion. Overall, the data show that residues comprising the fusion peptide pocket are important in triggering pH-dependent activation of the H5 HA protein.

**Code(s) de classement** : 002A05C10

**Descripteur(s) anglais**

- **Descripteur(s)** : Avian influenzavirus; Influenza A virus; Peptides; Regulation(control); pH; Hemagglutinin; Protein; Virology
- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus

**Descripteur(s) français**

- **Descripteur(s)** : Influenzavirus aviaire; Virus grippal A; Peptide; Régulation; pH; Hémagglutinine; Protéine; Virologie
- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus

**Localisation** : INIST-13592, 354000186762060150

**Origine de la notice** : INIST

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Intranasal Administration of Alpha Interferon Reduces Seasonal Influenza A Virus Morbidity in Ferrets

Titre : Intranasal Administration of Alpha Interferon Reduces Seasonal Influenza A Virus Morbidity in Ferrets

Auteur(s) : KUGEL (Daniela); KOCHS (Georg); OBOJES (Karola); ROTH (Joachim); KOBINGER (Gary P.); KOBASA (Darwyn); HALLER (Otto); STAEHELI (Peter); VON MESSLING (Veronika)

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Source : Journal of virology; vol. 83; no. 8; pp. 3843-3851
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 53 ref.

Résumé : The type I interferon (IFN) response represents one of the first lines of defense against influenza virus infections. In this study, we assessed the protective potential of exogenous IFN-a against seasonal and highly pathogenic influenza viruses in ferrets. Intranasal treatment with IFN-a several hours before infection with the H1N1 influenza A virus strain A/USSR/90/77 reduced viral titers in nasal washes at least 100-fold compared to mock-treated controls. IFN-treated animals developed only mild and transient respiratory symptoms, and the characteristic fever peak seen in mock-treated ferrets 2 days after infection was not observed. Repeated application of IFN-a substantially increased the protective effect of the cytokine treatment. IFN-a did not increase survival after infection with the highly pathogenic H5N1 avian influenza A virus strain A/Vietnam/ 1203/2004; However, viral titers in nasal washes were significantly reduced at days 1 and 3 postinfection. Our study shows that intranasal application of IFN- alpha can protect ferrets from seasonal influenza viruses, which replicate mainly in the upper respiratory tract, but not from highly pathogenic influenza viruses, which also disseminate to the lung. Based on these results, a more intensive evaluation of IFN-a as an emergency drug against pandemic influenza A is warranted.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Fissipedia; Carnivora; Mammalia; Vertebrata; Cytokine

Descripteur(s) français
Desc. génériques : Virus grippal A; Voie intranasale; Morbidité; Furet; Virologie; Interféron alpha

Localisation : INIST-13592, 354000186762060410
Origine de la notice : INIST
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Positively Charged Compact Quantum Dot-DNA Complexes for Detection of Nucleic Acids

Titre : Positively Charged Compact Quantum Dot-DNA Complexes for Detection of Nucleic Acids

Auteur(s) : LEE (Junghan); CHOI (Youngseon); KIM (Junwon); PARK (Eunjung); RITA SONG

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Source : ChemPhysChem : (Print); vol. 10; no. 5; pp. 806-811
ISSN : 1439-4235
Date de publication : 2009
Pays de publication : DEU
Langue(s) : ENG
Type de document : P
Nombre de références : 17 ref.

Résumé : Novel QD-DNA complexes are prepared by simple electrostatic interaction between pegylated amine-functionalized CdSe/ZnS quantum dots (QDs) and DNA. The cationic nature of the amine functionality on the QD surface allows for formation of an electrostatic complex with negatively charged DNA. The presence of polyethylene glycol (PEG5000) molecules on the QD leads to enhanced stability and decreased nonspecific adsorption of DNA on the QD surface. Unlike assembly of QD-DNA based on hydrogen bonding, the present QD probes tend to be more strongly stabilized during the hybridization process by increasing the overall negative charges. In addition, the DNA loading efficiency can be modulated by changing the pH of the reaction medium. The fluorescence of the QD is quenched up to 90% by complexation with 5'-TAMRA-modified oligonucleotide (TAMRA=carboxytetramethylrhodamine) through fluorescence resonance energy transfer (FRET). With the FRET pair we selected, the R0 value was calculated to be 5.5 nm and r is about 5 nm. This quenching of QD fluorescence is then reversed on binding of unlabeled target DNA. The maximum recovery of QD fluorescence is 60%. The QD-DNA probe (5DNA/ QD) exhibits selective photoluminescence (PL) recovery in the presence of target oligonucleotide with a PL ratio of 3 for complementary versus noncomplementary. The present QD-DNA probes also show the capability to detect the synthetic 100-mer oligonucleotide derived from H5N1 influenza virus when present at concentrations as low as 200 nM in the solution.

Code(s) de classement : 001C01J02; 002A02C03

Descripteur(s) anglais
- Descripteur(s) : Quantum dot; DNA; Complexes; Acids; Recognition; Nanoparticle; Oligonucleotide

Descripteur(s) français
- Descripteur(s) : Point quantique; DNA; Complexe; Acide; Reconnaissance; Nanoparticule; Oligonucléotide

Localisation : INIST-27010, 354000196137520110
Origine de la notice : INIST
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Stockpiling Drugs for an Avian Influenza Outbreak: Examining the Surge in Oseltamivir Prescriptions During Heightened Media Coverage of the Potential for a Worldwide Pandemic

**Titre** : Stockpiling Drugs for an Avian Influenza Outbreak: Examining the Surge in Oseltamivir Prescriptions During Heightened Media Coverage of the Potential for a Worldwide Pandemic

**Auteur(s)** : GASINK (Leanne B.); LINKIN (Darren R.); FISHMAN (Neil O.); BILKER (Warren B.); WEINER (Mark G.); LAUTENBACH (Ebbing)

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**Source** : Infection control and hospital epidemiology; vol. 30; no. 4; pp. 370-376

**ISSN** : 0899-823X

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 12 ref.

**Résumé** : OBJECTIVE. During fall 2005, personal stockpiling of oseltamivir for use during an outbreak of H5N1 influenza virus infection was widely reported. The present study aimed to identify indications for oseltamivir prescriptions to determine whether oseltamivir that was not intended for seasonal influenza was inappropriately consumed and to compare persons who were likely to have stockpiled oseltamivir and those who did not with respect to their knowledge, understanding, concerns, and expectations regarding avian influenza. DESIGN. Survey to evaluate usage patterns for oseltamivir and assess views about avian influenza. SUBJECTS. A total of 109 outpatients who received a prescription for oseltamivir between September 1, 2005, and December 31, 2005, and 825 matched control subjects. RESULTS. Of 109 prescriptions, 36 (33.0%) were prescribed for patients with appropriate indications. Sixty-eight (62.4%) of 109 patients identified as having received oseltamivir and 440 (53.3%) of 825 individuals identified as not having received it responded to the questionnaire. Only 2 prescription recipients whose oseltamivir was not intended for immediate consumption reported that they had consumed the oseltamivir. Persons who probably intended to stockpile oseltamivir were older and more often white than those unlikely to stockpile it. They also reported greater worry about avian influenza and more often expected avian influenza to spread to the United States than those unlikely to stockpile, but there were no significant differences in responses to other questionnaire items. CONCLUSIONS. A large proportion of the oseltamivir prescriptions written in fall 2005 were probably intended for personal stockpiling. Similarities in participants' responses to questionnaire items suggest that educational campaigns may not be an effective method to curtail stockpiling of antimicrobial medications during an infectious threat. Promoting appropriate prescribing practices among providers may be a better means by which to minimize personal stockpiling.

**Code(s) de classement** : 002B30A11; 002B05C02C; 002B02S05

**Descripteur(s) anglais**

- Avian influenza; Oseltamivir; Epidemic; Medical prescription; Public health; Antiviral
- Viral disease; Infection; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor; Neuraminidase inhibitor

**Descripteur(s) français**

- Grippe aviaire; Osélamivir; Epidémie; Prescription médicale; Santé publique; Antiviral; Pandémie

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Desc. génériques : Virose; Infection; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme; Inhibiteur neuraminidase

Localisation : INIST-19430, 354000187398630090
Origine de la notice : INIST
Copyright de notice : © 2009 INIST-CNRS. All rights reserved.
HPLC-based quantification of haemagglutinin in the production of egg-and MDCK cell-derived influenza virus seasonal and pandemic vaccines

Titre : HPLC-based quantification of haemagglutinin in the production of egg-and MDCK cell-derived influenza virus seasonal and pandemic vaccines

Auteur(s) : KAPTEYN (J. C.); PORRE (A. M.); DE ROND (E. J. P.); HESSELS (W. B.); TIJMS (M. A.); KESSEN (H.); SLOTBOOM (A. M. E.); OERLEMANS (M. A.); SMIT (D.); VAN DER LINDEN (J.); SCHOEN (P.); THUS (J. L. G.)

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Source : Vaccine; vol. 27; no. 9; pp. 1468-1477
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 15 ref.

Résumé : The haemagglutinin(HA)contentisanimportantspecificationofinfluenzavaccines. Recently, a reversed-phase high performance liquid chromatography (RP-HPLC) method for quantification of HA in PER.C6® cell culture-based whole virus vaccines has been reported, having a high sensitivity, precision, broad range, and high sample throughput [KapteynJC, Drissi Saidi M, Dijkstra R, Kars C, Tjon CMS-K, Weverling CJ et al. Haemagglutinin quantification and identification of influenza A&B strains propagated in PER.C6® cells: a novel RP-HPLC method. Vaccine 2006;24:3137-44]. This RP-HPLC assay is based on measuring the peak area of HA1, the hydrophilic subunit of HA, which turned out to be proportional to the amount of HA analyzed. Here, we present data demonstrating that this RP-HPLC method is also highly suitable for HA quantification of active and BPL- or formaldehyde-inactivated egg-based and MDCK cell-based whole virus samples, including egg allantoic harvest, and in final (monovalent) subunit vaccines, including those for pandemic H5N1 strains and for virosomal vaccines. In addition, the RP-HPLC assay was demonstrated to be a very powerful tool in the early stages of seasonal influenza vaccine production, when homologous serial radial immunodiffusion (SRID) reagents are not yet available, enabling fast and reliable viral growth studies in eggs in order to select the best growing virus strains or reassortants for the production of the seasonal trivalent influenza vaccine. Because of its high sensitivity, the RP-HPLC assay has shown its enormous value in supporting small scale MDCK-based (H5N1) influenza virus production models. Finally, the observed differences between HA1 molecules from various HA subtypes in UV absorbance, FLD response, and in the actual retention times in RP-HPLC are discussed in relation to the primary structure of the HA1 molecules studied.

Code(s) de classement : 002A05F04; 002A05C10

Describeur(s) anglais
Descripteur(s) : Influenzavirus; HPLC chromatography; Quantitative analysis; Hemagglutinin; Vaccine; Influenza
Desc. génériques : Orthomyxoviridae; Virus; Viral disease; Infection

Describeur(s) français
Descripteur(s) : Influenzavirus; Chromatographie HPLC; Analyse quantitative; Hémagglutinine; Vaccin; Grippe
Desc. génériques : Orthomyxoviridae; Virus; Viros; Infection

Localisation : INIST-20289, 354000187461990250
Origine de la notice : INIST
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A TLR3 ligand that exhibits potent inhibition of influenza virus replication and has strong adjuvant activity has the potential for dual applications in an influenza pandemic

Titre : A TLR3 ligand that exhibits potent inhibition of influenza virus replication and has strong adjuvant activity has the potential for dual applications in an influenza pandemic

Auteur(s) : LAU (Yuk-Fai); TANG (Lay-Hoon); OOI (Eng-Eong)
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Source : Vaccine; vol. 27; no. 9; pp. 1354-1364
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 57 ref.

Résumé : The appearance and spread of the H5N1 highly pathogenic avian influenza (HPAI) raise concern of a possible pandemic. Current preventive measures include the development of a pre-pandemic influenza vaccine and stockpiling of neuraminidase inhibitors. However, their benefits can be significantly reduced by mutations in the hemagglutinin or neuraminidase resulting in antigenic changes and the appearance of drug-resistance, respectively. Drugs that target the innate immune system to achieve a 'heightened antiviral' state represent another class of antiviral agents that could contribute to the control and treatment of influenza infection. In this study, PIKA (a stabilized dsRNA) provides broad-spectrum prophylaxis against a number of influenza A viruses. In addition, when PIKA was admixed with influenza vaccine preparations, including a formalin-inactivated whole-virion H5 vaccine, significant adjuvanting effect leading to accelerated viral clearance was observed in a murine model. These biological effects appear to be mediated by the ability of PIKA to promote the maturation of dendritic cells, including up-regulation of co-stimulatory molecules, such as CD80 and CD86, and the induction of various cytokines and chemokines. Toll-like receptor 3 (TLR3) was shown to recognize PIKA in a concentration-dependent manner. The potency and versatility in its activities make PIKA an attractive candidate for use in an influenza pandemic.

Code(s) de classement : 002A05F04; 002A05C10

Desc. génériques : Orthomyxoviridae; Virus; Viral disease; Infection

Localisation : INIST-20289, 354000187461990110
Origine de la notice : INIST
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Immunological assessment of plant-derived avian flu H5/HA1 variants

Titre : Immunological assessment of plant-derived avian flu H5/HA1 variants

Auteur(s) : SPITSIN (S.); ANDRIANOV (V.); POGREBNYAK (N.); SMIRNOV (Y.); BORISJUK (N.); PORTOCARRERO (C.); VEGUILA (V.); KOPROWSKI (H.); GOLOVKIN (M.)

Affiliation(s) : Biotechnology Foundation Laboratories, Thomas Jefferson University, Philadelphia, PA 19107-6799, USA; Centers for Disease Control and Prevention, Atlanta, GA 30333, USA

Source : Vaccine; vol. 27; no. 9; pp. 1289-1292

ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 19 ref.

Résumé : Polypeptide variants of the HA1 antigenic domain of the H5N1 avian influenza virus hemagglutinin (HA) molecule were produced in plants using transient and stable expression systems and fused with His/c-myc tags or with mouse or human Fc antibody fragments. The resulting peptides were purified and used for intramuscular immunization of mice. While the recombinant HA1 variants induced a significant serum humoral immune response in the mice, none of the HA1 preparations induced virus-neutralizing antibodies. Fusion with the Fc fragment improved overall yield of the constructs and allowed purification requiring only a single step, but led to no detectable fusion-related enhancement of immunogenicity or quality of immune response.

Code(s) de classement : 002A05F04

Descriptor(s) anglais
Descriptor(s) : Subunit; Vaccine; Avian influenza
Desc. généraux : Infection; Viral disease

Descriptor(s) français
Descriptor(s) : Sousunité; Vaccin; Grippe aviaire
Desc. généraux : Infection; Virose

Localisation : INIST-20289, 354000187461990020
Origine de la notice : INIST
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A universal epitope-based influenza vaccine and its efficacy against H5N1

Titre : A universal epitope-based influenza vaccine and its efficacy against H5N1

Auteur(s) : ADAR (Y.); SINGER (Y.); LEVI (R.); TZEHOVAL (E.); PERK (S.); BANET-NOACH (C.); NAGAR (S.); ARNON (R.); BEN-YEDIDIA (T.)

Affiliation(s) : Israel Institute for Biological Research, Ness Ziona, ISR; BiondVax Pharmaceuticals Ltd., 14 Einstein St, Ness Ziona, ISR; Department of Immunology, the Weizmann Institute of Science, Rehovot, ISR; Kimron Veterinary Institute, Beit Dagan, ISR

Source : Vaccine; vol. 27; no. 15; pp. 2099-2107
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 56 ref.

Résumé : Previous studies have shown that a recombinant vaccine expressing four highly conserved influenza virus epitopes has a potential for a broad spectrum, cross-reactive vaccine; it induced protection against H1, H2 and H3 influenza strains. Here, we report on the evaluation of an epitope-based vaccine in which six conserved epitopes, common to many influenza virus strains are expressed within a recombinant flagellin that serves as both a carrier and adjuvant. In an HLA-A2.1 transgenic mice model, this vaccine induced both humoral and cellular responses and conferred some protection against lethal challenge with the highly pathogenic H5N1 avian influenza strain. Hence, it is expected to protect against future strains as well. The data presented, demonstrate the feasibility of using an array of peptides for vaccination, which might pave the way to an advantageous universal influenza virus vaccine that does not require frequent updates and/or annual immunizations.

Code(s) de classement : 002A05F04

Descripteur(s) anglais
Antigenic determinant; Vaccine; Efficiency; Peptides; Flagellin; Influenza A

Desc. généraux : Viral disease; Infection

Descripteur(s) français
Déterminant antigénique; Vaccin; Efficacité; Peptide; Flagelline; Grippe A

Desc. généraux : Virose; Infection

Localisation : INIST-20289, 354000184875390040
Origine de la notice : INIST
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Enhanced protective immunity against H5N1 influenza virus challenge by vaccination with DNA expressing a chimeric hemagglutinin in combination with an MHC class I-restricted epitope of nucleoprotein in mice

**Titre :** Enhanced protective immunity against H5N1 influenza virus challenge by vaccination with DNA expressing a chimeric hemagglutinin in combination with an MHC class I-restricted epitope of nucleoprotein in mice

**Auteur(s) :** PAN TAO; MENGCHENG LUO; RUANGANG PAN; DAWEI LING; SIYU ZHOU; PO TIEN; ZISHU PAN

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**Source :** Antiviral research; vol. 81; no. 3; pp. 253-260

**ISSN :** 0166-3542

**CODEN :** ARSRDR

**Date de publication :** 2009

**Pays de publication :** NLD

**Langue(s) :** ENG

**Type de document :** P

**Nombre de références :** 1 p.

**Résumé :** DNA vaccination is an effective means of eliciting both humoral and cellular immune responses. The hemagglutinin (HA) surface protein of influenza A virus is a major target of protective antibody responses induced by virus infection or by vaccination and is widely considered to be the antigen of choice for an influenza vaccine. Cytotoxic T lymphocyte (CTL) responses directed against the conserved nucleoprotein (NP) are thought to play an important role in clearing virus and promoting survival and recovery from influenza. In this study, we developed a novel DNA vaccine approach using a chimeric plasmid consisting of the HA of H5N1 influenza virus in which an MHC class I-restricted NP-specific CTL epitope (NP147-155) was inserted. Immunogenicity and antiviral efficacy of this vaccine was assessed in mouse models. A similar level of HA expression was achieved in 293T cells transfected with pHANP147-155 compared to that with pHAN. Besides eliciting the specific anti-HA antibody responses, vaccination using pHANP147-155 in mice induced NP epitope-specific CD8+ T cell responses, which are generally not inducible by vaccination with pHAN alone. After H5N1 influenza virus challenge, BALB/c mice vaccinated with pHANP147-155 exhibited reduced inflammation severity and lung viral titers compared to those vaccinated with pHAN. Our work may contribute to improvement of HA-based influenza DNA vaccines.

**Code(s) de classement :** 002B02S05

**Descriputeur(s) anglais**

- **Descriputeur(s) :** Immunoprotection; Genetic vaccine; Hemagglutinin; Drug combination; Class I histocompatibility antigen; Antigenic determinant; Nucleoprotein; Animal; Mouse; Cytotoxic T lymphocyte; T-Lymphocyte; Cytotoxicity; Influenzavirus A(H5N1)
- **Desc. génériques :** Rodentia; Mammalia; Vertebrata

**Descriputeur(s) français**

- **Descriputeur(s) :** Immunoprotection; Vaccin génétique; Hémagglutinine; Association médicamenteuse; Antigène histocompatibilité classe I; Déterminant antigénique; Nucléoprotéine; Animal; Souris; Lymphocyte T cytotoxique; Lymphocyte T; Cytotoxicité; Influenzavirus A(H5N1)
- **Desc. génériques :** Rodentia; Mammalia; Vertebrata

**Localisation :** INIST-18839, 354000184863580090

**Origine de la notice :** INIST

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Recombinant fowlpox virus vector-based vaccine completely protects chickens from H5N1 avian influenza virus

Titre : Recombinant fowlpox virus vector-based vaccine completely protects chickens from H5N1 avian influenza virus

Auteur(s) : CHUANLING QIAO; YONGPING JIANG; GUOBIN TIAN; XIURONG WANG; CHENGJUN LI; XIAOGUANG XIN; HUALAN CHEN; KANGZHEN YU

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Source : Antiviral research; vol. 81; no. 3; pp. 234-238
ISSN : 0166-3542
CODEN : ARSRDR
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 1/2 p.

Résumé : With the widespread presence of influenza virus H5N1 in poultry and wildlife species, particularly migrating birds, vaccination has become an important control strategy for avian influenza (AI). In this study, the immune efficacy and hemagglutination inhibition (HI) antibody responses induced by a recombinant fowlpox virus (FPV) vector-based rFPV-HA-NA vaccine was evaluated in SPF and commercial chickens. Four-week old SPF chickens vaccinated with one dose of vaccine containing 2 × 103 plaque forming units (PFU) of virus were completely protected from H5N1 AI virus 1 week after vaccination, and protective immunity lasted for at least 40 weeks. Two-week old commercial layer chickens were vaccinated with the rFPV-HA-NA vaccine and boosted with the same dose of vaccine following an interval of 18 weeks. The HI antibody titers higher than 4 log 2 lasted for at least 52 weeks after the booster immunization. We also examined the efficacy of the rFPV-HA-NA vaccine in SPF chickens administrated by different routes. The results showed that effective application of rFPV-HA-NA vaccine in poultry may be restricted to wing-web puncture, intramuscular or subcutaneous injection. These results demonstrate that the rFPV-HA-NA vaccine is effective in the prevention of infection of H5N1 AI virus.

Code(s) de classement : 002B02S05

Descripteur(s) anglais
  - Descripteur(s) : Recombinant virus; Avipoxvirus; Vector; Vaccine; Prevention; Immunoprophylaxis; Chicken; Avian influenza virus; Immune response; Influenzavirus A(H5N1)
  - Desc. génériques : Chordopoxvirinae; Poxviridae; Virus; Aves; Vertebrata; Influenzavirus A; Orthomyxoviridae; Veterinary

Descripteur(s) français
  - Descripteur(s) : Virus recombinant; Avipoxvirus; Vecteur; Vaccin; Prévention; Immunoprophylaxie; Poulet; Influenzavirus aviaire; Réponse immune; Influenzavirus A(H5N1)
  - Desc. génériques : Chordopoxvirinae; Poxviridae; Virus; Aves; Vertebrata; Influenzavirus A; Orthomyxoviridae; Vétérinaire

Localisation : INIST-18839, 354000184863580060
Origine de la notice : INIST
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Serological reports of human infections of H7 and H9 avian influenza viruses in northern China

Titre : Serological reports of human infections of H7 and H9 avian influenza viruses in northern China

Auteur(s) : NA JIA; DE VLAS (Sake J.); LIU (Yun-Xi); ZHANG (Jiu-Song); LIN ZHAN; DANG (Rong-Li); MA (Yong-Hong); WANG (Xian-Jun); TI LIU; YANG (Guo-Ping); WEN (Qing-Li); RICHARDUS (Jan H.); SHAN LU; CAO (Wu-Chun)

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Source : Journal of clinical virology; vol. 44; no. 3; pp. 225-229

ISSN : 1386-6532

Date de publication : 2009

Pays de publication : NLD

Langue(s) : ENG

Type de document : P

Nombre de références : 40 ref.

Résumé : Background: H7 and H9 subtype avian influenza viruses pose a similar threat to humans as H5 virus. Objectives: This study aims to identify the potential existence of H7 and H9 avian influenza infections in farmers and in poultry workers in northern China regions with highly pathogenic avian influenza (HPAI) H5N1 outbreaks. Study design: Sera were collected from farmers in Xinjiang Uygur autonomous region and Liaoning province and poultry workers in Shandong province. Sera from healthy residents in Shanxi province were used as the controls. H7 and H9 virus infections were examined by hemagglutination inhibition (HI) assay using horse erythrocytes. The titer equal to or greater than 1:160 was considered positive. Results: A total of 583 sera collected from farmers in Xinjiang were tested, and 10 (1.7%) were positive for H9 virus infection. Out of 200 sera collected from Liaoning, two (1.0%) were infected by H9 virus. No H7 virus infection was detected in the above serum samples. Neither H7 nor H9 virus infection was identified in 277 poultry workers of Shandong and in 407 residents of Shanxi. Conclusions: Although H9 virus infection was limited in farmers from Xinjiang and Liaoning, a public health alert is needed as novel pandemic influenza strains may develop unnoticed given the presence of subclinical infections, and the possibility of re-assortment with prevailing H5N1 virus in these regions.

Code(s) de classement : 002A05C10; 002B05C02J; 002A05C06

Descripteur(s) anglais

Descripteur(s) : Human; Avian influenzavirus; Serology; China; Prevalence; Epidemiology; Subtype; Microbiology; Virology; Avian influenzavirus

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Asia; Zoopathogen; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Homme; Influenzavirus aviaire; Sérologie; Chine; Prévalence; Épidémiologie; Soustype; Microbiologie; Virologie; Grippe aviaire

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Asie; Zoopathogène; Virose; Infection

Localisation : INIST-26272, 354000184847260090
Multiorgan distribution of human influenza A virus strains observed in a mouse model

Titre : Multiorgan distribution of human influenza A virus strains observed in a mouse model

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Source : Archives of virology; vol. 154; no. 3; pp. 409-419
ISSN : 0304-8608
Date de publication : 2009
Pays de publication : AUT
Langue(s) : ENG
Type de document : P
Nombre de références : 42 ref.

Résumé : Multiorgan spread and pathogenesis of influenza infection with three human influenza A viruses was studied in mice. Mouse-adapted viruses A/Dunedin/4/73(H3N2), A/Mississippi/l/85(H3N2), and A/PR/8/34(H1N1) differed considerably in virulence (p.f.u./LD50): 79,000 p.f.u. for Dunedin, 5,000 p.f.u. for Mississippi, and 65 p.f.u. for PR/8, which qualified Dunedin as low virulent, Mississippi as intermediate, and PR/8 as highly virulent. All three viruses were detected in lungs, heart, and thymus by cultivation and RT-PCR. Moreover, vRNA of all viruses was found in liver and spleen, of Dunedin and PR/8 also in kidneys and that of Dunedin and Mississippi in blood. Only vRNA of Dunedin was demonstrated in brain. Lung damage accompanied by histopathological changes and thymus reduction were most extensive after infection with the highly virulent virus PR/8. We assume that the ability to spread to multiple organs may be a more common property of influenza viruses in mammalian hosts than previously believed.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Descripteur(s) : Human; Influenza A virus; Strain; Animal model
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) français
Descripteur(s) : Homme; Virus grippal A; Souche; Modèle animal
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST-6355, 354000187370240040
Origine de la notice : INIST
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Pathogenesis of 1918 Pandemic and H5N1 Influenza Virus Infections in a Guinea Pig Model: Antiviral Potential of Exogenous Alpha Interferon To Reduce Virus Shedding

Titre : Pathogenesis of 1918 Pandemic and H5N1 Influenza Virus Infections in a Guinea Pig Model: Antiviral Potential of Exogenous Alpha Interferon To Reduce Virus Shedding

Auteur(s) : VAN HOEVEN (Neal); BELSER (Jessica A.); SZRETTER (Kristy J.); HUI ZENG; STAEHELI (Peter); SWAYNE (David E.); KATZ (Jacqueline M.); TUMPEY (Terrence M.)
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Source : Journal of virology; vol. 83; no. 7; pp. 2851-2861
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 86 ref.

Résumé : Although highly pathogenic avian influenza H5N1 viruses have yet to acquire the ability to transmit efficiently among humans, the increasing genetic diversity among these viruses and continued outbreaks in avian species underscore the need for more effective measures for the control and prevention of human H5N1 virus infection. Additional small animal models with which therapeutic approaches against virulent influenza viruses can be evaluated are needed. In this study, we used the guinea pig model to evaluate the relative virulence of selected avian and human influenza A viruses. We demonstrate that guinea pigs can be infected with avian and human influenza viruses, resulting in high titers of virus shedding in nasal washes for up to 5 days postinoculation (p.i.) and in lung tissue of inoculated animals. However, other physiologic indicators typically associated with virulent influenza virus strains were absent in this species. We evaluated the ability of intranasal treatment with human alpha interferon (α-IFN) to reduce lung and nasal wash titers in guinea pigs challenged with the reconstructed 1918 pandemic H1N1 virus or a contemporary H5N1 virus. IFN treatment initiated 1 day prior to challenge significantly reduced or prevented infection of guinea pigs by both viruses, as measured by virus titer determination and seroconversion. The expression of the antiviral Mx protein in lung tissue correlated with the reduction of virus titers. We propose that the guinea pig may serve as a useful small animal model for testing the efficacy of antiviral compounds and that α-IFN treatment may be a useful antiviral strategy against highly virulent strains with pandemic potential.

Code(s) de classement : 002A05C10; 002A05C04

Descripteur(s) anglais
- Description : Guinea pig; Pathogenesis; Animal; Models; Antiviral; Exogenous; Dissemination; Virology; Influenza A; Alpha interferon; Influenzavirus A(H5N1)
- Description générique : Rodentia; Mammalia; Vertebrata; Cytokine; Viral disease; Infection

Descripteur(s) français
- Description : Cobaye; Pathogénie; Animal; Modèle; Antiviral; Exogène; Dissémination; Virologie; Grippe A; Interféron alpha; Influenzavirus A(H5N1)
- Description générique : Rodentia; Mammalia; Vertebrata; Cytokine; Virose; Infection

Localisation : INIST-13592, 354000187037030060
Origine de la notice : INIST
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Genetic correlation between H3N2 human and swine influenza viruses

Titre : Genetic correlation between H3N2 human and swine influenza viruses

Auteur(s) : LEI SUN; GUIHONG ZHANG; YUELONG SHU; XUEMEI CHEN; YIPING ZHU; LIMIN YANG; GUANGPENG MA; KITAMURA (Yoshihiro); WENJUN LIU

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Source : Journal of clinical virology; vol. 44; no. 2; pp. 141-144

ISSN : 1386-6532

Date de publication : 2009

Pays de publication : NLD

Langue(s) : ENG

Type de document : P

Nombre de références : 17 ref.

Résumé : Background: H3N2 is one of the main subtypes of influenza virus which circulates in human and swine population throughout the world. Objectives: To investigate the genetic correlation between H3N2 human and swine influenza viruses from the same region during the same season. Study design: Five H3N2 human and four H3N2 swine influenza viruses were isolated from Guangdong province of China in the winter of 2005. The molecular evolution of eight gene segments was analyzed. Results: In the phylogenetic trees of gene segments, all H3N2 human isolates along with the 2000's human isolates formed a cluster, and most of the H3N2 swine isolates along with the 1990's human isolates formed another cluster except that the M and NS gene of A/Swine/Guangdong/01/2005 and the PA gene of A/Swine/Guangdong/02/2005 fell into the cluster of the classical swine influenza virus, indicating the reassortment between H3N2 human and H1N1 swine influenza viruses. Conclusions: In this study, H3N2 swine influenza viruses in 2005 did not originate from the 2000's H3N2 human influenza viruses, but from the 1990's H3N2 human isolates. In addition, the reassortment of H3N2 human and H1N1 swine influenza virus in pigs was common in recent years.

Code(s) de classement : 002A05C10; 002B05C02J; 002A05C05

Descriptor(s) anglais

Descriptor(s) : Human; Swine; Influenzavirus; Genetics; Subtype; Microbiology; Virology; Influenza

Desc. génériques : Artiodactyla; Ungulata; Mammalia; Vertebrata; Orthomyxoviridae; Virus; Veterinary; Viral disease; Infection

Descriptor(s) français

Descriptor(s) : Homme; Porcin; Influenzavirus; Génétique; Soustype; Microbiologie; Virologie; Grippe

Desc. génériques : Artiodactyla; Ungulata; Mammalia; Vertebrata; Orthomyxoviridae; Virus; Vétérinaire; Virose; Infection

Localisation : INIST-26272, 354000187354160090

Origine de la notice : INIST

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Detection of Molecular Markers of Antiviral Resistance in Influenza A (H5N1) Viruses Using a Pyrosequencing Method

Titre : Detection of Molecular Markers of Antiviral Resistance in Influenza A (H5N1) Viruses Using a Pyrosequencing Method

Auteur(s) : DEYDE (Varough M.); NGUYEN (Tung); BRIGHT (Rick A.); BALISH (Amanda); BO SHU; LINDSTROM (Stephen); KLIMOV (Alexander I.); GUBAREVA (Larisa V.)

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Source : Antimicrobial agents and chemotherapy; vol. 53; no. 3; pp. 1039-1047
ISSN : 0066-4804
CODEN : AACHAX
Date de publication : 2009
Pays de publication : USA
Type de document : P
Nombre de références : 49 ref.

Résumé : Resistance of influenza viruses to antiviral drugs can emerge following medication or may result from natural variation. Two classes of anti-influenza virus drugs targeting either the M2 protein (amantadine and rimantadine) or neuraminidase (NA; oseltamivir and zanamivir) are currently licensed. These drugs are expected to be important in controlling the early stages of a potential pandemic. In the present study, we describe how a pyrosequencing method can be used to rapidly detect established molecular markers of resistance to M2 blockers and NA inhibitors in influenza A (H5N1) viruses. The residues L26, V27, A30, S31, and G34 in the M2 protein were targeted for pyrosequencing. The NA residues for pyrosequencing analysis included the established markers of drug resistance (H274 and N294), as well as residues of less certain relevance (V116, I117, Q136, K150, and L222). A single pair of pyro-reverse transcription (RT)-PCR primers was designed to allow amplification of an approximately 600-nucleotide-long amplicon of the NA genes of H5N1 viruses from various clades/subclades associated with infections in humans. The sensitivity of the assay was demonstrated by the successful pyrosequencing of RNA extracted from samples of serially diluted (10^-5 to 10^-7) virus stocks with initial concentrations ranging from 10^5 to 10^8 PFU/ml. The markers of resistance were detected in samples with threshold cycle values ranging from 32 to 37, as determined by real-time RT-PCR. The pyrosequencing approach may provide a valuable tool for rapid detection of markers of drug resistance in H5N1 viruses and facilitate the elucidation of the role of such changes in natural and acquired drug resistance.
Efficacy of live attenuated influenza vaccine in children: A meta-analysis of nine randomized clinical trials

**Titre** : Efficacy of live attenuated influenza vaccine in children: A meta-analysis of nine randomized clinical trials

**Auteur(s)** : RHORER (Janelle); AMBROSE (Christopher S.); DICKINSON (Stephanie); HAMILTON (Holli); OLEKA (Napoleon A.); MALINOSKI (Frank J.); WITTES (Janet)

**Affiliation(s)** : Statistics Collaborative, Inc, Washington, DC, USA; MedImmune, Inc, Gaithersburg, MD, USA; Indiana University, Bloomington, IN, USA

**Source** : Vaccine; vol. 27; no. 7; pp. 1101-1110

**ISSN** : 0264-410X

**CODEN** : VACCDE

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 38 ref.

**Résumé** : Nine randomized clinical trials, including approximately 25,000 children aged 6-71 months and 2000 children aged 6-17 years, have evaluated the efficacy of live attenuated influenza vaccine (LAIV) against culture-confirmed influenza as compared to placebo or trivalent inactivated vaccine (TIV). We conducted meta-analyses, based on Mantel-Haenszel relative risks from fixed effect models, to provide an estimate of vaccine efficacy (VE). Relative to placebo, year 1 VE for two doses in vaccine-naive young children was 77% (95% CI: 72%, 80%; P<0.001) against antigenically similar strains and 72% against strains regardless of antigenic similarity. Efficacy was 85%, 76%, and 73% against antigenically similar A/H1N1, A/H3N2, and B, respectively. Year 1 VE of one dose against antigenically similar strains in vaccine-naive children was 60%; efficacy of one dose in previously vaccinated children in year 2 of the various studies was 87%. In head-to-head trials comparing two doses of TIV and LAIV, vaccine-naive children who received two doses of LAIV experienced 46% fewer cases of influenza illness caused by antigenically similar strains. Similarly, for studies including older children who had been previously vaccinated, those receiving one LAIV dose experienced 35% fewer cases of influenza illness than those receiving one TIV dose. LAIV showed high VE versus placebo with no evidence of difference by age or by circulating subtype. In these studies, LAIV was more effective than TIV.

**Code(s) de classement** : 002A05F04

**Descriptor(s) anglais**
- Descripteur(s) : Efficiency; Attenuated strain; Vaccine; Child; Metaanalysis; Clinical trial; Influenza A
- Desc. génériques : Human; Viral disease; Infection

**Descriptor(s) français**
- Descripteur(s) : Efficacité; Souche atténuée; Vaccin; Enfant; Métanaalyse; Essai clinique; Grippe A
- Desc. génériques : Homme; Virose; Infection

**Localisation** : INIST-20289, 354000184824640220

**Origine de la notice** : INIST

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Plant-derived hemagglutinin protects ferrets against challenge infection with the A/Indonesia/05/05 strain of avian influenza

Titre : Plant-derived hemagglutinin protects ferrets against challenge infection with the A/Indonesia/05/05 strain of avian influenza

Auteur(s) : SHOJI (Yoko); HONG BI; MUSIYCHUK (Konstantin); RHEE (Amy); HORSEY (April); ROY (Gouropal); GREEN (Brian); SHAMLLOUL (Moneim); FARRANCE (Christine E.); TAGGART (Barbara); MYTLE (Nutan); UGULAVA (Natalia); RABINDRAN (Shailaja); METT (Vadim); CHICHESTER (Jessica A.); YUSIBOV (Vidadi)

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Source : Vaccine; vol. 27; no. 7; pp. 1087-1092
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 35 ref.

Résumé : The global spread of highly pathogenic avian influenza virus (H5N1 subtype) has promoted efforts to develop human vaccines against potential pandemic outbreaks. However, current platforms for influenza vaccine production are cumbersome, limited in scalability and often require the handling of live infectious virus. We describe the production of hemagglutinin from the A/Indonesia/05/05 strain of H5N1 influenza virus by transient expression in plants, and demonstrate the immunogenicity and protective efficacy of the vaccine candidate in animal models. Immunization of mice and ferrets with plant-derived hemagglutinin elicited serum hemagglutinin-inhibiting antibodies and protected the ferrets against challenge infection with a homologous virus. This demonstrates that plant-derived H5 HA is immunogenic in mice and ferrets, and can induce protective immunity against infection with highly pathogenic avian influenza virus. Plants could therefore be suitable as a platform for the rapid, large-scale production of influenza vaccines in the face of a pandemic.

Code(s) de classement : 002A05F04

Descripteur(s) anglais
Descripteur(s) : Hemagglutinin; Indonesia; Strain; Pathogenicity; Vaccine; Avian influenza
Desc. généraux : Asia; Infection; Viral disease

Descripteur(s) français
Descripteur(s) : Hémagglutinine; Indonésie; Souche; Pouvoir pathogène; Vaccin; Grippe aviaire
Desc. généraux : Asie; Infection; Virose

Localisation : INIST-20289, 354000184824640200
Origine de la notice : INIST
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Willingness of healthcare workers to accept voluntary stockpiled H5N1 vaccine in advance of pandemic activity

Titre : Willingness of healthcare workers to accept voluntary stockpiled H5N1 vaccine in advance of pandemic activity

Auteur(s) : PAREEK (Manish); CLARK (Tristan); DILLON (Helen); KUMAR (Rajesh); STEPHENSON (Lain)
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Source : Vaccine; vol. 27; no. 8; pp. 1242-1247
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
 Pays de publication : GBR
Type de document : P
Nombre de références : 24 ref.

Résumé : Healthcare workers may be at risk during the next influenza pandemic. Priming with stockpiled vaccine may protect staff and reduce nosocomial transmission. Despite campaigns to increase seasonal influenza vaccine coverage, uptake among healthcare workers is generally low; creating uncertainty whether they would participate in pre-pandemic vaccine programmes. We conducted a cross-sectional questionnaire survey of healthcare workers in a UK hospital during, and 6 months after, a period of media reporting of an H5N1 outbreak at a commercial UK poultry farm. A total of 520 questionnaires were returned, representing 20% of frontline workforce. More respondents indicated willingness to accept stockpiled H5N1 vaccine during the period of media attention than after (166/262, 63.4% vs. 134/258, 51.9%; p=0.009). Following multivariate analysis, factors associated with willingness to accept H5N1 vaccine included: previous seasonal vaccine (OR 6.2, 95% CI 3.0-12.8, p < 0.0001), awareness of occupational seasonal vaccine campaigns (OR 2.2, 95% CI 1.4-3.5, p = 0.001), belief that seasonal vaccine benefits themselves (OR 2.5, 95% CI 1.6-4.0, p < 0.0001) or the hospital (OR 3.6, 95% CI 2.3-5.8, p < 0.0001), belief that pandemic risk is high/moderate (OR 14.1, 95% CI 7.6-26.1, p < 0.0001) and would threaten healthcare workers (OR 2.9, 95% CI 1.8-4.5, p < 0.0001). Those who would not accept vaccine (220 respondents, 42.7%) if offered before the pandemic do not perceive pandemic influenza as a serious threat, and have concerns regarding vaccine safety. A majority of healthcare workers are amenable to accept stockpiled H5N1 vaccine if offered in advance of pandemic activity.

Code(s) de classement : 002A05F04

Descriputeur(s) anglais
Describeur(s) : Vaccine; Vaccination; Influenza
Desc. génériques : Viral disease; Infection

Descriputeur(s) français
Describeur(s) : Vaccin; Vaccination; Grippe
Desc. génériques : Virose; Infection

Localisation : INIST-20289, 354000184834130120
Origine de la notice : INIST
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Immune Response to Influenza Vaccine in Children With Inflammatory Bowel Disease

**Titre:** Immune Response to Influenza Vaccine in Children With Inflammatory Bowel Disease

**Auteurs:** YING LU; JACOBSON (Denise L.); ASHWORTH (Lori A.); GRAND (Richard J.); MEYER (Anthony L.); MCNEAL (Monica M.); GREGAS (Matt C.); BURCHETT (Sandra K.); BOUSVAROS (Athos)

**Affiliation(s):** Division of Gastroenterology, Hepatology, and Nutrition, Inflammatory Bowel Disease Center, Children's Hospital Boston, Boston, Massachusetts, USA; Department of Pediatrics, Harvard Medical School, Boston, Massachusetts, USA; Center for Biostatistics and AIDS Research, Harvard School of Public Health, Boston, Massachusetts, USA; Laboratory for Specialized Clinical Studies, Cincinnati Children's Hospital Medical Center, Cincinnati, Ohio, USA; Clinical Research Program, Department of Neurology, Children's Hospital Boston, Harvard Medical School, Boston, Massachusetts, USA; Division of Infectious Diseases, Children's Hospital Boston, Boston, Massachusetts, USA

**Source:** The American journal of gastroenterology; vol. 104; no. 2; pp. 444-453

**ISSN:** 0002-9270

**Date de publication:** 2009

**Pays de publication:** GBR

**Langue(s):** ENG

**Type de document:** P

**Nombre de références:** 37 ref.

**Résumé:** OBJECTIVES: Patients with inflammatory bowel disease (IBD) frequently receive immunosuppressive therapy. The immune response in these patients to vaccines has not been well studied. We conducted a prospective, open label study to evaluate the serologic response to influenza vaccine in children with IBD. METHODS: Serum was obtained from 146 children and young adults with IBD (96 Crohn's disease, 47 ulcerative colitis, and 3 indeterminate colitis) for baseline influenza titer, immediately followed by immunization with trivalent (A/Solomon Islands/3/2006 (H1N1), A/Wisconsin/67/2005 (H3N2), and B/Malaysia/2506/2004 (B)) inactivated influenza vaccine. Patients returned for repeat titers 3-9 weeks later. Seroprotection against each influenza strain was defined as hemagglutination inhibition titer >=40. Patients were categorized as nonimmunosuppressed (NIS; aminosalicylates only, antibiotics only, or no therapy) or immunosuppressed (IS; any immunosuppressive agent). IS patients were further subcategorized as: (i) tacrolimus, (ii) tumor necrosis factor-a (TNF-a) inhibitor, (3) immunomodulator, and (4) corticosteroids only. RESULTS: More patients were seroprotected against strains A/H1N1 and A/H3N2 than B strain (P<0.02), regardless of immunosuppression status. The proportion of seroprotected patients and geometric mean titers at post-vaccination were similar between NIS and IS groups for all three strains. Subanalysis of patients not seroprotected at baseline showed that those receiving anti-TNF therapy were less likely to be seroprotected against strain B (14%) compared to patients in the NIS group (39%, P=0.025). There were no serious vaccine-associated adverse events. CONCLUSIONS: Influenza vaccination produces a high prevalence of seroprotection in IBD patients, particularly against A strains. The vaccine is well tolerated. Routine influenza vaccination in IBD patients is recommended, irrespective of whether patients receive immunosuppressive medications.

**Code(s) de classement:** 002B13B03; 002B05C02C

**Descripteur(s) anglais**

- **Description(s) :** Influenza; Crohn disease; Ulcerative colitis; Immune response; Immunoprophylaxis; Prevention; Vaccine; Child; Gastroenterology
- **Desc. génériques :** Viral disease; Infection; Human; Digestive diseases; Intestinal disease; Inflammatory disease

**Descripteur(s) français**

- **Description(s) :** Grippe; Entérite de Crohn; Rectocolite ulcérohémorragique; Réponse immune; Immunoprophylaxie; Prévention; Vaccin; Enfant; Gastroentérologie
- **Desc. génériques :** Virose; Infection; Homme; Pathologie de l'appareil digestif; Pathologie de l'intestin; Maladie

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inflammatoire

Localisation : INIST-11062, 354000185532490270
Origine de la notice : INIST
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Effect of dexamethasone on acute respiratory distress syndrome induced by the H5N1 virus in mice

Titre : Effect of dexamethasone on acute respiratory distress syndrome induced by the H5N1 virus in mice

Auteur(s) : XU (T.); QIAO (J.); ZHAO (L.); HE (G.); LI (K.); WANG (J.); TIAN (Y.); WANG (H.)
Affiliation(s) : Dept of Pathophysiology, College of Veterinary Medicine, China Agricultural University, Beijing, CHN; Dept of Veterinary Medicine, College of Animal Science, Hebei North University, Hebei Province, CHN

Source : The European respiratory journal; vol. 33; no. 4; pp. 852-860
ISSN : 0903-1936
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 35 ref.

Résumé : Glucocorticoids are widely used in the treatment of different inflammatory diseases. The present study was performed to investigate the effect of dexamethasone (DEX) on acute respiratory distress syndrome (ARDS) induced by the H5N1 viral infection in mice. BALB/c mice, 6-8 weeks old, were divided into three groups with 80 mice in each. The infected group and the DEX-treated infected group were inoculated intranasally with 1 x 10^2 50% mouse infectious dose of A/Chicken/Hebei/108/2002 (H5N1) viruses, with daily intraperitoneal injections of PBS, or 2.5 mg.kg^-1 DEX at days 3-14 post inoculation, respectively. The control group received noninfectious allantoic fluid and a daily intraperitoneal injection of PBS. In H5N1-infected mice, DEX treatment did not improve the mortality (17 out of 20 versus 16 out of 20 deaths in the DEX-treated infected group versus the infected group), and did not alleviate clinical signs, including weight loss, decreased food intake and inactivity. There was no significant amelioration of the hypoxaemia and ARDS-associated pathological changes in DEX-treated infected mice, as assessed by blood gas analysis and histological score. Furthermore, DEX therapy did not inhibit inflammatory cellular infiltration and cytokine release (interleukin-6 and tumour necrosis factor-a) in bronchoalveolar lavage fluid induced by the H5N1 infection. In conclusion, dexamethasone treatment (2.5 mg.kg^-1) from days 3-14 post inoculation has no beneficial effect on acute respiratory distress syndrome caused by the H5N1 infection in mice.

Code(s) de classement : 002B11D; 002B05C02C

Description(s) anglais
- Descripteur(s) : Respiratory distress; Avian influenza; Dexamethasone; Acute; Influenza A virus; Animal; Mouse; Cytokine; Pneumology
- Desc. génériques : Viral disease; Infection; Influenzavirus A; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Respiratory disease

Description(s) français
- Descripteur(s) : Détresse respiratoire; Grippe aviaire; Dexaméthasone; Aigu; Virus grippal A; Animal; Souris; Cytokine; Pneumologie
- Desc. génériques : Virose; Infection; Influenzavirus A; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Pathologie de l'appareil respiratoire

Localisation : INIST-4275, 354000185559540230
Origine de la notice : INIST
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Incorporation of LpxL1, a detoxified lipopolysaccharide adjuvant, in influenza H5N1 virosomes increases vaccine immunogenicity

Titre : Incorporation of LpxL1, a detoxified lipopolysaccharide adjuvant, in influenza H5N1 virosomes increases vaccine immunogenicity

Auteur(s) : DE VRIES (J. J. C.); BUNGENER (L.); TER VEER (W.); VAN ALPHEN (L.); VAN DER LEY (P.); WILSCHUT (J.); HUCKRIEDE (A.)
Affiliation(s) : Department of Medical Microbiology, Molecular Virology Section, University Medical Center Groningen and University of Croningen, Groningen, NLD; Netherlands Vaccine Institute (NVI), Bilthoven, NLD

Source : Vaccine; vol. 27; no. 6; pp. 947-955
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 42 ref.

Résumé : The increasing number of human influenza H5N1 infections accentuates the need for the development of H5N1 vaccine candidates to prevent a potential influenza pandemic. The use of adjuvants in such vaccines can contribute significantly to antigen dose-sparing. In this study, we evaluated the capacity of the nontoxic Neisseria meningitidis lipopolysaccharide analog LpxL1 to function as an adjuvant for an influenza H5N1 virosomal vaccine. Inactivated influenza H5N1 virus (NIBRG-14) was used to construct virosomes (reconstituted virus envelopes) with LpxL1 incorporated in the virosomal membrane thus combining the influenza hemagglutinin (HA) antigen and the adjuvant in the same particle. Mice were immunized in a one- or two-dose immunization regimen with H5N1 virosomes with or without incorporated LpxL1. After a single immunization, H5N1 virosomes with incorporated LpxL1 induced significantly enhanced H5N1-specific total IgG titers as compared to non-adjuvanted virosomes but hemagglutination inhibition (HI) titers remained low. In the two-dose immunization regimen, LpxL1-modified H5N1 virosomes induced HI titers above 40 which were significantly higher than those obtained with non-adjuvanted virosomes. Incorporation of LpxL1 had little effect on virosome-induced IgG1 levels, but significantly increased IgG2a levels in both the one- and two-dose immunization regimen. Compared to non-adjuvanted virosomes, LpxL1-modified virosomes induced similar numbers of IFN gamma -producing T cells but decreased numbers of IL-4-producing T cells irrespective of the number of immunizations. We conclude that LpxL1 incorporated in H5N1 influenza virosomes has the capacity to function as a potent adjuvant particularly stimulating Thi-type immune reactions.

Code(s) de classement : 002A05F04

Descripteur(s) anglais
Desc. génériques : Viral disease; Infection

Descripteur(s) français
Desc. génériques : Virose; Infection

Localisation : INIST-20289, 354000185561350180
Origine de la notice : INIST
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Molecular characterization and epidemiology of the highly pathogenic avian influenza H5N1 in Nigeria

Titre : Molecular characterization and epidemiology of the highly pathogenic avian influenza H5N1 in Nigeria

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Source : Epidemiology and infection; vol. 137; no. 4; pp. 456-463
ISSN : 0950-2688
CODEN : EPINEU
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 23 ref.

Résumé : Avian influenza caused infection and spread throughout Nigeria in 2006. Carcass samples (lung, liver, spleen, heart, trachea and intestine) from the different regions of Nigeria were processed for virus isolation. Infective allantoic fluids were tested for avian influenza viruses (AIV) and Newcastle disease virus using monospecific antisera. Thirty-five isolates were generated and characterized molecularly using the haemagglutinin gene. The molecular analysis indicated that different sublineages of the highly pathogenic avian influenza (HPAI) H5N1 viruses spread throughout Nigeria. We compared the Nigerian isolates with others from Africa and results indicated close similarities between isolates from West Africa and Sudan. Some of the analysed viruses showed genetic drift, and the implications of these for future epidemiology and ecology of avian influenza in Africa require further evaluation. The spread of primary outbreaks was strongly linked to trade (legal and illegal), live bird markets, inappropriate disposal, and poorly implemented control measures. No strong correlation existed between wild birds and HPAI H5N1 in Nigeria.

Code(s) de classement : 002A05

Descripteur(s) anglais
Desc. génériques : Africa; Infection; Viral disease

Descripteur(s) français
Desc. génériques : Afrique; Infection; Virose

Localisation : INIST-6056, 354000187323060020
Origine de la notice : INIST
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Transmission of Influenza Virus via Aerosols and Fomites in the Guinea Pig Model

Titre : Transmission of Influenza Virus via Aerosols and Fomites in the Guinea Pig Model

Auteur(s) : MUBAREKA (Samira); LOWEN (Anice C.); STEEL (John); COATES (Allan L.); GARCIA-SASTRE (Adolfo); PALESE (Peter)

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Source : The Journal of infectious diseases; vol. 199; no. 6; pp. 858-865
ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 33 ref.

Résumé : Limited data on the relative contributions of different routes of transmission for influenza virus are available. Person-to-person transmission is central to seasonal and pandemic spread; nevertheless, the modes of spread are a matter of ongoing debate. Resolution of this discussion is paramount to the development of effective control measures in health care and community settings. Using the guinea pig model, we demonstrated that transmission of influenza A/Panama/2007/1999 (H3N2) virus through the air is efficient, compared with spread through contaminated environmental surfaces (fomites). We also examined the aerosol transmission efficiencies of 2 human influenza virus A strains and found that A/Panama/2007/1999 influenza virus transmitted more efficiently than A/Texas/36/1991 (H1N1) virus in our model. The data provide new and much-needed insights into the modes of influenza virus spread and strain-specific differences in the efficiency of transmission.

Code(s) de classement : 002A05C10; 002B05

Descriptor(s) anglais
Desc. génériques : Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata

Descriptor(s) français
Desc. génériques : Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata

Localisation : INIST-2052, 354000187323710130
Origine de la notice : INIST
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Simple, Sensitive, and Swift Sequencing of Complete H5N1 Avian Influenza Virus Genomes

Titre : Simple, Sensitive, and Swift Sequencing of Complete H5N1 Avian Influenza Virus Genomes

Auteur(s) : HOPER (Dirk); HOFFMANN (Bernd); BEER (Martin)
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Source : Journal of clinical microbiology : (Print); vol. 47; no. 3; pp. 674-679
ISSN : 0095-1137
CODEN : JCMIDW
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 11 ref.

Résumé : The spread of highly pathogenic avian influenza A virus (HPAIV) of subtype H5N1 demands fast and reliable methods for in-depth, full-length sequence analysis. For this purpose, we designed a simple and sensitive method for the preparation of sequencing libraries from H5N1 HPAIV diagnostic RNA samples for sequencing with the Genome Sequencer FLX instrument. The method presented seamlessly integrates high-throughput pyrosequencing with the Roche/454 instrument into diagnostics without the need for additional equipment or molecular biological techniques besides standard PCR and the Genome Sequencer FLX sample preparation and sequencing pipeline.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Descripteur(s) : Avian influenzavirus; Genome; Microbiology
Desc. généraires : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen

Descripteur(s) français
Descripteur(s) : Influenzavirus aviaire; Génome; Microbiologie
Desc. généraires : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogène

Localisation : INIST-17088, 354000185548250230
Origine de la notice : INIST
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Practical Considerations for High-Throughput Influenza A Virus Surveillance Studies of Wild Birds by Use of Molecular Diagnostic Tests

Titre : Practical Considerations for High-Throughput Influenza A Virus Surveillance Studies of Wild Birds by Use of Molecular Diagnostic Tests

Auteur(s) : MUNSTER (Vincent J.); BAAS (Chantal); LEXMOND (Pascal); BESTEBROER (Theo M.); GULDEMEESTER (Judith); BEYER (Walter E. P.); DE WIT (Emmie); SCHUTTEN (Martin); RIMMELZWAAN (Guus F.); OSTERHAUS (Albert D. M. E.); FOUCHIER (Ron A. M.)

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Source : Journal of clinical microbiology : (Print); vol. 47; no. 3; pp. 666-673
ISSN : 0095-1137
CODEN : JCMIDW
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 41 ref.

Résumé : Influenza A virus surveillance studies of wild bird populations are essential to improving our understanding of the role of wild birds in the ecology of low-pathogenic avian influenza viruses and their potential contribution to the spread of H5N1 highly pathogenic avian influenza viruses. Whereas the primary results of such surveillance programs have been communicated extensively, practical considerations and technical implementation options generally receive little attention. In the present study, the data obtained from 39,490 samples were used to compare the impacts of variables such as the sampling procedure, storage and transport conditions, and the choice of molecular and classical diagnostic tests on the outcome of the results. Molecular diagnostic tests allowed estimation of the virus load in samples, which has implications for the ability to isolate virus. Virus isolation in embryonated eggs was more sensitive than virus isolation in cell cultures. Storage and transport conditions had less of an impact on diagnostics by the use of molecular tests than by the use of classical approaches. These findings indicate that molecular diagnostic tests are more sensitive and more reliable than classical tests. In addition, molecular diagnostic tests facilitated analyses in real time and allowed the discrimination of H5 influenza viruses with low and high pathogenicities without the need for virus isolation. Critical assessment of the methods used in large surveillance studies like this will facilitate comparison of the results between studies. Moreover, the lessons learned from current large-scale influenza A virus surveillance activities could be valuable for other pathogen surveillance programs in the future.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Descripteur(s) : Influenza A virus; Aves; High throughput screening; Microbiology
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Vertebrata

Descripteur(s) français

Descripteur(s) : Virus grippal A; Aves; Criblage haut débit; Microbiologie
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Vertebrata

Localisation : INIST-17088, 354000185548250220
Origine de la notice : INIST
Copyright de notice : © 2009 INIST-CNRS. All rights reserved.
Pathogenesis of H5N1 Influenza Virus Infections in Mice and Ferret Models Differs According to Respiratory Tract or Digestive System Exposure

Titre : Pathogenesis of H5N1 Influenza Virus Infections in Mice and Ferret Models Differs According to Respiratory Tract or Digestive System Exposure

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Source : The Journal of infectious diseases; vol. 199; no. 5; pp. 717-725
ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 40 ref.

Résumé : Background. Epidemiologic, clinical, and laboratory data suggest that H5N1 influenza viruses are transmitted through and predominantly affect the respiratory system of mammals. Some data suggest digestive system involvement. However, direct evidence of alimentary transmission and infection in mammals is lacking. Methods. Infection with and pathogenesis of 4 H5N1 viruses were assessed in mice and ferrets inoculated intranasally or intragastrically with virus in liquid. In addition, ferrets were fed infected raw chicken meat or minced meat administered into the stomach by gavage with a tube. Results. Only one virus, A/Whooper swan/Mongolia/244/05, was able to infect mice after intragastric inoculation in liquid, whereas no evidence of infection was observed in ferrets after intragastric inoculation. Consumption of infected meat by ferrets resulted in respiratory system infection only (due to A/Muscovy duck/Vietnam/209/05 and A/Whooper swan/Mongolia/244/05 viruses) or in both severe respiratory and systemic infection with predominant involvement of the liver, pancreas, and large and small intestine (due to A/Vietnam/1203/04 virus). Direct intragastric exposure to infected meat (A/Vietnam/1203/04 virus) resulted in lethal systemic disease mainly affecting the intestine, liver, and pancreas but not involving the lungs. Conclusions. Our results demonstrated that exposure of the digestive system to H5N1 influenza viruses could initiate infection either through the tonsils, with spread to respiratory tissues, or through intestinal infection, with spread to the liver and pancreas.

Code(s) de classement : 002A05C10; 002B05

Descripertoire(s) anglais
  - Description(s) : Influenzavirus; Pathogenesis; Animal model; Respiratory system; Respiratory tract; Digestive tract; Microbiology; Infection; Viral disease
  - Description(s) : Orthomyxoviridae; Virus

Descripertoire(s) français
  - Description(s) : Influenzavirus; Pathogénie; Modèle animal; Appareil respiratoire; Voie respiratoire; Tube digestif; Microbiologie; Infection; Virose
  - Description(s) : Orthomyxoviridae; Virus

Localisation : INIST-2052, 354000187283380170
Origine de la notice : INIST
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Infections With Oseltamivir-Resistant Influenza A(H1 N1) Virus in the United States

Titre : Infections With Oseltamivir-Resistant Influenza A(H1 N1) Virus in the United States

Auteur(s) : DHARAN (Nila J.); GUBAREVA (Larisa V.); MEYER (John J.); OKOMO-ADHIAMBO (Margaret); MCCLINTON (Reginald C.); MARSHALL (Steven A.); GEORGE (Kirsten St.); EPPERSON (Scott); BRAMMER (Lynnette); KLIMOV (Alexander I.); BRESEE (Joseph S.); FRY (Alicia M.)

Collectivité(s) auteur : Oseltamivir-Resistance Working Group, USA

Affiliation(s) : Epidemic Intelligence Service, Office of Workforce and Career Development Assigned to Influenza Division, USA; Influenza Division, Centers for Disease Control and Prevention, Atlanta, Georgia, USA; Arizona Department of Health Services, Phoenix, USA; Wyoming Department of Health, Cheyenne, USA; Wisconsin State Laboratory of Hygiene, Madison, USA; Wadsworth Center, New York State Department of Health, Albany, USA

Source : JAMA, the journal of the American Medical Association; vol. 301; no. 10; pp. 1034-1041
ISSN : 0098-7484
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 32 ref.

Résumé : Context During the 2007-2008 influenza season, oseltamivir resistance among influenza A(H1 N1) viruses increased significantly for the first time worldwide. Early surveillance data suggest that the prevalence of oseltamivir resistance among A(H1N1) viruses will most likely be higher during the 2008-2009 season. Objectives To describe patients infected with oseltamivir-resistant influenza A(H1 N1) virus and to determine whether there were any differences between these patients and patients infected with oseltamivir-susceptible A(H1 N1) virus in demographic or epidemiological characteristics, clinical symptoms, severity of illness, or clinical outcomes. Design, Setting, and Patients Influenza A(H1 N1) viruses that were identified and submitted to the Centers for Disease Control and Prevention by US public health laboratories between September 30, 2007, and May 17, 2008, and between September 28, 2008, and February 19, 2009, were tested as part of ongoing surveillance. Oseltamivir resistance was determined by neuraminidase inhibition assay and pyrose-quencing analysis. Information was collected using a standardized case form from patients with oseltamivir-resistant A(H1 N1) infections and a comparison group of patients with oseltamivir-susceptible A(H1N1) infections during 2007-2008. Main Outcome Measures Demographic and epidemiological information as well as clinical information, including symptoms, severity of illness, and clinical outcomes. Results During the 2007-2008 season, influenza A(H1N1) accounted for an estimated 19% of circulating influenza viruses in the United States. Among 1155 influenza A(H1N1) viruses tested from 45 states, 142 (12.3%) from 24 states were resistant to oseltamivir. Data were available for 99 oseltamivir-resistant cases and 182 oseltamivir-susceptible cases from this period. Among resistant cases, median age was 19 years (range, 1 month to 62 years), 5 patients (5%) were hospitalized, and 4 patients (4%) died. None reported oseltamivir exposure before influenza diagnostic sample collection. No significant differences were found between cases of oseltamivir-resistant and oseltamivir-susceptible influenza in demographic characteristics, underlying medical illness, or clinical symptoms. Preliminary data from the 2008-2009 influenza season identified resistance to oseltamivir among 264 of 268 influenza A(H1N1) viruses (98.5%) tested. Conclusions Oseltamivir-resistant A(H1 N1) viruses circulated widely in the United States during the 2007-2008 influenza season, appeared to be unrelated to oseltamivir use, and appeared to cause illness similar to oseltamivir-susceptible A(H1N1) viruses. Circulation of oseltamivir-resistant A(H1N1) viruses will continue, with a higher prevalence of resistance, during the 2008-2009 season.

Code(s) de classement : 002B01

Descripteur(s) anglais

Descripteur(s) : Infection; Resistance; Influenza A virus; Oseltamivir; United States; Medicine; Antiviral
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; North America; America; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor; Neuraminidase inhibitor

Descr ipteur(s) français

Descr ipteur(s) : Infection; Résistance; Virus grippal A; Oséltamivir; Etats-Unis; Médecine; Antiviral

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Amérique du Nord; Amérique; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme; Inhibiteur neuraminidase

Localisation : INIST-5051, 354000187335770070

Origine de la notice : INIST

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Morbidity and Mortality Associated With Nosocomial Transmission of Oseltamivir-Resistant Influenza A(H1N1) Virus

Titre : Morbidity and Mortality Associated With Nosocomial Transmission of Oseltamivir-Resistant Influenza A(H1N1) Virus

Auteur(s) : GOOSKENS (Jairo); JONGES (Marcel); CLAAS (Eric C. J.); MEIJER (Adam); VAN DEN BROEK (Peterhans J.); KROES (Aloys C. M.)

Affiliation(s) : Department of Medical Microbiology, Center of Infectious Diseases, Leiden University Medical Center, Leiden, NLD; Section of Virology, National Institute for Public Health and the Environment, Bilthoven, NLD; Department of Infectious Diseases, Center of Infectious Diseases, Leiden University Medical Center, Leiden, NLD

Source : JAMA, the journal of the American Medical Association; vol. 301; no. 10; pp. 1042-1046

ISSN : 0098-7484

Date de publication : 2009

Pays de publication : USA

Langue(s) : ENG

Type de document : P

Nombre de références : 12 ref.

Résumé : Context The sudden emergence and rapid spread of oseltamivir-resistant influenza A(H1 N1) viruses with neuraminidase (NA) gene H274Y amino acid substitution is the hallmark of global seasonal influenza since January 2008. Viruses carrying this mutation are widely presumed to exhibit attenuated pathogenicity, compromised transmission, and reduced lethality. Objective To investigate nosocomial viral transmission in a cluster of patients with influenza A(H1N1) virus infection. Design, Setting, and Patients Descriptive outbreak investigation of 2 hematopoietic stem cell transplant recipients and an elderly patient who developed hospital-acquired influenza A virus infection following exposure to an index patient with community-acquired H274Y-mutated influenza A(H1N1) virus infection in a medical ward at a Dutch university hospital in February 2008. The investigation included a review of the medical records, influenza virus polymerase chain reaction and culture, phenotypic oseltamivir and zanamivir susceptibility determination, and hemagglutinin chain 1 (HA1) gene and NA gene sequence analysis. Main Outcome Measure Phylogenetic relationship of patient cluster influenza A(H1N1) viruses and other 2007-2008 seasonal influenza A(H1N1) viruses. Results Viral HA1 and NA gene sequence analysis from the 4 patients revealed indistinguishable nucleotide sequences and phylogenetic clustering of H274Y-mutated, oseltamivir-resistant influenza A(H1N1) virus, confirming nosocomial transmission. Influenza virus pneumonia (3 patients) and attributable mortality (2 patients) during active infection was observed in patients with lymphocytopenia at onset. Conclusion Seasonal oseltamivir-resistant influenza A(H1N1) viruses with NA gene H274Y mutation are transmitted and retain significant pathogenicity and lethality in high-risk patients.

Code(s) de classement : 002B01; 002B30A01A; 002B05A03

Descripteur(s) anglais

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor; Neuraminidase inhibitor

Descrip. associ. : Nosocomial infection; Epidemiology; Morbidity; Oseltamivir; Mortality; Association; Transmission; Resistance; Influenza A virus; Medicine; Antiviral

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor; Neuraminidase inhibitor

Descripteur(s) français

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme; Inhibiteur neuraminidase

Descrip. associ. : Infection nosocomiale; Epidémiologie; Morbidité; Osélétamivir; Mortalité; Association; Transmission; Résistance; Virus grippal A; Médecine; Antiviral

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme; Inhibiteur neuraminidase

Localisation : INIST-5051, 354000187335770080

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Identification of Amino Acid Substitutions in Avian Influenza Virus (H5N1) Matrix Protein 1 by Using Nanoelectrospray MS and MS/MS

**Titre** : Identification of Amino Acid Substitutions in Avian Influenza Virus (H5N1) Matrix Protein 1 by Using Nanoelectrospray MS and MS/MS

**Auteur(s)** : NING LIU; WENJUN SONG; LEE (Kim-Chung); PUIWANG; HONGLIN CHEN; ZONGWEI CAI

**Affiliation(s)** : Department of Chemistry, Hong Kong Baptist University, HKG; State Key Laboratory for Emerging Infectious Diseases, Department of Microbiology, The University of Hong Kong, HKG

**Source** : Journal of the American Society for Mass Spectrometry; vol. 20; no. 2; pp. 312-320
**ISSN** : 1044-0305
**Date de publication** : 2009
**Pays de publication** : USA
**Langue(s)** : ENG
**Type de document** : P
**Nombre de références** : 25 ref.

**Résumé** : Matrix protein 1 (M1), the major structural protein of the avian influenza virus, plays a critical role in regulation of viral RNA transcription via interaction with RNA and transportation of RNP cores. Mutations in M1 have been frequently observed in the highly virulent avian influenza H5N1 virus, which might be crucial to the pathogenic function. Here we report the characterization of mutated peptides in M1 purified from highly pathogenic avian influenza virus H5N1 by nanoelectrospray MS and MS/MS analyses on a quadrupole-time-of-flight mass spectrometer (Q-TOFMS). The specificity of tandem mass spectrometry allowed the identification of six amino acid (AA) substitutions in M1, including R95K, A166V, I168T, N207S, N224S, and R230K. Two commonly observed modifications such as oxidation and deamidation were accurately assigned in the protein. Bioinformatics analysis suggested some relationship between the amino acid substitution and structural property of M1 protein. Discussions on de novo sequencing of MS/MS spectra, especially in dealing with the AA substitutions, were provided.

**Code(s) de classement** : 002A05C03

**Descripteur(s) anglais**

- Qualitative analysis
- Analysis method
- Avian influenzavirus
- Mass spectrometry
- Aminoacid sequence
- Electrospray
- Isolation
- Purification
- Mutation
- Time of flight method
- Primary structure
- Peptide map
- Structural analysis
- Tandem mass spectrometry

**Descripteur(s) français**

- Analyse qualitative
- Méthode analyse
- Influenzavirus aviaire
- Spectrométrie masse
- Séquence aminoaide
- Electrospry
- Isolément
- Purification
- Mutation
- Méthodes temps vol
- Structure primaire
- Carte peptidique
- Analyse structurale
- Protéine M1
- Spectrométrie masse tandem

**Localisation** : INIST-22160, 354000185394610170
**Origine de la notice** : INIST
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Monoclonal Antibodies against the Fusion Peptide of Hemagglutinin Protect Mice from Lethal Influenza A Virus H5N1 Infection

**Titre** : Monoclonal Antibodies against the Fusion Peptide of Hemagglutinin Protect Mice from Lethal Influenza A Virus H5N1 Infection

**Auteur(s)** : PRABHU (Nayana); PRABAKARAN (Mookkan); HO (Hui-Ting); VELUMANI (Sumathy); JIA QIANG; GOUTAMA (Michael); KWANG (Jimmy)

**Affiliation(s)** : Animal Health Biotechnology, Temasek Life Sciences Laboratory, National University of Singapore, Singapore 117604, SGP; Tridel Biosciences International Pte. Ltd., 101 Cecil Street, Singapore 069533, SGP; Department of Microbiology, Faculty of Medicine, National University of Singapore, Singapore, SGP

**Source** : Journal of virology; vol. 83; no. 6; pp. 2553-2562

**ISSN** : 0022-538X

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 42 ref.

**Résumé** : The HA2 glycopolypeptide (gp) is highly conserved in all influenza A virus strains, and it is known to play a major role in the fusion of the virus with the endosomal membrane in host cells during the course of viral infection. Vaccines and therapeutics targeting this HA2 gp could induce efficient broad-spectrum immunity against influenza A virus infections. So far, there have been no studies on the possible therapeutic effects of monoclonal antibodies (MAbs), specifically against the fusion peptide of hemagglutinin (HA), upon lethal infections with highly pathogenic avian influenza (H5N1) virus. We have identified MAb 1C9, which binds to GLFGAIAGF, a part of the fusion peptide of the HA2 gp. We evaluated the efficacy of MAb 1C9 as a therapy for influenza A virus infections. This MAb, which inhibited cell fusion in vitro when administered passively, protected 100% of mice from challenge with five 50% mouse lethal doses of HPAI H5N1 influenza A viruses from two different clades. Furthermore, it caused earlier clearance of the virus from the lung. The influenza virus load was assessed in lung samples from mice challenged after pretreatment with MAb 1C9 (24 h prior to challenge) and from mice receiving early treatment (24 h after challenge). The study shows that MAb 1C9, which is specific to the antigenically conserved fusion peptide of HA2, can contribute to the cross-clade protection of mice infected with H5N1 virus and mediate more effective recovery from infection.

**Code(s) de classement** : 002A05C10; 002A05C07

**Descripteur(s) anglais**
- **Desc. anglais** : Mouse; Influenza A virus; Monoclonal antibody; Peptides; Hemagglutinin; Prevention; Animal; Virology; Influenza A; Influenzavirus A(H5N1)
- **Desc. généraux** : Rodentia; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Viral disease; Infection

**Descripteur(s) français**
- **Desc. français** : Souris; Virus grippal A; Anticorps monoclonal; Peptide; Hémagglutinine; Prévention; Animal; Virologie; Grippe A; Influenzavirus A(H5N1)
- **Desc. généraux** : Rodentia; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Virose; Infection

**Localisation** : INIST-13592, 354000187328270150

**Origine de la notice** : INIST

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Molecular evolution of human influenza A viruses in a local area
during eight influenza epidemics from 2000 to 2007

Titre : Molecular evolution of human influenza A viruses in a local area during eight influenza epidemics from 2000 to 2007

Auteur(s) : ZARAKET (Hassan); SAITO (Reiko); SATO (Isamu); SUZUKI (Yasushi); DANJUAN LI; DAPAT (Clyde); CAPERIG-DAPAT (Isolde); OGUMA (Taeko); SASAKI (Asami); SUZUKI (Hiroshi)

Affiliation(s) : Division of Public Health, Department of Infectious Disease Control and International Medicine, Graduate School of Medical and Dental Sciences, Niigata University, 1-757, Asahimachi-Dori, Niigata, Niigata 951-8510, JPN; Yoiko Pediatric Clinic, Niigata, Niigata, JPN

Source : Archives of virology; vol. 154; no. 2; pp. 285-295
ISSN : 0304-8608
Date de publication : 2009
Pays de publication : AUT
Langue(s) : ENG
Type de document : P
Nombre de références : 48 ref.

Résumé : A total of 1,041 human influenza A virus isolates were collected at a clinic in Niigata, Japan, during eight influenza seasons from 2000 to 2007. The H3N2 subtype accounted for 75.4% of the isolates, and the rest were H1N1. Extremely high rates of amantadine-resistant strains of H3N2 subtype were observed in 2005/2006 (100%) and 2006/2007 (79.4%), while amantadine-resistant strains of H1N1 subtype were only detected in 2006/ 2007 (48.2%). Sequence and phylogenetic analysis of the HA1 subunit of the hemagglutinin (HA) gene revealed a characteristic linear trunk in the case of H3N2 viruses and a multi-furcated tree in the case of H1N1 and showed a higher sequence diversity among H3N2 strains than H1N1 strains. Mutations in the HA1 from both subtypes were mainly found in the globular region, and only one-third of these were retained for two or more successive years. Higher diversity of H3N2 viruses was mainly attributable to a higher fixation rate of non-synonymous mutations and to a lesser extent to a higher nucleotide substitution rate than for H1N1. Our analysis showed evidence of four positively selected sites in the HA1 of H1 and five sites in that of H3, four of which were novel. Finally, acquisition or loss of N-glycosylation sites was shown to contribute to the evolution of influenza A virus, especially in the case of H3N2, which had a higher tendency to acquire new glycosylation sites.

Code(s) de classement : 002A05C10

Descriptor(s) anglais
Descriptor(s) : Human; Influenza A virus; Molecular evolution; Epidemic; Influenza
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Viral disease; Infection

Descriptor(s) français
Descriptor(s) : Homme; Virus grippal A; Evolution moléculaire; Epidémie; Gripppe
Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Virole; Infection

Localisation : INIST-6355, 354000185474070120
Origine de la notice : INIST
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Pathological lesions and viral localization of Influenza A (H5N1) virus in experimentally infected Chinese rhesus macaques: implications for pathogenesis and viral transmission

Titre: Pathological lesions and viral localization of Influenza A (H5N1) virus in experimentally infected Chinese rhesus macaques: implications for pathogenesis and viral transmission

Auteur(s): YUNXIN CHEN; WEI DENG; CHUNSHI JIA; XIAOWEI DAI; HUA ZHU; QI KONG; LAN HUANG; YALI LIU; CHUNMEI MA; JIAMEI LI; CHONG XIAO; YING LIU; QIANG WEI; CHUAN QIN

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Source: Archives of virology; vol. 154; no. 2; pp. 227-233
ISSN: 0304-8608
Date de publication: 2009
Langue(s): ENG
Type de document: P
Nombre de références: 25 ref.

Résumé: Chinese rhesus macaques infected with influenza virus A/Tiger/Harbin/01/2002 (H5N1) developed acute interstitial pneumonia with diffuse alveolar damage. The results of virus isolation, reverse transcriptase polymerase chain reaction, immunohistochemistry, and in situ hybridization showed that the lung was the major target organ of the H5N1 virus infection. No virus was detected in the extra-pulmonary organs. The results of immunohistochemistry and in situ hybridization also showed that pneumocytes and macrophages of the lower airway, not the ciliary epithelium of the trachea and bronchi, were the chief target cells in the lung tissue of the infected Chinese rhesus macaque. Our data indicate that the Chinese rhesus macaque is suitable as a new primate model for H5N1 virus research, especially for the study of H5N1 virus transmission. The predilection of the H5N1 virus to infect the lower airway suggests that the failure of the virus to attach to the ciliary epithelium of the trachea and bronchi may be a limiting factor in human-to-human transmissibility of the H5N1 virus.

Code(s) de classement: 002A05C10; 002A05C04

Desc. génériques: Influenzavirus A; Orthomyxoviridae; Virus; Simioidea; Primates; Mammalia; Vertebrata

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Dose Sparing Strategy With Intradermal Influenza Vaccination in Patients With Solid Cancer

Titre : Dose Sparing Strategy With Intradermal Influenza Vaccination in Patients With Solid Cancer

Auteur(s) : YU MI JO; JOON YOUNG SONG; IN SOOK HWANG; LEE (Jacob); SANG CHEUL OH; JUN SUK KIM; SUNG RAN KIM; WOO JOO KIM; HEE JIN CHEONG

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Source : Journal of medical virology; vol. 81; no. 4; pp. 722-727
ISSN : 0146-6615
CODEN : JMVIDB
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 1/4 p.

Résumé : Influenza vaccine is considered to reduce influenza-related morbidity and mortality in patients with underlying chronic medical conditions. Because of fear of vaccine shortage during an influenza pandemic, several antigen sparing strategies have been investigated. The immunogenicity of intradermal influenza vaccination with one half the antigenic contents was compared to that of conventional intramuscular vaccination in patients with solid cancer, and adverse events were assessed after vaccination. There was no significant difference between the injection routes in the hemagglutinin inhibition (HI) response and increase in the titer of A/H1N1, A/H3N2, and B 4-6 weeks after the vaccination; seroconversion factors increased by more than 2.5-fold. Seroresponse rates were more than 40% and seroprotection rates were above 70% against all three influenza strains irrespective of the vaccination routes. No serious events were observed, and local skin reactions were more frequent in the intradermal injection recipients (32.7% vs. 9.1%). This study shows that intradermal injection of one half the dose of a commercial influenza vaccine elicits immune responses comparable to those elicited by a full dose of intramuscular vaccine among cancer patients, and it can be tolerated without serious adverse reactions.

Code(s) de classement : 002A05C10; 002B05C02J; 002A05C07

Describeur(s) anglais
- Descripteur(s) : Human; Influenza; Vaccination; Vaccine; Malignant tumor
- Desc. généraux : Viral disease; Infection; Cancer

Describeur(s) français
- Descripteur(s) : Homme; Grippe; Vaccination; Vaccin; Tumeur maligne
- Desc. généraux : Virose; Infection; Cancer

Localisation : INIST-17422, 354000186975410210
Origine de la notice : INIST
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Comparison of the performance of the rapid antigen detection actim Influenza A&B test and RT-PCR in different respiratory specimens

Titre : Comparison of the performance of the rapid antigen detection actim Influenza A&B test and RT-PCR in different respiratory specimens

Auteur(s) : GHEBREMEDHIN (B.); ENGELMANN (I.); KÖNIG (W.); KÖNIG (B.)
Affiliation(s) : University Clinic Magdeburg, Institute of Medical Microbiology, Magdeburg, DEU; Institute of Virology, Hannover Medical School, Hannover, DEU

Source : Journal of medical microbiology; vol. 58; no. 3; pp. 365-370
ISSN : 0022-2615
CODEN : JMMIAV
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 1/2 p.

Résumé : Nowadays, influenza antigen detection test kits are used most frequently to detect influenza A or B virus to establish the diagnosis of influenza rapidly and initiate appropriate therapy. This study was conducted to evaluate the performance of the actim Influenza A&B test (Medix Biochemica). Overall, 473 respiratory specimens were analysed in the actim Influenza A&B test and the results were compared with those from an RT-PCR assay; 461 of these samples originated from paediatric patients aged 7 weeks to 6.5 years either with influenza-related symptoms or from the intensive care unit, and 12 samples originated from adults with underlying lung or haematological diseases. Diagnosis of influenza A or B virus could be established using the actim Influenza A&B test (9/473 samples for influenza A virus and 6/473 for influenza B virus). RT-PCR revealed 23 patients with influenza virus (13/473 for influenza A virus and 10/473 for influenza B virus). The sensitivity and specificity of the actim Influenza A&B test were 65 and 100% compared with the RT-PCR assay. However, 32 external quality assessment samples containing seven different strains of influenza A subtypes H1N1 and H3N2 and the avian H5N1 were detected correctly by the actim Influenza A&B test. No cross-reactivity to a range of bacterial, fungal and other viral pathogens was observed. In conclusion, the actim Influenza A&B test is reliable for positive results due to its high specificity. Nevertheless, negative results from this test need to be confirmed by a more sensitive assay because of the low sensitivity observed with diagnostic samples.

Code(s) de classement : 002A05; 002B05

Descriptor(s) anglais
- Descriptor(s) : Antigen; Detection; Reverse transcription polymerase chain reaction; Microbiology; Influenza A; Influenza B
- Desc. génériques : Viral disease; Infection

Descriptor(s) français
- Descriptor(s) : Antigène; Détection; Réaction chaîne polymérase RT; Microbiologie; Grippe A; Grippe B
- Desc. génériques : Virose; Infection

Localisation : INIST-988B, 354000185448340140
Origine de la notice : INIST
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Augmentation de la résistance à l'oseltamivir; More resistance to oseltamivir (Tamiflu)

**Titre** : Augmentation de la résistance à l'oseltamivir; More resistance to oseltamivir (Tamiflu)

**Source** : The Medical letter on drugs and therapeutics : (Edition française); vol. 31; no. 4; pp. 13-14

**ISSN** : 0253-8512

**Date de publication** : 2009

**Pays de publication** : CHE

**Langue(s)** : FRE

**Type de document** : P

**Nombre de références** : 4 ref.

**Code(s) de classement** : 002B02S05

**Descripteur(s) anglais**

- **Desc. génériques** : Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor; Neuraminidase inhibitor

**Descripteur(s) français**

- **Desc. génériques** : Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Inhibiteur enzyme; Inhibiteur neuraminidase

**Localisation** : INIST-17102F, 354000186512330010

**Origine de la notice** : INIST

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Multiplex Assay for Simultaneously Typing and Subtyping Influenza Viruses by Use of an Electronic Microarray

**Titre** : Multiplex Assay for Simultaneously Typing and Subtyping Influenza Viruses by Use of an Electronic Microarray

**Auteur(s)** : YING HUANG; HUONG TANG; DUFFY (Stuart); YUWEN HONG; NORMAN (Sylvia); GHOSH (Madhu); JIE HE; BOSE (Michael); HENRICKSON (Kelly J.); JIANG FAN; KRAFT (Andrea J.); WEISBURG (William G.); MATHER (Elizabeth L.)

**Affiliation(s)** : Nanogen, Inc, San Diego, California 92121, USA; Department of Pediatrics, Medical College of Wisconsin, Milwaukee, Wisconsin 53226, USA; Midwest Respiratory Virus Program, Medical College of Wisconsin, Milwaukee, Wisconsin 53226, USA

**Source** : Journal of clinical microbiology : (Print); vol. 47; no. 2; pp. 390-396

**ISSN** : 0095-1137

**CODEN** : JCMIDW

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 27 ref.

**Résumé** : We report on the use of an electronic microarray to simultaneously type influenza A and B viruses and to distinguish influenza A virus subtypes H1N1 and H3N2 from the potentially pandemic avian virus subtype H5N1. The assay targets seven genes: the H1, H3, H5, N1, and N2 genes of influenza A virus; the matrix protein M1 gene of influenza A virus; and the nonstructural protein (NS) gene of influenza B virus. By combining a two-step reverse transcription-multiplex PCR with typing and subtyping on the electronic microarray, the assay achieved an analytical sensitivity of 102 to 103 copies of transcripts per reaction for each of the genes. The assay correctly typed and subtyped 15 different influenza virus isolates, including two influenza B virus, five A/H1N1, six A/H3N2, and two A/H5N1 isolates. In addition, the assay correctly identified 8 out of 10 diluted, archived avian influenza virus specimens with complete typing and subtyping information and 2 specimens with partial subtyping information. In a study of 146 human clinical specimens that had previously been shown to be positive for influenza virus or another respiratory virus, the assay showed a clinical sensitivity of 96% and a clinical specificity of 100%. The assay is a rapid, accurate, user-friendly method for simultaneously typing and subtyping influenza viruses.

**Code(s) de classement** : 002A05

**Descripteur(s) anglais**
- **Descriputeur(s) :** Typing; Microbiology; Influenza
- **Desc. génériques :** Viral disease; Infection

**Descripteur(s) français**
- **Descriputeur(s) :** Typage; Microbiologie; Grippe
- **Desc. génériques :** Virose; Infection

**Localisation** : INIST-17088, 354000185468390160

**Origine de la notice** : INIST

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Design and Validation of a Microarray for Detection, Hemagglutinin Subtyping, and Pathotyping of Avian Influenza Viruses

**Titre** : Design and Validation of a Microarray for Detection, Hemagglutinin Subtyping, and Pathotyping of Avian Influenza Viruses

**Auteur(s)** : GALL (Astrid); HOFFMANN (Bernd); HARDER (Timm); GRUND (Christian); HOPER (Dirk); BEER (Martin)

**Affiliation(s)** : Institute of Diagnostic Virology, Friedrich-Loeffler-Institut, Stidufer 10, Greifswald-Insel Riems 17493, DEU

**Source** : Journal of clinical microbiology : (Print); vol. 47; no. 2; pp. 327-334

**ISSN** : 0095-1137

**CODEN** : JCMIDW

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 42 ref.

**Résumé** : Continuing threats of devastating outbreaks in poultry and of human infections caused by highly pathogenic avian influenza virus (HPAIV) H5N1 emphasize the need for the further development of rapid and reliable methods of virus detection and characterization. Here we report on the design and comprehensive validation of a low-density microarray as a diagnostic tool for the detection and typing of avian influenza virus (AIV). The array consists of one probe for the conserved matrix gene and 97 probes targeting the HA0 cleavage-site region. Following fragment amplification by a generic PCR approach, the array enables AIV detection, hemagglutinin (HA) subtyping, and pathotyping within a single assay. For validation, a panel of 92 influenza A viruses which included 43 reference strains representing all 16 HA subtypes was used. All reference strains were correctly typed with respect to their HA subtypes and pathotypes, including HPAIV H5N1/Asia, which caused outbreaks in Germany in 2006 and 2007. In addition, differentiation of strains of the Eurasian and North American lineages of the H5 and H7 subtypes was possible. The sensitivity of the microarray for the matrix gene is comparable to that of real-time reverse transcription-PCR (RT-PCR). It is, however, 10- to 100-fold lower than that of real-time RT-PCR with respect to HA subtyping and pathotyping. The specificity of the array was excellent, as no pathogens relevant for differential diagnosis yielded a positive reaction. Validation with field samples included 19 cloacal swab specimens from wild and domestic birds. Influenza A virus was verified in all samples, whereas the HA subtypes could be determined for 14 samples. The results demonstrate that the microarray assay described complements current methods and can accelerate the diagnosis and characterization of AIV.

**Code(s) de classement** : 002A05C10

**Description(s) anglais**

- **Description(s) :** Avian influenza virus; Detection; Hemagglutinin; Microbiology
- **Desc. génériques :** Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen

**Description(s) français**

- **Description(s) :** Influenzavirus aviaire; Détection; Hémagglutinine; Microbiologie
- **Desc. génériques :** Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogène

**Localisation** : INIST-17088, 354000185468390060

**Origine de la notice** : INIST

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Design of Multiplexed Detection Assays for Identification of Avian Influenza A Virus Subtypes Pathogenic to Humans by SmartCycler Real-Time Reverse Transcription-PCR

**Titre** : Design of Multiplexed Detection Assays for Identification of Avian Influenza A Virus Subtypes Pathogenic to Humans by SmartCycler Real-Time Reverse Transcription-PCR

**Auteur(s) :** WEI WANG; PEIJUN REN; MARDI (Sek); LILI HOU; TSAI (Cheguo); KWOK HUNG CHAN; CHENG (Peter); JUN SHENG; BUCHY (Philippe); BING SUN; TOYODA (Tetsuya); LIM (Wilina); MALIK PEIRIS (J. S.); ZHOU (Paul); DEUBEL (Vincent)

**Affiliation(s) :** Institut Pasteur of Shanghai, Chinese Academy of Sciences, Shanghai Institute of Biological Sciences, Shanghai, CHN; Institut Pasteur du Cambodge, Phnom Penh, KHM; Department of Microbiology, the University of Hong Kong, HKG; Public Health Laboratory Services Branch, Centre for Health Protection, Department of Health, HKG; Shanghai Nanxiang Hospital, Shanghai, CHN; HKU-Pasteur Research Centre, HKG

**Source** : Journal of clinical microbiology : (Print); vol. 47; no. 1; pp. 86-92

**ISSN** : 0095-1137

**CODEN** : JCMIDW

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 56 ref.

**Résumé** : Influenza A virus (IAV) epidemics are the result of human-to-human or poultry-to-human transmission. Tracking seasonal outbreaks of IAV and other avian influenza virus (AIV) subtypes that can infect humans, aquatic and migratory birds, poultry, and pigs is essential for epidemiological surveillance and outbreak alerts. In this study, we performed four real-time reverse transcription-PCR (rRT-PCR) assays for identification of the IAV M and hemagglutinin (HA) genes from six known AIVs infecting pigs, birds, and humans. IAV M1 gene-positive samples tested by single-step rRT-PCR and a fluorogenic Sybr green I detection system were further processed for H5 subtype identification by using two-primer-set multiplex and Sybr green I rRT-PCR assays. H5 subtype-negative samples were then tested with either a TaqMan assay for subtypes H1 and H3 or a TaqMan assay for subtypes H2, H7, and H9 and a beacon multiplex rRT-PCR identification assay. The four-tube strategy was able to detect 10 RNA copies of the HA genes of subtypes H1, H2, H3, H5, and H7 and 100 RNA copies of the HA gene of subtype H9. At least six H5 clades of H5N1 viruses isolated in Southeast Asia and China were detected by that test. Using rRT-PCR assays for the M1 and HA genes in 202 nasopharyngeal swab specimens from children with acute respiratory infections, we identified a total of 39 samples positive for the IAV M1 gene and subtypes H1 and H3. When performed with a portable SmartCycler instrument, the assays offer an efficient, flexible, and reliable platform for investigations of IAV and AIV in remote hospitals and in the field.

**Code(s) de classement** : 002A05C10

**Descripteur(s) anglais**

- **Descriputeur(s) aviaire** : Avian influenzavirus; Influenza A virus; Human; Detection; Identification; Subtype; Pathogenicity; Real time; Reverse transcription polymerase chain reaction; Microbiology
- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen

**Descripteur(s) français**

- **Descriputeur(s) aviaire** : Influenzavirus aviaire; Virus grippal A; Homme; Détection; Identification; Soustype; Pouvoir pathogène; Temps réel; Réaction chaîne polymérase RT; Microbiologie
- **Desc. génériques** : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogènes

**Localisation** : INIST-17088, 354000185468210100

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PB2 Protein of a Highly Pathogenic Avian Influenza Virus Strain A/chicken/Yamaguchi/7/2004 (H5N1) Determines Its Replication Potential in Pigs

**Titre :** PB2 Protein of a Highly Pathogenic Avian Influenza Virus Strain A/chicken/Yamaguchi/7/2004 (H5N1) Determines Its Replication Potential in Pigs

**Auteur(s) :** MANZOOR (Rashid); SAKODA (Yoshihiro); NOMURA (Naoki); TSUDA (Yoshimi); OZAKI (Hiroichi); OKAMATSU (Masatoshi); KIDA (Hiroshi)

**Affiliation(s) :** Laboratory of Microbiology, Department of Disease Control, Graduate School of Veterinary Medicine, Hokkaido University, Sapporo 060-0818, JPN; Department of Veterinary Microbiology, Faculty of Agriculture, Tottori University, Tottori 680-8553, JPN; Research Center for Zoonosis Control, Hokkaido University, Sapporo 001-0020, JPN

**Source :** Journal of virology; vol. 83; no. 4; pp. 1572-1578

**ISSN :** 0022-538X

**Date de publication :** 2009

**Pays de publication :** USA

**Langue(s) :** ENG

**Type de document :** P

**Nombre de références :** 58 ref.

**Résumé :** It has been shown that not all but most of the avian influenza viruses replicate in the upper respiratory tract of pigs (H. Kida et al., J. Gen. Virol. 75:2183-2188, 1994). It was shown that A/chicken/Yamaguchi/7/2004 (H5N1) [Ck/Yamaguchi/04 (H5N1)] did not replicate in pigs (N. Isoda et al., Arch. Virol. 151:1267-1279, 2006). In the present study, the genetic basis for this host range restriction was determined using reassortant viruses generated between Ck/Yamaguchi/04 (H5N1) and A/swine/Hokkaido/2/1981 (H1N1) [Sw/Hokkaido/81 (H1N1)]. Two in vivo-generated single-gene reassortant virus clones of the H5N1 subtype (virus clones 1 and 2), whose PB2 gene was of Sw/Hokkaido/81 (H1N1) origin and whose remaining seven genes were of Ck/ Yamaguchi/04 (H5N1) origin, were recovered from the experimentally infected pigs. The replicative potential of virus clones 1 and 2 was further confirmed by using reassortant virus (rg-Ck-Sw/PB2) generated by reverse genetics. Interestingly, the PB2 gene of Ck/Yamaguchi/04 (H5N1) did not restrict the replication of Sw/ Hokkaido/81 (H1N1), as determined by using reassortant virus rg-Sw-Ck/PB2. The rg-Sw-Ck/PB2 virus replicated to moderate levels and for a shorter duration than parental Sw/Hokkaido/81 (H1N1). Sequencing of two isolates recovered from the pigs inoculated with rg-Sw-Ck/PB2 revealed either the D256G or the E627K amino acid substitution in the PB2 proteins of the isolates. The D256G and E627K mutations enhanced viral polymerase activity in the mammalian cells, correlating with replication of virus in pigs. These results indicate that the PB2 protein restricts the growth of Ck/Yamaguchi/04 (H5N1) in pigs.

**Code(s) de classement :** 002A05C10; 002A05C04

**Desc. génériques :** Influenzavirus A; Orthomyxoviridae; Virus; Aves; Vertebrata; Artiodactyla; Ungulata; Mammalia; Veterinary

**Localisation :** INIST-13592, 354000185451040040

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Live Attenuated Influenza Viruses Containing NS1 Truncations as Vaccine Candidates against H5N1 Highly Pathogenic Avian Influenza

**Titre** : Live Attenuated Influenza Viruses Containing NS1 Truncations as Vaccine Candidates against H5N1 Highly Pathogenic Avian Influenza

**Auteur(s)** : STEEL (John); LOWEN (Anice C.); PENA (Lindomar); ANGEL (Matthew); SOLORZANO (Alicia); ALBRECHT (Randy); PEREZ (Daniel R.); GARCIA-SASTRE (Adolfo); PALESE (Peter)

**Affiliation(s)** : Department of Microbiology, Mount Sinai School of Medicine, 1 Gustave Levy PI, New York, New York 10029-6574, USA; Department of Veterinary Medicine, University of Maryland, College Park, and Virginia-Maryland Regional College of Veterinary Medicine, 8075 Greenmead Drive, College Park, Maryland 20742-3711, USA; Department of Medicine, Division of Infectious Diseases, Mount Sinai School of Medicine, 1 Gustave Levy PI, New York, New York 10029-6574, USA; Global Health and Emerging Pathogens Institute, Mount Sinai School of Medicine, 1 Gustave Levy PI, New York, New York 10029-6574, USA

**Source** : Journal of virology; vol. 83; no. 4; pp. 1742-1753

**ISSN** : 0022-538X

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 37 ref.

**Résumé** : Due to the high mortality associated with recent, widely circulating strains of H5N1 influenza virus in poultry, the recurring introduction of H5N1 viruses from birds to humans, and the difficulties in H5N1 eradication by elimination of affected flocks, an effective vaccine against HPAI (highly pathogenic avian influenza) is highly desirable. Using reverse genetics, a set of experimental live attenuated vaccine strains based on recombinant H5N1 influenza virus A/Viet Nam/1203/04 was generated. Each virus was attenuated through expression of a hemagglutinin protein in which the polybasic cleavage site had been removed. Viruses were generated which possessed a full-length NS1 or a C-terminally truncated NS1 protein of 73, 99, or 126 amino acids. Viruses with each NS genotype were combined with a PB2 polymerase gene which carried either a lysine or a glutamic acid at position 627. We predicted that glutamic acid at position 627 of PB2 would attenuate the virus in mammalian hosts, thus increasing the safety of the vaccine. All recombinant viruses grew to high titers in 10-day-old embryonated chicken eggs but were attenuated in mammalian cell culture. Induction of high levels of beta interferon by all viruses possessing truncations in the NS1 protein was demonstrated by interferon bioassay. The viruses were each found to be highly attenuated in a mouse model. Vaccination with a single dose of any virus conferred complete protection from death upon challenge with a mouse lethal virus expressing H5N1 hemagglutinin and neuraminidase proteins. In a chicken model, vaccination with a single dose of a selected virus encoding the NS1 1-99 protein completely protected chickens from lethal challenge with homologous HPAI virus A/Viet Nam/1203/04 (H5N1) and provided a high level of protection from a heterologous virus, A/egret/Egypt/01/06 (H5N1). Thus, recombinant influenza A/Viet Nam/1203/04 viruses attenuated through the introduction of mutations in the hemagglutinin, NS1, and PB2 coding regions display characteristics desirable for live attenuated vaccines and hold potential as vaccine candidates in poultry as well as in mammalian hosts.

**Code(s) de classement** : 002A05C10; 002A05C07; 002A05C04

**Descripteur(s) anglais**

- Attenuated strain; Vaccine; Pathogenicity; Virology; Avian influenza; Influenzavirus A(H5N1)
- Infection; Viral disease

**Descripteur(s) français**

- Souche atténuée; Vaccin; Pouvoir pathogène; Virologie; Grippe aviaire; Influenzavirus A(H5N1)
- Infection; Virose
Localisation : INIST-13592, 354000185451040210
Origine de la notice : INIST
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Influenza A Virus Polymerase Is an Integral Component of the CPSF30-NS1A Protein Complex in Infected Cells

Titre : Influenza A Virus Polymerase Is an Integral Component of the CPSF30-NS1A Protein Complex in Infected Cells

Auteur(s) : KUO (Rei-Lin); KRUG (Robert M.)
Affiliation(s) : Institute for Cellular and Molecular Biology, Section of Molecular Genetics and Microbiology, University of Texas at Austin, Austin, Texas 78712, USA

Source : Journal of virology; vol. 83; no. 4; pp. 1611-1616
ISSN : 0022-538X
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 22 ref.

Résumé : The NS1A protein of influenza A virus binds the cellular CPSF30 protein, thereby inhibiting the 3'-end processing of all cellular pre-mRNAs, including beta interferon pre-mRNA. X-ray crystallography identified the CPSF30-binding pocket on the influenza virus A/Udorn/72 (Ud) NS1A protein and the critical role of two hydrophobic NS1A amino acids outside the pocket, F103 and M106, in stabilizing the CPSF30-NS1A complex. Although the NS1A protein of the 1997 H5N1 influenza A/Hong Kong/483/97 (HK97) virus contains L (not F) at position 103 and I (not M) at position 106, it binds CPSF30 in vivo to a significant extent because cognate (HK97) internal proteins stabilize the CPSF30-NS1A complex in infected cells. Here we show that the cognate HK97 polymerase complex, containing the viral polymerase proteins (PB1, PB2, and PA) and the nucleocapsid protein (NP), is responsible for this stabilization. The noncognate Ud polymerase complex cannot carry out this stabilization, but it can stabilize CPSF30 binding to a mutated (F103L M106I) cognate Ud NS1A protein. These results suggested that the viral polymerase complex is an integral component of the CPSF30-NS1A protein complex in infected cells even when the cognate NS1A protein contains F103 and M106, and we show that this is indeed the case. Finally, we show that cognate PA protein and NP, but not cognate PB1 and PB2 proteins, are required for stabilizing the CPSF30-NS1A complex, indicating that the NS1A protein interacts primarily with its cognate PA protein and NP in a complex that includes the cellular CPSF30 protein.

Code(s) de classement : 002A05C10

Descriptor(s) anglais
- Descripteur(s) : Influenza A virus; Protein; Infected cell; Virology
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus

Descriptor(s) français
- Descripteur(s) : Virus grippal A; Protéine; Cellule infectée; Virologie
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST-13592, 354000185451040080
Origine de la notice : INIST
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Estimation of the basic reproductive number (R0) for epidemic, highly pathogenic avian influenza subtype H5N1 spread

**Titre** : Estimation of the basic reproductive number (R0) for epidemic, highly pathogenic avian influenza subtype H5N1 spread

**Auteur(s)** : WARD (M. P.); MAFTEI (D.); APOSTU (C.); SURU (A.)

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**Source** : Epidemiology and infection; vol. 137; no. 2; pp. 219-226

**ISSN** : 0950-2688

**CODEN** : EPINEU

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 29 ref.

**Résumé** : Three different methods were used for estimating the basic reproductive number (R0) from data on 110 outbreaks of highly pathogenic avian influenza (HPAI) subtype H5N1 that occurred in village poultry in Romania, 12 May to 6 June 2006. We assumed a village-level infectious period of 7 days. The methods applied were GIS-based identification of nearest infectious neighbour (based on either Euclidean or road distance), the method of epidemic doubling time, and a susceptible-infectious (SI) modelling approach. In general, the estimated basic reproductive numbers were consistent: 2.14, 1.95, 2.68 and 2.21, respectively. Although the true basic reproductive number in this epidemic is unknown, results suggest that the use of a range of methods might be useful for characterizing epidemics of infectious diseases. Once the basic reproductive number has been estimated, better control strategies and targeted surveillance programmes can be designed.
Avian influenza vaccines: a practical review in relation to their application in the field with a focus on the Asian experience

Titre : Avian influenza vaccines: a practical review in relation to their application in the field with a focus on the Asian experience

Auteur(s) : PEYRE (M.); FUSHENG (G.); DESVAUX (S.); ROGER (F.)
Affiliation(s) : French Agricultural Research Center for International Development (CIRAD), AGIRs (Animal and Integrated Risk Management), Montpellier, FRA; FAO Office, Beijing, CHN; CIRAD, AGIRs-PRISE Consortium in Vietnam, National Institute of Veterinary Research, Hanoi, VNM

Source : Epidemiology and infection; vol. 137; no. 1; pp. 1-21
ISSN : 0950-2688
CODEN : EPINEU
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 106 ref.

Résumé : Vaccination can be a useful tool for the control of avian influenza (AI) outbreaks, but its use is prohibited in most of the countries worldwide because of its interference with AI surveillance tests and its negative impact on poultry trade. AI vaccines currently in use in the field increase host resistance to the disease but have a limited impact on the virus transmission. To control or eradicate the disease, a carefully conceived vaccination strategy must be accompanied by strict biosecurity measures. Some countries have authorized vaccination under special circumstances with contradictory results, from control and disease eradication (Italy) to endemicity and antigenic drift of the viral strain (Mexico). Extensive vaccination programmes are ongoing in South East Asia to control the H5N1 epidemic. This review provides practical information on the available AI vaccines and associated diagnostic tests, the vaccination strategies applied in Asia and their impact on the disease epidemiology.

Code(s) de classement : 002A05F04

Descriptor(s) anglais
Description(s) : Vaccine; Review; Microbiology; Epidemiology; Human; Avian influenza; Influenza A
Desc. génériques : Infection; Viral disease

Descriptor(s) français
Description(s) : Vaccin; Article synthèse; Microbiologie; Epidémiologie; Homme; Grippe aviaire; Grippe A
Desc. génériques : Infection; Virose

Localisation : INIST-6056, 354000184209280010
Origine de la notice : INIST
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Activity of the Oral Neuraminidase Inhibitor A-322278 against the Oseltamivir-Resistant H274Y (A/H1N1) Influenza Virus Mutant in Mice

Titre : Activity of the Oral Neuraminidase Inhibitor A-322278 against the Oseltamivir-Resistant H274Y (A/H1N1) Influenza Virus Mutant in Mice

Auteur(s) : BAZ (Mariana); ABED (Yacine); NEHME (Benjamin); BOIVIN (Guy)
Affiliation(s) : Research Center in Infectious Diseases, CHUQ-CHUL, and Laval University, Québec City, Québec, CAN

Source : Antimicrobial agents and chemotherapy; vol. 53; no. 2; pp. 791-793
ISSN : 0066-4804
CODEN : AACHAX
Date de publication : 2009
Pays de publication : USA
Type de document : P
Nombre de références : 13 ref.

Résumé : The new oral neuraminidase (NA) inhibitor A-322278 was evaluated in mice infected with influenza A/H1N1 wild-type virus or the oseltamivir-resistant (H274Y mutant) virus. A-322278 decreased mortality rates and lung virus titers significantly more than oseltamivir in mice infected with the NA H274Y mutant when therapy was started 4 h before or even 48 h after infection.

Code(s) de classement : 002B02S

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Exo- alpha -sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Enzyme inhibitor

Desc. génériques : Activité biologique; Voie orale; Inhibiteur neuraminidase; Osélétamivir; Résistance; Virus grippal A; Mutation; Animal; Souris; Antiviral

Localisation : INIST-13334, 354000184201340590
Origine de la notice : INIST
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Influenza-pseudotyped Gag virus-like particle vaccines provide broad protection against highly pathogenic avian influenza challenge

**Titre** : Influenza-pseudotyped Gag virus-like particle vaccines provide broad protection against highly pathogenic avian influenza challenge

**Auteur(s)** : HAYNES (Joel R.); DOKKEN (Leslie); WILEY (James A.); CAWTHON (Andrew G.); BIGGER (John); HARMSEN (Allen G.); RICHARDSON (Charles)

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**Source** : Vaccine; vol. 27; no. 4; pp. 530-541

**ISSN** : 0264-410X

**CODEN** : VACCDE

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 54 ref.

**Résumé** : Influenza-pseudotyped Gag virus-like particles (VLPs) were produced via the expression of influenza hemagglutinin (HA), neuraminidase (NA) and the murine leukemia virus Gag product in the baculovirus-insect cell expression system. Hemagglutination specific activities of sucrose gradient-purified VLPs were similar to those of egg-grown influenza viruses but particle morphologies were gamma retrovirus-like in the form of consistent 100 nm spheres. Immunization of mice and ferrets demonstrated robust immunogenicity and protection from challenge with no measurable morbidity. Ferret data were striking in that immunization with H5N1 VLPs representing either A/Vietnam/1203/04 or A/Indonesia/5/05 resulted in solid protection against highly pathogenic A/Vietnam/1203/04 challenge with no detectable virus in the upper respiratory tract post-challenge in either group. H1N1 VLP immunization of ferrets resulted in partial protection against H5N1 challenge with markedly accelerated virus clearance from the upper respiratory tract relative to controls. The immunogenicity of influenza-pseudotyped VLPs was not dependent on the adjuvant properties of replication competent contaminating baculovirus. These data demonstrate robust vaccine protection of Gag-based, influenza-pseudotyped VLPs carrying a variety of influenza antigens and suggest applicability toward a number of additional respiratory viruses.

**Code(s) de classement** : 002A05F04; 002A05C10

**Descrip teur(s) anglais**

- **Descrip teur(s)** : Influenzavirus; Virus like particle; Vaccine; Pathogenicity; Avian influenza; Flu-like syndrome
- **Desc. génériques** : Orthomyxoviridae; Virus; Infection; Viral disease

**Descrip teur(s) français**

- **Descrip teur(s)** : Influenzavirus; Particule type viral; Vaccin; Pouvoir pathogène; Grippe aviaire; Syndrome pseudogrippal
- **Desc. génériques** : Orthomyxoviridae; Virus; Infection; Virose

**Localisation** : INIST-20289, 354000184207870050

**Origine de la notice** : INIST

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Developing New Antiviral Agents for Influenza Treatment: What Does the Future Hold?; Antiviral Therapy for Influenza: Challenging the Status Quo

**Titre** : Developing New Antiviral Agents for Influenza Treatment: What Does the Future Hold?; Antiviral Therapy for Influenza: Challenging the Status Quo

**Auteur(s) :** HAYDEN (Frederick); HAYDEN (Frederick G.), ed.; MCGEER (Allison J.), ed.; MONTO (Arnold S.), ed.

**Affiliation(s) :** Global Influenza Programme, World Health Organization, Geneva, CHE; University of Virginia School of Medicine, Charlottesville, CHE; Global Influenza Programme, World Health Organization, Geneva, CHE; University of Virginia School of Medicine, Charlottesville, USA; Department of Laboratory Medicine and Pathobiology, Medicine and Public Health Sciences, University of Toronto, and Division of Infection Control, Mount Sinai Hospital, Toronto, CAN; Department of Epidemiology, School of Public Health, and the University of Michigan Bioterrorism Preparedness Initiative, University of Michigan, Ann Arbor, USA

**Source** : Clinical infectious diseases; vol. 48; no. SUP1
**ISSN** : 1058-4838
**CODEN** : CIDIEL

**Date de publication** : 2009

**Langue(s)** : ENG

**Pays de publication** : USA

**Type de document** : P

**Nombre de références** : 77 ref.

**Résumé** : Antiviral agents for the treatment of influenza are urgently needed to circumvent the limitations of current drugs in several critical areas: high frequencies of resistance to M2 inhibitors among currently circulating strains and variable frequencies of resistance to oseltamivir among A(H1N1) strains, limited efficacy of treatment and treatment-emergent antiviral resistance in cases of avian influenza A(H5N1) illness in humans, and lack of parenteral agents for seriously ill patients. Two neuraminidase inhibitors (NAIs), zanamivir and per-amivir, have undergone or are undergoing clinical trials for use by intravenous or intramuscular administration, and one long-acting NAI, designated CS-8958, is under study for use by inhalation. Advances in understanding the mechanisms involved in influenza virus replication have revealed a number of potential targets that might be exploited in the development of new agents. Among these agents are T-705, a polymerase inhibitor, and DAS181, an attachment inhibitor. Combination therapy with currently available agents is supported by data from animal models but has received limited clinical study to date.

**Code(s) de classement** : 002B05C02C; 002B02S05

**Description(s) anglais**

*Description(s) :* Influenza; Antiviral; Treatment

*Desc. génériques :* Viral disease; Infection

**Description(s) français**

*Description(s) :* Grippe; Antiviral; Traitement

*Desc. génériques :* Virose; Infection

**Localisation** : INIST-18407, 354000186379270010

**Origine de la notice** : INIST

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Protection of chickens against H5N1 highly pathogenic avian influenza virus infection by live vaccination with infectious laryngotracheitis virus recombinants expressing H5 hemagglutinin and N1 neuraminidase

**Titre** : Protection of chickens against H5N1 highly pathogenic avian influenza virus infection by live vaccination with infectious laryngotracheitis virus recombinants expressing H5 hemagglutinin and N1 neuraminidase

**Auteur(s)** : PAVLOVA (Sophia P.); VEITS (Jutta); KEIL (Günther M.); METTENLEITER (Thomas C.); FUCHS (Walter)

**Affiliation(s)** : Institute of Molecular Biology, Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Greifswald-Insel Riems, DEU

**Source** : Vaccine; vol. 27; no. 5; pp. 773-785

**ISSN** : 0264-410X

**CODEN** : VACCDE

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 58 ref.

**Résumé** : Attenuated vaccine strains of the alphaherpesvirus causing infectious laryngotracheitis of chickens (ILTV, gallid herpesvirus 1) can be used for mass application. Previously, we showed that live virus vaccination with recombinant ILTV expressing hemagglutinin of highly pathogenic avian influenza viruses (HPAIV) protected chickens against ILT and fowl plague caused by HPAIV carrying the corresponding hemagglutinin subtypes [Lüschow D, Werner O, Mettenleiter TC, Fuchs W. Protection of chickens from lethal avian influenza A virus infection by live-virus vaccination with infectious laryngotracheitis virus recombinants expressing the hemagglutinin (H5) gene. Vaccine 2001;19(30):4249-59; Veits J, Lüschow D, Kindermann K, Werner O, Teifke JP, Mettenleiter TC, et al. Deletion of the non-essential ULO gene of infectious laryngotracheitis (ILT) virus leads to attenuation in chickens, and ULO mutants expressing influenza virus haemagglutinin (H7) protect against ILT and fowl plague. J Gen Virol 2003;84(12):3343-52]. However, protection against H5N1 HPAIV was not satisfactory. Therefore, a newly designed dUTPase-negative ILTV vectorwasusedforrapidinsertionofthe H5-hemagglutinin, or N1-neuraminidase genes of a recent H5N1 HPAIV isolate. Compared to our previous constructs, protein expression was considerably enhanced by insertion of synthetic introns downstream of the human cytomegalovirus immediate-early promoter within the 5’-nontranslated region of the transgenes. Deletion of the viral dUTPase gene did not affect in vitro replication of the ILTV recombinants, but led to sufficient attenuation in vivo. After a single ocular immunization, all chickens developed H5- or N1-specific serum antibodies. Nevertheless, animals immunized with N1-ILTV died after subsequent H5N1 HPAIV challenge, although survival times were prolonged compared to non-vaccinated controls. In contrast, all chickens vaccinated with either H5-ILTV alone, or H5- and N1-ILTV simultaneously, survived without showing any clinical signs. Real-time RT-PCR indicated limited challenge virus replication after vaccination with H5-ILTV only, which was completely blocked after coimmunization with N1-ILTV. Thus, chickens can be protected from H5N1 HPAIV-induced disease by live vaccination with an attenuated hemagglutinin-expressing ILTV recombinant, and efficacy can be further increased by coadministration of an ILTV mutant expressing neuraminidase. Furthermore, chickens vaccinated with ILTV vectors can be easily differentiated from influenza virus-infected animals by the absence of serum antibodies against the AIV nucleoprotein.

**Code(s) de classement** : 002A05F04; 002A05C10

**Descripteur(s) anglais**

*Descripteur(s)* : Chicken; Avian influenzavirus; Pathogenicity; Vaccination; Recombinant virus; Hemagglutinin;
Exo- alpha -sialidase; Infection

**Desc. génériques** : Aves; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Glycosidases; Glycosylases; Hydrolases; Enzyme; Poultry; Veterinary; Zoopathogen; Farming animal

**Description(s) français**

**Descrip...**

**Description(s)** : Poulet; Influenzavirus aviaire; Pouvoir pathogène; Vaccination; Virus recombinant; Hémagglutinine; Exo- alpha -sialidase; Infection

**Desc. génériques** : Aves; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Glycosidases; Glycosylases; Hydrolases; Enzyme; Volaille; Vétérinaire; Zoopathogène; Animal élevage

**Localisation** : INIST-20289, 354000184171630220
**Origine de la notice** : INIST

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Prime-boost vaccination with a fowlpox vector and an inactivated avian influenza vaccine is highly immunogenic in Pekin ducks challenged with Asian H5N1 HPAI

Titre : Prime-boost vaccination with a fowlpox vector and an inactivated avian influenza vaccine is highly immunogenic in Pekin ducks challenged with Asian H5N1 HPAI

Auteur(s) : STEENSELS (M.); BUBLOT (M.); VAN BORM (S.); DE VRIESE (J.); LAMBRECHT (B.); RICHARD-MAZET (A.); CHANAVAT-BIZZINI (S.); DUBOEUF (M.); LE GROS (F.-X.); VAN DEN BERG (T.)

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Source : Vaccine; vol. 27; no. 5; pp. 646-654
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 59 ref.

Résumé : The efficacy of different vaccination schedules was evaluated in 17-day-old Pekin ducks using an experimental inactivated whole virus vaccine based on the H5N9 A/chicken/Italy/22A/98 isolate (H5N9-lt) and/or a fowlpox recombinant (vFP-H5) expressing a synthetic HA gene from an Asian H5N1 isolate (A/chicken/Indonesia/7/2003). Full protection against clinical signs and shedding was induced by the different vaccination schemes. However, the broadest antibody response and the lowest antibody increase after challenge were observed in the group of ducks whose immune system was primed with the fowlpox vectored vaccine and boosted with the inactivated vaccine, suggesting that this prime-boost strategy induced optimal immunity against H5N1 and minimal viral replication after challenge in ducks. In addition, this prime-boost vaccination scheme was shown to be immunogenic in 1-day-old ducklings.

Code(s) de classement : 002A05F04

Descr. français

Localisation : INIST-20289, 354000184171630060
Origine de la notice : INIST
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Readiness exercise to combat avian influenza

Titre : Readiness exercise to combat avian influenza

Auteur(s) : SEET (R. C.-S.); LIM (E. C. H.); OH (V. M. S.); ONG (B. K. C.); GOH (K. T.); FISHER (D. A.); HO (K. Y.); YEOH (K. G.)

Affiliation(s) : Department of Medicine, Yong Loo Lin School of Medicine, National University of Singapore, SGP; Department of Medicine, National University Hospital, SGP; Medical Affairs, National University Hospital, SGP

Source : QJM : (Oxford. 1994. Print); vol. 102; no. 2; pp. 133-137
ISSN : 1460-2725
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 19 ref.

Résumé : Aim: To examine the readiness of our hospital for the potential pandemic threat of avian influenza, we developed and implemented simulation case scenarios in our hospital. Methods: Two volunteers, who assumed the identity of 'actual' patients, were trained to simulate acute respiratory symptoms following a visit to an avian influenza-affected area, and their identities and locations were kept confidential prior to the readiness exercise. A team of auditors was stationed at high-risk areas to assess adherence to the use of personal protective equipment (PPE) and infection control procedures. Results: A total of 324 healthcare workers and 84 administrators participated in this hospital-wide exercise. Following disclosure of their symptoms, the 'patients' were masked and isolated in negative-pressure rooms. A quarantine order was enforced on 38 inpatients and 45 healthcare workers who were present in the affected wards at the time of the exercise, which mandated the use of PPE. Although all affected healthcare workers were competent in the use of PPE, we observed breaches in PPE and isolation procedures in eight medical and nursing students, and 10 healthcare attendants. The exercise concluded after H5N1 tests returned negative. Conclusions: We recommend the use of case simulation as an effective means of assessing potential breaches in infection control procedures.

Code(s) de classement : 002B01; 002B05C02C

Description(s) anglais

Descriputeur(s) : Avian influenza; Motivation; Physical exercise; Medicine
Desc. génériques : Viral disease; Infection

Description(s) français

Descriputeur(s) : Grippe aviaire; Motivation; Exercice physique; Médecine
Desc. génériques : Virose; Infection

Localisation : INIST-5050, 354000184177910070
Origine de la notice : INIST
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Differential patterns of amantadine-resistance in influenza A (H3N2) and (H1N1) isolates in Toronto, Canada

Titre : Differential patterns of amantadine-resistance in influenza A (H3N2) and (H1N1) isolates in Toronto, Canada

Auteur(s) : HIGGINS (Rachel R.); ESHAGHI (A.); BURTON (L.); MAZZULLI (T.); DREWS (S. J.)
Affiliation(s) : Central Public Health Laboratory, Toronto, ON, CAN; Mount Sinai Hospital, Toronto, ON, CAN; Department of Pathobiology and Laboratory Medicine, University of Toronto, Toronto, ON, CAN

Source : Journal of clinical virology; vol. 44; no. 1; pp. 91-93
ISSN : 1386-6532
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 9 ref.

Résumé : Background: Molecular methods were used to characterize influenza A (H1N1) and (H3N2) strains and to identify amantadine-resistance. Objectives: To compare proportions of amantadine-resistant influenza A (H1N1) and (H3N2) isolates in the Greater Toronto Area. Study design: Isolates of influenza A (H1N1) and (H3N2) were strain typed using molecular methods. Pyrosequencing for point mutations in the transmembrane domain of the M2 proton channel was undertaken. Proportions of amantadine-resistant and susceptible isolates were compared using the The Fisher's exact test. Results: 96% of the 49 influenza A (H3N2) isolates and none of the influenza A (H1N1) tested carried a point mutation in the M gene coding for the M2 protein. Influenza A (H3N2) isolates were more likely to carry an amantadine-resistance associated mutation than influenza A (H1N1) isolates (Fishers's exact test, P < 0.0001). Conclusions:: Characterization of amantadine-resistance in influenza A (H1N1) isolates should utilize a variety of different methods including sub-typing, strain typing, and direct sequencing for point mutations associated with amantadine-resistance.

Code(s) de classement : 002A05C10; 002B05C02J

Descripteur(s) anglais
Desc. génériques : North America; America; Viral disease; Infection

Descripteur(s) français
Desc. génériques : Amérique du Nord; Amérique; Virose; Infection

Localisation : INIST-26272, 354000184149620220
Origine de la notice : INIST
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Recombinant Modified Vaccinia Virus Ankara Expressing the Hemagglutinin Gene Confers Protection against Homologous and Heterologous H5N1 Influenza Virus Infections in Macaques

**Titre** : Recombinant Modified Vaccinia Virus Ankara Expressing the Hemagglutinin Gene Confers Protection against Homologous and Heterologous H5N1 Influenza Virus Infections in Macaques

**Auteur(s)** : KREIJTZ (J. H. C. M.); SUEZER (Y.); DE MUTSERT (G.); VAN DEN BRAND (J. M. A.); VAN AMERONGEN (G.); SCHNIEDEL (B. S.); KUIKEN (T.); FOUCHEIR (R. A. M.); LOWER (J.); OSTERHAUS (A. D. M. E.); SUTTER (G.); RIMMELZWAAN (G. F.)

**Affiliation(s)** : Department of Virology, Erasmus Medical Center, Rotterdam, NLD; Paul-Ehrlich-Institut, Langen, DEU

**Source** : The Journal of infectious diseases; vol. 199; no. 3; pp. 405-413

**ISSN** : 0022-1899

**CODEN** : JIDIAQ

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 49 ref.

**Résumé** : Background. Highly pathogenic avian influenza viruses of the H5N1 subtype have been responsible for an increasing number of infections in humans since 2003. More than 60% of infected individuals die, and new infections are reported frequently. In light of the pandemic threat caused by these events, the rapid availability of safe and effective vaccines is desirable. Modified vaccinia virus Ankara (MVA) expressing the hemagglutinin (HA) gene of H5N1 viruses is a promising candidate vaccine that induced protective immunity against infection with homologous and heterologous H5N1 influenza virus in mice. Methods. In the present study, we evaluated a recombinant MVA vector expressing the HA gene of H5N1 influenza virus A/Vietnam/194/04 (MVA-HA-VN/04) in nonhuman primates. Cynomolgus macaques were immunized twice and then were challenged with influenza virus A/Vietnam/1194/04 (clade 1) or A/Indonesia/5/05 (clade 2.1) to assess the level of protective immunity. Results. Immunization with MVA-HA-VN/04 induced (cross-reactive) antibodies and prevented virus replication in the upper and lower respiratory tract and the development of severe necrotizing bronchointerstitial pneumonia. Conclusion. Therefore, MVA-HA-VN/04 is a promising vaccine candidate for the induction of protective immunity against highly pathogenic H5N1 avian influenza viruses in humans.

**Code(s) de classement** : 002A05C10; 002B05

**Desc. génériques** : Orthopoxvirus; Chordopoxvirinae; Poxviridae; Virus; Orthomyxoviridae

**Desc. génériques** : Orthopoxvirus; Chordopoxvirinae; Poxviridae; Virus; Orthomyxoviridae

**Localisation** : INIST-2052, 354000185176730150

**Origine de la notice** : INIST

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Antibody Persistence after 2-Dose Priming and Booster Response to a Third Dose of an Inactivated, Adjuvanted, Whole-Virion H5N1 Vaccine

Titre : Antibody Persistence after 2-Dose Priming and Booster Response to a Third Dose of an Inactivated, Adjuvanted, Whole-Virion H5N1 Vaccine

Auteur(s) : LIN (Jiang-Tao); LI (Chang-Gui); XU WANG; NAN SU; YAN LIU; QIU (Yuan-Zheng); MENG YANG; CHEN (Jiang-Ting); FANG (Han-Hua); DONG (Xiao-Ping); YIN (Wei-Dong); FENG (Zi-Jian)

Affiliation(s) : China-Japan Friendship Hospital, CHN; National Institute for the Control of Pharmaceuticals and Biological Products, CHN; Sinovac Biotech Ltd, CHN; State Key Laboratory for Infectious Disease Prevention and Control, National Institute for Viral Disease Control and Prevention, CHN; Chinese Center for Disease Control and Prevention, Beijing, CHN

Source : The Journal of infectious diseases; vol. 199; no. 2; pp. 184-187

ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 15 ref.

Résumé : An inactivated, alum-adjuvanted, whole-virion H5N1 vaccine had been evaluated previously. Hemagglutination inhibition (HI) assays showed that the antibody levels declined significantly, with 4.8%-20.8% and 0%-18.8% of participants retaining sero-protection (HI titer >=1:40) 6 and 12 months after the second dose, respectively. A third dose of the same vaccine given 12 months after the second dose significantly boosted immune responses. Thirty days after the third dose in the 1.25-, 2.5-, 5-, and 10- μg dose groups, 29.4%, 31.3%, 78.6%, and 90.0% of participants had HI titers >= 1:40, and 52.9%, 81.2%, 92.9%, and 100% of participants had microneutralization titers >= 1:40, respectively. Both the 5- μg and 10- μg doses met European Union criteria. (ClinicalTrials.gov identifier: NCT00660257.).

Code(s) de classement : 002A05; 002B05

Descripteur(s) anglais

Descripteur(s) : Antibody; Booster vaccination; Inactivated strain; Immunological adjuvant; Microbiology; Infection

Descripteur(s) français

Descripteur(s) : Anticorps; Rappel vaccination; Souche inactivée; Adjuvant immunologique; Microbiologie; Infection

Localisation : INIST-2052, 354000184122140040
Origine de la notice : INIST
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Component-Specific Effectiveness of Trivalent Influenza Vaccine as Monitored through a Sentinel Surveillance Network in Canada, 2006-2007. Commentary

Title: Component-Specific Effectiveness of Trivalent Influenza Vaccine as Monitored through a Sentinel Surveillance Network in Canada, 2006-2007. Commentary

Authors: JACKSON (Lisa A.), comment.; SKOWRONSKI (Danuta M.); DE SERRES (Gaston); DICKINSON (Jim); PETRIC (Martin); MAK (Annie); FONSECA (Kevin); KWINDT (Trijntje L.); CHAN (Tracy); BASTIEN (Nathalie); CHAREST (Hugues); YAN LI

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Source: The Journal of infectious diseases; vol. 199; no. 2
ISSN: 0022-1899
CODEN: JIDIAQ
Date de publication: 2009
Pays de publication: USA
Langue(s): ENG
Type de document: P
Nombre de références: 58 ref.

Résumé: Background. Trivalent inactivated influenza vaccine (TIV) is reformulated annually to contain representative strains of 2 influenza A subtypes (H1N1 and H3N2) and 1 B lineage (Yamagata or Victoria). We describe a sentinel surveillance approach to link influenza variant detection with component-specific vaccine effectiveness (VE) estimation. Methods. The 2006-2007 TIV included A/NewCaledonia/20/1999(H1N1)-like, A/Wisconsin/67/2005 (H3N2)-like, and B/Malaysia/2506/2004(Victoria)-like components. Included participants were individuals 3>=9 years of age who presented within 1 week after influenzalike illness onset to a sentinel physician between November 2006 and April 2007. Influenza was identified by real-time reverse-transcriptase polymerase chain reaction and/or culture. Isolates were characterized by hemagglutination inhibition assay (HI) and HA1 gene sequence. VE was estimated as 1 - [odds ratio for influenza in vaccinated versus nonvaccinated persons]. Results. A total of 841 participants contributed: 69 (8%) were >=65 years of age; 166 (20%) received the 2006-2007 TIV. Influenza was detected in 337 subjects (40%), distributed as follows: A/H3N2, 242 (72%); A/H1N1,55 (16%); and B, 36 (11%). All but 1 of the A/H1N1 isolates were well matched, half of A/H3N2 isolates were strain mismatched, and all B isolates were lineage-level mismatched to vaccine. Age-adjusted estimated VE for A/H1N1, A/H3N2, and B components was 92% (95% CI, 40%-91%), 41% (95% CI, 6%-63%), and 19% (95% CI, -112% to 69%), respectively, with an overall VE estimate of 47% (95% CI, 18%- 65%). Restriction of the analysis to include only working-age adults resulted in lower VE estimates with wide confidence intervals but similar component-specific trends. Conclusions. Sentinel surveillance provides a broad platform to link new variant detection and the composite of circulating viruses to annual monitoring of component-specific VE.

Code(s) de classement: 002A05F04; 002B05

Desc. génériques: North America; America; Viral disease

Desc. génériques: Amérique du Nord; Amérique; Virose
Broad Cross-Protection against H5N1 Avian Influenza Virus Infection by Means of Monoclonal Antibodies that Map to Conserved Viral Epitopes

Titre : Broad Cross-Protection against H5N1 Avian Influenza Virus Infection by Means of Monoclonal Antibodies that Map to Conserved Viral Epitopes

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Source : The Journal of infectious diseases; vol. 199; no. 1; pp. 49-58
ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 41 ref.

Résumé : Background. Passive immunization with human H5 antisera or H5-specific monoclonal antibodies (MAbs) has potential as an effective treatment for acute H5N1 influenza virus infection, but its efficacy against antigenically diverse H5N1 viruses is unconfirmed. Methods. Cross-protection against antigenically diverse H5N1 strains with H5-specific MAbs, generated by successive immunization of antigenically distinct strains, was evaluated in mice. Results. A panel of 52 broadly cross-reactive H5 specific MAbs were generated and characterized. One of these MAbs, 13D4, has been demonstrated to protect mice against lethal challenge by 4 H5N1 strains representing the current major genetic populations, clades 1, 2.1, 2.2, and 2.3, even at a stage of infection when H5N1 virus has disseminated beyond the pulmonary system. Complete neutralization of virus in lung tissue of infected animals was observed 24 h after treatment with 13D4. Mapping of this MAb with escape mutants showed it to bind to 2 conserved, possibly critical, sites of H5N1 hemagglutinin, 152 and 182. Conclusion. Generation of broadly cross-protective MAbs against H5N1 influenza virus may be optimized by selecting MAbs that target conserved sites in hemagglutinin. H5 MAbs such as 13D4 may prove to have therapeutic value in controlling infection due to current and future H5N1 variants.

Code(s) de classement : 002A05C10; 002B05; 002A05F04

Descripteur(s) anglais
- Descripteur(s) : Avian influenzavirus; Cross protection; Monoclonal antibody; Antigenic determinant; Microbiology; Infection
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen

Descripteur(s) français
- Descripteur(s) : Influenzavirus aviaire; Protection croisée; Anticorps monoclonal; Déterminant antigénique; Microbiologie; Infection
- Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogène

Localisation : INIST-2052, 35400184112400060
Origine de la notice : INIST
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Immunohistochemical detection of Influenza virus infection in formalin-fixed tissues with anti-H5 monoclonal antibody recognizing FFWTILKP

Titre : Immunohistochemical detection of Influenza virus infection in formalin-fixed tissues with anti-H5 monoclonal antibody recognizing FFWTILKP

Auteur(s) : FANG HE; QINGYUN DU; YUENFERN HO; KWANG (Jimmy)
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Source : Journal of virological methods; vol. 155; no. 1; pp. 25-33
ISSN : 0166-0934
CODEN : JVMEDH
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 1/2 p.

Résumé : The worldwide outbreak of avian influenza among poultry species and humans is associated with the H5N1 subtype of avian influenza A virus (AIV). This highlighted the need to develop safe H5 AIV diagnostic methods. 7H10, an H5-specific monoclonal antibody (Mab), can be used for immunohistochemical (IHC) staining for formalin-fixed tissue. An assortment of H5N1 tissue specimens infected naturally in paraffin sections from Asia, between years 2002-2006, including one human specimen, were tested. 7H10 detected H5 infection in all of these tissue samples infected naturally. In addition, 24 different human H5N1 isolates from Indonesia, 5 H5 isolates and 3 non-H5 isolates from Asia were inoculated into BALB/C mice and chicken embryos. Among these influenza viruses, 7H10 detected 28 of the 29 H5 virus strains by immunohistochemical staining, while none of non-H5 strains used in this study could be detected by 7H10, confirming its specificity to H5. Further, the eight-residue-long linear epitope, “FFWTILKP”, identified through epitope mapping, enables 7H10 to detect >98.3% of H5 subtype viruses reported worldwide before 2007. This study describes a specific H5 diagnostic system with minimal possibility of exposure to live virus based on immunohistochemical staining.

Code(s) de classement : 002A05C09

Descripteur(s) anglais

Descripteur(s) : Influenzavirus; Immunohistochemistry; Detection; Monoclonal antibody; Staining; Microbiology; Method; Virology; Viral disease
Desc. génériques : Orthomyxoviridae; Virus; Infection

Descripteur(s) français

Descripteur(s) : Influenzavirus; Immunohistochimie; Détection; Anticorps monoclonal; Coloration échantillon; Microbiologie; Méthode; Virologie; Virose
Desc. génériques : Orthomyxoviridae; Virus; Infection

Localisation : INIST-18295, 354000184139640040
Origine de la notice : INIST
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Évaluation de la préparation à une pandémie grippale par un exercice de terrain au centre hospitalier universitaire de Nîmes; Pandemic influenza: Training in the Nîmes university hospital

Titre : Évaluation de la préparation à une pandémie grippale par un exercice de terrain au centre hospitalier universitaire de Nîmes; Pandemic influenza: Training in the Nîmes university hospital

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Source : Médecine et maladies infectieuses; vol. 39; no. 2; pp. 116-124
ISSN : 0399-077X
CODEN : MMAIB5
Date de publication : 2009
Pays de publication : FRA
Langue(s) : FRE
Langue(s) du résumé : eng
Type de document : P
Nombre de références : 13 ref.

Résumé : Objectif. - Tester l'application des mesures barrières et l'organisation de l'établissement lors d'une pandémie grippale, dans une démarche éducative, en application du programme national de « formations pandémie grippale » et de l'annexe « Grippe » du Plan Blanc d'établissement. Méthode. - Un exercice de terrain a été réalisé le 18 décembre 2007 dans deux secteurs de haute densité virale et un secteur de basse densité. Il s'appliquait à toute personne dans ces secteurs, sans perturber l'activité normale de soins. Résultats. - Deux cent quarante-cinq personnes ont été évaluées. Soixante-quinze pour cent du personnel avaient suivi la formation dispensée dans l'établissement. L'hygiène des mains était conforme aux procédures dans 32 % des cas, correcte dans 44 %, insuffisante dans 24 %. L'application du masque était incorrecte dans 21 % des cas. Ces mesures ont été perçues facilement supportables pour 36 % du personnel, pénibles pour 54 % et difficilement supportables pour 10 %. La mauvaise étanchéité du masque FFP2 (dotation nationale), selon la morphologie du visage, sa mauvaise tolérance, le manque de points d'eau et le regroupement de personnes ont été notés. Conclusion. - L'exercice a été satisfaisant avec une bonne participation des différents acteurs. Cependant, il a mis en évidence des dysfonctionnements inattendus comme l'application des mesures barrières. Aussi, le masque FFP2 coqué n'était pas efficace pour tout le personnel, ce qui posera problème en période pandémique. Il n'existe pas de masque adapté aux enfants. Enfin, cet exercice a permis d'orienter les actions correctives à mener et complète les différents « exercices sur table » réalisés dans d'autres établissements de soins.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais
- Descripteur(s) : Influenza; Teaching hospital; Hospital; Microbiology; Influenzavirus A(H5N1)
- Desc. génériques : Viral disease; Infection

Descripteur(s) français
- Descripteur(s) : Grippe; Centre hospitalier universitaire; Hôpital; Microbiologie; Pandémie; Influenzavirus A(H5N1)
- Desc. génériques : Virose; Infection

Localisation : INIST-15434, 354000186440890060
Origine de la notice : INIST
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Neuraminidase Inhibitor Resistance after Oseltamivir Treatment of Acute Influenza A and B in Children. Commentary

**Titre** : Neuraminidase Inhibitor Resistance after Oseltamivir Treatment of Acute Influenza A and B in Children. Commentary

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**Source** : Clinical infectious diseases; vol. 48; no. 4; pp. 389-399

**ISSN** : 1058-4838

**CODEN** : CIDIEL

**Date de publication** : 2009

**Pays de publication** : USA

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 49 ref.

**Résumé** : Background. Oseltamivir, a specific influenza neuraminidase inhibitor, is an effective treatment for seasonal influenza. Emergence of drug-resistant influenza viruses after treatment has been reported, particularly in children in Japan, where the dosing schedule is different from that used throughout the rest of the world. We investigated the emergence of drug-resistant infection in children treated with a tiered weight-based dosing regimen. Methods. We analyzed sequential clinical nasopharyngeal samples, obtained before and after tiered weight-based oseltamivir therapy, from children with acute influenza during 2005-2007. We isolated viruses, tested for drug resistance with use of a fluorescence-based neuraminidase inhibition assay, performed neuraminidase gene sequencing, and determined quantitative viral loads. Results. Sixty-four children (34 with influenza A subtype H3N2, 11 with influenza A subtype H1N1, and 19 with influenza B virus) aged 1-12 years (median age, 3 years, 1 month) were enrolled. By days 4-7 after initiation of treatment, of 64 samples tested, 47 (73.4%) and 26 (40.6%) had virus detectable by reverse-transcriptase polymerase chain reaction and culture, respectively. By days 8-12 after initiation of treatment, of 53 samples tested, 18 (33.9%) and 1 (1.8%) had virus detectable by reverse-transcriptase polymerase chain reaction and culture, respectively. We found no statistically significant differences in the reduction of viral shedding or time to clearance of virus between viral subtypes. Antiviral-resistant viruses were recovered from 3 (27.3%) of 11 children with influenza A subtype H1N1, 1 (2.9%) of 34 children with influenza A subtype H3N2, and 0 (0%) of 19 children with influenza B virus, all of whom were treated with oseltamivir (P = .004). There was no evidence of prolonged illness in children infected with drug-resistant virus. Conclusions. Drug resistance emerges at a higher rate in influenza A subtype H1N1 virus than in influenza A subtype H3N2 or influenza B virus after tiered weight-based oseltamivir therapy. Virological surveillance for patterns of drug resistance is essential for determination of antiviral treatment strategies and for composition of pandemic preparedness stockpiles.

**Code(s) de classement** : 002B05C02C; 002B02S05

**Descrip. génériques** : Viral disease; Infection; Glycosidases; Glycosylases; Hydrolases; Enzyme; Human; Enzyme inhibitor; Neuraminidase inhibitor

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Antiviral

Desc. génériques : Virose; Infection; Glycosidases; Glycosylases; Hydrolases; Enzyme; Homme; Inhibiteur enzyme; Inhibiteur neuraminidase

Localisation : INIST-18407, 354000186444100020
Origine de la notice : INIST
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Molecular and phylogenetic analysis of the H5N1 avian influenza virus caused the first highly pathogenic avian influenza outbreak in poultry in the Czech Republic in 2007

Titre : Molecular and phylogenetic analysis of the H5N1 avian influenza virus caused the first highly pathogenic avian influenza outbreak in poultry in the Czech Republic in 2007

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Source : Veterinary microbiology : (Amsterdam); vol. 133; no. 3; pp. 257-263
ISSN : 0378-1135
CODEN : VMICDQ
Date de publication : 2009
Pays de publication : NLD
Langue(s) : ENG
Type de document : P
Nombre de références : 3/4 p.

Résumé : On 19th July 2007 re-occurrence of the H5N1 highly pathogenic avian influenza (HPAI) virus was noticed in Europe. The index strain of this novel H5N1 lineage was identified in the Czech Republic where it caused historically the first HPAI outbreak in commercial poultry. In the present study we performed molecular and phylogenetic analysis of the index strain of the re-emerging H5N1 virus lineage along with the Czech and the Slovak H5N1 strains collected in 2006 and established the evolutionary relationships to additional viruses circulated in Europe in 2005-2006. Our analysis revealed that the Czech and the Slovak H5N1 viruses collected during 2006 were separated into two subclades 2.2.1 and 2.2.2, which predominated in Europe during 2005-2006. On the contrary the newly emerged H5N1 viruses belonged to a clearly distinguishable sub-clade 2.2.3. Within the sub-clade 2.2.3 the Czech H5N1 strains showed the closest relationships to the simultaneously circulated viruses from Germany, Romania and Russia (Krasnodar) in 2007 and were further clustered with the viruses from Afghanistan and Mongolia circulated in 2006. The origin of the Czech 2007 H5N1 HPAI strains was also discussed.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Descripteur(s) : Avian influenzavirus; Phylogeny; Pathogenicity; Poultry; Czech Republic; Microbiology; Veterinary; Avian influenza

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Europe; Zoopathogen; Viral disease; Infection; Farming animal

Descripteur(s) français

Descripteur(s) : Influenzavirus aviaire; Phylogénèse; Pouvoir pathogène; Volaille; République tchèque; Microbiologie; Vétérinaire; Grippe aviaire

Desc. génériques : Influenzavirus A; Orthomyxoviridae; Virus; Europe; Zoopathogène; Virose; Infection; Animal élevage

Localisation : INIST-16884, 354000186345690050
Origine de la notice : INIST
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Safety and efficacy of a novel microneedle device for dose sparing intradermal influenza vaccination in healthy adults

Titre: Safety and efficacy of a novel microneedle device for dose sparing intradermal influenza vaccination in healthy adults

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Source: Vaccine; vol. 27; no. 3; pp. 454-459
ISSN: 0264-410X
CODEN: VACCDE
Date de publication: 2009
Pays de publication: GBR
Langue(s): ENG
Type de document: P
Nombre de références: 42 ref.

Résumé: Background: Intradermal vaccine delivery has been shown to induce good immune responses with low vaccine doses. Technologies for drug-delivery which specifically target the skin may render intradermal vaccination more accessible. Methods: We conducted a prospective, randomized trial in 180 intended-to-treat healthy adults. Study objectives were to evaluate the safety and immunogenicity of low-dose intradermal (ID) influenza vaccines delivered using a novel microneedle device (MicronJet). This device replaces a conventional needle, and is designed specifically for intradermal delivery. Subjects were randomly assigned to receive either the full-dose standard flu shot (containing 15 μg hemagglutinin per strain) delivered intramuscularly using a conventional needle (IM group), a medium dose intradermal injection (6 μg hemagglutinin per strain) delivered with the MicronJet (ID2 group), or a low-dose intradermal injection (3 μg hemagglutinin per strain) delivered with the MicronJet (ID1 group). A marketed influenza vaccine for the 2006/2007 influenza season (αRIX® by GSK Biologicals) was used for all injections. Adverse events were recorded over a 42-day period. Immunogenicity was evaluated by changes in hemagglutination inhibition (HAI) antibody titer, and by comparing geometric mean titers (GMTs), seroconversion, and seroprotection rates between the study groups. Results: Local reactions were significantly more frequent following intradermal vaccination, but were mild and transient in nature. At 21 days after injection, GMT fold increase was 22, 18, and 22 in the ID1, ID2, and IM groups respectively for the H1N1 strain; 9, 9, and 16 for the H3N2 strain and 9, 13, and 11 for strain B. The CPMP criteria for re-licensure of seasonal influenza vaccines were met in full for all study groups. Conclusions: Low-dose influenza vaccines delivered intradermally using microneedles elicited immunogenic responses similar to those elicited by the full-dose intramuscular vaccination. The microneedle injection device used in this study was found to be effective, safe, and reliable.

Code(s) de classement: 002A05F04

Descriptor(s) anglais
   Desc. généraux: Viral disease; Infection

Descriptor(s) français
   Desc. généraux: Virose; Infection

Localisation: INIST-20289, 354000186432890160
Origine de la notice: INIST
Copyright de notice: © 2009 INIST-CNRS. All rights reserved.
Efficacy of Soap and Water and Alcohol-Based Hand-Rub Preparations against Live H1N1 Influenza Virus on the Hands of Human Volunteers

Titre : Efficacy of Soap and Water and Alcohol-Based Hand-Rub Preparations against Live H1N1 Influenza Virus on the Hands of Human Volunteers

Auteur(s) : LINDSAY GRAYSON (M.); MELVANI (Sharmila); DRUCE (Julian); BARR (Lan G.); BALLARD (Susan A.); JOHNSON (Paul D. R.); MASTORAKOS (Tasoula); BIRCH (Christopher)

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Source : Clinical infectious diseases; vol. 48; no. 3; pp. 285-291
ISSN : 1058-4838
CODEN : CIDIEL
Date de publication : 2009
Pays de publication : USA
Langue(s) : ENG
Type de document : P
Nombre de références : 32 ref.

Résumé : Background. Although pandemic and avian influenza are known to be transmitted via human hands, there are minimal data regarding the effectiveness of routine hand hygiene (HH) protocols against pandemic and avian influenza. Methods. Twenty vaccinated, antibody-positive health care workers had their hands contaminated with 1 mL of 107 tissue culture infectious dose (TCID)50/0.1 mL live human influenza A virus (H1N1; A/New Caledonia/20/99) before undertaking 1 of 5 HH protocols (no HH [control], soap and water hand washing [SW], or use of 1 of 3 alcohol-based hand rubs [61.5% ethanol gel, 70% ethanol plus 0.5% chlorhexidine solution, or 70% isopropanol plus 0.5% chlorhexidine solution]). H1N1 concentrations were assessed before and after each intervention by viral culture and real-time reverse-transcriptase polymerase chain reaction (PCR). The natural viability of H1N1 on hands for >60 min without HH was also assessed. Results. There was an immediate reduction in culture-detectable and PCR-detectable H1N1 after brief cutaneous air drying—14 of 20 health care workers had H1N1 detected by means of culture (mean reduction, 103-4 TCID50/0.1 mL), whereas 6 of 20 had no viable H1N1 recovered; all 20 health care workers had similar changes in PCR test results. Marked antiviral efficacy was noted for all 4 HH protocols, on the basis of culture results (14 of 14 had no culturable H1N1; P<.002) and PCR results (P<.001; cycle threshold value range, 33.3-39.4), with SW statistically superior (P<.001) to all 3 alcohol-based hand rubs, although the actual difference was only 1-100 virus copies/μL. There was minimal reduction in H1N1 after 60 min without HH. Conclusions. HH with SW or alcohol-based hand rub is highly effective in reducing influenza A virus on human hands, although SW is the most effective intervention. Appropriate HH may be an important public health initiative to reduce pandemic and avian influenza transmission.

Code(s) de classement : 002B05C02C

Desc. génériques : Virose; Infection
Isolation and pathotyping of H9N2 avian influenza viruses in Indian poultry

Title: Isolation and pathotyping of H9N2 avian influenza viruses in Indian poultry

Authors: NAGARAJAN (S.); RAJUKUMAR (K.); TOSH (C.); RAMASWAMY (V.); PUROHIT (K.); SAXENA (G.); BEHERA (P.); PATTNAIK (B.); PRADHAN (H. K.); DUBEY (S. C.)

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Source: Veterinary microbiology: (Amsterdam); vol. 133; no. 1-2; pp. 154-163

Resume: A total of 1246 faecal and tissue samples collected/received from 119 farms located in various states of India were processed for isolation of avian influenza viruses (AIV) during 2003-2004 as part of a program to monitor AIV infection in Indian poultry population. Avian influenza virus was isolated for the first time in India from poultry farms with history of drop in egg production, respiratory illness and increased mortality in Haryana state. A total of 29 H9N2 AIV isolates were obtained from the states of Punjab, Haryana, Uttar Pradesh, Gujarat, and Orissa and Union Territory Delhi. Subtyping was done by HI, RT-PCR and neuraminidase inhibition assay. Pathotyping of six representative isolates by intravenous pathogenicity index (0.0/3.0) in 6-8 weeks old chicken, trypsin dependency in cell culture and HA cleavage site analysis (335RSSR*GLF341) confirmed that these isolates are low pathogenic. Nucleotide sequence analysis of the HA gene showed that the Indian isolates are very closely related (95.0-99.6%) and shared a homology of 92-96% with H9N2 isolates from Germany and Asian regions other than that of mainland China. Deduced amino acid sequences showed the presence of L226 (234 in H9 numbering) which indicates a preference to binding of a (2-6) sialic acid receptors. Two of the six isolates had 7 glycosylation sites in the HA1 cleaved protein and the remaining four had 5 sites. Phylogenetic analysis showed that they share a common ancestor Qa/HK/G1/97 isolate which had contributed internal genes of H5N1 virus circulating in Vietnam. Further characterization of Indian H9N2 isolates is required to understand their nature and evolution.

Code(s) de classement: 002A05C10

Descriptor(s) anglais

Desc. génériques: Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen; Viral disease; Infection; Farming animal

Descriptor(s) français

Desc. génériques: Influenzavirus aviaire; Isolément; Volaille; Microbiologie; Vétérinaire; Grippe aviaire

Localisation: INIST-16884, 354000184026450170

Origine de la notice: INIST

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Pathogenicity of highly pathogenic avian influenza viruses of H5N1 subtype isolated in Thailand for different poultry species

Titre : Pathogenicity of highly pathogenic avian influenza viruses of H5N1 subtype isolated in Thailand for different poultry species

Auteur(s) : SAITO (Takehiko); WATANABE (Chiaki); TAKEMAE (Nobuhiro); CHAISINGH (Arunee); UCHIDA (Yuko); BURANATHAI (Chantanees); SUZUKI (Hiroyumi); OKAMATSU (Masatoshi); IMADA (Tadao); PARCHARIYANON (Sujira); TRAIWANATAM (Nimit); YAMAGUCHI (Shigeo)

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Source : Veterinary microbiology : (Amsterdam); vol. 133; no. 1-2; pp. 65-74

Résumé : Highly pathogenic avian influenza (HPAI) viruses of the H5N1 subtype have caused several rounds of outbreaks in Thailand. In this study, we used 3 HPAI viruses isolated in Thailand in January 2004 from chicken, quail, and duck for genetic and pathogenetic studies. Sequence analysis of the entire genomes of these isolates revealed that they were genetically similar to each other. Chickens, quails, domestic ducks, and cross-bred ducks were inoculated with these isolates to evaluate their pathogenicity to different host species. A/chicken/Yamaguchi/7/04 (H5N1), an HPAI virus isolated in Japan, was also used in the chicken and quail studies for comparison. All four isolates were shown to be highly pathogenic to chickens and quails, with 100% mortality by 10^6 EID50 inoculants of the viruses. They caused sudden death in chickens and quails within 2-4 days after inoculation. The mean death times (MDT) of quails infected with the Thai isolates were shorter than those of chickens infected with the same isolates. Mortality against domestic and cross-bred ducks ranged from 50 to 75% by intranasal inoculation with the 106 EID50 viruses. Neurological symptoms were observed in most of the inoculated domestic ducks and appeared less severe in the cross-bred ducks. The MDT's of the ducks infected with the Thai isolates were 4.8-6 days post-inoculation. Most of the surviving ducks infected with the Thai isolates had sero-converted until 14 dpi. Our study illustrated the pathobiology of the Thai isolates against different poultry species and would provide useful information for improving control strategies against HPAI.
Histopathology and growth kinetics of influenza viruses (H1N1 and H3N2) in the upper and lower airways of guinea pigs

**Titre** : Histopathology and growth kinetics of influenza viruses (H1N1 and H3N2) in the upper and lower airways of guinea pigs

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**Source** : Journal of general virology; vol. 90; no. p. 2; pp. 386-391

**ISSN** : 0022-1317

**CODEN** : JGVIAY

**Date de publication** : 2009

**Pays de publication** : GBR

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 3/4 p.

**Résumé** : Recent investigations have shown that guinea pigs are important for the study of influenza A virus (IAV) transmission. However, very little is known about IAV replication and histopathology in the guinea pig respiratory tract. Here, we describe viral growth kinetics, target cells and histopathology in the nasosinus, trachea and lungs of IAV-infected guinea pigs. We found that guinea pigs infected with either A/Puerto Rico/8/34 (H1N1) or A/Hong Kong/8/68 (H3N2) developed a predominantly upper airway infection with high nasal viral titres. IAV grew to moderate titres in the lungs but induced marked inflammatory responses, resulting in severe bronchopneumonia and alveolitis. Although non-lethal at the high dose of 2×10^6 p.f.u., infections with these IAV strains were associated with reduced weight gain. IAV infection in guinea pigs is characterized by extensive viral replication in the ciliated nasal epithelial cells followed by heavy nasal mucus secretion.

**Code(s) de classement** : 002A05C10

**Description(s) anglais**

*Description(s)* : Guinea pig; Anatomic pathology; Histopathology; Kinetics; Influenza; Respiratory tract; Animal; Microbiology

*Desc. génériques* : Rodentia; Mammalia; Vertebrata; Viral disease; Infection

**Description(s) français**

*Description(s)* : Cobaye; Anatomopathologie; Histopathologie; Cinétique; Grippe; Voie respiratoire; Animal; Microbiologie

*Desc. génériques* : Rodentia; Mammalia; Vertebrata; Virose; Infection

**Localisation** : INIST-13533, 354000184122300120

**Origine de la notice** : INIST

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Anti-Influenza Drugs: The Development of Sialidase Inhibitors; Antiviral Strategies

**Titre** : Anti-Influenza Drugs: The Development of Sialidase Inhibitors; Antiviral Strategies

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**Source** : Handbook of experimental pharmacology; vol. 189; pp. 111-154

**ISSN** : 0171-2004

**Date de publication** : 2009

**Pays de publication** : DEU

**Langue(s)** : ENG

**Type de document** : P

**Nombre de références** : 9 p.1/4

**Résumé** : Viruses, particularly those that are harmful to humans, are the ‘silent terrorists’ of the twenty-first century. Well over four million humans die per annum as a result of viral infections alone. The scourge of influenza virus has plagued mankind throughout the ages. The fact that new viral strains emerge on a regular basis, particularly out of Asia, establishes a continual socio-economic threat to mankind. The arrival of the highly pathogenic avian influenza H5N1 heightened the threat of a potential human pandemic to the point where many countries have put in place ‘preparedness plans’ to defend against such an outcome. The discovery of the first designer influenza virus sialidase inhibitor and anti-influenza drug Relenza™, and subsequently Tamiflu™, has now inspired a number of continuing efforts towards the discovery of next generation anti-influenza drugs. Such drugs may act as ‘first-line-of-defence’ against the spread of influenza infection and buy time for necessary vaccine development particularly in a human pandemic setting. Furthermore, the fact that influenza virus can develop resistance to therapeutics makes these continuing efforts extremely important. An overview of the role of the virus-associated glycoprotein sialidase (neuraminidase) and some of the most recent developments towards the discovery of anti-influenza drugs based on the inhibition of influenza virus sialidase is provided in this chapter.

**Code(s) de classement** : 002B05C02C

**Descripteur(s) anglais**

- **Desc. génériques** : Viral disease; Infection; Glycosidases; Glycosylases; Hydrolases; Enzyme; Orthomyxoviridae; Virus; Neuraminidase inhibitor

**Descripente(s) français**

- **Desc. génériques** : Virose; Infection; Glycosidases; Glycosylases; Hydrolases; Enzyme; Orthomyxoviridae; Virus; Inhibiteur neuraminidase

**Localisation** : INIST-21230, 354000185001330050

**Origine de la notice** : INIST

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Indigenous sources of 2007-2008 H5N1 avian influenza outbreaks in Thailand

Titre : Indigenous sources of 2007-2008 H5N1 avian influenza outbreaks in Thailand

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Source : Journal of general virology; vol. 90; no. p. 1; pp. 216-222
ISSN : 0022-1317
CODEN : JGVIAY
Date de publication : 2009
Pays de publication : GBR
Langue(s) : ENG
Type de document : P
Nombre de références : 3/4 p.

Résumé : Outbreaks of H5N1 avian influenza show strong seasonality. It is not clear where the source of virus originates from in each new outbreak season. This study sought to understand the nature of viral resurgence in recent outbreak seasons in Thailand, where the epidemic is relatively well controlled. In such a situation, indigenous viruses surviving the inter-outbreak season would have to pass through a bottleneck. In order to look for evidence of the bottleneck effect, viral genome sequences from recent outbreaks in the country were analysed. H5N1 avian influenza viruses were isolated from six outbreaks in the rainy season and winter of 2007 through to early 2008. Most of the outbreaks were in the Yom-Nan River basin in the southern part of the northern region of the country. Sequences of these viral isolates were identified as clade 1, genotype Z, similar to viruses from previous years in the central region of the country. The sequences clustered into two groups, one of which was closely related to viruses isolated from the same area in July 2006. These analyses indicated that there was a strong bottleneck effect on the virus population and that only a few lineages remained in the area. In addition, evidence of reassortment among these viruses was found. These indicated re-emergence of viruses from a small pool of indigenous sources that had been silently perpetuated over the dry summer months. Therefore, an approach to eradicate H5N1 avian influenza from the area by eliminating these local reservoirs may be feasible and should be seriously considered.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
  Desc. généraux : Asia; Infection; Viral disease

Descripteur(s) français
  Desc. généraux : Asie; Infection; Virose
Maladies infectieuses : Nouveautés en médecine 2008 (Première partie); Infectious diseases

Titre : Maladies infectieuses : Nouveautés en médecine 2008 (Première partie); Infectious diseases

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Source : Revue médicale suisse ; vol. 5; no. 185; pp. 29-34
ISSN : 1660-9379
Date de publication : 2009
Pays de publication : CHE
Langue(s) : FRE
Langue(s) du résumé : eng
Type de document : P
Nombre de références : 51 ref.

Résumé : En 2008, une série de données ont suggéré que les changements climatiques et la globalisation des modes de vie pouvaient influencer l'épidémiologie des maladies infectieuses. Ces études montrent l'extension en direction de l'Europe des zones d'endémie de la fièvre de Crimée-Congo (Kosovo, Turquie, Grèce, Bulgarie), de la leishmaniose (Chypre) et de l'infection au virus du chikungunya (Italie). L'article est complété par des commentaires sur le Plasmodium knowlesi, nouvellement identifié comme une cause de malaria sévère chez l'homme et par des données récentes sur la transmission interhumaine du virus de la grippe aviaire H5N1. Il mentionne également quelques données nouvelles sur la paralysie de Bell et sur deux vaccins (varicella-zoster et pneumocoque) et propose une liste des recommandations de pratique clinique les plus récentes.

Code(s) de classement : 002B05E02B3; 002B10D02

Descripteur(s) anglais

- Descripteur(s) : Herpes zoster; Chikungunya virus; Dengue; Leishmaniasis; Europe; Cyprus; Immunoprophylaxis; Italy; Congo-Crimean haemorrhagic fever; Facial paralysis; Vaccine; Elderly; Avian influenza; Pneumococcal infection; Virulent strain; Treatment; Epidemiology; Malaria; Diagnosis; Recommendation; Facial nerve
- Desc. génériques : Viral disease; Infection; Alphavirus; Togaviridae; Virus; Arbovirus disease; Protozoal disease; Parasitosis; Asia; Human; Streptococcal infection; Bacteriosis; Skin disease; Nervous system diseases; Cranial nerve disease; ENT disease; Motor system disorder; Public health

Descripteur(s) français

- Descripteur(s) : Zona; Virus Chikungunya; Dengue; Leishmaniose; Europe; Chypre; Immunoprophylaxie; Italie; Fièvre hémorragique Crimeée Congo; Paralysie faciale; Vaccin; Personne âgée; Grippe aviaire; Pneumococcie; Souche virulente; Traitement; Epidémiologie; Paludisme; Diagnostic; Recommandation; Nerf facial
- Desc. génériques : Virose; Infection; Alphavirus; Togaviridae; Virus; Arbovirose; Protozoose; Parasitose; Asie; Homme; Streptococcie; Bactériose; Pathologie de la peau; Pathologie du système nerveux; Pathologie des nerfs crâniens; Pathologie ORL; Trouble moteur; Santé publique

Localisation : INIST-27566, 354000184713500050
Origine de la notice : INIST
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