Grippe Aviaire

Decembre 2008

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080342409
PASCAL

Heterologous HA DNA vaccine prime-inactivated influenza vaccine boost is more effective than using DNA or inactivated vaccine alone in eliciting antibody responses against H1 or H3 serotype influenza viruses

Titre : Heterologous HA DNA vaccine prime-inactivated influenza vaccine boost is more effective than using DNA or inactivated vaccine alone in eliciting antibody responses against H1 or H3 serotype influenza viruses

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Source : Vaccine . 2008; 26 (29-30) : 3626-3633
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Nombre de références : 23 ref.

Résumé : The trivalent inactivated vaccine (TIV) is used to prevent seasonal influenza virus infection in humans, however, the immunogenicity of this vaccine may be influenced by the priming effect of previous influenza vaccinations or exposure to antigenically related influenza viruses. The current study examines the immunogenicity of a clinically licensed TIV in rabbits naive to influenza antigens. Animals were immunized with either the licensed TIV, a bivalent (H1 and H3) HA DNA vaccine or the combination of both. Temporal and peak level serum anti-influenza virus IgG responses were determined by enzyme-linked immunosorbent assay (ELISA). Functional antibody responses were measured by hemagglutination inhibition and microneutralizationagainsteitherA/NewCaledonia//20/99(H1 N1) or A/Panama/2007/99(H3N2) influenza viruses. Our results demonstrate that the immunogenicity of the TIV is low in sero-negative animals. More significantly, the heterologous DNA prime-TIV boost regimen was more immunogenic than the homologous prime-boost using either TIV or DNA vaccines alone. This finding justifies further investigation of HA DNA vaccines as a priming immunogen for the next generation of vaccines against seasonal or pandemic influenza virus infections.

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

Descripteur(s) anglais
Descripteur(s) : Influenzavirus; Genetic vaccine; Inactivated strain; Humoral immunity; Immune response; Serotype; Protein; Influenza
Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Orthomyxoviridae; Virus; Viral disease; Infection
Descripteur(s) français
Descripteur(s) : Influenzavirus; Vaccin genetique; Souche inactivee; Immunite humorale; Reponse immune; Serotype; Proteine; Grippe
Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquee; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Orthomyxoviridae; Virus; Virose; Infection

080342416
PASCAL

Antibody and T-cell responses to a virosomal adjuvanted H9N2 avian influenza vaccine : Impact of distinct additional adjuvants

Titre : Antibody and T-cell responses to a virosomal adjuvanted H9N2 avian influenza vaccine : Impact of distinct additional adjuvants

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Source : Vaccine . 2008; 26 (29-30) : 3640-3646
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Nombre de références : 63 ref.

Résumé : A highly efficacious vaccine is required to counteract a threat of an avian influenza pandemic. Increasing the potency of vaccines by adjuvation is essential not only to overcome generally low immunogenicity of pandemic strains, but also to allow dose sparing and as such to make it feasible to satisfy huge global production demands. In this study we evaluated the ability of four distinct adjuvants to further increase immune responses to a virosomal adjuvanted avian H9N2 influenza vaccine in mice. Currently registered adjuvants aluminium phosphate, aluminium hydroxide and MF59, as well as a novel promising adjuvant MATRIX-M were included in the study. Our results demonstrate that all adjuvants significantly increased the H9N2 haemagglutinin (HA) inhibition and ELISA antibody titers induced with the virosomal adjuvanted vaccine. The adjuvants exhibited different effect on the isotype of virus specific antibodies, with MATRIX-M inducing the most pronounced skewing to IgG2a, i.e. towards Th1 type of response. While the virosomal adjuvanted pandemic influenza vaccine efficiently induced CD4<sup>+ T-cell response, with no further increase upon adjuvation, the CD8<sup>+ T-cell responses induced with virosomal adjuvanted vaccine could be significantly improved upon additional adjuvation with MATRIX-M or MF59. All adjuvants demonstrated a dose sparing effect, i.e. in combination with the virosomal adjuvanted pandemic influenza vaccine they increased immune responses to comparable level independent of the tested vaccine dose. In conclusion, our results demonstrate that immune responses to a virosomal adjuvanted pandemic influenza vaccine can be further enhanced by add-on adjuvants, with MATRIX-M being overall the most potent adjuvant in combination with virosomes, followed by MF59 and finally aluminium-based adjuvants.

Code(s) de classement : 002A05F04

Descripteur(s) anglais
Descripteur(s) : Humoral immunity; Immune response; Cellular immunity; Immunological adjuvant; Vaccine; Avian influenza
Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Infection; Viral disease
Descripteur(s) français
Descripteur(s) : Immunite humorale; Reponse immune; Immunite cellulaire; Adjuvant immunologique; Vaccin; Grippe aviaire
Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquee; Microbiologie; Sciences biologiques; Infection; Virose

080342422
PASCAL

Optimal allocation of pandemic influenza vaccine depends on age, risk and timing

Titre : Optimal allocation of pandemic influenza vaccine depends on age, risk and timing

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Source : Vaccine . 2008; 26 (29-30) : 3742-3749
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Nombre de références : 31 ref.

Résumé : The limited production capacity for vaccines raises the question what the best strategy is for allocating the vaccine to mitigate an influenza pandemic. We developed an age-structured model for spread of an influenza pandemic and validated it against observations from the Asian flu pandemic. Two strategies were evaluated: vaccination can be implemented at the start of the influenza pandemic, or vaccination will be implemented near the peak of it. Our results suggest prioritizing individuals with a high-risk of complications if a vaccine becomes available during a pandemic. If available at the start, vaccinating school children might be considered since this results in slightly lower expected number of deaths.

Code(s) de classement : 002A05F04

Descripteur(s) anglais
Descripteur(s) : Vaccine; Age; Modeling; Models; Influenza
Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Viral disease; Infection
Descripteur(s) français
Descripteur(s) : Vaccin; Age; Modelisation; Modele; Grippe
Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquee; Microbiologie; Sciences biologiques; Virose; Infection

Localisation : INIST, Shelf number 20289, INIST No. 354000161791120260
Origine de la notice : INIST

080342460
PASCAL

High titer growth of human and avian influenza viruses in an immortalized chick embryo cell line without the need for exogenous proteases

Titre : High titer growth of human and avian influenza viruses in an immortalized chick embryo cell line without the need for exogenous proteases

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Source : Vaccine . 2008; 26 (29-30) : 3778-3782
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Nombre de références : 22 ref.

Résumé : The current method of growing influenza virus for vaccine production is through the use ofembryonated chicken eggs. This manufacturing system yields a low concentration of virus per egg, requires significant downstream production for purification, and demands a considerable amount of time for production. We have demonstrated an immortalized chick embryo cell line, termed PBS-1, is capable of growing unmodified recent isolates of human and avian influenza A and B viruses to extremely high titers. In many cases, PBS-1 cells out perform primary chick embryo kidney (CEK) cells, Madin-Darby Canine Kidney (MDCK) cells and African green monkey kidney cells (Vero) in growth of recent influenza isolates. PBS-1 cells are free of any exogenous agents, are non-tumorigenic, and are readily adaptable to a variety of culture conditions, including growth on microcarrier beads. Influenza viruses grown in PBS-1 cells are released into the culture fluid without the need for exogenous proteases, thus simplifying downstream processing. In addition to offering a significant improvement in vaccine production, PBS-1 cells should prove valuable in diagnostics and as a cell line of choice for influenza virus research.

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

Descripteur(s) anglais
Descripteur(s) : Human; Avian influenzavirus; Embryo; Cell line; Peptidases; Vaccine; Influenza
Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Hydrolases; Enzyme; Zoopathogen; Viral disease; Infection
Descripteur(s) français
Descripteur(s) : Homme; Influenzavirus aviaire; Embryon; Lignee cellulaire; Peptidases; Vaccin; Grippe
Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquee; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Hydrolases; Enzyme; Zoopathogene; Virose; Infection

Localisation : INIST, Shelf number 20289, INIST No. 354000161791120310
Origine de la notice : INIST

080348122
PASCAL

Grippe saisonniere, grippe aviaire, grippe pandemique : connaissances et attitudes. 9es Journees Nationales d' Infectiologie. Marseille, 4, 5 et 6 juin 2008; Seasonal influenza, avian influenza, pandemic influenza : knowledge and behavior

Titre : Grippe saisonniere, grippe aviaire, grippe pandemique : connaissances et attitudes. 9es Journees Nationales d' Infectiologie. Marseille, 4, 5 et 6 juin 2008; Seasonal influenza, avian influenza, pandemic influenza : knowledge and behavior

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Source : Medecine et maladies infectieuses Supplement. 2008; 38 (2) : S71-S73
Informations congrès : *Journees Nationales d' Infectiologie, *9, *Marseille France, *2008-06-04
ISSN : 1166-8237
Date de publication : 2008
Pays de publication : France
Langue(s) : French
Type de document : Serial; *Conference-Meeting
Nombre de références : 4 ref.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais
Descripteur(s) : Avian influenza; Knowledge; Attitude; Seasonal variation; Behavior; Tropical medicine; Microbiology
Desc. génériques : Virology; Infectious diseases; Medical sciences; Viral disease; Infection; Epidemiology
Descripteur(s) français
Descripteur(s) : Grippe aviaire; Connaissance; Attitude; Variation saisonniere; Comportement; Medecine tropicale; Microbiologie; Pandemie
Desc. génériques : Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection; Epidemiologie

Localisation : INIST, Shelf number 15434S, INIST No. 354000200278850170
Origine de la notice : INIST

080348126
PASCAL

Grippe aviaire : actualite epidemiologique et veille sanitaire. 9es Journees Nationales d' Infectiologie. Marseille, 4, 5 et 6 juin 2008; Avian influenza in human beings : epidemiological update and monitoring

Titre : Grippe aviaire : actualite epidemiologique et veille sanitaire. 9es Journees Nationales d' Infectiologie. Marseille, 4, 5 et 6 juin 2008; Avian influenza in human beings : epidemiological update and monitoring

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Source : Medecine et maladies infectieuses Supplement. 2008; 38 (2) : S124-S125
Informations congrès : *Journees Nationales d' Infectiologie, *9, *Marseille France, *2008-06-04
ISSN : 1166-8237
Date de publication : 2008
Pays de publication : France
Langue(s) : French
Type de document : Serial; *Conference-Meeting

Code(s) de classement : 002B05C02C

Descripteur(s) anglais
Descripteur(s) : Avian influenza; Epidemiology; Surveillance; Human; Tropical medicine; Microbiology
Desc. génériques : Virology; Infectious diseases; Medical sciences; Viral disease; Infection
Descripteur(s) français
Descripteur(s) : Grippe aviaire; Epidemiologie; Surveillance; Homme; Medecine tropicale; Microbiologie; Pandemie
Desc. génériques : Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection

Localisation : INIST, Shelf number 15434S, INIST No. 354000200278850330
Origine de la notice : INIST

The potential of a protease activation mutant of a highly pathogenic avian influenza virus for a pandemic live vaccine

Titre : The potential of a protease activation mutant of a highly pathogenic avian influenza virus for a pandemic live vaccine

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Source : Vaccine . 2008; 26 (7) : 956-965
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Nombre de références : 36 ref.

Résumé : The most effective countermeasure against a pandemic originating from a highly pathogenic avian influenza virus (HPAIV) is immunoprophylaxis of the human population. We present here a new approach for the development of a pandemic HPAIV live vaccine. Using reverse genetics, we replaced the polybasic hemagglutinin cleavage site of an H7N7 HPAIV with an elastase motif. This mutant was strictly elastase-dependent, grew equally well as the wild-type in cell culture and was attenuated in mice unlike the lethal wild-type. Immunization at 10<sup>6pfu dosage protected mice against disease and induced sterile immunity; vaccination with homosubtypic or heterosubtypic reassortants led to cross-protection. These observations demonstrate that a mutated hemagglutinin requiring elastase cleavage can serve as an attenuating component of a live vaccine against HPAIV.

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

Descripteur(s) anglais
Descripteur(s) : Avian influenzavirus; Influenza A virus; Inactivated strain; Mutation; Pathogenicity; Vaccine; Genetics; Influenza
Desc. génériques : Virology; Microbiology; Biological sciences; Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen; Viral disease; Infection
Descripteur(s) français
Descripteur(s) : Influenzavirus aviaire; Virus grippal A; Souche inactivee; Mutation; Pouvoir pathogene; Vaccin; Genetique; Grippe
Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Immunologie; Pharmacologie; Microbiologie appliquee; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogene; Virose; Infection

Localisation : INIST, Shelf number 20289, INIST No. 354000161886670120
Origine de la notice : INIST

080369815
PASCAL

La grippe H5N1. Conferences du centenaire de la SPE. 20-21 juin 2008, Paris; Asia : Avian influenza H5N1

Titre : La grippe H5N1. Conferences du centenaire de la SPE. 20-21 juin 2008, Paris; Asia : Avian influenza H5N1

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Source : Bulletin de la Societe de pathologie exotique. 2008; 101 (3) : 238-242
Informations congrès : *Conferences du centenaire de la SPE (Societe de Pathologie Exotique), *Paris France, *2008-06-20
ISSN : 0037-9085
CODEN : BSPEAM
Date de publication : 2008
Pays de publication : France
Langue(s) : French
Langue(s) du résumé : English
Type de document : Serial; *Conference-Meeting
Nombre de références : 23 ref.

Résumé : L' emergence des premiers cas humains de grippe aviaire a Hong Kong en 1997 a fait resurgir la crainte d' une nouvelle pandemie venue du continent asiatique. Malgre une mobilisation internationale considerable visant d' abord a l' eradiquer, puis a limiter sa diffusion, le virus aviaire hautement pathogene A/H5N 1 a pu se propager en Asie, en Europe et en Afrique par des flambees epizootiques successives affectant les oiseaux migrateurs et les oiseaux d' elevage La transmission de l' animal a l' homme reste peu frequente, mais l' infection est redoutable avec un taux de letalite superieur a 60 % des cas confirmes. Pres de la moitie des pays touches par l' epizootie est en Asie. Avec 87 % des cas confirmes dans le monde et 91 % des deces, c' est aussi le continent qui paye le plus lourd tribut humain. Comme les pays voisins du Sud-Est asiatique, le Cambodge a ete plusieurs fois touche par la grippe aviaire au cours des dernieres annees. Les mesures appliquees pour enrayer la propagation du virus A/H5N1 dans les elevages avicoles, pour changer le comportement des eleveurs et pour assainir le commerce des volailles illustrent toute la complexite de la lutte contre cette zoonose. Parallelement, la mise en place d' une surveillance de la grippe chez l' homme, reposant sur un systeme de declaration et sur un reseau d' hopitaux sentinelles connectes a l' Institut Pasteur du Cambodge, place ce petit pays au coeur du grand dispositif international dont la vigilance devrait permettre de detecter dans les meilleurs delais tout evenement mutationnel pouvant aboutir a l' emergence d' un variant pandemique.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais
Descripteur(s) : Avian influenza; Influenza A; South east Asia; Epizootics; Surveillance; Epidemiology; Public health; Cambodia; Tropical medicine; Influenzavirus AH5N1
Desc. génériques : Virology; Infectious diseases; Medical sciences; Viral disease; Infection; Asia
Descripteur(s) français
Descripteur(s) : Grippe aviaire; Grippe A; Asie du sud est; Epizootie; Surveillance; Epidemiologie; Sante publique; Cambodge; Medecine tropicale; Influenzavirus AH5N1
Desc. génériques : Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection; Asie

Localisation : INIST, Shelf number 832, INIST No. 354000198078420050
Origine de la notice : INIST

080368877
PASCAL

Concerns of using sialidase fusion protein as an experimental drug to combat seasonal and pandemic influenza

Titre : Concerns of using sialidase fusion protein as an experimental drug to combat seasonal and pandemic influenza

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Source : Journal of antimicrobial chemotherapy Print. 2008; 62 (2) : 219-223
ISSN : 0305-7453
CODEN : JACHDX
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Nombre de références : 38 ref.

Résumé : Sialidase fusion protein is reported to have great potential to combat seasonal and pandemic influenza, because it may prevent influenza virus infection by removing all sialic acid receptors from host cells. Meanwhile, recent studies have demonstrated that absence of a2-6 sialic acid does not protect a cell from influenza infection, and influenza virus can infect desialylated cells, suggesting that accessible surface sialic acid is dispensable for influenza virus infection. In addition, studies using animal models have shown that neuraminidase promotes adherence and invasion of Streptococcus pneumoniae, because cleavage of sialic acid from host cells exposes cryptic receptors for S. pneumoniae. The purpose of this article is to comment on the benefits and potential risks of using sialidase fusion protein as an experimental drug to combat seasonal and pandemic influenza.

Code(s) de classement : 002B02S; 002B05C02C; 002B05B02E

Descripteur(s) anglais
Descripteur(s) : Exo <alpha> sialidase; Fusion protein; Drug; Seasonal variation; Influenza; Influenzavirus; Secondary; Bacterial pneumonia; Animal model
Desc. génériques : Infectious diseases; Pharmacology; Medical sciences; Virology; Infectious diseases; Medical sciences; Pneumology; Respiratory system; Bacteriology; Infectious diseases; Medical sciences; Glycosidases; Glycosylases; Hydrolases; Enzyme; Viral disease; Infection; Orthomyxoviridae; Virus; Respiratory disease; Lung disease
Descripteur(s) français
Descripteur(s) : Exo <alpha> sialidase; Proteine fusion; Medicament; Variation saisonniere; Grippe; Influenzavirus; Secondaire; Pneumonie bacterienne; Modele animal; Pandemie
Desc. génériques : Maladies infectieuses; Pharmacologie; Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Pneumologie; Appareil respiratoire; Bacteriologie; Maladies infectieuses; Sciences medicales; Glycosidases; Glycosylases; Hydrolases; Enzyme; Virose; Infection; Orthomyxoviridae; Virus; Pathologie de l' appareil respiratoire; Pathologie des poumons

Localisation : INIST, Shelf number 17084, INIST No. 354000197702480020
Origine de la notice : INIST

080363614
PASCAL

Modelling control measures to reduce the impact of pandemic influenza among schoolchildren

Titre : Modelling control measures to reduce the impact of pandemic influenza among schoolchildren

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Source : Epidemiology and infection. 2008; 136 (8) : 1035-1045
ISSN : 0950-2688
CODEN : EPINEU
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Nombre de références : 37 ref.

Résumé : We coupled the Wells-Riley equation and the susceptible-exposed-infected-recovery (SEIR) model to quantify the impact of the combination of indoor air-based control measures of enhanced ventilation and respiratory masking in containing pandemic influenza within an elementary school. We integrated indoor environmental factors of a real elementary school and aetiological characteristics of influenza to estimate the age-specific risk of infection (P) and basic reproduction number (R<sub>0). We combined the enhanced ventilation rates of 0.5, 1, 1.5, and 2/h and respiratory masking with 60%, 70%, 80%, and 95% efficacies, respectively, to predict the reducing level of R<sub>0. We also took into account the critical vaccination coverage rate among schoolchildren. Age-specific P and R<sub>0 were estimated respectively to be 0.29 and 16.90; 0.56 and 16.11; 0.59 and 12.88; 0.64 and 16.09; and 0.07 and 2.80 for five age groups 4-6, 7-8, 9-10, 11-12, and 25-45 years, indicating pre-schoolchildren have the highest transmission potential. We conclude that our integrated approach, employing the mechanism of transmission of indoor respiratory infection, population-dynamic transmission model, and the impact of infectious control programmes, is a powerful tool for risk profiling prediction of pandemic influenza among schoolchildren.

Code(s) de classement : 002A05

Descripteur(s) anglais
Descripteur(s) : School age; Microbiology; Epidemiology; Human; Influenza
Desc. génériques : Microbiology; Biological sciences; Viral disease; Infection
Descripteur(s) français
Descripteur(s) : Age scolaire; Microbiologie; Epidemiologie; Homme; Grippe
Desc. génériques : Microbiologie; Sciences biologiques; Virose; Infection

Localisation : INIST, Shelf number 6056, INIST No. 354000197611550040
Origine de la notice : INIST

Asparagine 631 Variants of the Chicken Mx Protein Do Not Inhibit Influenza Virus Replication in Primary Chicken Embryo Fibroblasts or In Vitro Surrogate Assays

Titre : Asparagine 631 Variants of the Chicken Mx Protein Do Not Inhibit Influenza Virus Replication in Primary Chicken Embryo Fibroblasts or In Vitro Surrogate Assays

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Source : Journal of virology. 2008; 82 (15) : 7533-7539
ISSN : 0022-538X
Date de publication : 2008
Pays de publication : United States
Langue(s) : English
Type de document : Serial
Nombre de références : 43 ref.

Résumé : Whether chicken Mx inhibits influenza virus replication is an important question with regard to strategies aimed at enhancing influenza resistance in domestic flocks. The Asn631 polymorphism of the chicken Mx protein found in the Shamo (SHK) chicken line was previously reported to be crucial for the antiviral activity of this highly polymorphic chicken gene. Our aims were to determine whether cells from commercial chicken lines containing Asn631 alleles were resistant to influenza virus infection and to investigate the effects that other polymorphisms might have on Mx function. Unexpectedly, we found that the Asn631 genotype had no impact on multicycle replication of influenza virus (A/WSN/33 H1N1) in primary chicken embryo fibroblast lines. Furthermore, expression of the Shamo (SHK) chicken Mx protein in transfected 293T cells did not inhibit viral gene expression (A/PR/8/34 H1N1, A/Duck/England/62 H4N6, and A/Duck/Singapore/97 H5N3). Lastly, in minireplicon systems (A/PR/8/34 and A/Turkey/England/50-92/91 H5N1), which were highly sensitive to inhibition by the murine Mxl and human MxA proteins, respectively, Shamo chicken Mx also proved ineffective in the context of avian as well as mammalian cell backgrounds. Our findings demonstrate that Asn631 chicken Mx alleles do not inhibit influenza virus replication of the five strains tested here and efforts to increase the frequency of Asn631 alleles in commercial chicken populations are not warranted. Nevertheless, chicken Mx variants with anti-influenza activity might still exist. The flow cytometry and minireplicon assays described herein could be used as efficient functional screens to identify such active chicken Mx alleles.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Descripteur(s) : Chicken; Influenzavirus; Asparagine; Replication; Embryo; Fibroblast; In vitro; Virology
Desc. génériques : Virology; Microbiology; Biological sciences; Aves; Vertebrata; Orthomyxoviridae; Virus; Veterinary
Descripteur(s) français
Descripteur(s) : Poulet; Influenzavirus; Asparagine; Replication; Embryon; Fibroblaste; In vitro; Virologie; Proteine Mx
Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Aves; Vertebrata; Orthomyxoviridae; Virus; Veterinaire

Localisation : INIST, Shelf number 13592, INIST No. 354000200359610280
Origine de la notice : INIST

080360539
PASCAL

Genetic diversity-independent neutralization of pandemic viruses (e.g. HIV), potentially pandemic (e.g. H5N1 strain of influenza) and carcinogenic (e.g. HBV and HCV) viruses and possible agents of bioterrorism (variola) by enveloped virus neutralizing compounds (EVNCs). Genetic and Immune Correlates of the HIV Infection and Vaccine-Induced Immunity

Titre : Genetic diversity-independent neutralization of pandemic viruses (e.g. HIV), potentially pandemic (e.g. H5N1 strain of influenza) and carcinogenic (e.g. HBV and HCV) viruses and possible agents of bioterrorism (variola) by enveloped virus neutralizing compounds (EVNCs). Genetic and Immune Correlates of the HIV Infection and Vaccine-Induced Immunity

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Source : Vaccine . 2008; 26 (24) : 3055-3058
Informations congrès : *International Symposium Genetic and Immune Correlates of the HIV Infection and Vaccine-Induced Immunity, *1, *Budapest Hungary, *2007-06-10
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial; *Conference-Meeting
Nombre de références : 18 ref.

Résumé : Genetic diversity and hypermutation contribute to difficulties in developing a vaccine against viruses like HIV and influenza. There are currently no known immune correlates of protection against HIV. This has made the development of a vaccine against HIV that would provide sterilizing immunity in the near future an impossible task. The abandonment of a recent AIDS vaccine human trial due to a failure to elicit a protective sterilising immune response confirms that empirical attempts to develop a vaccine may result in failures. Also the difficulty in predicting the next pandemic strain of influenza may make it difficult to respond rapidly should there be an outbreak. Therefore, it is time to explore broad spectrum agents that can target either the lipid portion of the envelope or the sugar moieties of the glycoproteins or the rafts (regions within viral and cell envelopes where a higher concentration of the glycoproteins exist). Broad spectrum agents that can serve as disrafters or neutralize the viral infectivity by binding to the envelope lipid or sugar moieties will not be affected by the vagaries of hypermutation of surface antigens. This is because the post-translation modification is a host function. Presented here is a review of recently reported agents present in pomegranate juice (polyphenols, beta-sitosterol, sugars and ellagic acid) and fulvic acid, described here as the envelope virus neutralising compounds (EVNCs) and complex molecules like lectins and mucins. Pomegranate juice was previously reported to inactivate HIV and further shown by our group to inactivate influenza, herpes viruses and poxviruses. A formulation consisting of fulvic acid, a complex mixture of compounds was previously reported to render vaccinia virus, HIV and SARS virus non-infectious. Recently, both fulvic acid and pomegranate juice have been shown to inactivate genetically diverse strains of influenza including H5N1, further confirming the broad spectrum nature of these agents. How EVNCs will be used in developing a vaccine achieving sterilizing immunity or prophylaxis needs to be researched. <Copyright> 2007 Elsevier Ltd. All rights reserved.

Code(s) de classement : 002A05F04; 002A05C10; 002B04

Descripteur(s) anglais

Descripteur(s) : Human immunodeficiency virus; Hepatitis B virus; Hepatitis C virus; Variola virus; Genetic diversity; Neutralization; Strain; Carcinogen; Bioterrorism; Hemagglutinin; Subtype; Treatment; Influenza

Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Oncology; Medical sciences; Lentivirus; Retroviridae; Virus; Orthohepadnavirus; Hepadnaviridae; Hepacivirus; Flaviviridae; Orthopoxvirus; Chordopoxvirinae; Poxviridae; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Virus immunodeficience humaine; Virus hepatite B; Virus hepatite C; Virus variole; Diversite genetique; Neutralisation; Souche; Carcinogene; Bioterrorisme; Hemagglutinine; Soustype; Traitement; Grippe

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquee; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Cancerologie; Sciences medicales; Lentivirus; Retroviridae; Virus; Orthohepadnavirus; Hepadnaviridae; Hepacivirus; Flaviviridae; Orthopoxvirus; Chordopoxvirinae; Poxviridae; Virose; Infection

Localisation : INIST, Shelf number 20289, INIST No. 354000197887780110
Origine de la notice : INIST

Acute Respiratory Infections in a Recently Arrived Traveler to Your Part of the World

Titre : Acute Respiratory Infections in a Recently Arrived Traveler to Your Part of the World

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Source : Chest . 2008; 134 (1) : 163-171
ISSN : 0012-3692
CODEN : CHETBF
Date de publication : 2008
Pays de publication : United States
Langue(s) : English
Type de document : Serial
Nombre de références : 69 ref.

Résumé : Many acute infectious pulmonary diseases have incubation periods that are long enough for travelers to have symptoms after returning home to a health-care system that is not familiar with "foreign" infections. Respiratory infections have a relatively limited repertoire of clinical manifestations, so that there is often nothing characteristic enough about a specific infection to make the diagnosis obvious. Thus, the pathway to the diagnosis of infections that are not endemic in a region relies heavily on taking a thorough history of both itinerary and of specific exposures. One important caveat is that on occasion, the history of a recent trip creates an element of "tunnel vision" in the evaluating health-care provider. It is tempting to relate a person's problem to that recent trip; however, when evaluating recent returnees, it is always important to remember that the travel may have nothing to do with the patient's presentation. Recent travel may add diagnostic considerations to the list of possibilities, but an astute clinician must not disregard the possibility that the patient's illness has nothing to do with the recent trip.

Code(s) de classement : 002B11; 002B12; 002B05C02C; 002B05D02K3

Descripteur(s) anglais
Descripteur(s) : Infection; Avian influenza; Coccidioidomycosis; Histoplasmosis; Legionellosis; Loeffler syndrome; Melioidosis; Plague; Acute; Human; Travel; World; Airplane; Toxicity; Safety; Complication; Psittacosis; Q fever; Schistosomiasis; Sin Nombre virus; Eosinophilia; Tuberculosis; Anesthesia; Circulatory system; Cardiology; Hantavirus pulmonary syndrome
Desc. génériques : Pneumology; Respiratory system; Medical sciences; Cardiovascular system; Medical sciences; Virology; Infectious diseases; Medical sciences; Mycology; Infectious diseases; Medical sciences; Viral disease; Mycosis; Bacteriosis; Yersiniosis; Chlamydiosis; Rickettsial infection; Rickettsialosis; Trematode disease; Helminthiasis; Parasitosis; Hantavirus; Bunyaviridae; Virus; Mycobacterial infection; Respiratory disease; Immunopathology; Lung disease; Hemopathy
Descripteur(s) français
Descripteur(s) : Infection; Grippe aviaire; Coccidioidomycose; Histoplasmose; Legionellose; Syndrome de Loeffler; Melioidose; Peste; Aigu; Homme; Voyage; Monde; Avion; Toxicite; Securite; Complication; Psittacose; Fievre Q; Schistosomiase; Virus Sin Nombre; Eosinophilie; Tuberculose; Anesthesie; Appareil circulatoire; Cardiologie; Syndrome pulmonaire a hantavirus
Desc. génériques : Pneumologie; Appareil respiratoire; Sciences medicales; Systeme cardiovasculaire; Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Mycologie; Maladies infectieuses; Sciences medicales; Virose; Mycose; Bacteriose; Yersiniose; Chlamydiose; Rickettsiose; Rickettsialose; Trematodose; Helminthiase; Parasitose; Hantavirus; Bunyaviridae; Virus; Mycobacteriose; Pathologie de l' appareil respiratoire; Immunopathologie; Pathologie des poumons; Hemopathie

Localisation : INIST, Shelf number 7627, INIST No. 354000197664770220

080359102
PASCAL

The Spanish flu in Denmark

Titre : The Spanish flu in Denmark

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Source : Scandinavian journal of infectious diseases. 2008; 40 (6-7) : 538-546
ISSN : 0036-5548
CODEN : SJIDB7
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Nombre de références : 44 ref.

Résumé : The spread of H5N1 influenza and the similarity between this avian virus and the Spanish flu virus causes fear of a new influenza pandemic, but data from the Spanish flu may also be of guidance in planning for preventive measures. Using data on influenza cases, influenza deaths and total deaths for Denmark and for Danish towns from 1917 to 1921, and population data from the 1916 and 1921 censuses, we analysed incident cases, cumulative, age-specific and age-standardized rates. Overall, more than 900,000 persons contracted flu during the y 1918-1920, and 1 out of 50 patients died from the disease. An early wave of the flu occurred in the capital and major towns, but not in peripheral towns. Influenza incidence in 1918 peaked at age 5-15 y, closely followed by the age groups 1-5 y and 15-65 y, but the influenza mortality was highest in the age groups 0-1 y and 15-65 y, with a peak mortality at age 20-34 y producing a W curve for mortality by age. The background for the better outcome in children aged 1-15 y as well as for the disease immunity in the elderly population should be further investigated.

Code(s) de classement : 002B05C

Descripteur(s) anglais
Descripteur(s) : Denmark; Infection; Microbiology; Spanish flu
Desc. génériques : Virology; Infectious diseases; Medical sciences; Europe; Viral disease
Descripteur(s) français
Descripteur(s) : Danemark; Infection; Microbiologie; Grippe espagnole
Desc. génériques : Virologie; Maladies infectieuses; Sciences medicales; Europe; Virose

Localisation : INIST, Shelf number 14662, INIST No. 354000197598520150
Origine de la notice : INIST

080357879
PASCAL

Rapid isothermal detection assay : a probe amplification method for the detection of nucleic acids

Titre : Rapid isothermal detection assay : a probe amplification method for the detection of nucleic acids

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Source : Diagnostic microbiology and infectious disease. 2008; 60 (2) : 133-141
ISSN : 0732-8893
CODEN : DMIDDZ
Date de publication : 2008
Pays de publication : United States
Langue(s) : English
Type de document : Serial
Nombre de références : 3/4 p.

Résumé : Simple, accurate, and stable diagnostic tests are essential to control viral infectious diseases such as avian influenza virus. The current technologies are often inaccessible to people who need them, mainly because of the specialized equipment and the need for highly trained technologists. Here, we describe a rapid isothermal nucleic acid detection assay (RIDA) that can be used to detect both DNA and RNA targets. Using chemically modified probes, we designed a lateral-flow (LF) immunoassay that can be used in combination with RIDA for equipment-free nucleic acid target detection. RIDA is a "probe amplification" assay that uses the single-strand nicking activity of restriction nicking endonucleases to repeatedly cleave synthetic probes hybridizing to the same target sequences. In the RIDA-LF combined assay, chemically labeled probes are covalently conjugated to magnetic microbeads, which is propitious to separate cleaved probes from the reaction solution. The cleaved probes in the solution are then detected with an LF immunoassay. The real-time assay shows that RIDA is able to specifically detect target sequences in 5 to 15 min. The RIDA-LF combined assay can specifically detect nucleic acid targets without sophisticated equipment. In this report, our data suggest that RIDA is a flexible simple assay that could be applied for point-of-care detection. The modified-RIDA described in this report further extends the application of this technology.

Code(s) de classement : 002A05B14

Descripteur(s) anglais
Descripteur(s) : Bacteria; Detection; Amplification; Method; Nucleic acid
Desc. génériques : Bacteriology; Microbiology; Biological sciences
Descripteur(s) français
Descripteur(s) : Bacterie; Detection; Amplification; Methode; Acide nucleique
Desc. génériques : Bacteriologie; Microbiologie; Sciences biologiques

Localisation : INIST, Shelf number 20217, INIST No. 354000161894180010
Origine de la notice : INIST

080357436
PASCAL

Epidemiologic Characterization of the 1918 Influenza Pandemic Summer Wave in Copenhagen : Implications for Pandemic Control Strategies

Titre : Epidemiologic Characterization of the 1918 Influenza Pandemic Summer Wave in Copenhagen : Implications for Pandemic Control Strategies

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Source : The Journal of infectious diseases. 2008; 197 (2) : 270-278
ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2008
Pays de publication : United States
Langue(s) : English
Type de document : Serial
Nombre de références : 39 ref.

Résumé : Background. The 1918-1919 A/H1N1 influenza pandemic killed <equivalent sign>50 million people worldwide. Historical records suggest that an early pandemic wave struck Europe during the summer of 1918. Methods. We obtained surveillance data that were compiled weekly, during 1910-1919, in Copenhagen, Denmark; the records included medically treated influenza-like illnesses (ILIs), hospitalizations, and deaths by age. We used a Serfling seasonal regression model to quantify excess morbidity and mortality, and we estimated the reproductive number (R) for the summer, fall, and winter pandemic waves. Results. A large epidemic occurred in Copenhagen during the summer of 1918; the age distribution of deaths was characteristic of the 1918-1919 A/H1N1 pandemic overall. That summer wave accounted for 29%-34% of all excess ILIs and hospitalizations during 1918, whereas the case-fatality rate (0.3%) was many-fold lower than that of the fall wave (2.3%). Similar patterns were observed in 3 other Scandinavian cities. R was substantially higher in summer (2.0-5.4) than in fall (1.2-1.6) in all cities. Conclusions. The Copenhagen summer wave may have been caused by a precursor A/H 1 N 1 pandemic virus that transmitted efficiently but lacked extreme virulence. The R measured in the summer wave is likely a better approximation of transmissibility in a fully susceptible population and is substantially higher than that found in previous US studies. The summer wave may have provided partial protection against the lethal fall wave.

Code(s) de classement : 002A05B11

Descripteur(s) anglais
Descripteur(s) : Epidemic; Epidemiology; Influenza
Desc. génériques : Bacteriology; Microbiology; Biological sciences; Viral disease; Infection
Descripteur(s) français
Descripteur(s) : Epidemie; Epidemiologie; Grippe
Desc. génériques : Bacteriologie; Microbiologie; Sciences biologiques; Virose; Infection

Localisation : INIST, Shelf number 2052, INIST No. 354000183428250120
Origine de la notice : INIST

The relationship between encephalitis lethargica and influenza : A critical analysis

Titre : The relationship between encephalitis lethargica and influenza : A critical analysis

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Source : Journal of neurovirology. 2008; 14 (3) : 177-185
ISSN : 1355-0284
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Nombre de références : 2 p.1/2

Résumé : Since encephalitis lethargica's (EL) prevalence in the 1920s, epidemiologic and clinical debate has persisted over whether EL was caused by, potentiated by, or merely coincident with the Spanish influenza pandemic. Epidemiologic analyses generally suggest that the disorders were coincidental. Beginning in the 1970s, modern experiments on archival brain samples mainly failed to confirm a direct relationship between influenza and EL. These experimental studies have technical limitations, e.g., the appropriateness of antibodies, polymerase chain reaction (PCR) primers and controls, and the extreme paucity and age of available material. These factors render the case against influenza less decisive than currently perceived. Nevertheless, there is little direct evidence supporting influenza in the etiology of EL. Almost 100 years after the EL epidemic, its etiology remains enigmatic, raising the possibility of a recurrence of EL in a future influenza pandemic.

Code(s) de classement : 002B05C02A; 002B05C02C

Descripteur(s) anglais
Descripteur(s) : Encephalitis; Avian influenza; Nervous system diseases; Influenza A; Epidemic
Desc. génériques : Neurology; Nervous system; Virology; Infectious diseases; Medical sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection; Cerebral disorder; Central nervous system disease
Descripteur(s) français
Descripteur(s) : Encephalite; Grippe aviaire; Pathologie du systeme nerveux; Grippe A; Epidemie
Desc. génériques : Neurologie; Systeme nerveux; Virologie; Maladies infectieuses; Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection; Pathologie de l' encephale; Pathologie du systeme nerveux central

Localisation : INIST, Shelf number 26734, INIST No. 354000196399300010
Origine de la notice : INIST

080372386
PASCAL

Positive selection at the receptor-binding site of haemagglutinin H5 in viral sequences derived from human tissues

Titre : Positive selection at the receptor-binding site of haemagglutinin H5 in viral sequences derived from human tissues

Auteur(s) : KONGCHANAGUL Alita; SUPTAWIWAT Ornpreya; KANRAI Pumaree; UIPRASERTKUL Mongkol; PUTHAVATHANA Pilaipan; AUEWARAKUL Prasert
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Source : Journal of general virology. 2008; 89 (p. 8) : 1805-1810
ISSN : 0022-1317
CODEN : JGVIAY
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Nombre de références : 3/4 p.

Résumé : Highly pathogenic H5N1 avian influenza virus has spread through at least 45 countries in three continents. Despite the ability to infect and cause severe disease in humans, the virus cannot transmit efficiently from human to human. The lack of efficient transmission indicates the incompletion of the adaptation of the avian virus to the new host species. The required mutations for the complete adaptation and the emergence of a potential pandemic virus are likely to originate and be selected within infected human tissues. Differential receptor preference plays an important role in the species-tropism of avian influenza. We have analysed quasispecies of sequences covering the receptor-binding domain of the haemagglutinin gene of H5N1 viruses derived from fatal human cases. We employed a likelihood ratio test to identify positive-selection sites within the quasispecies. Nine of seventeen positive-selection sites identified in our analyses were found to be located within or flanking the receptor-binding domain. Some of these mutations are known to alter receptor-binding specificity. This suggests that our approach could be used to screen for mutations with significant functional impact. Our data provide new candidate mutations for the viral adaptation to a human host, and a new approach to search for new genetic markers of potential pandemic viruses.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Descripteur(s) : Human; Biological receptor; Binding site; Hemagglutinin; Microbiology
Desc. génériques : Virology; Microbiology; Biological sciences
Descripteur(s) français
Descripteur(s) : Homme; Recepteur biologique; Site fixation; Hemagglutinine; Microbiologie
Desc. génériques : Virologie; Microbiologie; Sciences biologiques

Localisation : INIST, Shelf number 13533, INIST No. 354000197723190020
Origine de la notice : INIST

080412134
PASCAL

Genotypic diversity of H5N1 highly pathogenic avian influenza viruses

Titre : Genotypic diversity of H5N1 highly pathogenic avian influenza viruses

Auteur(s) : ZHAO Zi Ming; SHORTRIDGE Kennedy F; GARCIA Maricarmen; YI GUAN; WAN Xiu Feng
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Source : Journal of general virology. 2008; 89 (p. 9) : 2182-2193
ISSN : 0022-1317
CODEN : JGVIAY
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Nombre de références : 3/4 p.

Résumé : Besides enormous economic losses to the poultry industry, recent H5N1 highly pathogenic avian influenza viruses (HPAIVs) originating in eastern Asia have posed serious threats to public health. Up to April 17, 2008, 381 human cases had been confirmed with a mortality of more than 60%. Here, we attempt to identify potential progenitor genes for H5N1 HPAIVs since their first recognition in 1996; most were detected in the Eurasian landmass before 1996. Combinations among these progenitor genes generated at least 21 reassortants (named H5N1 progenitor reassortant, H5N1-PR1-21). H5N1-PR1 includes A/Goose/Guangdong/1/1996(H5N1). Only reassortants H5N1-PR2 and H5N1-PR7 were associated with confirmed human cases: H5N1-PR2 in the Hong Kong H5N1 outbreak in 1997 and H5N1-PR7 in laboratory confirmed human cases since 2003. H5N1-PR7 also contains a majority of the H5N1 viruses causing avian influenza outbreaks in birds, including the first wave of genotype Z, Qinghai-like and Fujian-like virus lineages. Among the 21 reassortants identified, 13 are first reported here. This study illustrates evolutionary patterns of H5N1 HPAIVs, which may be useful toward pandemic preparedness as well as avian influenza prevention and control.

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

Descripteur(s) anglais
Descripteur(s) : Avian influenzavirus; Pathogenicity; Microbiology; Influenzavirus AH5N1
Desc. génériques : Virology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus
Descripteur(s) français
Descripteur(s) : Influenzavirus aviaire; Pouvoir pathogene; Microbiologie; Influenzavirus AH5N1
Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST, Shelf number 13533, INIST No. 354000196332970150
Origine de la notice : INIST

080411833
PASCAL

Influenza Virus Protecting RNA : an Effective Prophylactic and Therapeutic Antiviral

Titre : Influenza Virus Protecting RNA : an Effective Prophylactic and Therapeutic Antiviral

Auteur(s) : DIMMOCK Nigel J; RAINSFORD Edward W; SCOTT Paul D; MARRIOTT Anthony C
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Source : Journal of virology. 2008; 82 (17) : 8570-8578
ISSN : 0022-538X
Date de publication : 2008
Pays de publication : United States
Langue(s) : English
Type de document : Serial
Nombre de références : 32 ref.

Résumé : Another influenza pandemic is inevitable, and new measures to combat this and seasonal influenza are urgently needed. Here we describe a new concept in antivirals based on a defined, naturally occurring defective influenza virus RNA that has the potential to protect against any influenza A virus in any animal host. This "protecting RNA" (244 RNA) is incorporated into virions which, although noninfectious, deliver the RNA to those cells of the respiratory tract that are naturally targeted by infectious influenza virus. A 120-ng intranasal dose of this 244 protecting virus completely protected mice against a simultaneous challenge of 10 50% lethal doses with influenza A/WSN (H1N1) virus. The 244 virus also protected mice against strong challenge doses of all other subtypes tested (i.e., H2N2, H3N2, and H3N8). This prophylactic activity was maintained in the animal for at least 1 week prior to challenge. The 244 virus was 10- to 100-fold more active than previously characterized defective influenza A viruses, and the protecting activity was confirmed to reside in the 244 RNA molecule by recovering a protecting virus entirely from cloned cDNA. There was a clear therapeutic benefit when the 244 virus was administered 24 to 48 h after a lethal challenge, an effect which has not been previously observed with any defective virus. Protecting virus reduced, but did not abolish, replication of challenge virus in mouse lungs during both prophylactic and therapeutic treatments. Protecting virus is a novel antiviral, having the potential to combat human influenza virus infections, particularly when the infecting strain is not known or is resistant to antiviral drugs.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Descripteur(s) : Influenzavirus; Prevention; Treatment; Antiviral; Virology
Desc. génériques : Virology; Microbiology; Biological sciences; Orthomyxoviridae; Virus
Descripteur(s) français
Descripteur(s) : Influenzavirus; Prevention; Traitement; Antiviral; Virologie
Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Orthomyxoviridae; Virus

Localisation : INIST, Shelf number 13592, INIST No. 354000196331490320
Origine de la notice : INIST

080411056
PASCAL

The 1918 "Spanish Flu" in Spain

Titre : The 1918 "Spanish Flu" in Spain

Auteur(s) : TRILLA Antoni; TRILLA Guillem; DAER Carolyn
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Source : Clinical infectious diseases. 2008; 47 (5) : 668-673
ISSN : 1058-4838
CODEN : CIDIEL
Date de publication : 2008
Pays de publication : United States
Langue(s) : English
Type de document : Serial
Nombre de références : 40 ref.

Résumé : The 1918-1919 influenza pandemic was the most devastating epidemic in modern history. Here, we review epidemiological and historical data about the 1918-1919 influenza epidemic in Spain. On 22 May 1918, the epidemic was a headline in Madrid's ABC newspaper. The infectious disease most likely reached Spain from France, perhaps as the result of the heavy railroad traffic of Spanish and Portuguese migrant workers to and from France. The total numbers of persons who died of influenza in Spain were officially estimated to be 147,114 in 1918, 21,235 in 1919, and 17,825 in 1920. However, it is likely that >260,000 Spaniards died of influenza; 75% of these persons died during the second period of the epidemic, and 45% died during October 1918 alone. The Spanish population growth index was negative for 1918 (net loss, 83,121 persons). Although a great deal of evidence indicates that the 1918 A(H1N1) influenza virus unlikely originated in and spread from Spain, the 1918-1919 influenza pandemic will always be known as the Spanish flu.

Code(s) de classement : 002B05C

Descripteur(s) anglais
Descripteur(s) : Spain; Infection; Spanish flu
Desc. génériques : Virology; Infectious diseases; Medical sciences; Europe; Viral disease
Descripteur(s) français
Descripteur(s) : Espagne; Infection; Grippe espagnole
Desc. génériques : Virologie; Maladies infectieuses; Sciences medicales; Europe; Virose

Localisation : INIST, Shelf number 18407, INIST No. 354000197471050100
Origine de la notice : INIST

080409785
PASCAL

Factors associated with case fatality of human H5N1 virus infections in Indonesia : a case series. Commentary

Titre : Factors associated with case fatality of human H5N1 virus infections in Indonesia : a case series. Commentary

Auteur(s) : BIRD Sheila M, comment; FARRAR Jeremy, comment; NYOMAN KANDUN I; TRESNANINGSIH Erna; PURBA Wilfried H; LEE Vernon; SAMAAN Gina; HARUN Syahrial; SONI Eka; SEPTIAWATI Chita; SETIAWATI Tetty; SARIWATI Elvieda; WANDRA Toni
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Source : Lancet British edition. 2008; 372 (9640) : 696-697, 744-749 8 p.
ISSN : 0140-6736
CODEN : LANCAO
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Type de document : article; comments
Nombre de références : 29 ref.

Résumé : Background Indonesia has had the most human cases of highly pathogenic avian influenza A (H5N1) and one of the highest case-fatality rates worldwide. We described the factors associated with H5N1 case-fatality in Indonesia. Methods Between June, 2005, and February, 2008, there were 127 confirmed H5N1 infections. Investigation teams were deployed to investigate and manage each confirmed case; they obtained epidemiological and clinical data from case-investigation reports when possible and through interviews with patients, family members, and key individuals. Findings Of the 127 patients with confirmed H5N1 infections, 103 (81%) died. Median time to hospitalisation was 6 days (range 1-16). Of the 122 hospitalised patients for whom data were available, 121 (99%) had fever, 107 (88%) cough, and 103 (84%) dyspnoea on reaching hospital. However, for the first 2 days after onset, most had non-specific symptoms; only 31 had both fever and cough, and nine had fever and dyspnoea. Median time from onset to oseltamivir treatment was 7 days (range 0-21 days); treatment started within 2 days for one patient who survived, four (36.4%) of 11 receiving treatment within 2-4 days survived, six (37-5%) of 16 receiving treatment within 5-6 days survived, and ten (18.5%) of 44 receiving treatment at 7 days or later survived (p=0.03). Initiation of treatment within 2 days was associated with significantly lower mortality than was initiation at 5-6 days or later than 7 days (p<0 0001). Mortality was lower in clustered than unclustered cases (odds ratio 33.3, 95% CI 3.13-273). Treatment started at a median of 5 days (range 0-13 days) from onset in secondary cases in clusters compared with 8 days (range 4-16) for primary cases (p=0.04). Interpretation Development ofbetter diagnostic methods and improved case management might improve identification of patients with H5N1 influenza, which could decrease mortality by allowing for earlier treatment with oseltamivir.

Code(s) de classement : 002B01; 002B05C

Descripteur(s) anglais
Descripteur(s) : Cause; Mortality; Death; Human; Viral disease; Indonesia; Medicine; Influenzavirus AH5N1
Desc. génériques : Medical sciences; Virology; Infectious diseases; Medical sciences; Infection; Asia
Descripteur(s) français
Descripteur(s) : Cause; Mortalite; Mort; Homme; Virose; Indonesie; Medecine; Influenzavirus AH5N1
Desc. génériques : Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Infection; Asie

Localisation : INIST, Shelf number 5004, INIST No. 354000196330080150

080408320
PASCAL

Cell-Based Influenza Vaccines : Progress to Date

Titre : Cell-Based Influenza Vaccines : Progress to Date

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Source : Drugs Basel. 2008; 68 (11) : 1483-1491
ISSN : 0012-6667
CODEN : DRUGAY
Date de publication : 2008
Pays de publication : New Zealand
Langue(s) : English
Type de document : Serial
Nombre de références : 77 ref.

Résumé : Human vaccines against influenza have been available for almost 60 years and, until recently, were prepared almost entirely from viruses grown in the allantoic cavity of 9- to 11-day-old embryonated chicken eggs. Manufacture involving eggs is not sufficiently flexible to allow vaccine supplies to be rapidly expanded, especially in the face of an impending pandemic. Other problems may arise from the infections of progenitor flocks that adversely affect egg supplies, and from the manufacturing process itself, where breakdowns in sterility can occur from the occasional contamination of large batches of viral allantoic fluid. In addition, egg-grown viruses exhibit differences in antigenicity from viruses isolated in mammalian cell lines from clinical specimens. These concerns and the probable need for greatly expanded manufacturing capability in the future have been brought into focus in recent years by the limited spread of H5N1 avian influenza infections to humans in several Asian countries. Alternative approaches involving the use of accredited anchorage-dependent and -independent preparations of the African Green monkey kidney (Vero), Madin-Darby canine kidney (MDCK) and other cell lines have been pursued by several manufacturers in recent years. Yields comparable with those obtained in embryonated eggs have been achieved. These improvements have occurred in parallel with newer technologies that allow the growth of cells in newer synthetic media that do not contain animal serum, in order to allay the concerns of regulators about the potential for spread of transmissible spongiform encephalopathies.

Code(s) de classement : 002B05C02C; 002B02S05; 002A05F04

Descripteur(s) anglais
Descripteur(s) : Production; Influenza; Vaccine; State of the art; Review; Case history; Embryonic cell; Chicken; Established cell line; Synthetic medium
Desc. génériques : Virology; Infectious diseases; Medical sciences; Virology; Infectious diseases; Pharmacology; Medical sciences; Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Viral disease; Infection; Aves; Vertebrata
Descripteur(s) français
Descripteur(s) : Production; Grippe; Vaccin; Etat actuel; Article synthese; Historique; Cellule embryonnaire; Poulet; Lignee cellulaire etablie; Milieu synthetique
Desc. génériques : Virologie; Maladies infectieuses; Sciences medicales; Virologie; Maladies infectieuses; Pharmacologie; Sciences medicales; Immunologie; Pharmacologie; Microbiologie appliquee; Microbiologie; Sciences biologiques; Virose; Infection; Aves; Vertebrata

Localisation : INIST, Shelf number 15326, INIST No. 354000197428740020
Origine de la notice : INIST

080406325
PASCAL

Evaluation of the Safety and Immunogenicity of a Booster (Third) Dose of Inactivated Subvirion H5N1 Influenza Vaccine in Humans

Titre : Evaluation of the Safety and Immunogenicity of a Booster (Third) Dose of Inactivated Subvirion H5N1 Influenza Vaccine in Humans

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Source : The Journal of infectious diseases. 2008; 197 (4) : 580-583
ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2008
Pays de publication : United States
Langue(s) : English
Type de document : Serial
Nombre de références : 11 ref.

Résumé : Previously, we evaluated 2 doses of H5N1 influenza vaccine in persons 18-64 years of age (placebo and 7.5-, 15-, 45-, or 90-<mu>g doses), separated by 28 days. In this study, 337 participants received a third dose, 6 months thereafter. Microneutralization (MN) and hemagglutination-inhibition geometric mean titers (GMTs) of antibody declined before the third dose. Twenty-eight days after the third dose, 78%, 67%, 43%, and 31% of recipients in the 90-, 45-, 15-, and 7.5-<mu>g-dose groups had a MN GMT >=1:40, respectively. Five months later, MN GMTs were significantly greater than those after the second dose.

Code(s) de classement : 002B05C02C; 002A05C07

Descripteur(s) anglais
Descripteur(s) : Human; Influenza A virus; Toxicity; Immunogenicity; Booster vaccination; Inactivated strain; Influenza; Avian influenza
Desc. génériques : Virology; Infectious diseases; Medical sciences; Immunology; Pharmacology; Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Infection; Viral disease
Descripteur(s) français
Descripteur(s) : Homme; Virus grippal A; Toxicite; Immunogenicite; Rappel vaccination; Souche inactivee; Grippe; Grippe aviaire
Desc. génériques : Virologie; Maladies infectieuses; Sciences medicales; Immunologie; Pharmacologie; Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Infection; Virose

Localisation : INIST, Shelf number 2052, INIST No. 354000183599510120
Origine de la notice : INIST

080402554
PASCAL

Hyperinduction of Cyclooxygenase-2-Mediated Proinflammatory Cascade : A Mechanism for the Pathogenesis of Avian Influenza H5N1 Infection

Titre : Hyperinduction of Cyclooxygenase-2-Mediated Proinflammatory Cascade : A Mechanism for the Pathogenesis of Avian Influenza H5N1 Infection

Auteur(s) : LEE Suki M Y; CHEUNG Chung Yan; NICHOLLS John M; HUI Kenrie P Y; LEUNG Connie Y H; UIPRASERTKUL Mongkol; TIPOE George L; LAU Yu Lung; POON Leo L M; IP Nancy Y; YI GUAN; MALIK PEIRIS J S
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Source : The Journal of infectious diseases. 2008; 198 (4) : 525-535
ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2008
Pays de publication : United States
Langue(s) : English
Type de document : Serial
Nombre de références : 28 ref.

Résumé : The mechanism for the pathogenesis of H5N1 infection in humans remains unclear. This study reveals that cyclooxygenase-2 (COX-2) was strongly induced in H5N1-infected macrophages in vitro and in epithelial cells of lung tissue samples obtained during autopsy of patients who died of H5N1 disease. Novel findings demonstrated that COX-2, along with tumor necrosis factor a and other proinflammatory cytokines were hyperinduced in epithelial cells by secretory factors from H5N-infected macrophages in vitro. This amplification of the proinflammatory response is rapid, and the effects elicited by the H5N-triggered proinflammatory cascade are broader than those arising from direct viral infection. Furthermore, selective COX-2 inhibitors suppress the hyperinduction of cytokines in the proinflammatory cascade, indicating a regulatory role for COX-2 in the H5N1-hyperinduced host proinflammatory cascade. These data provide a basis for the possible development of novel therapeutic interventions for the treatment of H5N1 disease, as adjuncts to antiviral drugs.

Code(s) de classement : 002A05; 002B05

Descripteur(s) anglais
Descripteur(s) : Cyclooxygenase 2; Mechanism; Pathogenesis; Microbiology; Infection; Avian influenza
Desc. génériques : Microbiology; Biological sciences; Infectious diseases; Medical sciences; Oxidoreductases; Enzyme; Viral disease
Descripteur(s) français
Descripteur(s) : Cyclooxygenase 2; Mecanisme; Pathogenie; Microbiologie; Infection; Grippe aviaire
Desc. génériques : Microbiologie; Sciences biologiques; Maladies infectieuses; Sciences medicales; Oxidoreductases; Enzyme; Virose

Localisation : INIST, Shelf number 2052, INIST No. 354000196441120100
Origine de la notice : INIST

080400336
PASCAL

Highly pathogenic avian influenza virus subtype H5N1 in ducks in the Northern part of Cameroon

Titre : Highly pathogenic avian influenza virus subtype H5N1 in ducks in the Northern part of Cameroon

Auteur(s) : NJOUOM Richard; AUBIN Jean Thierry; LUCIENNE BELLA Assumpta; MOUSSA DEMSA Baschirou; ROUQUET Pierre; GAKE Bouba; NGANGNOU Andre; FOUPOUAPOUOGNIGNI Yacouba; VAN DER WERF Sylvie; ROCOURT Jocelyne; ROUSSET Dominique
Affiliation(s) : Laboratoire de Virologie, Centre Pasteur du Cameroun, Yaounde, Cameroon; Centre Collaborateur de l'O.M.S. pour les References et la Recherche sur lesVirus de la Grippe et d'autres Virus Respiratoires, Institut Pasteur, Paris, France; Ministere de la Sante Publique, Yaounde, Cameroon; Ministere de l'Elevage, des Peches et des Industries Animales, Yaounde, Cameroon; Annexe de Garoua, Centre Pasteur du Cameroun, Garoua, Cameroon; Laboratoire National Veterinaire, Garoua, Cameroon

Source : Veterinary microbiology Amsterdam. 2008; 130 (3-4) : 380-384
ISSN : 0378-1135
CODEN : VMICDQ
Date de publication : 2008
Pays de publication : Netherlands
Langue(s) : English
Type de document : Serial
Type de document : short-communication
Nombre de références : 1/4 p.

Résumé : Highly pathogenic avian influenza (HPAI) virus was first detected in Cameroon in February 2006. Analysis of NA sequences of the virus demonstrated that it is closely related to the H5N1 isolates from Northern Nigeria, Sudan and Ivory Coast, suggesting a common virus ancestor.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Descripteur(s) : Avian influenzavirus; Pathogenicity; Subtype; Cameroon; Microbiology; Veterinary
Desc. génériques : Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Africa; Zoopathogen
Descripteur(s) français
Descripteur(s) : Influenzavirus aviaire; Pouvoir pathogene; Soustype; Cameroun; Microbiologie; Veterinaire
Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Afrique; Zoopathogene

Localisation : INIST, Shelf number 16884, INIST No. 354000196430800170
Origine de la notice : INIST

080400323
PASCAL

Generation and evaluation of reassortant influenza vaccines made by reverse genetics for H9N2 avian influenza in Korea

Titre : Generation and evaluation of reassortant influenza vaccines made by reverse genetics for H9N2 avian influenza in Korea

Auteur(s) : JAE MIN SONG; YOUN JEONG LEE; OK MI JEONG; HYUN MI KANG; HYE RYOUNG KIM; JUN HUN KWON; JAE HONG KIM; BAIK LIN SEONG; YONG JOO KIM
Affiliation(s) : National Veterinary Research & Quarantine Service, Anyang6dong, Manangu, Anyang City, Gyeonggi-do 430-824, Korea, Republic of; College of Veterinary Medicine, Seoul National University, Seoul, Korea, Republic of; Department of Biotechnology, College of Engineering, Yonsei University, Seoul, Korea, Republic of

Source : Veterinary microbiology Amsterdam. 2008; 130 (3-4) : 268-276
ISSN : 0378-1135
CODEN : VMICDQ
Date de publication : 2008
Pays de publication : Netherlands
Langue(s) : English
Type de document : Serial
Nombre de références : 3/4 p.

Résumé : The prevalence and continuous evolution of H9N2 avian influenza viruses in poultry have necessitated the use of vaccines in veterinary medicine. Because of the inadequate growth properties of some strains, additional steps are needed for producing vaccine seed virus. In this study, we generated three H9N2/PR8 reassortant viruses using a total cDNA plasmid-transfection system, as an alternative strategy for developing an avian influenza vaccine for animals. We investigated the vaccine potency of the reassortant viruses compared with the existing vaccine strain which was adapted by the 20th serial passages in embryonated eggs with A/Ck/Kor/01310/01 (H9N2). The H9N2/PR8 reassortant viruses, containing the internal genes of the high-yielding PR8 strain and the surface gene of the A/Ck/Kor/01310/01 strain, could be propagated in eggs to the same extent as existing vaccine strain without additional processing. Similar to vaccine strain, the H9N2/PR8 reassortant viruses induced hemagglutination-inhibiting antibodies in chickens and prevented virus shedding and replication in multiple organs in response to homologous infection. However, due to the continuing evolution and increasing biologic diversity of H9N2 influenza in Korea, the vaccine provided only partial protection against currently isolates. Taken together, our results suggest that the H9N2/PR8 reassortant virus can be used as a seed virus for avian influenza vaccines in poultry farm. Considering the constant genetic changes in H9 strains isolated in Korea, this reverse genetic system may offer a prompt and simple way to change the vaccine seed virus and mitigate the impact of unexpected influenza outbreaks.

Code(s) de classement : 002A05C10

Descripteur(s) anglais
Descripteur(s) : Avian influenzavirus; Genetic vaccine; Korea; Genetics; Microbiology; Veterinary; Avian influenza; Genetic reassortment
Desc. génériques : Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Asia; Infection; Viral disease; Zoopathogen
Descripteur(s) français
Descripteur(s) : Influenzavirus aviaire; Vaccin genetique; Coree; Genetique; Microbiologie; Veterinaire; Grippe aviaire; Reassortiment genetique
Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Asie; Infection; Virose; Zoopathogene

Localisation : INIST, Shelf number 16884, INIST No. 354000196430800060
Origine de la notice : INIST

080398488
PASCAL

Progress in identifying virulence determinants of the 1918 H1N1 and the Southeast Asian H5N1 influenza A viruses

Titre : Progress in identifying virulence determinants of the 1918 H1N1 and the Southeast Asian H5N1 influenza A viruses

Auteur(s) : EASIER Christopher F; AGUILAR Patricia V
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Source : Antiviral research. 2008; 79 (3) : 166-178
ISSN : 0166-3542
CODEN : ARSRDR
Date de publication : 2008
Pays de publication : Netherlands
Langue(s) : English
Type de document : Serial
Nombre de références : 2 p.1/4

Résumé : The 1918 pandemic H1 N1 influenza virus and the recently emerged Southeast Asian H5N1 avian influenza virus are unique among influenza A virus isolates in their high virulence for humans and their lethality for a variety of animal species without prior adaptation. Reverse genetic studies have implicated several viral genes as virulence determinants. For both the 1918 and H5N1 viruses, the hemagglutinin and the polymerase complex contribute to high virulence. Non-structural proteins NS1 and PB1-F2, which block host antiviral responses, also influence pathogenesis. Additionally, recent studies correlate high levels of viral replication and induction of strong proinflammatory responses with the high virulence of these viruses. Defining how individual viral proteins promote enhanced replication, inflammation and severe disease will provide insight into the pathogenesis of severe influenza virus infections and suggest novel therapeutic approaches.

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

Descripteur(s) anglais
Descripteur(s) : Virulence; Influenza; Treatment; Influenzavirus A; Pathogenesis; Antiviral; Replication; Immunopathology; Gene; Influenzavirus AH5N1
Desc. génériques : Virology; Infectious diseases; Pharmacology; Medical sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection; Orthomyxoviridae; Virus; Genetics
Descripteur(s) français
Descripteur(s) : Virulence; Grippe; Traitement; Influenzavirus A; Pathogenie; Antiviral; Replication; Immunopathologie; Gene; Influenzavirus AH1N1; Pandemie; Influenzavirus AH5N1
Desc. génériques : Virologie; Maladies infectieuses; Pharmacologie; Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection; Orthomyxoviridae; Virus; Genetique

Localisation : INIST, Shelf number 18839, INIST No. 354000197393340020
Origine de la notice : INIST

080396806
PASCAL

Using influenza-like illness data to reconstruct an influenza outbreak

Titre : Using influenza-like illness data to reconstruct an influenza outbreak

Auteur(s) : COOLEY Philip; GANAPATHI Laxminarayana; GHNEIM George; HOLMBERG Scott; WHEATON William; HOLLINGSWORTH Craig R
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Source : Mathematical and computer modelling. 2008; 48 (5-6) : 929-939
ISSN : 0895-7177
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Nombre de références : 11 ref.

Résumé : The objective of this study was to reconstruct the type A influenza epidemic that occurred in the Research Triangle Park (RTP) region of North Carolina during the 2003-04 flu season. We describe an agent-based influenza transmission model that uses Influenza-like Illness (ILI) data gathered from state agencies to estimate model parameters. The design of the model is similar to models represented in the literature that have been used to predict the impact of pandemic avian influenza in Southeast Asia and in the continental United States and to assess containment strategies. The focus of this model is to reconstruct a historical epidemic that left traces of its impact in the form of an ILI epidemic curve. In this context, the work assumes aspects of a curve fitting exercise.

Code(s) de classement : 001A02I02; 001A02E; 001A02B01B; 001A02I01D

Descripteur(s) anglais
Descripteur(s) : Numerical approximation; Smoothing methods; Curve fitting; Applied mathematics; Mathematical model; Computer aided analysis; Scientific computation; Triangle
Desc. génériques : Scientific computation; Mathematics; Mathematics; Mathematics; Numerical analysis; Mathematics
Descripteur(s) français
Descripteur(s) : Approximation numerique; Methode lissage; Ajustement courbe; Mathematiques appliquees; Modele mathematique; Analyse assistee; Calcul scientifique; 05Bxx; 65D10; Triangle
Desc. génériques : Calcul scientifique; Mathematiques; Mathematiques; Mathematiques; Analyse numerique; Mathematiques

Localisation : INIST, Shelf number 18808, INIST No. 354000196482380230
Origine de la notice : INIST

080392481
PASCAL

How will Australian general practitioners respond to an influenza pandemic? A qualitative study of ethical values

Titre : How will Australian general practitioners respond to an influenza pandemic? A qualitative study of ethical values

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Source : Medical journal of Australia. 2008; 189 (3) : 148-150
ISSN : 0025-729X
CODEN : MJAUAJ
Date de publication : 2008
Pays de publication : Australia
Langue(s) : English
Type de document : Serial
Nombre de références : 12 ref.

Résumé : Objectives: To explore general practitioners' perceptions of their preparedness for an influenza pandemic, the changes they would make to their practice, and the ethical justifications for their planned actions. Design and setting: A qualitative study was performed among South Australian GPs between March and October 2007. A semi-structured interview was carried out with each participant in his or her practice, and the interviews were audio-recorded, transcribed and analysed thematically. Participants: 10 GPs were recruited: five from a metropolitan Division and five from a rural Division of General Practice. Results: Some participants felt they would not be able to cope with an influenza pandemic, while others felt it would simply mean an increase in their workloads. Most respondents considered creating separate waiting rooms, moving the reception desk outside of the practice and delaying all non-urgent consultations in order to deal with a pandemic more effectively. Respondents mentioned the conflict between their various roles and responsibilities as a primary source of tension when thinking about the way they would organise their work in the event of a pandemic. A number of GPs said they would not practise in the event of a pandemic, as they felt their responsibility to their families outweighed that to their patients. Conclusions: Professional codes of ethics should include guidance about the scope of the duty to treat during infectious disease outbreaks. The community has to uphold the value of reciprocity, and ensure that GPs and their families are provided with support during a pandemic and are given the opportunity to be actively involved in pandemic preparedness planning.

Code(s) de classement : 002B01; 002B31

Descripteur(s) anglais
Descripteur(s) : Australia; General practitioner; Ethics; Public health
Desc. génériques : Medical sciences; Ethics; Medical sciences; Oceania
Descripteur(s) français
Descripteur(s) : Australie; Medecin generaliste; Ethique; Sante publique; Grippe pandemique
Desc. génériques : Sciences medicales; Ethique; Sciences medicales; Oceanie

Localisation : INIST, Shelf number 3557, INIST No. 354000196253680070
Origine de la notice : INIST

080392249
PASCAL

Phase I and II randomised trials of the safety and immunogenicity of a prototype adjuvanted inactivated split-virus influenza A (H5N1) vaccine in healthy adults

Titre : Phase I and II randomised trials of the safety and immunogenicity of a prototype adjuvanted inactivated split-virus influenza A (H5N1) vaccine in healthy adults

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Source : Vaccine . 2008; 26 (33) : 4160-4167
ISSN : 0264-410X
CODEN : VACCDE
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Nombre de références : 17 ref.

Résumé : Objective: The primary objective was to evaluate the safety and immunogenicity of a prototype inactivated, split-virus H5N1 (avian influenza A) vaccine. A secondary objective was to assess the cross-reactivity of immune responses to two variant clade 2 H5N1 strains. Methods: In two randomised, dose comparison, parallel assignment, multicentre trials conducted in Australia, healthy adult volunteers received two doses of 7.5 <mu>g or 15 <mu>g H5 haemagglutinin (HA) vaccine <plus or minus sign>AIPO<sub>4 adjuvant (phase I trial; N= 400) or two doses of 30 <mu>g or 45 <mu>g H5 HA with AIPO<sub>4 adjuvant (phase II trial; N=400). Revaccination with a booster dose was offered 6 months after dose 2 (phase I trial only). Main outcome measures were the change in immunogenicity at each follow-up visit from baseline, measured using HA inhibition (HI) and virus microneutralisation (MN) assays, and the frequency and nature of adverse events (AEs). Computer generated tables were used to randomly allocate treatments; participants and investigators were blinded to treatment allocation. Findings: All formulations were well-tolerated; no unexpected serious adverse events were reported. Two doses of 30 <mu>g or 45 <mu>g H5 HA adjuvanted formulations elicited the highest immune responses, with considerable MN antibody (>=1:20) persistence up to 6 months post-vaccination. The 7.5 and 15 <mu>g formulations (<plus or minus sign>adjuvant) were less immunogenic than the higher dose formulations; HI and MN antibody titres decreased to near pre-vaccination levels at 6 months but were restored to post-dose 2 levels after the booster dose. Immune responses in the phase I trial demonstrated modest levels of cross-protective MN antibodies against two currently circulating, distinct clade 2 H5N1 strains. Interpretation: Two doses of prototype 30 (<mu>g or 45 <mu>g aluminium-adjuvanted, clade 1 H5N1 vaccines were immunogenic and well-tolerated with considerable 6-month antibody persistence. The prototype H5N1 vaccine also elicited modest levels of cross-protective MN antibodies against variant clade 2 H5N1 strains ClinicalTrials.gov identifiers: NCT00136331, NCT00320346; Funding: CSL Limited, Australia.

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

Descripteur(s) anglais
Descripteur(s) : Influenza A virus; Phase II trial; Phase I trial; Immunogenicity; Immunological adjuvant; Vaccine; Adult; Avian influenza
Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Virology;

Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Human; Infection; Viral disease
Descripteur(s) français
Descripteur(s) : Virus grippal A; Essai clinique phase II; Essai clinique phase I; Immunogenicite; Adjuvant immunologique; Vaccin; Adulte; Grippe aviaire
Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquee; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Homme; Infection; Virose

Localisation : INIST, Shelf number 20289, INIST No. 354000196247830100
Origine de la notice : INIST

080388447
PASCAL

Prioritization of Influenza Pandemic Vaccination to Minimize Years of Life Lost

Titre : Prioritization of Influenza Pandemic Vaccination to Minimize Years of Life Lost

Auteur(s) : MILLER Mark A; VIBOUD Cecile; OLSON Donald R; GRAIS Rebecca F; RABAA Maia A; SIMONSEN Lone
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Source : The Journal of infectious diseases. 2008; 198 (3) : 305-311
ISSN : 0022-1899
CODEN : JIDIAQ
Date de publication : 2008
Pays de publication : United States
Langue(s) : English
Type de document : Serial
Nombre de références : 50 ref.

Résumé : Background. How to allocate limited vaccine supplies in the event of an influenza pandemic is currently under debate. Conventional vaccination strategies focus on those at highest risk for severe outcomes, including seniors, but do not consider (1) the signature pandemic pattern in which mortality risk is shifted to younger ages, (2) likely reduced vaccine response in seniors, and (3) differences in remaining years of life with age. Methods. We integrated these factors to project the age-specific years of life lost (YLL) and saved in a future pandemic, on the basis of mortality patterns from 3 historical pandemics, age-specific vaccine efficacy, and the 2000 US population structure. Results. For a 1918-like scenario, the absolute mortality risk is highest in people <45 years old; in contrast, seniors (those >=65 years old) have the highest mortality risk in the 1957 and 1968 scenarios. The greatest YLL savings would be achieved by targeting different age groups in each scenario; people <45 years old in the 1918 scenario, people 45-64 years old in the 1968 scenario, and people >45 years old in the 1957 scenario. Conclusions. Our findings shift the focus of pandemic vaccination strategies onto younger populations and illustrate the need for real-time surveillance of mortality patterns in a future pandemic. Flexible setting of vaccination priority is essential to minimize mortality.

Code(s) de classement : 002A05; 002B05

Descripteur(s) anglais
Descripteur(s) : Vaccination; Microbiology; Infection; Influenza
Desc. génériques : Microbiology; Biological sciences; Infectious diseases; Medical sciences; Viral disease
Descripteur(s) français
Descripteur(s) : Vaccination; Microbiologie; Infection; Grippe
Desc. génériques : Microbiologie; Sciences biologiques; Maladies infectieuses; Sciences medicales; Virose

Localisation : INIST, Shelf number 2052, INIST No. 354000197713030020
Origine de la notice : INIST

080388361
PASCAL

Development of reverse transcription loop-mediated isothermal amplification for rapid detection of H9 avian influenza virus

Titre : Development of reverse transcription loop-mediated isothermal amplification for rapid detection of H9 avian influenza virus

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Source : Journal of virological methods. 2008; 151 (2) : 200-203
ISSN : 0166-0934
CODEN : JVMEDH
Date de publication : 2008
Pays de publication : Netherlands
Langue(s) : English
Type de document : Serial
Type de document : research-paper
Nombre de références : 1/2 p.

Résumé : Reverse transcription loop-mediated isothermal amplification (RT-LAMP) is a unique gene amplification method that can be completed within 45 min at 63<degree>C. In this study, RT-LAMP was used to develop a rapid and sensitive laboratory diagnostic system for the H9 subtype of avian influenza virus (AIV). The experiment results from the reference strains demonstrated that the established RT-LAMP sensitivity was 10-fold higher than that of RT-PCR, with the detection limit of 10 copies per reaction, and no cross-reactivity was observed from the samples of other related viruses including H5N1, H3N2 subtype of AIV and Newcastle disease virus. Furthermore, a total of 112 clinical samples were tested by RT-LAMP, RT-PCR, and virus isolation, respectively. All of the 85 positive specimens identified by virus isolation were also positive by RT-LAMP, while 7 of these samples were missed by RT-PCR. These results suggest that the present RT-LAMP system may provide a new avenue for the recognition of H9 subtype virus, and may be employed to screen for potential carriers in wild and domestic birds.

Code(s) de classement : 002A05C09

Descripteur(s) anglais
Descripteur(s) : Avian influenzavirus; Transcription; Amplification; Detection; Subtype; Reverse transcription polymerase chain reaction; Microbiology; Method; Virology; Influenza
Desc. génériques : Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Viral disease; Infection
Descripteur(s) français
Descripteur(s) : Influenzavirus aviaire; Transcription; Amplification; Detection; Soustype; Reaction chaine polymerase RT; Microbiologie; Methode; Virologie; Grippe
Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Virose; Infection

Localisation : INIST, Shelf number 18295, INIST No. 354000196399060060
Origine de la notice : INIST

080387528
PASCAL

Analyses of the 1957 (Asian) influenza pandemic in the United Kingdom and the impact of school closures

Titre : Analyses of the 1957 (Asian) influenza pandemic in the United Kingdom and the impact of school closures

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Source : Epidemiology and infection. 2008; 136 (2) : 166-179
ISSN : 0950-2688
CODEN : EPINEU
Date de publication : 2008
Pays de publication : United Kingdom
Langue(s) : English
Type de document : Serial
Nombre de références : 27 ref.

Résumé : Many countries plan to close schools during a future influenza pandemic, although the potential impact is poorly understood. We apply a model of the transmission dynamics of pandemic influenza to consultation, serological and clinical data from the United Kingdom from the 1957 (Asian) influenza pandemic, to estimate the basic reproduction number (R<sub>0), the proportion of infected individuals who experience clinical symptoms and the impact of school/nursery closures. The R<sub>0 for Asian influenza was about 1-8 and 60-65% of infected individuals were estimated to have experienced clinical symptoms. During a future pandemic, closure of schools/nurseries could reduce the epidemic size only by a very small amount (<10%) if R<sub>0 is high (e.g. 2.5 or 3<sup>.5), and modest reductions, e.g. 22% might be possible if it is low (1<sup>.8) and schools are closed early, depending on assumptions about contact patterns. Further data on contact patterns and their dependence on school closures are needed.

Code(s) de classement : 002A05C06

Descripteur(s) anglais
Descripteur(s) : Human; United Kingdom; Epidemiology; Epidemic; Prevention; Influenza
Desc. génériques : Virology; Microbiology; Biological sciences; Europe; Viral disease; Infection
Descripteur(s) français
Descripteur(s) : Homme; Royaume Uni; Epidemiologie; Epidemie; Prevention; Grippe
Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Europe; Virose; Infection

Localisation : INIST, Shelf number 6056, INIST No. 354000175121960030
Origine de la notice : INIST

080377161
PASCAL

Gestion d' une epidemie par un service de sante au travail : exemple de la pandemie grippale. 30<sup>e Congres national de medecine et sante au travail. Tours, 3 au 6 juin 2008; Management of an epidemic by an occupational health service : Example of the influenza pandemic

Titre : Gestion d' une epidemie par un service de sante au travail : exemple de la pandemie grippale. 30<sup>e Congres national de medecine et sante au travail. Tours, 3 au 6 juin 2008; Management of an epidemic by an occupational health service : Example of the influenza pandemic

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Source : Archives des maladies professionnelles et de l'environnement. 2008; 69 (2) : 341-344
Informations congrès : *Congres national de medecine et sante au travail, *30, *Tours France, *2008-06-03
ISSN : 1775-8785
Date de publication : 2008
Pays de publication : France
Langue(s) : French
Type de document : Serial; *Conference-Meeting
Nombre de références : 5 ref.

Code(s) de classement : 002B05C02C; 002B05A02

Descripteur(s) anglais
Descripteur(s) : Management; Epidemic; Public health; Health service; Work place; Epidemiology; Influenza; Occupational medicine; Firm; Human; France
Desc. génériques : Virology; Infectious diseases; Medical sciences; Infectious diseases; Medical sciences; Viral disease; Infection; Europe
Descripteur(s) français
Descripteur(s) : Gestion; Epidemie; Sante publique; Service sante; Lieu travail; Epidemiologie; Grippe; Medecine du travail; Entreprise; Homme; France; Pandemie; Grippe pandemique
Desc. génériques : Virologie; Maladies infectieuses; Sciences medicales; Maladies infectieuses; Sciences medicales; Virose; Infection; Europe

Localisation : INIST, Shelf number 738, INIST No. 354000183154900410
Origine de la notice : INIST