

Grippe Aviaire

Septembre 2008

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ACUTE KIDNEY INJURY IN EMERGING, NON-TROPICAL INFECTIONS

Titre : ACUTE KIDNEY INJURY IN EMERGING, NON-TROPICAL INFECTIONS

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Descripteur(s) : Acute kidney injury; Hantavirus; Congo Crimean haemorrhagic fever; Emerging disease; Ehrlichia infection; Severe acute respiratory syndrome; Hemorrhagic fever with renal syndrome; Rhabdomyolysis; Human; Legionnaires disease; Avian influenza

Desc. génériques : Nephrology; Urinary system; Medical sciences; Bunyaviridae; Virus; Arbovirus disease; Viral disease; Infection; Rickettsialosis; Bacteriosis; Urinary system disease; Kidney disease; Respiratory disease; Lung disease; Legionellosis; Pneumonia; Striated muscle disease

Descripteur(s) français

Descripteur(s) : Lésion rénale aiguë; Hantavirus; Fièvre hémorragique Crimée Congo; Maladie émergente; Ehrlichiose; Syndrome respiratoire aigu sévère; Fièvre hémorragique avec syndrome rénal; Rhabdomyolyse; Homme; Maladie des légionnaires; Grippe aviaire; Néphropathie épidémique

Desc. génériques : Néphrologie; Appareil urinaire; Sciences médicales; Bunyaviridae; Virus; Arbovirose; Virose; Infection; Rickettsialose; Bactériose; Pathologie de l'appareil urinaire; Pathologie du rein; Pathologie de l'appareil respiratoire; Pathologie des poumons; Légionellose; Pneumonie; Pathologie du muscle strié

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Impact of Severe Acute Respiratory Syndrome and the Perceived Avian Influenza Epidemic on the Increased Rate of Influenza Vaccination Among Nurses in Hong Kong

Titre : Impact of Severe Acute Respiratory Syndrome and the Perceived Avian Influenza Epidemic on the Increased Rate of Influenza Vaccination Among Nurses in Hong Kong

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Pays de publication : United States

Langue(s) : English

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Résumé : OBJECTIVE. To determine the rate of influenza vaccination and the factors associated with the vaccination's acceptance among nurses in Hong Kong. DESIGN. Cross-sectional survey. PARTICIPANTS. Nurses practicing between 2003 and 2007. METHODS. A questionnaire was sent to all nurses registered with any of the 3 nursing associations that participated in this study. RESULTS. A total of 941 completed questionnaires were available for analysis, though not all nurses responded to every question (response rate, 33.5%-36.3%). Vaccination rates in 2006 and 2007 were 57.2% and 46.2%, respectively. Nurses who were vaccinated in 2006 were more likely to get vaccinated in 2007 ($P<.01$); 56% of the nurses perceived influenza vaccine as being effective against influenza. The perceived effectiveness of influenza vaccine was a consistent predictor of rates of vaccination in 2006 (odds ratio OR, 8.47 95% confidence interval {CI}, 6.13-11.70; $P<.01$) and 2007 (OR, 6.05 95% CI, 3.79-9.67; $P<.01$). Concern about contracting avian influenza was a predictor of the vaccination rate in 2006 but not in 2007 (OR, 1.47 95% CI, 1.03-2.09; $P<.05$), as was the perceived lack of control over avian influenza infection (OR, 1.52 95% CI, 1.06-2.18; $P<.05$). CONCLUSIONS. The overall influenza vaccination rate for nurses in Hong Kong was about 50%. It was affected by the perceived threat of an impending outbreak. The attitudes of nurses toward the effectiveness of and rationale for vaccination were a major barrier to increasing the rate of vaccination.

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

Descripteur(s) anglais

Descripteur(s) : Severe acute respiratory syndrome; Avian influenza; Immunoprophylaxis; Epidemic; Vaccination; Nurse; Hong Kong; Public health

Desc. génériques : Public health; Medical sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection; China; Asia; Respiratory disease; Lung disease; Prevention; Health care staff

Descripteur(s) français

Descripteur(s) : Syndrome respiratoire aigu severe; Grippe aviaire; Immunoprophylaxie; Epidemie; Vaccination; Infirmier; Hong Kong; Sante publique

Desc. génériques : Sante publique; Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection; Chine; Asie; Pathologie de l' appareil respiratoire; Pathologie des poumons; Prevention; Equipe soignante

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Avian influenza : Lessons from history

Titre : Avian influenza : Lessons from history

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Date de publication : 2008

Pays de publication : Ireland

Langue(s) : English

Type de document : Serial

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Descripteur(s) anglais

Descripteur(s) : Avian influenza; Resuscitation; Intensive care

Desc. génériques : Resuscitation; Intensive care medicine; Medical sciences; Toxicology; Medical sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Grippe aviaire; Reanimation; Soins intensif

Desc. génériques : Reanimation; Soins intensifs; Sciences medicales; Toxicologie; Sciences medicales; Virose; Infection

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Effects of Adjuvants on the Safety and Immunogenicity of an Avian Influenza H5N1 Vaccine in Adults

Titre : Effects of Adjuvants on the Safety and Immunogenicity of an Avian Influenza H5N1 Vaccine in Adults

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Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 14 ref.

Résumé : Background. Influenza A H5N1 viruses pose a significant threat to human health. Methods. We conducted a multicenter, randomized, double-blind study in 394 healthy adults. Subjects were randomly assigned to receive 2 intramuscular doses of either saline placebo; influenza A/Vietnam/1203/2004(H5N1) vaccine alone at 45, 30, or 15 μ g per dose; vaccine at 15 or 7.5 μ g per dose with MF59; or vaccine at 30, 15, or 7.5 μ g per dose with aluminum hydroxide. Subjects were followed up for safety and blood samples were obtained to determine antibody responses. Results. The vaccine formulations were well tolerated but local adverse effects were common; the incidence of these effects increased in a dose-dependent manner and was increased by the addition of adjuvants. The addition of MF59 increased the antibody response, whereas the addition of aluminum hydroxide did not. The highest antibody responses were seen in the group that received 15 μ g of vaccine per dose with MF59, in which 63% of subjects achieved the predetermined endpoint (hemagglutination-inhibition titer ≥ 40) 28 days after the second dose, compared with 29% in the group that received the highest dose (45 μ g per dose) of vaccine alone. Conclusions. A 2-dose regimen of subvirion influenza A (H5N1) vaccine was well tolerated. The antibody responses to 15 μ g of A/H5 vaccine with MF59 were higher than the responses to 45 μ g of vaccine alone.

Code(s) de classement : 002A05F04

Descripteur(s) anglais

Descripteur(s) : Immunological adjuvant; Toxicity; Immunogenicity; Vaccine; Adult; Avian influenza

Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Human; Infection; Viral disease

Descripteur(s) français

Descripteur(s) : Adjuvant immunologique; Toxicité; Immunogénicité; Vaccin; Adulte; Grippe aviaire

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquée; Microbiologie; Sciences biologiques; Homme; Infection; Virose

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Infectious diseases and governance of global risks through public communication and participation : Poverty and human development

Titre : Infectious diseases and governance of global risks through public communication and participation : Poverty and human development

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Langue(s) du résumé : Italian

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Résumé : In recent years a succession of health emergencies connected with the threat of new, possibly global, infectious diseases has stimulated the attention of the mass media, the scientific community, and international public opinion, setting a tough test for the institutions whose job is to manage the risks. On the basis of experience in the fields of AIDS, BSE, SARS and bird flu, this study discusses the strong and weak points of governance procedures for health risks. In particular, the paper illustrates how risk management can be improved by adopting practices and procedures which actively involve the public in dealing with the emergency, by taking a transparent and accessible approach to communication with the public (including the provision of information about the risks) and by fostering the unrestricted exchange of scientific knowledge among researchers. Lastly, the text shows how the analysis of these themes provides starting points for understanding the crisis in the current relationship between science and society.

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Descripteur(s) anglais

Descripteur(s) : Infection; Risk factor; Risk; Communication; Participation; Medicine; Italy

Desc. génériques : Medical sciences; Europe

Descripteur(s) français

Descripteur(s) : Infection; Facteur risque; Risque; Communication; Participation; Medecine; Italie

Desc. génériques : Sciences medicales; Europe

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Phylogenetic analyses of highly pathogenic avian influenza virus isolates from Germany in 2006 and 2007 suggest at least three separate introductions of H5N1 virus

Titre : Phylogenetic analyses of highly pathogenic avian influenza virus isolates from Germany in 2006 and 2007 suggest at least three separate introductions of H5N1 virus

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Résumé : In spring 2006, highly pathogenic avian influenza virus (HPAIV) of subtype H5N1 was detected in Germany in 343 dead wild birds, as well as in a black swan (*Cygnus atratus*) kept in a zoo, three stray cats, one stone marten (*Martes foina*), and in a single turkey farm. In 2007 (June-July) the virus reoccurred in 96 wild birds at six geographically separate locations in the Southeast of Germany. In addition, a backyard mixed duck and goose holding was affected. Real-time RT-PCR Hoffmann, B., Harder, T., Starick, E., Depner, K., Werner, O., Beer, M., 2007. Rapid and highly sensitive pathotyping of avian influenza A H5N1 virus by using real-time reverse transcription-PCR. *J. Clin. Microbiol.* 45, 600-603 and nucleotide sequencing confirmed that these H5-viruses belonged to the Qinghai lineage of HPAIV H5N1 (clade 2.2). For a more detailed analysis, the hemagglutinin and neuraminidase genes of 27 selected German H5N1 viruses isolated 2006 or 2007 and originating from different regions and animal species were sequenced and analysed phylogenetically. As a result, three closely related but distinguishable H5N1 subclades could be defined: In 2006 a 'Northern type' (subclade 2.2.2), representing virus isolates from the German federal states Mecklenburg-Western Pomerania, Schleswig-Holstein, Brandenburg, and Lower Saxony, and a 'Southern type' (subclade 2.2.1) from Baden-Wuerttemberg and Bavaria were detected. Interestingly, representatives of both types were present in Central Germany and caused the outbreak in turkeys (subclade 2.2.2) and in a case in a tufted duck (*Aythya fuligula*) (subclade 2.2.1) in Saxony. Furthermore, one isolate from the South of Germany was identified as 2.2.2 and vice versa a 2.2.1-like isolate was found in Northern Germany. H5N1 viruses isolated in 2007 belonged to a third type (subclade 2.2.3) which was not detected in 2006. Our data suggest the introduction of three distinct H5N1 variants into the wild bird population of Germany. The source of these viruses and the exact time of introduction remain obscure. Based on the identification of closely related H5N1 viruses from Southern and Central Russia, a recent introduction via wild birds on winter escape from these regions, early in 2006 constitutes the most likely scenario for the 2006 outbreaks. The viruses detected in 2007 most likely represent another new incursion from an as yet unknown source.

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Descripteur(s) anglais

Descripteur(s) : Avian influenzavirus; Phylogeny; Pathogenicity; Isolate; Germany; Molecular epidemiology; Genotype; Avian influenza

Desc. génériques : Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Europe; Zoonopathogen; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Influenzavirus aviaire; Phylogénèse; Pouvoir pathogène; Isolat; Allemagne; Épidémiologie moléculaire; Génotype; Grippe aviaire

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Europe; Zoopathogène; Virose; Infection

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Genetic Evolution of Swine Influenza A (H3N2) Viruses in China from 1970 to 2006

Titre : Genetic Evolution of Swine Influenza A (H3N2) Viruses in China from 1970 to 2006

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Type de document : Serial

Nombre de références : 36 ref.

Résumé : Pigs are susceptible to both human and avian influenza viruses and have been proposed to be intermediate hosts, or mixing vessels, for the generation of pandemic influenza viruses through reassortment or adaptation to the mammalian host. In this study, we summarize and report for the first time the coexistence of wholly human-like H3N2 viruses, double-reassortant H3N2 viruses, and triple-reassortant H3N2 viruses in pigs in China by analyzing the eight genes of swine influenza A (H3N2) viruses found in China from 1970 to 2006. In 1970, the first wholly human-like H3N2 (Hong Kong/68-like) viruses were isolated from pigs in Taiwan, and then in the next years Victoria/75-like, Sydney/97-like, New York/99-like, and Moscow/99-like swine H3N2 viruses were regularly isolated in China. In the 1980s, two triple-reassortant viruses were isolated from pigs. Recently, the double-reassortant viruses containing genes from the human (HA and NA) and avian (PB2, PB1, PA, NP, M, and NS) lineages and the triple-reassortant viruses containing genes from the human (HA and NA), classical swine (NP), and avian (PB2, PB1, PA, M, and NS) lineages emerged in pigs in China. The coexistence of wholly human-like and reassortant viruses provides farther evidence that pigs serve as intermediate hosts, or mixing vessels, and emphasizes the importance of reinforcing swine influenza virus surveillance in China.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Descripteur(s) : Swine; Influenza A virus; Genetics; China

Desc. génériques : Virology; Microbiology; Biological sciences; Artiodactyla; Ungulata; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Asia; Veterinary

Descripteur(s) français

Descripteur(s) : Porcin; Virus grippal A; Genetique; Chine

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Artiodactyla; Ungulata; Mammalia; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Asie; Veterinaire

Localisation : INIST, Shelf number 17088, INIST No. 354000183280550370

Origine de la notice : INIST

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Rapid Differentiation of Influenza A Virus Subtypes and Genetic Screening for Virus Variants by High-Resolution Melting Analysis

Titre : Rapid Differentiation of Influenza A Virus Subtypes and Genetic Screening for Virus Variants by High-Resolution Melting Analysis

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ISSN : 0095-1137

CODEN : JCMIDW

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 39 ref.

Résumé : We assessed the use of high-resolution melting (HRM) analysis for the rapid identification of influenza A virus subtypes and the detection of newly emerging virus variants. The viral matrix gene was amplified by LightCycler real-time reverse transcription-PCR (RT-PCR) in the presence of the LCGreen I fluorescent dye. Upon optimization of the assay conditions, all the major influenza A virus subtypes, including H1N1, H3N2, H5N1, H7N3, and H9N2, were amplifiable by this method and had a PCR product length of 179 bp. Real-time RT-PCR of in vitro-transcribed H3N2 RNA revealed a standard curve for quantification with a linear range (correlation coefficient = 0.9935) across at least 8 log units of RNA concentrations and a detection limit of $10^{3.3}$ copies of viral RNA. We performed HRM analysis of the PCR products with the HR-1 instrument and used the melting profiles as molecular fingerprints for virus subtyping. The virus subtypes were identified from the high-resolution derivative plot obtained by heteroduplex formation between the PCR products of the viral isolates tested and those of the reference viral isolates. The melting profiles were consistent with minimal interassay variability. Hence, an HRM database and a working protocol were established for the identification of these five influenza A virus subtypes. When this protocol was used to test 21 clinical influenza A virus isolates, the results were comparable to those obtained by RT-PCR with hemagglutinin-specific primer sets. Sequence variants of the clinical isolates ($n = 4$) were also revealed by our HRM analytical scheme. This assay requires no multiplexing or hybridization probes and provides a new approach for influenza A virus subtyping and genetic screening of virus variants in a clinical virology laboratory.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Descripteur(s) : Influenza A virus; Subtype; Genetics

Desc. génériques : Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) français

Descripteur(s) : Virus grippal A; Soustype; Genetique

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST, Shelf number 17088, INIST No. 354000183280550400

Origine de la notice : INIST

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Seasonal and Pandemic Influenza : A 2007 Update on Challenges and Solutions

Titre : Seasonal and Pandemic Influenza : A 2007 Update on Challenges and Solutions

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Source : Clinical infectious diseases. 2008; 46 (7) : 1024-1031

ISSN : 1058-4838

CODEN : CIDIEL

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 49 ref.

Résumé : The second annual Seasonal and Pandemic Influenza Conference, which took place in February 2007 in Arlington, Virginia, focused on recent progress in basic and clinical research regarding preparedness for outbreaks of influenza. Sporadic outbreaks of avian influenza A in Asia and the Middle East remind us that the threat of another influenza pandemic remains real. Although the exact mechanisms underlying avian influenza A human pathogenicity remain unclear, preclinical studies in animal models provide insights into the mechanisms of avian influenza A virus infection and transmission from bird to human and, rarely, from human to human. With regard to prevention, developmental studies of adjuvant-supplemented vaccines indicate promising immunogenicity and cross-reactivity. The pipeline of new antiviral agents in development is also increasing, including a new neuraminidase inhibitor and agents aimed at completely new targets. Global strategic planning efforts focus on assuring sufficient stocks of vaccines and antiviral agents, as well as timely nonpharmacological interventions to potentially delay or contain spread of an outbreak. These initiatives will also help control outbreaks of seasonal influenza.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Influenza A; Seasonal variation

Desc. génériques : Virology; Infectious diseases; Medical sciences; Viral disease; Infection; Epidemiology

Descripteur(s) français

Descripteur(s) : Grippe A; Variation saisonniere; Pandemie

Desc. génériques : Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection; Epidemiologie

Localisation : INIST, Shelf number 18407, INIST No. 354000183778210090

Origine de la notice : INIST

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Antivirals and the Control of Influenza Outbreaks

Titre : Antivirals and the Control of Influenza Outbreaks

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Source : Clinical infectious diseases. 2007; 45 (10) : 1362-1368

ISSN : 1058-4838

CODEN : CIDIEL

Date de publication : 2007

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 44 ref.

Résumé : During annual influenza epidemics, outbreaks of influenza in closed institutions are common. Among healthy children or young adults, such outbreaks are uncommonly associated with serious morbidity or mortality; however, in hospitals and nursing homes, attack rates as high as 60% and case-fatality rates as high as 50% have been reported. Annual influenza vaccination of both patients or residents and hospital and nursing home staff has had a substantial impact on mortality and has reduced the number of outbreaks. Nonpharmacologic interventions (e.g., handwashing and contact isolation of case patients) may reduce the spread of influenza, although evidence for their efficacy is lacking. Nonetheless, long-term care facilities for the elderly population with high vaccination rates and better-than-average infection-control programs have a 25%-50% chance of experiencing an influenza outbreak each year, with an expected resident attack rate of 35%-40%. Thus, antiviral drugs have been increasingly used to mitigate the impact of influenza outbreaks. There are 2 classes of antiviral drugs that are active against influenza: adamantanes and neuraminidase inhibitors. Drugs of the 2 classes appear to be equally effective for the treatment and prophylaxis of susceptible influenza A virus strains. However, adamantanes are not active against influenza B virus, and an increasing proportion of influenza A isolates are resistant to adamantanes. Adamantanes are associated with higher rates of adverse events than are neuraminidase inhibitors. There is substantial evidence that antiviral prophylaxis is effective in terminating outbreaks of seasonal influenza in closed institutions. If stockpiles are adequate, antiviral drugs are likely to be even more important in mitigating the impact of influenza transmission in health care institutions during the next influenza pandemic.

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

Descripteur(s) anglais

Descripteur(s) : Influenza; Antiviral; Check; Epidemic

Desc. génériques : Virology; Infectious diseases; Medical sciences; Virology; Infectious diseases; Pharmacology; Medical sciences; Viral disease; Infection; Prevention

Descripteur(s) français

Descripteur(s) : Grippe; Antiviral; Controle; Epidemie

Desc. génériques : Virologie; Maladies infectieuses; Sciences médicales; Virologie; Maladies infectieuses; Pharmacologie; Sciences médicales; Virose; Infection; Prevention

Localisation : INIST, Shelf number 18407, INIST No. 354000183778130160

Origine de la notice : INIST

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Issues Relevant to the Adoption and Modification of Hospital Infection-Control Recommendations for Avian Influenza (H5N1 Infection) in Developing Countries

Titre : Issues Relevant to the Adoption and Modification of Hospital Infection-Control Recommendations for Avian Influenza (H5N1 Infection) in Developing Countries

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CODEN : CIDIEL

Date de publication : 2007

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 55 ref.

Résumé : The reemergence of avian influenza (H5N1 infection) has heightened concern for a potential human influenza pandemic. Recommendations regarding preparation for a global avian influenza pandemic are available, and it is imperative that health care workers participate in preparedness planning and training. In developing countries, health care worker preparedness training should address the modes of avian influenza transmission and specify how to implement appropriate infection-control strategies to prevent and control the spread of avian influenza. We provide evidence for avian influenza transmission methods and identify prevention strategies relevant to infection control for hospitals in developing countries. Pandemic influenza preparedness plans must include health care administrative support, mechanisms to rapidly create temporary isolation facilities, systems to restrict access to exposed health care workers, and plans to involve specialists to screen and identify cases early, to provide for continuous monitoring to ensure adherence to optimal infection-control practices, and to provide regular feedback to health care workers.

Code(s) de classement : 002B05A03; 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Nosocomial infection; Avian influenza; Check; Recommendation; Developing countries; Influenzavirus AH5N1

Desc. génériques : Infectious diseases; Medical sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection; Prevention

Descripteur(s) français

Descripteur(s) : Infection nosocomiale; Grippe aviaire; Controle; Recommandation; Pays en developpement; Influenzavirus AH5N1

Desc. génériques : Maladies infectieuses; Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection; Prevention

Localisation : INIST, Shelf number 18407, INIST No. 354000183778130110

Origine de la notice : INIST

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PREPARING FOR AN INFLUENZA PANDEMIC IN ITALY : RESOURCES AND PROCEDURES IN PAEDIATRIC HOSPITAL UNITS

Titre : PREPARING FOR AN INFLUENZA PANDEMIC IN ITALY : RESOURCES AND PROCEDURES IN PAEDIATRIC HOSPITAL UNITS

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Source : Euro surveillance. 2007; 12 (7-9) : 255-257

ISSN : 1025-496X

Date de publication : 2007

Pays de publication : France

Langue(s) : English

Type de document : Serial

Nombre de références : 12 ref.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Influenza; Italy; Hospital; Child; Public health; Sanitary surveillance

Desc. génériques : Virology; Infectious diseases; Medical sciences; Viral disease; Infection; Europe; Human

Descripteur(s) français

Descripteur(s) : Grippe; Italie; Hopital; Enfant; Sante publique; Surveillance sanitaire; Pandemie

Desc. génériques : Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection; Europe; Homme

Localisation : INIST, Shelf number 26438, INIST No. 354000173694720140

Origine de la notice : INIST

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HUMAN INFLUENZA A/H5N1 ("PRE-PANDEMIC") VACCINES : INFORMING POLICY DEVELOPMENT IN EUROPE

Titre : HUMAN INFLUENZA A/H5N1 ("PRE-PANDEMIC") VACCINES : INFORMING POLICY DEVELOPMENT IN EUROPE

Auteur(s) : TEAM Influenza

Source : Euro surveillance. 2007; 12 (7-9) : 264-265

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Date de publication : 2007

Pays de publication : France

Langue(s) : English

Type de document : Serial

Nombre de références : 12 ref.

Code(s) de classement : 002B05

Descripteur(s) anglais

Descripteur(s) : Immunoprophylaxis; Prevention; Vaccine; Policy; Human; Europe; Infection; Public health; Sanitary surveillance; Influenzavirus AH5N1

Desc. génériques : Infectious diseases; Medical sciences

Descripteur(s) français

Descripteur(s) : Immunoprophylaxie; Prevention; Vaccin; Politique; Homme; Europe; Infection; Sante publique; Surveillance sanitaire; Pandemie; Influenzavirus AH5N1

Desc. génériques : Maladies infectieuses; Sciences medicales

Localisation : INIST, Shelf number 26438, INIST No. 354000173694720180

Origine de la notice : INIST

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Responding to Simulated Pandemic Influenza in San Antonio, Texas

Titre : Responding to Simulated Pandemic Influenza in San Antonio, Texas

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Source : Infection control and hospital epidemiology. 2008; 29 (4) : 320-326

ISSN : 0899-823X

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 36 ref.

Résumé : **OBJECTIVE.** To describe the results of a simulation study of the spread of pandemic influenza, the effects of public health measures on the simulated pandemic, and the resultant adequacy of the surge capacity of the hospital infrastructure and to investigate the adequacy of key elements of the national pandemic influenza plan to reduce the overall attack rate so that surge capacity would not be overwhelmed. **DESIGN.** We used 2 discrete-event simulation models: the first model simulates the contact and disease transmission process, as affected by public health interventions, to produce a stream of arriving patients, and the second model simulates the diagnosis and treatment process and determines patient outcomes. **SETTING.** Hypothetical scenarios were based on the response plans, infrastructure, and demographic data of the population of San Antonio, Texas. **RESULTS.** Use of a mix of strategies, including social distancing, antiviral medications, and targeted vaccination, may limit the overall attack rate so that demand for care would not exceed the capacity of the infrastructure. Additional simulations to assess social distancing as a sole mitigation strategy suggest that a reduction of infectious community contacts to half of normal levels would have to occur within approximately 7 days. **CONCLUSIONS.** Under ideal conditions, the mix of strategies may limit demand, which can then be met by community surge capacity. Given inadequate supplies of vaccines and antiviral medications, aggressive social distancing alone might allow for the control of a local epidemic without reliance on outside support.

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

Descripteur(s) anglais

Descripteur(s) : Influenza; Texas; Public health

Desc. génériques : Public health; Medical sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection; United States; North America; America

Descripteur(s) français

Descripteur(s) : Grippe; Texas; Santé publique; Pandémie

Desc. génériques : Santé publique; Sciences médicales; Virologie; Maladies infectieuses; Sciences médicales; Virose; Infection; Etats Unis; Amérique du Nord; Amérique

Localisation : INIST, Shelf number 19430, INIST No. 354000173698450060

Origine de la notice : INIST

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Ecology of H3 avian influenza viruses in Korea and assessment of their pathogenic potentials

Titre : Ecology of H3 avian influenza viruses in Korea and assessment of their pathogenic potentials

Auteur(s) : SONG Min Suk; OH Taek Kyu; HO JIN MOON; YOO Dai Woon; EUN HO LEE; LEE Jong Soo; KIM Chul Jung; YOO Gi Jo; KIM Hyunggee; CHOI Young Ki

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Source : Journal of general virology. 2008; 89 (p. 4) : 949-957

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 : To determine the genetic origins of novel H3 avian influenza viruses of chickens and ducks in Korea, genetic characterization of H3 avian influenza viruses isolated from live poultry markets and migratory aquatic birds in South Korea during 2004-2006 was conducted. Phylogenetic analysis revealed that at least four novel genotypes of H3N2 and two genotypes of H3N6 avian influenza viruses were co-circulating in backyard poultry of Korea. The viruses were reassortants between H9N2 viruses of Korean chickens and unknown influenza viruses of migratory birds. Genetic comparison of H3 viruses from live bird markets with those from wild bird isolates revealed that certain gene segments of wild bird isolates are related closely to those of Korean group H9N2 viruses isolated from live poultry markets in 2003. Furthermore, animal-challenge studies demonstrated that the pathogenicity of certain avian H3 influenza viruses was altered due to reassortment, leading to H3 avian influenza viruses in Korea that can potentially expand their host range to include mammals. These studies emphasize the continuing need to monitor backyard poultry at live poultry markets to better understand interspecies transmission and the emergence of novel influenza viruses that have the potential to infect humans.

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

Descripteur(s) anglais

Descripteur(s) : Avian influenza virus; Korea; Evaluation; Pathogenicity; Microbiology

Desc. génériques : Virology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Asia

Descripteur(s) français

Descripteur(s) : Influenzavirus aviaire; Coree; Evaluation; Pouvoir pathogene; Microbiologie

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Asie

Localisation : INIST, Shelf number 13533, INIST No. 354000183767240130

Origine de la notice : INIST

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Protection of cats against lethal influenza H5N1 challenge infection

Titre : Protection of cats against lethal influenza H5N1 challenge infection

Auteur(s) : VAHLENKAMP Thomas W; HARDER Timm C; GIESE Matthias; FENGSHENG LIN; TEITKE Jens P; KLOPFLEISCH Robert; HOFFMANN Ralf; TARPEY Ian; BEER Martin; METTENLEITER Thomas C
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Source : Journal of general virology. 2008; 89 (p. 4) : 968-974

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 avian influenza virus (HPAIV) H5N1 of Asian origin continues to circulate in poultry and wild birds, causing considerable concern for veterinary and public health in Asia, Europe and Africa. Natural transmission of HPAIV H5N1 from poultry to humans, resulting in infections associated with high mortality, and from poultry or wild birds to large felids and domestic cats has been reported. Experimental infection of cats with HPAIV H5N1 derived from a human patient resulted in lethal disease. The role of cats in the adaptation of HPAIV H5N1 to mammals and vaccination regimens for the eventual protection of cats, however, remain to be elucidated. Here, it was shown that cats can be protected against a lethal high-dose challenge infection by an inactivated, adjuvanted heterologous H5N6 avian influenza virus vaccine. The challenge HPAIV H5N1 was derived from a naturally infected cat. In non-vaccinated cats, low-dose exposure resulted in asymptomatic infections with minimal virus excretion. As diseased cats can transmit the infection to naive contact animals, the epidemiological role of H5N1 -infected cats in endemically infected areas as a link between wild birds, poultry and humans needs close inspection, and vaccination of cats should be considered to reduce possible human exposure.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Descripteur(s) : Animal; Influenza; Microbiology

Desc. génériques : Virology; Microbiology; Biological sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Animal; Grippe; Microbiologie

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Virose; Infection

Localisation : INIST, Shelf number 13533, INIST No. 354000183767240150

Origine de la notice : INIST

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Epitope mapping of the hemagglutinin molecule of a highly pathogenic H5N1 influenza virus by using monoclonal antibodies

Titre : Epitope mapping of the hemagglutinin molecule of a highly pathogenic H5N1 influenza virus by using monoclonal antibodies

Auteur(s) : KAVERIN Nikolai V; RUDNEVA Irina A; GOVORKOVA Elena A; TIMOFEEVA Tatyana A; SHILOV Aleksandr A; KOCHERGIN NIKITSKY Konstantin S; KRYLOV Piotr S; WEBSTER Robert G

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Source : Journal of virology. 2007; 81 (23) : 12911-12917

ISSN : 0022-538X

Date de publication : 2007

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 31 ref.

Résumé : We mapped the hemagglutinin (HA) antigenic epitopes of a highly pathogenic H5N1 influenza virus on the three-dimensional HA structure by characterizing escape mutants of a recombinant virus containing A/Vietnam/1203/04 (H5N1) AHA and neuraminidase genes in the genetic background of A/Puerto Rico/8/34 (H1N1) virus. The mutants were selected with a panel of eight anti-HA monoclonal antibodies (MAbs), seven to A/Vietnam/1203/04 (H5N1) virus and one to A/Chicken/Pennsylvania/8125/83 (H5N2) virus, and the mutants' HA genes were sequenced. The amino acid changes suggested three MAb groups: four MAbs reacted with the complex epitope comprising parts of the antigenic site B of H3 HA and site Sa of H1 HA, two MAbs reacted with the epitope corresponding to the antigenic site A in H3 HA, and two MAbs displayed unusual behavior: each recognized amino acid changes at two widely separate antigenic sites. Five changes were detected in amino acid residues not previously reported as changed in H5 escape mutants, and four others had substitutions not previously described. The HA antigenic structure differs substantially between A/Vietnam/1203/04 (H5N1) virus and the low-pathogenic A/Mallard/Pennsylvania/10218/84 (H5N2) virus we previously characterized (N. V. Kaverin et al., J. Gen. Virol. 83:2497-2505, 2002). The hemagglutination inhibition reactions of the MAbs with recent highly pathogenic H5N1 viruses were consistent with the antigenic-site amino acid changes but not with clades and subclades based on H5 phylogenetic analysis. These results provide information on the recognition sites of the MAbs widely used to study H5N1 viruses and demonstrate the involvement of the HA antigenic sites in the evolution of highly pathogenic H5N1 viruses, findings that can be critical for characterizing pathogenesis and vaccine design.

Code(s) de classement : 002A05C10; 002A05C04; 002A05C07

Descripteur(s) anglais

Descripteur(s) : Influenza A virus; Antigenic determinant; Hemagglutinin; Pathogenicity; Monoclonal antibody; Virology

Desc. génériques : Virology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Immunology; Pharmacology; Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) français

Descripteur(s) : Virus grippal A; Determinant antigenique; Hemagglutinine; Pouvoir pathogene; Anticorps monoclonal; Virologie

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Immunologie; Pharmacologie; Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST, Shelf number 13592, INIST No. 354000173576180200
Origine de la notice : INIST
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RespiFinder : a New Multiparameter Test To Differentially Identify Fifteen Respiratory Viruses

Titre : RespiFinder : a New Multiparameter Test To Differentially Identify Fifteen Respiratory Viruses

Auteur(s) : REIJANS Martin; DINGEMANS Gijs; KLAASSEN Corne H; MEIS Jacques F; KEIJDENER Judith; MULDER Brit; EADIE Kimberly; VAN LEEUWEN Willem; VAN BELKUM Alex; HORREVORTS Alphons M; SIMONS Guus

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Langue(s) : English

Type de document : Serial

Nombre de références : 36 ref.

Résumé : Broad-spectrum analysis for pathogens in patients with respiratory tract infections is becoming more relevant as the number of potential infectious agents is still increasing. Here we describe the new multiparameter RespiFinder assay, which is based on the multiplex ligation-dependent probe amplification (MLPA) technology. This assay detects 15 respiratory viruses in one reaction. The MLPA reaction is preceded by a preamplification step which ensures the detection of both RNA and DNA viruses with the same specificity and sensitivity as individual monoplex real-time reverse transcription-PCRs. The RespiFinder assay was validated with 144 clinical samples, and the results of the assay were compared to those of cell culture and a respiratory syncytial virus (RSV)-specific immunochromatography assay (ICA). Compared to the cell culture results, the RespiFinder assay showed specificities and sensitivities of 98.2% and 100%, respectively, for adenovirus; 96.4% and 100%, respectively, for human metapneumovirus; 98.2% and 100%, respectively, for influenza A virus (InfA); 99.1% and 100%, respectively, for parainfluenza virus type 1 (PIV-1); 99.1% and 80%, respectively, for PIV-3; 90.1% and 100%, respectively, for rhinovirus; and 94.6% and 100%, respectively, for RSV. Compared to the results of the RSV-specific ICA, the RespiFinder assay gave a specificity and a sensitivity of 82.4% and 80%, respectively. PIV-2, PIV-4, influenza B virus, InfA H5N1, and coronavirus 229E were not detected in the clinical specimens tested. The use of the RespiFinder assay resulted in an increase in the diagnostic yield compared to that obtained by cell culture (diagnostic yields, 60% and 35.5%, respectively). In conclusion, the RespiFinder assay provides a user-friendly and high-throughput tool for the simultaneous detection of 15 respiratory viruses with excellent overall performance statistics.

Code(s) de classement : 002A05

Descripteur(s) anglais

Descripteur(s) : Identification; Microbiology

Desc. génériques : Microbiology; Biological sciences

Descripteur(s) français

Descripteur(s) : Identification; Microbiologie

Desc. génériques : Microbiologie; Sciences biologiques

Localisation : INIST, Shelf number 17088, INIST No. 354000183024560120

Origine de la notice : INIST

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Le virus de la grippe aviaire sera-t-il humain ?

Titre : Le virus de la grippe aviaire sera-t-il humain ?

Auteur(s) : THOMAS Yves; WUNDERLI Werner; CHERPILLOD Pascal; KAISER Laurent

Source : REVUE MEDICALE SUISSE. 2007; 3 (106) : 918-923

ISSN : 1660-9379

Date de publication : 2007

Pays de publication : Switzerland

Langue(s) : French

Type de document : Serial

Résumé : Depuis 1997 apparait regulierement chez l' homme un virus Influenza d' origine aviaire a l' origine d' infections respiratoires severes conduisant a un deces dans 50% des cas. Le virus Influenza A (H5N1) a l' origine de cette maladie circule tant chez les oiseaux sauvages que domestiques. Des millions de volailles ont regulierement ete infectees ou abattues par mesure de precaution sur trois continents : Asie, Afrique et Europe. Le virus H5N1, comme les virus Influenza en general, a la capacite d' adapter son genome tres facilement et rapidement. Grace a cette propriete, il pourrait passer directement du monde aviaire aux humains. Le present article resume et discute nos connaissances permettant d' evaluer le risque d' une nouvelle pandémie. R.A.

Code(s) de classement : 002B30A11

Descripteur(s) anglais

Descripteur(s) : Influenza; Risk analysis; Prevention; Contagion

Desc. génériques : Public health; Medical sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Grippe; Analyse risque; Prevention; Contagion

Desc. génériques : Sante publique; Sciences medicales; Virose; Infection

Localisation : BDSP/SAPHIR, Shelf number 61875

Origine de la notice : BDSP

Pandemie de grippe : quel role pour les medecins de premier recours ?

Titre : Pandemie de grippe : quel role pour les medecins de premier recours ?

Auteur(s) : ZANETTI Giorgio; HUGONNET Stephane; TROILLET Nicolas; STAEGER Philippe; SUDRE Philippe; MASSEREY Eric

Source : REVUE MEDICALE SUISSE. 2007; 3 (106) : 910-914

ISSN : 1660-9379

Date de publication : 2007

Pays de publication : Switzerland

Langue(s) : French

Type de document : Serial

Résumé : La survenue d' une pandémie de grippe semble, a terme, un evenement ineluctable. La grippe aviaire causee par le virus Influenza A H5N1 est actuellement la situation qui risque le plus de degenerer en pandémie. Sa dissemination stimule donc d' importants efforts de planification. L' implication des medecins de premier recours en cas de pandémie grippale est essentielle tant en raison de l' ampleur presumee de l' enjeu que de la competence de ces medecins a y repondre. Le but de cet article est d' illustrer quel serait leur role dans cette situation, et de presenter les deux principales options envisagees pour organiser leur travail : l' integration des praticiens dans un systeme ambulatoire dedie, specifiquement organise pour la pandémie grippale, ou leur contribution dans les cabinets medicaux existants moyennant des adaptations. R.A.

Code(s) de classement : 002B30A11

Descripteur(s) anglais

Descripteur(s) : Epidemic; Influenza; Primary health care; Communicable disease; Prevention

Desc. génériques : Public health; Medical sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Epidemie; Grippe; Soins sante primaire; Maladie contagieuse; Prevention

Desc. génériques : Sante publique; Sciences medicales; Virose; Infection

Localisation : BDSP/SAPHIR, Shelf number 61867

Origine de la notice : BDSP

Maladies infectieuses (sauf sida) : nouveautés en médecine 2006

Titre : Maladies infectieuses (sauf sida) : nouveautés en médecine 2006

Auteur(s) : ZANETTI Giorgio

Source : REVUE MEDICALE SUISSE. 2007; 3 (93) : 26-29

ISSN : 1660-9379

Date de publication : 2007

Pays de publication : Switzerland

Langue(s) : French

Type de document : Serial

Résumé : L' actualité infectiologique est surtout épidémiologique. Le virus Influenza A H5N1 poursuit sa dissémination. Il n' est pas adapté à l' homme, mais les progrès scientifiques confirment son potentiel pandémique. Le Chikungunya a pris des proportions impressionnantes autour de l' océan indien. De nouveaux staphylocoques dorés résistants se propagent dans la communauté. Enfin, une souche très virulente de Clostridium difficile apparaît en Amérique du Nord et en Europe. Les nouveautés thérapeutiques sont rares. Plusieurs publications encouragent l' utilisation rationnelle des antibiotiques à disposition, par exemple par la prescription différée en cas d' otite moyenne aiguë ou l' utilisation appropriée des cultures urinaires chez les patients âgés. Un vaccin contre le virus du papillome humain offre désormais une protection efficace contre le cancer du col utérin. R.A.

Code(s) de classement : 002B30A11

Descripteur(s) anglais

Descripteur(s) : Infection; Emerging disease; Chemotherapy; Epidemiology

Desc. génériques : Public health; Medical sciences; Treatment

Descripteur(s) français

Descripteur(s) : Infection; Maladie émergente; Chimiothérapie; Épidémiologie

Desc. génériques : Santé publique; Sciences médicales; Traitement

Localisation : BDSP/SAPHIR, Shelf number 60837

Origine de la notice : BDSP

Se prémunir contre la grippe aviaire : pour collaborateurs et clients des pharmacies

Titre : Se prémunir contre la grippe aviaire : pour collaborateurs et clients des pharmacies

Auteur(s) : MUTSCH Matthias

Source : PHARMAJOURNAL . 2008; 146 (3) : 23-24

ISSN : 1661-8785

Date de publication : 2008

Pays de publication : Switzerland

Langue(s) : French

Type de document : Serial

Résumé : Cet article fait une synthèse des principaux points dont il faut tenir compte dans les pharmacies publiques en cas de pandémie de grippe aviaire

Code(s) de classement : 002B30A11

Descripteur(s) anglais

Descripteur(s) : Chemist; Prevention

Desc. génériques : Public health; Medical sciences

Descripteur(s) français

Descripteur(s) : Pharmacien; Prevention

Desc. génériques : Santé publique; Sciences médicales

Localisation : BDSP/SAPHIR, Shelf number 64283

Origine de la notice : BDSP

Detection and isolation of H5N1 influenza virus from large volumes of natural water

Titre : Detection and isolation of H5N1 influenza virus from large volumes of natural water

Auteur(s) : KHALENKOV Alexey; GRAEME LAVER W; WEBSTER Robert G

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Source : Journal of virological methods. 2008; 149 (1) : 180-183

ISSN : 0166-0934

CODEN : JVMEDH

Date de publication : 2008

Pays de publication : Netherlands

Langue(s) : English

Type de document : Serial

Type de document : short-communication

Nombre de références : 1/2 p.

Résumé : Various species of aquatic or wetlands birds can be the natural reservoir of avian influenza A viruses of all hemagglutinin (HA) subtypes. Shedding of the virus into water leads to transmission between waterfowl and is a major threat for epidemics in poultry and pandemics in humans. Concentrations of the influenza virus in natural water reservoirs are often too low to be detected by most methods. The procedure was designed to detect and isolate low concentrations of the influenza virus in large volumes of water without the need for costly installations and reagents. The virus was adsorbed onto formalin-fixed erythrocytes and subsequently isolated in chicken embryos. Sensitivity of the method was determined using a reverse-genetic H5N1 virus. A concentration as low as 0.03 of the 50% egg infection dose per milliliter (EID₅₀/ml) of the initial volume of water was effectively detected. The probability of detection was >13%, which is comparable to that of detecting the influenza virus M-gene by PCR amplification. The method can be used by field workers, ecologists, ornithologists, and researchers who need a simple method to isolate H5N1 influenza virus from natural reservoirs. The detection and isolation of virus in embryonated chicken eggs may help epidemiologic, genetic, and vaccine studies.

Code(s) de classement : 002A05C09

Descripteur(s) anglais

Descripteur(s) : Influenzavirus; Detection; Isolation; Hemagglutination; Microbiology; Method; Virology

Desc. génériques : Virology; Microbiology; Biological sciences; Orthomyxoviridae; Virus

Descripteur(s) français

Descripteur(s) : Influenzavirus; Detection; Isolement; Hemagglutination; Microbiologie; Methode; Virologie

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Orthomyxoviridae; Virus

Localisation : INIST, Shelf number 18295, INIST No. 354000183354230270

Origine de la notice : INIST

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The effect of sample type, temperature and RNAlater<<sup>T^M on the stability of avian influenza virus RNA

Titre : The effect of sample type, temperature and RNAlater<<sup>T^M on the stability of avian influenza virus RNA

Auteur(s) : FORSTER Julie L; HARKIN Valerie B; GRAHAM David A; MCCULLOUGH Samuel J

Affiliation(s) : Veterinary Sciences Division, Agri-Food and Biosciences Institute, Stormont, Belfast BT4 3SD, Northern Ireland, United Kingdom

Source : Journal of virological methods. 2008; 149 (1) : 190-194

ISSN : 0166-0934

CODEN : JVMEDH

Date de publication : 2008

Pays de publication : Netherlands

Langue(s) : English

Type de document : Serial

Type de document : short-communication

Nombre de références : 1/2 p.

Résumé : As a result of continuing worldwide outbreaks of highly pathogenic avian influenza (HPAI) caused by the Asian lineage of H5N 1, surveillance of targeted avian species in selected regions has been implemented. In these wild bird surveys, the use of real-time reverse transcription (rRT)-PCR has proved to be an invaluable tool as a frontline screening assay for the detection of avian influenza virus (AIV) RNA. However, verification of HPAI diagnosis, particularly in a primary outbreak situation, requires confirmation by a national, community or world reference laboratory. This may necessitate freezing and thawing of samples, sub-sampling and transportation to the reference laboratory. The deleterious effects of such handling on the infectivity of virus and the yield of viral RNA have been observed. The objective of this study was to investigate the effects of freezing and thawing, time, sample type and transportation on the yield of AIV RNA. Additionally, the effect of the RNA stabilisation agent, RNAlater<<sup>T^M was investigated. It was demonstrated that the quality of AIV RNA in faecal homogenate was markedly reduced by freezing and thawing, but that treatment with RNAlater<<sup>T^M protected the viral RNA from deterioration. When using RNAlater<<sup>T^M even low titre AIV samples were protected from the detrimental effects of time and transportation conditions.

Code(s) de classement : 002A05C09

Descripteur(s) anglais

Descripteur(s) : Avian influenzavirus; Temperature; Real time; Reverse transcription polymerase chain reaction; Microbiology; Method; Virology

Desc. génériques : Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) français

Descripteur(s) : Influenzavirus aviaire; Temperature; Temps reel; Reaction chaine polymerase RT; Microbiologie; Methode; Virologie

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST, Shelf number 18295, INIST No. 354000183354230290

Origine de la notice : INIST

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Quantifying the transmission potential of pandemic influenza

Titre : Quantifying the transmission potential of pandemic influenza

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Source : Physics of life reviews. 2008; 5 (1) : 50-77

ISSN : 1571-0645

Date de publication : 2008

Pays de publication : Netherlands

Langue(s) : English

Type de document : Serial

Nombre de références : 168 ref.

Résumé : This article reviews quantitative methods to estimate the basic reproduction number of pandemic influenza, a key threshold quantity to help determine the intensity of interventions required to control the disease. Although it is difficult to assess the transmission potential of a probable future pandemic, historical epidemiologic data is readily available from previous pandemics, and as a reference quantity for future pandemic planning, mathematical and statistical analyses of historical data are crucial. In particular, because many historical records tend to document only the temporal distribution of cases or deaths (i.e. epidemic curve), our review focuses on methods to maximize the utility of time-evolution data and to clarify the detailed mechanisms of the spread of influenza. First, we highlight structured epidemic models and their parameter estimation method which can quantify the detailed disease dynamics including those we cannot observe directly. Duration-structured epidemic systems are subsequently presented, offering firm understanding of the definition of the basic and effective reproduction numbers. When the initial growth phase of an epidemic is investigated, the distribution of the generation time is key statistical information to appropriately estimate the transmission potential using the intrinsic growth rate. Applications of stochastic processes are also highlighted to estimate the transmission potential using similar data. Critically important characteristics of influenza data are subsequently summarized, followed by our conclusions to suggest potential future methodological improvements.

Code(s) de classement : 002B30A01A1

Descripteur(s) anglais

Descripteur(s) : Transmission; Epidemiology; Reproduction; Models; Review; Quantitative analysis; Influenza; Influenzavirus

Desc. génériques : Public health; Medical sciences; Viral disease; Infection; Orthomyxoviridae; Virus

Descripteur(s) français

Descripteur(s) : Transmission; Epidemiologie; Reproduction; Modele; Article synthese; Analyse quantitative; Grippe; Influenzavirus; Pandemie

Desc. génériques : Sante publique; Sciences medicales; Virose; Infection; Orthomyxoviridae; Virus

Localisation : INIST, Shelf number 27673, INIST No. 354000183536650030

Origine de la notice : INIST

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Probable limited person-to-person transmission of highly pathogenic avian influenza A (H5N1) virus in China. Commentaries

Titre : Probable limited person-to-person transmission of highly pathogenic avian influenza A (H5N1) virus in China. Commentaries

Auteur(s) : STEIN James H, comment; CURRIER Judith S, comment; NGUYEN TRAN HIEN, comment; FARRAR Jeremy, comment; HORBY Peter, comment; HUA WANG; ZIJIAN FENG; YUELONG SHU; HONGJIE YU; LEI ZHOU; RONGQIANG ZU; YANG HUAI; JIE DONG; CHANGJUN BAO; LEYING WEN; HONG WANG; PENG YANG; WEI ZHAO; LIBO DONG; MINGHAO ZHOU; QIAOHONG LIAO; HAITAO YANG; MIN WANG; XIAOJUN LU; ZHIYANG SHI; WEI WANG; LING GU; FENGCAI ZHU; QUN LI; WEIDONG YIN; WEIZHONG YANG; DEXIN LI; UYEKI Timothy M; YU WANG

Affiliation(s) : Division of Cardiovascular Medicine, University of Wisconsin School of Medicine and Public Health, Madison, WI 53717, USA, United States; Division of Infectious Diseases, UCLA Center for Clinical AIDS Research and Education, University of California David Geffen School of Medicine, Los Angeles, CA, United States; National Institute of Hygiene and Epidemiology, Hanoi, Viet Nam; Hospital for Tropical Diseases and Oxford University, QUAN 5, Ho Chi Minh City, Viet Nam; National Institute for Infectious and Tropical Diseases and Oxford University, Hanoi, Viet Nam; Jiangsu Provincial Centre for Disease Control and Prevention, Nanjing, China; Office for Disease Control and Emergency Response, Chinese Centre for Disease Control and Prevention (China CDC), Beijing, China; State Key Laboratory for Infectious Disease Prevention and Control, National Institute for Viral Disease Control and Prevention, China CDC, Beijing, China; Jiangsu Provincial People's Hospital, Nanjing, China; Nanjing Secondary People's Hospital, Nanjing, China; Najing Centre for Disease Control and Prevention, Nanjing, China; Sinovac Biotech Co, Beijing, China; Influenza Division, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, United States

Source : Lancet British edition. 2008; 371 (9622) : 1392-1394, 1427-1434 11 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 : 62 ref.

Résumé : Background In December, 2007, a family cluster of two individuals infected with highly pathogenic avian influenza A (H5N1) virus was identified in Jiangsu Province, China. Field and laboratory investigations were implemented immediately by public-health authorities. Methods Epidemiological, clinical, and virological data were collected and analysed. Respiratory specimens from the patients were tested by reverse transcriptase (RT) PCR and by viral culture for the presence of H5N1 virus. Contacts of cases were monitored for symptoms of illness for 10 days. Any contacts who became ill had respiratory specimens collected for H5N1 testing by RT PCR. Sera were obtained from contacts for H5N1 serological testing by microneutralisation and horse red-blood-cell haemagglutinin inhibition assays. Findings The 24-year-old index case died, and the second case, his 52-year-old father, survived after receiving early antiviral treatment and post-vaccination plasma from a participant in an H5N1 vaccine trial. The index case's only plausible exposure to H5N1 virus was a poultry market visit 6 days before the onset of illness. The second case had substantial unprotected close exposure to his ill son. 91 contacts with close exposure to one or both cases without adequate protective equipment provided consent for serological investigation. Of these individuals, 78 (86%) received oseltamivir chemoprophylaxis and two had mild illness. Both ill contacts tested negative for H5N1 by RT PCR. All 91 close contacts tested negative for H5N1 antibodies. H5N1 viruses isolated from the two cases were genetically identical except for one non-synonymous nucleotide substitution. Interpretation Limited, non-sustained person-to-person transmission of H5N1 virus probably occurred in this family cluster. Funding Chinese Ministry of Science and Technology; US National Institute of Allergy and Infectious Diseases, National Institutes of Health; China-US

Collaborative Program on Emerging and Re-emerging Infectious Diseases.

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

Descripteur(s) anglais

Descripteur(s) : Avian influenza; Limit; Transmission from man to man; Pathogenesis; Pathogenic; Influenzavirus A; Influenza A virus; China; Medicine; Influenzavirus AH5N1

Desc. génériques : Medical sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection; Orthomyxoviridae; Virus; Asia

Descripteur(s) français

Descripteur(s) : Grippe aviaire; Limite; Transmission homme homme; Pathogenie; Pathogene; Influenzavirus A; Virus grippal A; Chine; Medecine; Influenzavirus AH5N1

Desc. génériques : Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection; Orthomyxoviridae; Virus; Asie

Localisation : INIST, Shelf number 5004, INIST No. 354000172678740080

Origine de la notice : INIST

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Comparison of vaccines for induction of heterosubtypic immunity to influenza A virus : Cold-adapted vaccine versus DNA prime-adenovirus boost strategies

Titre : Comparison of vaccines for induction of heterosubtypic immunity to influenza A virus : Cold-adapted vaccine versus DNA prime-adenovirus boost strategies

Auteur(s) : LO Chia Yun; ZHENGQI WU; MISPLON Julia A; PRICE Graeme E; PAPPAS Claudia; KONG Wing Pui; TUMPEY Terrence M; EPSTEIN Suzanne L

Affiliation(s) : Division of Cellular and Gene Therapies, Office of Cellular Tissue and Gene Therapies, Center for Biologics Evaluation and Research (CBER), Food and Drug Administration (FDA), 1401 Rockville Pike, HFM-730, Rockville, MD 20852-1448, United States; Influenza Division, Mailstop G-16, National Center for Immunization and Respiratory Diseases, Coordinating Center for Infectious Diseases, Centers for Disease Control and Prevention, 1600 Clifton Road, NE, Atlanta, GA 30333, United States; Vaccine Research Center, National Institute for Allergy and Infectious Diseases, Room 4504, National Institutes of Health, Bethesda, MD 20892, United States

Source : Vaccine . 2008; 26 (17) : 2062-2072

ISSN : 0264-410X

CODEN : VACCDE

Date de publication : 2008

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Nombre de références : 43 ref.

Résumé : Influenza epidemics or pandemics can arise for which strain- or subtype-matched vaccines are unavailable. Heterosubtypic immunity (Het-I) targeting conserved influenza A antigens could reduce morbidity and mortality during preparation of matched vaccines. Various vaccines inducing Het-I in animals have been studied separately using different viruses and conditions, but effectiveness for inducing Het-I has not been directly compared. The present studies compared immunization with cold-adapted (ca) viruses to DNA prime-recombinant adenovirus (rAd) boost vaccination to conserved antigens nucleoprotein (NP), matrix-2 (M2), or A/NP+M2. Both ca and DNA-rAd vaccinations induced antibody and T cell responses, and protected against lethal H1N1 challenge. Only A/NP+M2 DNA-rAd protected against challenge with highly pathogenic A/Vietnam/1203/2004 (H5N1); ca vaccine did not. Existing ca vaccines may provide some Het-I, but experimental vaccination focusing on conserved antigens was more effective in this model for protection against a divergent, highly pathogenic virus.

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

Descripteur(s) anglais

Descripteur(s) : Influenza A virus; Adenoviridae; Genetic vaccine; Influenza

Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Virus grippal A; Adenoviridae; Vaccin génétique; Grippe

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquée; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Virose; Infection

Localisation : INIST, Shelf number 20289, INIST No. 354000172681790040

Origine de la notice : INIST

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A vaccine prepared from a non-pathogenic H7N7 virus isolated from natural reservoir conferred protective immunity against the challenge with lethal dose of highly pathogenic avian influenza virus in chickens

Titre : A vaccine prepared from a non-pathogenic H7N7 virus isolated from natural reservoir conferred protective immunity against the challenge with lethal dose of highly pathogenic avian influenza virus in chickens

Auteur(s) : SAKABE Saori; SAKODA Yoshihiro; HARAGUCHI Yoshinari; ISODA Norikazu; SODA Kosuke; TAKAKUWA Hiroki; SAIJO Kazue; SAWATA Akira; KUME Katsumi; HAGIWARA Junko; TUCHIYA Kotaro; ZHIFENG LIN; SAKAMOTO Ryuichi; IMAMURA Takashi; SASAKI Takashi; KOKUMAI Norihide; KAWAOKA Yoshihiro; KIDA Hiroshi

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Source : Vaccine . 2008; 26 (17) : 2127-2134

ISSN : 0264-410X

CODEN : VACCDE

Date de publication : 2008

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Nombre de références : 24 ref.

Résumé : During 2001-2004, 41 H7 influenza viruses (2 H7N1 and 39 H7N7 strains) were isolated from fecal samples of migratory ducks that flew from Siberia in the autumn of each year to Japan and Mongolia. A phylogenetic analysis of the hemagglutinin (HA) genes of the nine representative isolates revealed that they belonged to the Eurasian lineage and the deduced amino acid sequence at the cleavage site of the HAs represented apathogenic profiles. One of the H7 isolates A/duck/Mongolia/736/02 (H7N7) was chosen from these H7 isolates for the preparation of the test vaccine. To improve the growth potential of A/duck/Mongolia/736/02 (H7N7) in chicken embryos, A/duck/Hokkaido/Vac-2/04 (H7N7) was generated by genetic reassortment between A/duck/Mongolia/736/02 (H7N7) as the donor of the PB2, PB1, PA, HA, NA, and NS genes and A/duck/Hokkaido/49/98 (H9N2) as that of NP and M genes. The test vaccine was prepared as follows; A/duck/Hokkaido/Vac-2/04 (H7N7) was propagated in chicken embryos and the virus in the allantoic fluid was inactivated and adjuvanted to form an oil-in-water emulsion. The test vaccine conferred immunity to chickens, completely protecting the manifestation of clinical signs against the challenge with lethal dose of H7 highly pathogenic avian influenza virus. These results indicate that influenza viruses isolated from natural reservoirs are useful for vaccine strains.

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

Descripteur(s) anglais

Descripteur(s) : Avian influenzavirus; Chicken; Vaccine; Pathogenicity; Natural immunity; Reservoir; Immunoprotection; Subtype

Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Aves; Vertebrata; Epidemiology; Zoopathogen; Poultry; Veterinary; Farming animal

Descripteur(s) français

Descripteur(s) : Influenzavirus aviaire; Poulet; Vaccin; Pouvoir pathogene; Immunité naturelle; Reservoir; Immunoprotection; Soustype

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquée; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Aves; Vertebrata; Epidemiologie; Zoopathogene; Volaille; Veterinaire; Animal elevage

Localisation : INIST, Shelf number 20289, INIST No. 354000172681790110

Origine de la notice : INIST

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The relative immunogenicity of DNA vaccines delivered by the intramuscular needle injection, electroporation and gene gun methods

Titre : The relative immunogenicity of DNA vaccines delivered by the intramuscular needle injection, electroporation and gene gun methods

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ISSN : 0264-410X

CODEN : VACCDE

Date de publication : 2008

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Nombre de références : 77 ref.

Résumé : Immunogenicity of DNA vaccines varies significantly due to many factors including the inherent immunogenicity of the protein antigen encoded in the DNA vaccine, the optimal immune responses that can be achieved in different animal models and in humans with different genetic backgrounds and, to a great degree, the delivery methods used to administer the DNA vaccines. Based on published results, only the gene gun-mediated delivery approach has been able to elicit protective levels of immune responses in healthy, adult volunteers by DNA immunization alone without the use of another vaccine modality as a boost. Recent results from animal studies suggest that electroporation is also effective in eliciting high level immune responses. However, there have been no reports to identify the similarities and differences between these two leading physical delivery methods for DNA vaccines against infectious disease targets. In the current study, we compared the relative immunogenicity of a DNA vaccine expressing a hemagglutinin (HA) antigen from an H5N1 influenza virus in two animal models (rabbit and mouse) when delivered by either intramuscular needle immunization (IM), gene gun (GG) or electroporation (EP). HA-specific antibody, T cell and B cell responses were analyzed. Our results indicate that, overall, both the GG and EP methods are more immunogenic than the IM method. However, EP and IM stimulated a Th-1 type antibody response and the antibody response to GG was Th-2 dominated. These findings provide important information for the further selection and optimization of DNA vaccine delivery methods for human applications.

Code(s) de classement : 002A05F04

Descripteur(s) anglais

Descripteur(s) : Immunogenicity; Genetic vaccine; Needle; Electroporation; Gene; Method; Antibody; T Lymphocyte; Influenza; B Lymphocyte

Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Immunogenicite; Vaccin genetique; Aiguille; Electroporation; Gene; Methode; Anticorps; Lymphocyte T; Grippe; Lymphocyte B

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquee; Microbiologie; Sciences biologiques; Virose; Infection

Localisation : INIST, Shelf number 20289, INIST No. 354000172681790080

Origine de la notice : INIST

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Genetic analysis of four porcine avian influenza viruses isolated from Shandong, China

Titre : Genetic analysis of four porcine avian influenza viruses isolated from Shandong, China

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Source : Archives of virology. 2008; 153 (1) : 211-217

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Date de publication : 2008

Pays de publication : Austria

Langue(s) : English

Type de document : Serial

Type de document : short-communication

Nombre de références : 20 ref.

Résumé : A Bayesian phylogenetic analysis of eight separate gene segments indicated A/Swine/Shandong/ 2/2003 (H5N1), A/Swine/Shandong/na/2003 (H9N2), A/Swine/Shandong/nb/2003 (H9N2) and A/Swine/Shandong/nc/2005 (H9N2) probably represent two multiple reassortant lineages, that had not been described before, with genes coming from H5N1, H9N2 and other lineages from poultry in Asia. Amino acid motifs within the haemagglutinin sequence of A/Swine/Shandong/nb/2003 suggested it may be able to infect people, whereas the sequences of the other three isolates suggested they would not have had that capability. Our analysis emphasizes the need for a comprehensive study of the interactions between H5N1 and H9N2 viruses in Asia that includes sequencing and phylogenetic investigation.

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

Descripteur(s) anglais

Descripteur(s) : Avian influenza virus; Genetics; China; Porcine influenza

Desc. génériques : Virology; Microbiology; Biological sciences; Genetics; Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Asia; Zoonoses; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Influenzavirus aviaire; Génétique; Chine; Grippe porcine

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Génétique; Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Asie; Zoonoses; Virus; Infection

Localisation : INIST, Shelf number 6355, INIST No. 354000173715850220

Origine de la notice : INIST

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Organisation de la reanimation en situation de pandémie de grippe aviaire; Organization of intensive care in case of avian flu pandemic

Titre : Organisation de la reanimation en situation de pandémie de grippe aviaire; Organization of intensive care in case of avian flu pandemic

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Source : Reanimation Paris 2001. 2008; 17 (3) : 286-296

ISSN : 1624-0693

Date de publication : 2008

Pays de publication : France

Langue(s) : French

Type de document : Serial

Nombre de références : 22 ref.

Code(s) de classement : 002B27B; 002B27C

Descripteur(s) anglais

Descripteur(s) : Avian influenza; Resuscitation; Intensive care

Desc. génériques : Resuscitation; Intensive care medicine; Medical sciences; Medical sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Grippe aviaire; Reanimation; Soins intensif

Desc. génériques : Reanimation; Soins intensifs; Sciences medicales; Sciences medicales; Virose; Infection

Localisation : INIST, Shelf number 26751, INIST No. 354000172722130140

Origine de la notice : INIST

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Evolution du taux de couverture vaccinale contre la grippe en France : de 2001 a 2006; Evolution of influenza vaccination coverage in France from 2001 to 2006

Titre : Evolution du taux de couverture vaccinale contre la grippe en France : de 2001 a 2006; Evolution of influenza vaccination coverage in France from 2001 to 2006

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Source : Medecine et maladies infectieuses. 2008; 38 (3) : 125-132

ISSN : 0399-077X

CODEN : MMAIB5

Date de publication : 2008

Pays de publication : France

Langue(s) : French

Langue(s) du résumé : English

Type de document : Serial

Nombre de références : 14 ref.

Résumé : Introduction. - Le risque d'une nouvelle pandémie a entraîné une prise de conscience d'un besoin d'une couverture vaccinale élevée contre la grippe saisonnière. Objectifs. - Analyser les tendances, comprendre les motivations ou les réticences et identifier les intentions de vaccination pour 2006/2007. Méthode. - Une enquête a été menée portant sur la période 2001 à 2006, en France, sur un échantillon de 9835 sujets représentatif de la population de plus de 15 ans. Un questionnaire postal identique a été utilisé. Résultats. - La couverture vaccinale antigrippale a faiblement augmenté, pour atteindre 24,2 % en 2005/2006. Chez les personnes de plus de 65 ans, elle a atteint 70,1 % en 2005/2006. Au cours des deux dernières saisons, le remboursement de la vaccination a été le principal motif de vaccination. L'âge, considérer la grippe comme une maladie grave et les recommandations du médecin de famille ou de l'infirmière étaient également des facteurs motivants. En 2005 à 2006, le risque de grippe aviaire n'a pas eu d'impact (2 %). Chez les personnes n'ayant jamais été vaccinées, les raisons évoquées étaient les suivantes : se sentir trop jeune pour être vacciné, n'avoir jamais envisagé une vaccination auparavant, absence de recommandation du médecin de famille. Parmi les personnes ayant précédemment été vaccinées les raisons de non-revaccination étaient l'oubli ou avoir eu un syndrome grippal malgré la vaccination. Conclusion. - Le taux de vaccination était stable entre 2001 et 2006. La France peut atteindre l'objectif international fixé par l'OMS (couverture vaccinale de 75 % chez les personnes âgées), mais des efforts sont à faire pour les autres catégories.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Influenza A; Evolution; Vaccination coverage; France; Vaccination; Prevention; Microbiology

Desc. génériques : Virology; Infectious diseases; Medical sciences; Viral disease; Infection; Europe

Descripteur(s) français

Descripteur(s) : Grippe A; Evolution; Couverture vaccinale; France; Vaccination; Prevention; Microbiologie

Desc. génériques : Virologie; Maladies infectieuses; Sciences médicales; Virose; Infection; Europe

Localisation : INIST, Shelf number 15434, INIST No. 354000172763050020

Origine de la notice : INIST

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NP, PB1, and PB2 Viral Genes Contribute to Altered Replication of H5N1 Avian Influenza Viruses in Chickens

Titre : NP, PB1, and PB2 Viral Genes Contribute to Altered Replication of H5N1 Avian Influenza Viruses in Chickens

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Source : Journal of virology. 2008; 82 (9) : 4544-4553

ISSN : 0022-538X

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 61 ref.

Résumé : The virulence determinants for highly pathogenic avian influenza viruses (AIVs) are considered multigenic, although the best characterized virulence factor is the hemagglutinin (HA) cleavage site. The capability of influenza viruses to reassort gene segments is one potential way for new viruses to emerge with different virulence characteristics. To evaluate the role of other gene segments in virulence, we used reverse genetics to generate two H5N1 recombinant viruses with differing pathogenicity in chickens. Single-gene reassortants were used to determine which viral genes contribute to the altered virulence. Exchange of the PB1, PB2, and NP genes impacted replication of the reassortant viruses while also affecting the expression of specific host genes. Disruption of the parental virus' functional polymerase complexes by exchanging PB1 or PB2 genes decreased viral replication in tissues and consequently the pathogenicity of the viruses. In contrast, exchanging the NP gene greatly increased viral replication and expanded tissue tropism, thus resulting in decreased mean death times. Infection with the NP reassortant virus also resulted in the upregulation of gamma interferon and inducible nitric oxide synthase gene expression. In addition to the impact of PB1, PB2, and NP on viral replication, the HA, NS, and M genes also contributed to the pathogenesis of the reassortant viruses. While the pathogenesis of AIVs in chickens is clearly dependent on the interaction of multiple gene products, we have shown that single-gene reassortment events are sufficient to alter the virulence of AIVs in chickens.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Descripteur(s) : Avian influenza virus; Chicken; Gene; Replication; Virology

Desc. génériques : Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Aves; Vertebrata; Veterinary

Descripteur(s) français

Descripteur(s) : Influenzavirus aviaire; Poulet; Gene; Replication; Virologie

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Aves; Vertebrata; Veterinaire

Localisation : INIST, Shelf number 13592, INIST No. 354000172771700350

Origine de la notice : INIST

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Infection Due to 3 Avian Influenza Subtypes in United States Veterinarians

Titre : Infection Due to 3 Avian Influenza Subtypes in United States Veterinarians

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Source : Clinical infectious diseases. 2007; 45 (1) : 4-9

ISSN : 1058-4838

CODEN : CIDIEL

Date de publication : 2007

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 16 ref.

Résumé : Background. Pandemic influenza virus strains originate in avian species. We examined veterinarians in the United States for evidence of previous avian influenza virus infection. Methods. We performed a controlled, cross-sectional seroprevalence study among 42 veterinarians and 66 healthy control subjects using serum samples collected from 2002 through 2004. Serum samples were tested using a microneutralization assay against 9 influenza A virus strains. Results. Using multivariable logistic regression modeling, veterinarians exposed to birds demonstrated statistically significant elevated titers against the H5, H6, and H7 avian influenza virus isolates, compared with control subjects. Conclusions. These data suggest that occupational exposure to avian species may increase veterinarians' risk of avian influenza virus infection. Veterinarians should be considered for priority access to vaccines and antiviral drugs in pandemic planning.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Avian influenza; Subtype; Typing; United States

Desc. génériques : Virology; Infectious diseases; Medical sciences; Viral disease; Infection; North America; America; Microbiological investigation

Descripteur(s) français

Descripteur(s) : Grippe aviaire; Soustype; Typage; Etats Unis

Desc. génériques : Virologie; Maladies infectieuses; Sciences médicales; Virose; Infection; Amérique du Nord; Amérique; Exploration microbiologique

Localisation : INIST, Shelf number 18407, INIST No. 354000172795070010

Origine de la notice : INIST

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Modulation of the immune responses in chickens by low-pathogenicity avian influenza virus H9N2

Titre : Modulation of the immune responses in chickens by low-pathogenicity avian influenza virus H9N2

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Source : Journal of general virology. 2008; 89 (p. 5) : 1288-1299

ISSN : 0022-1317

CODEN : JGVIAY

Date de publication : 2008

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Nombre de références : 1 p.1/2

Résumé : Most low-pathogenicity avian influenza (LPAI) viruses cause no or mild disease in avian species. Little is known about the mechanisms of host defence and the immune responses of avian influenza-infected birds. This study showed that chicken macrophages are susceptible to infection with LPAI H9N2 and H6N2 viruses and that infection led to apoptosis. In H9N2 virus-infected chicken macrophages, Toll-like receptor 7 responded to infection and mediated the cytokine responses. Whilst pro-inflammatory cytokines were largely upregulated, the interferon (IFN) response was fairly weak and IFN-inducible genes were differentially regulated. Among the regulated genes, major histocompatibility complex (MHC) antigens II were downregulated, which also occurred in the lungs of H9N2-infected chickens. Additionally, interleukin (IL)-4, IL-4 receptor and CD74 (MHC class II invariable chain) were also downregulated, all of which are pivotal in the activation of CD4⁺ helper T cells and humoral immunity. Remarkably, in H9N2 virus-infected chickens, the antibody response was severely suppressed. This was in contrast to the robust antibody response in chickens infected with H6N2 virus, in which expression of MHC class II antigens was upregulated. These data suggest that neutralizing antibodies and humoral immunity may not be developed efficiently in H9N2-infected chickens. These findings raise questions about how some LPAI viruses differentially regulate avian immune responses and whether they have similar effects on mammalian immune function.

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

Descripteur(s) anglais

Descripteur(s) : Chicken; Avian influenza virus; Immune response; Pathogenicity; Microbiology

Desc. génériques : Virology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Aves; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Veterinary

Descripteur(s) français

Descripteur(s) : Poulet; Influenzavirus aviaire; Réponse immunitaire; Pouvoir pathogène; Microbiologie

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Aves; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Vétérinaire

Localisation : INIST, Shelf number 13533, INIST No. 354000173749770230

Origine de la notice : INIST

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Pathology, Molecular Biology, and Pathogenesis of Avian Influenza A (H5N1) Infection in Humans

Titre : Pathology, Molecular Biology, and Pathogenesis of Avian Influenza A (H5N1) Infection in Humans

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Source : The American journal of pathology. 2008; 172 (5) : 1155-1170

ISSN : 0002-9440

CODEN : AJPAA4

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Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 112 ref.

Code(s) de classement : 002B24O; 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Avian influenza; Anatomic pathology; Molecular biology; Pathogenesis; Influenza A; Human

Desc. génériques : Medical sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Grippe aviaire; Anatomopathologie; Biologie moléculaire; Pathogenie; Grippe A; Homme

Desc. génériques : Sciences médicales; Virologie; Maladies infectieuses; Sciences médicales; Virose; Infection

Localisation : INIST, Shelf number 2047, INIST No. 354000172791840010

Origine de la notice : INIST

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Influenza Vaccination and the Elderly : Pandemic Preparedness

Titre : Influenza Vaccination and the Elderly : Pandemic Preparedness

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Source : Drugs and aging. 2008; 25 (3) : 179-186

ISSN : 1170-229X

Date de publication : 2008

Pays de publication : New Zealand

Langue(s) : English

Type de document : Serial

Nombre de références : 51 ref.

Résumé : Seasonal influenza causes significant morbidity and mortality in the elderly, the very young and those with chronic illness, despite the availability of effective vaccines. The mortality and morbidity attributed annually to seasonal influenza are small in comparison to the potential mortality and morbidity of a novel highly pathogenic human influenza A virus strain. The current influenza A/H5N1 virus that has caused epidemics in poultry and is evolving to find new niches needs only to become more efficiently transmitted from human to human to cause the next pandemic. Vaccination is the intervention with the potential to save the most lives when a pandemic occurs. Pandemic awareness and preparedness are essential to decrease the predicted chaos, death and illness arising from the next influenza pandemic.

Code(s) de classement : 002A05B12; 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Influenza; Vaccination; Prevention; Elderly; Review; Influenzavirus A; Influenzavirus B; Avian influenza; Mortality; United States; Pandemic

Desc. génériques : Immunology; Pharmacology; Bacteriology; Microbiology; Biological sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection; Human; Orthomyxoviridae; Virus; North America; America

Descripteur(s) français

Descripteur(s) : Grippe; Vaccination; Prevention; Personne agee; Article synthese; Influenzavirus A; Influenzavirus B; Influenzavirus aviaire; Mortalite; Etats Unis; Pandemie

Desc. génériques : Immunologie; Pharmacologie; Bacteriologie; Microbiologie; Sciences biologiques; Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection; Homme; Orthomyxoviridae; Virus; Amerique du Nord; Amerique

Localisation : INIST, Shelf number 26115, INIST No. 354000183000470010

Origine de la notice : INIST

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A Nationally Coordinated Laboratory System for Human Avian Influenza A (H5N1) in Thailand : Program Design, Analysis, and Evaluation

Titre : A Nationally Coordinated Laboratory System for Human Avian Influenza A (H5N1) in Thailand : Program Design, Analysis, and Evaluation

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Source : Clinical infectious diseases. 2008; 46 (9) : 1394-1400

ISSN : 1058-4838

CODEN : CIDIEL

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 24 ref.

Résumé : Background. The first phase of national surveillance for avian influenza (H5N1) human disease in Thailand occurred over a 4-month period that began on 1 December 2003. Subsequently, a nationally coordinated laboratory system (NCLS) for avian influenza (H5N1) was created to assess population-based surveillance, specimen procurement, case detection, and reporting at the national level. Methods. We conducted a pre- and postintervention study to evaluate the NCLS designed during the 6-week interval from 1 April through 15 May 2004. During the pre-NCLS period (1 December 2003 through 31 March 2004), 12 cases of human avian influenza (H5N1) were confirmed. During the post-NCLS period (16 May 2004 through 31 December 2006), interventions were implemented for human avian influenza (H5N1) surveillance, case detection, and expedited, computer-based reporting. Results. During the pre- and post-NCLS periods, 777 (85%) of 915 and 10,434 (95%) of 11,042 clinical respiratory specimens, respectively, were adequate for confirmatory testing ($P < .001$), the median time from procurement to results decreased from 17 days (range, 14-24 days) to 1.8 days (range, 0.25-4 days; $P < .001$), and the duration of specimen shipment decreased from 46.5 h to 21.1 h ($P < .001$). Thirteen cases of avian influenza (H5N1) were detected during the 31-month postintervention period. H5N1 reverse-transcriptase polymerase chain reaction and real-time reverse-transcriptase polymerase chain reaction sensitivity was 100% and specificity was 99.8%. Conclusions. The NCLS exemplifies a systematic approach to national surveillance for avian influenza A (H5N1). This NCLS program in Thailand serves as a model for human avian influenza (H5N1) preparedness that can be adopted or modified for use in other countries.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Avian influenza; Laboratory; Thailand; Human; Influenzavirus AH5N1

Desc. génériques : Virology; Infectious diseases; Medical sciences; Viral disease; Infection; Asia

Descripteur(s) français

Descripteur(s) : Grippe aviaire; Laboratoire; Thaïlande; Homme; Influenzavirus AH5N1

Desc. génériques : Virologie; Maladies infectieuses; Sciences médicales; Virose; Infection; Asie

Localisation : INIST, Shelf number 18407, INIST No. 354000183045850080

Origine de la notice : INIST

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Level of protection of chickens against highly pathogenic H5 avian influenza virus with Newcastle disease virus based live attenuated vector vaccine depends on homology of H5 sequence between vaccine and challenge virus

Titre : Level of protection of chickens against highly pathogenic H5 avian influenza virus with Newcastle disease virus based live attenuated vector vaccine depends on homology of H5 sequence between vaccine and challenge virus

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Source : Vaccine . 2008; 26 (19) : 2307-2313

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CODEN : VACCDE

Date de publication : 2008

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Type de document : short-communication

Nombre de références : 34 ref.

Résumé : Vaccination of poultry against avian influenza is of high priority, in particular after the dramatic spread of subtype H5N1 in Asia, Africa and Europe. Newcastle disease virus (NDV) has been developed as a vector for the expression of the main immunogen of avian influenza virus, hemagglutinin (HA). An NDV vector based vaccine has several advantages. It allows easy serological differentiation between infected and vaccinated animals by the detection of antibodies against non-HA influenza proteins. Moreover, it can be administered easily to large numbers of animals by spray or drinking water. We recently showed that chickens could be protected against infection with highly pathogenic avian influenza virus (HPAIV) A/chicken/Italy/8/98 (H5N2) after immunization with a recombinant Newcastle disease virus, NDVH5m, which expresses the homologous hemagglutinin. Here, we describe that immunization with NDVH5m conferred only partial protection against lethal infection with heterologous HPAIV A/duck/Vietnam/TG24-01/05 (H5N1). Comparison of amino acid sequences of both H5 proteins showed only 93.6% amino acid identity. Therefore, a new NDV recombinant (NDVH5Vm) was generated which expresses the H5 protein of HPAIV A/chicken/Vietnam/P41/05 (H5N1). This recombinant virus protected chickens against lethal infection with HPAIV H5N1 (Vietnam) already after one immunization. Our data thus show that application of a vector-based vaccine in the control of influenza may require adaptation of the vaccine to currently circulating viruses.

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

Descripteur(s) anglais

Descripteur(s) : Chicken; Avian influenzavirus; Newcastle disease virus; Pathogenicity; Attenuated strain; Vector; Vaccine; Homology; Avian influenza

Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Aves; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Rubulavirus; Paramyxovirinae; Paramyxoviridae; Mononegavirales; Poultry; Viral disease; Infection; Veterinary; Zoopathogen; Farming animal

Descripteur(s) français

Descripteur(s) : Poulet; Influenzavirus aviaire; Virus de la maladie de Newcastle; Pouvoir pathogene; Souche atténuee; Vecteur; Vaccin; Homologie; Grippe aviaire

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquée; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Aves; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus;

Rubulavirus; Paramyxovirinae; Paramyxoviridae; Mononegavirales; Volaille; Virose; Infection; Veterinaire;
Zoopathogene; Animal elevage

Localisation : INIST, Shelf number 20289, INIST No. 354000195837080020

Origine de la notice : INIST

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Alum boosts TH2-type antibody responses to whole-inactivated virus influenza vaccine in mice but does not confer superior protection

Titre : Alum boosts TH2-type antibody responses to whole-inactivated virus influenza vaccine in mice but does not confer superior protection

Auteur(s) : BUNGENER Laura; GEERAEDTS Felix; TER VEER Wouter; MEDEMA Jeroen; WILSCHUT Jan; HUCKRIEDE Anke

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Source : Vaccine . 2008; 26 (19) : 2350-2359

ISSN : 0264-410X

CODEN : VACCDE

Date de publication : 2008

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Type de document : research-paper

Nombre de références : 52 ref.

Résumé : Clinical trials with pandemic influenza vaccine candidates have focused on aluminium hydroxide as an adjuvant to boost humoral immune responses. In this study we investigated the effect of aluminium hydroxide on the magnitude and type of immune response induced by whole-inactivated virus (WIV) vaccine. Balb/c mice were immunized once with a range of antigen doses (0.04-5 μ g) of WIV produced from A/PR/8 virus, either alone or in combination with aluminium hydroxide. The hemagglutination inhibition (HI) titers of mice receiving WIV + aluminium hydroxide were 4-16-fold higher than HI titers in mice receiving the same dose of WIV alone, indicating the boosting effect of aluminium hydroxide. WIV induced a TH1 skewed humoral and cellular immune response, characterized by strong influenza-specific IgG2a responses and a high number of IFN γ -secreting T cells. In contrast, immunization with WIV adsorbed to aluminium hydroxide resulted in skewing of this response to a TH2 phenotype (high IgG1 levels and a low number of IFN γ -producing T cells). To assess the effect of the observed immune response skewing on viral clearance from the lungs mice immunized once with 1 μ g WIV without or with aluminium hydroxide were challenged with A/PR/8 virus 4 weeks later. The immunized mice showed a significant decrease in viral lung titers compared to control mice receiving buffer. However, despite higher antibody titers, mice immunized with WIV adsorbed to aluminium hydroxide suffered from more severe weight loss and had significantly higher virus loads in their lung tissue than mice receiving WIV alone. Major difference between these groups of mice was the type of immune response induced, TH2 instead of TH1, indicating that a TH1 response plays a major role in viral clearance.

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

Descripteur(s) anglais

Descripteur(s) : Influenzavirus; Mouse; T Lymphocyte; Th2 lymphocyte; Humoral immunity; Immune response; Inactivated strain; Vaccine; Immunological adjuvant; Aluminium; Influenza; Th1 lymphocyte

Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Helper cell; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Influenzavirus; Souris; Lymphocyte T; Lymphocyte Th2; Immunité humorale; Réponse immunitaire; Souche inactivée; Vaccin; Adjuvant immunologique; Aluminium; Grippe; Lymphocyte Th1

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquée; Microbiologie; Sciences biologiques;

Virologie; Microbiologie; Sciences biologiques; Orthomyxoviridae; Virus; Rodentia; Mammalia; Vertebrata; Cellule helper; Virose; Infection

Localisation : INIST, Shelf number 20289, INIST No. 354000195837080070

Origine de la notice : INIST

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Safety and reactogenicity profile of an adjuvanted H5N1 pandemic candidate vaccine in adults within a phase III safety trial

Titre : Safety and reactogenicity profile of an adjuvanted H5N1 pandemic candidate vaccine in adults within a phase III safety trial

Auteur(s) : RUMKE Hans C; BAYAS Jose Maria; DE JUANES Jose Ramon; CASO Covadonga; RICHARDUS Jan Hendrik; CAMPINS Magda; ROMBO Lars; DUVAL Xavier; ROMANENKO Viktor; SCHWARZ Tino F; FASSAKHOV Rustem; ABAD SANTOS Francisco; VON SONNENBURG Frank; DRAME Mamadou; SANGER Roland; BALLOU W Ripley

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Source : Vaccine . 2008; 26 (19) : 2378-2388

ISSN : 0264-410X

CODEN : VACCDE

Date de publication : 2008

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Type de document : research-paper

Nombre de références : 31 ref.

Résumé : A multicentre, randomized, phase III clinical trial in 5071 healthy adults was conducted to evaluate the safety and reactogenicity of a 15 μ g HA dose of a candidate oil-in-water emulsion-based adjuvant system (AS)-adjuvanted split-virion H5N1 (AS-H5N1) vaccine compared to a licensed seasonal influenza vaccine, FluarixTM. Stringent criteria were used to evaluate adverse events and reactogenicity profile. Overall, 96.7% of the 5071 vaccinated subjects completed the study. Significantly more participants in the AS-H5N1 vaccine group reported general or local adverse events. Pain was the most common symptom in both treatment groups. Less than 1% of subjects withdrew from the study due to adverse events and no withdrawals were due to serious adverse events related to vaccination. The safety and reactogenicity profile of the AS-H5N1 candidate vaccine can be considered clinically acceptable in the context of its use against pandemic influenza.

Code(s) de classement : 002A05F04

Descripteur(s) anglais

Descripteur(s) : Toxicity; Immunological adjuvant; Vaccine; Adult; Phase III trial; Influenza

Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Human; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Toxicité; Adjuvant immunologique; Vaccin; Adulte; Essai clinique phase III; Grippe

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquée; Microbiologie; Sciences biologiques; Homme; Virose; Infection

Localisation : INIST, Shelf number 20289, INIST No. 354000195837080100

Origine de la notice : INIST

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MegaRibavirin aerosol for the treatment of influenza A virus infections in mice

Titre : MegaRibavirin aerosol for the treatment of influenza A virus infections in mice

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Affiliation(s) : Department of Molecular Virology and Microbiology, Baylor College of Medicine, One Baylor Plaza, Mail Stop BCM-280, Houston, TX 77030, United States; MTM Research, LLC, Omaha, NE, United States

Source : Antiviral research. 2008; 78 (3) : 223-229

ISSN : 0166-3542

CODEN : ARSRDR

Date de publication : 2008

Pays de publication : Netherlands

Langue(s) : English

Type de document : Serial

Nombre de références : 3/4 p.

Résumé : While newer neuraminidase inhibitors have been used recently to treat influenza A and B virus infections, emergence of drug resistance poses potential problems. Previous ribavirin aerosol treatments of influenza were effective and drug resistance was not observed. To make ribavirin aerosol treatment a quicker process and limited to once or twice daily treatments, a MegaRibavirin formulation (100 mg of ribavirin/mL) was developed that when used with the Aerotech II nebulizer was effective in preventing death in a lethal influenza A virus mouse model. Aerosol generated using the Aerotech II nebulizer flowing at 10 L of air/min produced aerosol droplets that contained 2.3 mg of ribavirin/L with a mass median aerodynamic diameter of 1.8 μ m. Using this system for treatment, a single daily 30-min exposure on days 1-4 produced a survival rate of greater than 90%. Delaying the start of aerosol treatment for 48 or 72 h and treating once daily for 30 min for two days (days 2-3 and 3-4, respectively) still significantly increased the number of survivors and mean time to death. For the treatment of influenza in general and for pandemic avian influenza, the MegaRibavirin-Aerotech II method of aerosol treatment allows for short treatment periods, minimizes environmental issues and costs less.

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

Descripteur(s) anglais

Descripteur(s) : Aerosols; Inhalation; Treatment; Influenza A virus; Influenza A; Animal; Mouse; Ribavirin; Formulation; Antiviral; Daily dose

Desc. génériques : Virology; Infectious diseases; Pharmacology; Medical sciences; Virology; Infectious diseases; Medical sciences; Influenzavirus A; Orthomyxoviridae; Virus; Viral disease; Infection; Rodentia; Mammalia; Vertebrata; Nucleoside analog; Inosine monophosphate dehydrogenase inhibitor

Descripteur(s) français

Descripteur(s) : Aerosol; Inhalation; Traitement; Virus grippal A; Grippe A; Animal; Souris; Ribavirine; Formulation; Antiviral; Dose journaliere; Influenzavirus AH3N2

Desc. génériques : Virologie; Maladies infectieuses; Pharmacologie; Sciences médicales; Virologie; Maladies infectieuses; Sciences médicales; Influenzavirus A; Orthomyxoviridae; Virus; Virose; Infection; Rodentia; Mammalia; Vertebrata; Analogue de nucleoside; Inhibiteur de l'inosine monophosphate deshydrogenase

Localisation : INIST, Shelf number 18839, INIST No. 354000172682370060

Origine de la notice : INIST

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Application of DNA microarray technology to influenza A/Vietnam/1194/2004 (H5N1) vaccine safety evaluation

Titre : Application of DNA microarray technology to influenza A/Vietnam/1194/2004 (H5N1) vaccine safety evaluation

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Source : Vaccine . 2008; 26 (18) : 2270-2283

ISSN : 0264-410X

CODEN : VACCDE

Date de publication : 2008

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Nombre de références : 47 ref.

Résumé : We propose that cDNA microarray analysis can be used in the quality control of pandemic and endemic influenza vaccine. Based on the expression profiles of 76 genes in the rat lung one day after inoculation of influenza vaccine, we can distinguish whole-virion influenza vaccine (PDv: pandemic influenza vaccine and WPv: whole virion-particle vaccine) and sub-virion vaccine (HA vaccine) from saline. Among these 76 genes, we found genes up-regulated by influenza infection, as well as genes involved in the immune response, and interferon. Hierarchical clustering of each influenza vaccine by the expression profiles of these 76 genes matched data from current quality control tests in Japan, such as the abnormal toxicity test (ATT) and the leukopenic toxicity test (LTT). Thus, it can be concluded that cDNA microarray technology is an informative, rapid and highly sensitive method with which to evaluate the quality of influenza vaccines. Using DNA microarray system, consistent with the results of the ATT and LTT, it was clarified that there was no difference in vaccine quality between PDv and WPv.

Code(s) de classement : 002A05F04

Descripteur(s) anglais

Descripteur(s) : DNA chip; Vietnam; Vaccine; Toxicity; Influenza A

Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Asia; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Puce a DNA; Vietnam; Vaccin; Toxicite; Grippe A

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquee; Microbiologie; Sciences biologiques; Asie; Virose; Infection

Localisation : INIST, Shelf number 20289, INIST No. 354000183057310120

Origine de la notice : INIST

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Ethical Issues in Resource Triage. Mechanical Ventilation in Mass Casualty Scenarios. Part II of Two Special Issues

Titre : Ethical Issues in Resource Triage. Mechanical Ventilation in Mass Casualty Scenarios. Part II of Two Special Issues

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Source : Respiratory care. 2008; 53 (2) : 190-200

Informations congrès : *Mechanical Ventilation in Mass Casualty Scenarios. Respiratory Care Journal Conference, *40, *Reno, Nevada United States, *2007-07-16

ISSN : 0020-1324

CODEN : RECACP

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial; *Conference-Meeting

Type de document : article; comments

Nombre de références : 38 ref.

Résumé : Mass-care events, such as pandemic influenza, could reach such devastating proportions that there will be the need to make difficult triage decisions that will ultimately result in the deaths or severe disability of patients in large numbers. The method by which we determine how triage of scarce health care resources will be performed must be clearly defined prior to a disaster event. This paper will discuss several of the ethical principles that must be weighed in developing a mass-care triage plan, as well as steps to facilitate its implementation. Development of triage policies in such an event should be developed in an open and transparent manner, be reasonable in design, include the views of the critical stakeholders, and be responsive to and provide a mechanism for accountability, with a clearly defined goal of the just triage of limited health care resources. Planning failure will result in increased deaths from poor triage processes and substantial mistrust of the health care system and its practitioners.

Code(s) de classement : 002B27B; 002B16B

Descripteur(s) anglais

Descripteur(s) : Respiration; Disaster; Ethics; Resuscitation; Intensive care

Desc. génériques : Resuscitation; Intensive care medicine; Medical sciences; Neurology; Nervous system; Traumatology; Medical sciences

Descripteur(s) français

Descripteur(s) : Respiration; Sinistre; Ethique; Reanimation; Soins intensifs

Desc. génériques : Reanimation; Soins intensifs; Sciences médicales; Neurologie; Systeme nerveux; Traumatologie; Sciences médicales

Localisation : INIST, Shelf number 15553, INIST No. 354000161934770020

Origine de la notice : INIST

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Serologic and Genetic Characterization Analyses of a Highly Pathogenic Influenza Virus (H5N1) Isolated From an Infected Man in Shenzhen

Titre : Serologic and Genetic Characterization Analyses of a Highly Pathogenic Influenza Virus (H5N1) Isolated From an Infected Man in Shenzhen

Auteur(s) : XIAOWEN CHENG; CHUNLI WU; JIANFAN HE; XING LV; SHUNXIANG ZHANG; LI ZHOU; JINGWEN WANG; RIQIANG DENG; QINGXING LONG; XUNZHANG WANG; JINQUAN CHENG

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Source : Journal of medical virology. 2008; 80 (6) : 1058-1064

ISSN : 0146-6615

CODEN : JMVIDB

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 1/2 p.

Résumé : Highly pathogenic avian influenza (HPAI) H5N1 virus caused a wave of outbreaks in China during 2005-2006, resulting in a total of 20 cases of human infection in 14 provinces of China. On June 16, 2006, a case of H5N1 human infection was confirmed in Shenzhen. The virus isolated from the patient, A/Guangdong/2/06, was characterized genetically and the relationship between the tracheal virus load and the antibody titer of the infected man was analyzed. Serological analysis confirmed that the patient's neutralizing antibodies had been generated 2 weeks after the onset of symptoms. The patient's serum antibodies could efficiently neutralize A/Guangdong/2/06 infectivity in vitro. Phylogenetic analysis showed that the H5N1 virus of Shenzhen belonged to subclade 2.3.4, which contained viruses that were mainly responsible for the outbreaks in domestic poultry and in the cases of human infection in southern China. Homology and molecular characterization analysis revealed that all the segments of Shenzhen H5N1 virus still belonged to avian segments. Several specific amino acid residue mutations were detected.

Code(s) de classement : 002A05C10; 002B05C02J; 002A05C05; 002A05C04

Descripteur(s) anglais

Descripteur(s) : Influenza A virus; Human; Serology; Genetics; Pathogenicity; Infection; Influenza A

Desc. génériques : Virology; Microbiology; Biological sciences; Virology; Infectious diseases; Medical sciences; Genetics; Virology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Viral disease

Descripteur(s) français

Descripteur(s) : Virus grippal A; Homme; Serologie; Genetique; Pouvoir pathogene; Infection; Grippe A

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Virologie; Maladies infectieuses; Sciences medicales; Genetique; Virologie; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Virose

Localisation : INIST, Shelf number 17422, INIST No. 354000173767900190

Origine de la notice : INIST

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Human Influenza Virus Infection and Apoptosis Induction in Human Vascular Endothelial Cells

Titre : Human Influenza Virus Infection and Apoptosis Induction in Human Vascular Endothelial Cells

Auteur(s) : SUMIKOSHI Makoto; HASHIMOTO Koichi; KAWASAKI Yukihiro; SAKUMA Hiroko; SUZUTANI Tatsuo; SUZUKI Hitoshi; HOSOYA Mitsuaki

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Source : Journal of medical virology. 2008; 80 (6) : 1072-1078

ISSN : 0146-6615

CODEN : JMVIDB

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 1/2 p.

Résumé : Acute encephalopathy accompanying influenza virus infection results in brain and systemic organ failure mainly through vasogenic edema with high levels of inflammatory cytokines, such as blood tumor necrosis factor (TNF)- α and interleukin (IL)-6, as well as the cytochrome c apoptosis marker. A highly virulent strain of avian influenza virus causes fatal infection in chickens by infecting vascular endothelial cells in systemic organs, inducing apoptosis therein. To verify the possibility of apoptosis induction by human influenza virus in infected human vascular endothelial cells, purified influenza virus-infected human umbilical vein endothelial cells (HUVECs) were examined using a tissue culture method. When pre-treated with TNF- α , influenza virus (Philippine strain, H3N2) promoted TNF- α induced apoptosis of HUVECs. Viral replication was confirmed in HUVECs infected with the Philippine strain in the absence of TNF- α by measurement of the amount of infective virus in the culture supernatant using the tissue culture infectious dose (TCID) method, immunohistochemistry and real-time PCR. The number of influenza virus genomes in the infected HUVECs at 24 hr post-infection increased about fivefold compared to that just after virus adsorption. Many TUNEL-positive influenza virus-infected HUVECs were observed using the TUNEL method. Furthermore, cleaved caspase 3 was also detected in influenza virus-infected cells by immunofluorescence staining. These results demonstrated that human influenza virus can infect and replicate in human vascular endothelial cells and induce apoptosis therein.

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

Descripteur(s) anglais

Descripteur(s) : Human; Influenzavirus; Apoptosis; Cell death; Induction; Endothelial cell; Failure; Edema; Cytokine; Viral disease; Encephalopathy

Desc. génériques : Virology; Microbiology; Biological sciences; Virology; Infectious diseases; Medical sciences; Orthomyxoviridae; Virus; Cerebral disorder; Infection; Central nervous system disease; Nervous system diseases

Descripteur(s) français

Descripteur(s) : Homme; Influenzavirus; Apoptose; Mort cellulaire; Induction; Cellule endothéliale; Echec; Oedeme; Cytokine; Virose; Encephalopathie

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Virologie; Maladies infectieuses; Sciences médicales; Orthomyxoviridae; Virus; Pathologie de l'encephale; Infection; Pathologie du système nerveux central; Pathologie du système nerveux

Localisation : INIST, Shelf number 17422, INIST No. 354000173767900210

Origine de la notice : INIST

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From refuge to risk : Public libraries and children in World War I. Libraries in times of war, revolution, and social change

Titre : From refuge to risk : Public libraries and children in World War I. Libraries in times of war, revolution, and social change

Auteur(s) : KIMBALL Melanie A; RAYWARD W Boyd, ed; JENKINS Christine, ed

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Source : Library trends. 2007; 55 (3) : 454-463

ISSN : 0024-2594

CODEN : LIBTA3

Date de publication : 2007

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 1/4 p.

Notes : 19 notes

Résumé : During World War I public libraries in the United States functioned in multiple ways as civic spaces. This was particularly true of libraries in large, urban centers with diverse ethnic populations, many from countries involved in the conflict. For children, the library was a refuge that provided story hours, reading material, and space dedicated to their needs. Just before the end of the war, the influenza pandemic broke out and children were not allowed in the library building. In a few short months, the library went from being a refuge to being a health risk for children.

Code(s) de classement : 001A01C02B

Descripteur(s) anglais

Descripteur(s) : United States; War; Public library; Public space; Child; Infectious risk

Desc. génériques : Information sciences; Documentation; North America; America; Human

Descripteur(s) français

Descripteur(s) : Etats Unis; Guerre; Bibliotheque publique; Espace public; Enfant; Risque infectieux

Desc. génériques : Sciences de l'information; Documentation; Amerique du Nord; Amerique; Homme

Localisation : INIST, Shelf number 1503, INIST No. 354000145727710070

Origine de la notice : INIST

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Geostatistical visualisation and spatial statistics for evaluation of the dispersion of epidemic highly pathogenic avian influenza subtype H5N1

Titre : Geostatistical visualisation and spatial statistics for evaluation of the dispersion of epidemic highly pathogenic avian influenza subtype H5N1

Auteur(s) : WARD Michael P; MAFTEI Daniel; APOSTU Cristian; SURU Andrian

Affiliation(s) : College of Veterinary Medicine & Biomedical Sciences, Texas A&M University, College Station, Texas, United States; Regional Diagnostic Laboratory (DSVSA), Tulcea, ROU; Institute for Diagnosis and Animal Health (IDSV), Bucharest, ROU; National Animal Health and Food Safety Authority (ANSVSA), Bucharest, ROU

Source : Veterinary research Print. 2008; 39 (3) : 1-12

ISSN : 0928-4249

Date de publication : 2008

Pays de publication : France

Langue(s) : English

Type de document : Serial

Nombre de références : 33 ref.

Résumé : The aim of this study was to evaluate a range of statistical and geostatistical methods for their usefulness in providing insights into how highly pathogenic avian influenza (HPAI) subtype H5N1 might spread through a national population of village poultry. The insights gained allow the generation of disease dispersion hypotheses. The case study data set consisted of 161 outbreaks of HPAI subtype H5N1 in village poultry reported in Romania between October 2005 and June 2006. Reports of village outbreaks (%) occurred in three waves: October-December (14%), February-March (16%), and May-June (68%). Risk mapping - based on variography and kriging - was used to visualize the evolution of the epidemic. Outbreaks first appeared in eastern and southern Romania, particularly within an area that forms part of the Danube River Delta. The largest phase of the epidemic affected villages in all parts of central, southern, and eastern Romania, but outbreaks were clustered in central Romania. Outbreaks spread in an east to west direction. By using geostatistical visualisation and spatial statistics, the evolution of the epidemic could be characterised into two parts: disease introduction, local spread, and sporadic outbreaks, and long-distance disease spread with rapid epidemic propagation. This is consistent with the hypothesis that the environment and landscape (specifically the Danube River Delta) played a critical role in the introduction and initial spread of HPAI subtype H5N1 during the autumn and winter of 2005, and that the movement of poultry might have introduced the infection into central Romania during the spring and summer of 2006. Further research focusing on the spatio-temporal interface between the two parts of the epidemic might reveal how and why it progressed from a confined, local epidemic to a large, national epidemic. Such information would assist efforts to limit the global spread of HPAI subtype H5N1.

Code(s) de classement : 002A05

Descripteur(s) anglais

Descripteur(s) : Epidemic; Pathogenicity; Subtype; Poultry; Romania; Microbiology; Veterinary; Avian influenza

Desc. génériques : Microbiology; Biological sciences; Europe; Infection; Viral disease; Farming animal

Descripteur(s) français

Descripteur(s) : Epidemie; Pouvoir pathogene; Soustype; Volaille; Roumanie; Microbiologie; Veterinaire; Grippe aviaire

Desc. génériques : Microbiologie; Sciences biologiques; Europe; Infection; Virose; Animal elevage

Localisation : INIST, Shelf number 14119, INIST No. 354000183078440020

Origine de la notice : INIST

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Quantification of influenza virus hemagglutinins in complex mixtures using isotope dilution tandem mass spectrometry

Titre : Quantification of influenza virus hemagglutinins in complex mixtures using isotope dilution tandem mass spectrometry

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Source : Vaccine . 2008; 26 (20) : 2510-2520

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 : Influenza vaccination is the primary method for preventing influenza and its severe complications. Licensed inactivated vaccines for seasonal or pandemic influenza are formulated to contain a preset amount of hemagglutinin (HA), the critical antigen to elicit protection. Current methods to establish the HA concentration of vaccines rely on indirect measurements that are subject to considerable experimental variability. We present a liquid chromatography-tandem mass spectrometry (LC/MS/MS) method for the absolute quantification of viral proteins in a complex mixture. Through use of an isotope dilution approach, HA from viral subtypes H1, H3, H5, and B was determined both directly and rapidly. This method can be applied to purified virus preparations, to monovalent bulk concentrates, or to trivalent inactivated influenza vaccines with improved speed, sensitivity, precision, and accuracy. This LC/MS/MS approach may substantially increase the reliability of methods used to quantitate the amount of antigen in seasonal and pandemic influenza vaccines and reduce the time and effort to deliver influenza vaccines for public health use during the next influenza pandemic.

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

Descripteur(s) anglais

Descripteur(s) : Influenzavirus; Quantitative analysis; Hemagglutinin; Mass spectrometry MS/MS; Vaccine; 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; Analyse quantitative; Hemagglutinine; Spectrometrie masse tandem; Vaccin; Proteine; Grippe

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquee; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Orthomyxoviridae; Virus; Virose; Infection

Localisation : INIST, Shelf number 20289, INIST No. 354000195851170080

Origine de la notice : INIST

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Respecting, Enabling, and Involving All Personnel in a Sustainable Continuity of Operations Plan : Strategic management and productivity 2007

Titre : Respecting, Enabling, and Involving All Personnel in a Sustainable Continuity of Operations Plan : Strategic management and productivity 2007

Auteur(s) : WEST Tim; MILLER Steve; ZDUNEK Tom; MCKIBBEN Kim; PAUL Roger; ALBRIGHT David

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Source : Transportation research record. 2007; (2036) : 24-30

ISSN : 0361-1981

CODEN : TRREDM

Date de publication : 2007

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 12 ref.

Résumé : This paper describes implementation of a local government continuity of operations plan and pandemic influenza appendix through the first plan-train-exercise cycle. The potential for pandemic influenza was addressed by the Bernalillo County Public Works Division, New Mexico, as part of an all-hazards approach in continuity of operations planning. The continuity of operations planning process typically emphasizes loss of use of facilities. A pandemic scenario based on the 1918 influenza is used to determine whether adequate staff will be available to ensure that essential functions are performed. Staff reduction during an emergency requires difficult choices among what is "essential." It also requires redefinition of each member of the staff as currently or potentially providing an essential function. The paper describes how all personnel are involved in the continuity of operations plan. "All personnel" in this agency involves more than 200 employees with diverse job descriptions and skills. All personnel include political appointees, janitorial staff, civil engineers, field technicians, and clerical staff. Each person is considered an essential employee. Respect for each individual as an essential employee was demonstrated by enabling and involving each employee. Human factors addressed during the process included communication to ensure that all staff were informed, education to ensure that all staff could be trained, and organization to ensure that all staff were part of a team. The result of the approach is a near-term capability to maintain essential functions during a pandemic influenza. The effort also supports long-term, all-hazards local government capacity to maintain essential functions.

Code(s) de classement : 001D00E

Descripteur(s) anglais

Descripteur(s) : Planning; Durability; New Mexico; Script; Influenza

Desc. génériques : Applied sciences; United States; North America; America; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Planification; Durabilité; Nouveau Mexique; Scénario; Grippe

Desc. génériques : Sciences appliquées; Etats Unis; Amérique du Nord; Amérique; Virose; Infection

Localisation : INIST, Shelf number 10459B, INIST No. 354000161990780030

Origine de la notice : INIST

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Future novel threats and opportunities facing UK biodiversity identified by horizon scanning

Titre : Future novel threats and opportunities facing UK biodiversity identified by horizon scanning

Auteur(s) : SUTHERLAND William J; BAILEY Mark J; BAINBRIDGE Ian P; BRERETON Tom; DICK Jaimie T A; DREWITT Joanna; DULVY Nicholas K; DUSIC Nicholas R; FRECKLETON Robert P; GASTON Kevin J; GILDER Pam M; GREEN Rhys E; HEATHWAITE A Louise; JOHNSON Sally M; MACDONALD David W; MITCHELL Roger; OSBORN Daniel; OWEN Roger P; PRETTY Jules; PRIOR Stephanie V; PROSSER Havard; PULLIN Andrew S; ROSE Paul; STOTT Andrew; TEW Tom; THOMAS Chris D; THOMPSON Des B A; VICKERY Juliet A; WALKER Matt; WALMSLEY Clive; WARRINGTON Stuart; WATKINSON Andrew R; WILLIAMS Rich J; WOODROFFE Rosie; WOODROOF Harry J

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Source : Journal of applied ecology. 2008; 45 (3) : 821-833

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CODEN : JAPEAI

Date de publication : 2008

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Nombre de références : 1 p.1/4

Résumé : 1. Horizon scanning is an essential tool for environmental scientists if they are to contribute to the evidence base for Government, its agencies and other decision makers to devise and implement environmental policies. The implication of not foreseeing issues that are foreseeable is illustrated by the contentious responses to genetically modified herbicide-tolerant crops in the UK, and by challenges surrounding biofuels, foot and mouth disease, avian influenza and climate change. 2. A total of 35 representatives from organizations involved in environmental policy,

academia, scientific journalism and horizon scanning were asked to use wide consultation to identify the future novel or step changes in threats to, and opportunities for, biodiversity that might arise in the UK up to 2050, but that had not been important in the recent past. At least 452 people were consulted. 3. Cases for 195 submitted issues were distributed to all participants for comments and additions. All issues were scored (probability, hazard, novelty and overall score) prior to a 2-day workshop. Shortlisting to 41 issues and then the final 25 issues, together with refinement of these issues, took place at the workshop during another two rounds of discussion and scoring. 4. We provide summaries of the 25 shortlisted issues and outline the research needs. 5. We suggest that horizon scanning incorporating wide consultation with providers and users of environmental science is used by environmental policy makers and researchers. This can be used to identify gaps in knowledge and policy, and to identify future key issues for biodiversity, including those arising from outside the domains of ecology and biodiversity. 6. Synthesis and applications. Horizon scanning can be used by environmental policy makers and researchers to identify gaps in knowledge and policy. Drawing on the experience, expertise and research of policy advisors, academics and journalists, this exercise helps set the agenda for policy, practice and research.

Code(s) de classement : 002A14D01

Descripteur(s) anglais

Descripteur(s) : United Kingdom; Biodiversity; Conservation; Policy; Decision making; Environment; Risk

Desc. génériques : Applied ecology; Ecology; Biological sciences; Europe

Descripteur(s) français

Descripteur(s) : Royaume Uni; Diversité biologique; Conservation; Politique; Prise de décision; Environnement; Risque

Desc. génériques : Ecologie appliquée; Ecologie; Sciences biologiques; Europe

Localisation : INIST, Shelf number 11538, INIST No. 354000183097250090

Origine de la notice : INIST

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A Broadly Protective Vaccine against Globally Dispersed Clade 1 and Clade 2 H5N1 Influenza Viruses

Titre : A Broadly Protective Vaccine against Globally Dispersed Clade 1 and Clade 2 H5N1 Influenza Viruses

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Source : The Journal of infectious diseases. 2008; 197 (8) : 1185-1188

ISSN : 0022-1899

CODEN : JIDIAQ

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Type de document : short-communication

Nombre de références : 15 ref.

Résumé : Development of effective and immunogenic vaccines against highly pathogenic avian influenza H5N1 viruses with the potential to cause a pandemic is a public health priority. The global demand for a vaccine cannot be met in the event of an influenza pandemic because of the limited capacity to manufacture egg-derived vaccines as well as potential problems with the availability of embryonated eggs. Thus, there is an urgent need to develop alternative, egg-independent vaccines. We developed an adenoviral vector-based vaccine that contains hemagglutinin protein from clade 1 and clade 2 viruses, as well as conserved nucleoprotein, to broaden the vaccine coverage against H5N1 viruses.

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

Descripteur(s) anglais

Descripteur(s) : Vaccine; Microbiology; Infection; Influenza

Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Infectious diseases; Medical sciences; Viral disease

Descripteur(s) français

Descripteur(s) : Vaccin; Microbiologie; Infection; Grippe

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquée; Microbiologie; Sciences biologiques; Maladies infectieuses; Sciences médicales; Virose

Localisation : INIST, Shelf number 2052, INIST No. 354000172749530120

Origine de la notice : INIST

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Acute Febrile Respiratory Illness in the ICU* : Reducing Disease Transmission

Titre : Acute Febrile Respiratory Illness in the ICU* : Reducing Disease Transmission

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Source : Chest . 2008; 133 (5) : 1221-1231

ISSN : 0012-3692

CODEN : CHETBF

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 76 ref.

Résumé : Acute febrile respiratory illness (FRI) leading to respiratory failure is a common reason for admission to the ICU. Viral pneumonia constitutes a portion of these cases, and often the viral etiology goes undiagnosed. Emerging viral infectious diseases such as severe acute respiratory syndrome and avian influenza present with acute FRIs progressing to respiratory failure and ARDS. Therefore, early recognition of a viral cause of acute FRI leading to ARDS becomes important for protection of health-care workers (HCWs), lessening spread to other patients, and notification of public health officials. These patients often have longer courses of viral shedding and undergo higher-risk procedures that may potentially generate aerosols, such as intubation, bronchoscopy, bag-valve mask ventilation, noninvasive positive pressure ventilation, and medication nebulization, further illustrating the importance of early detection and isolation. A small number of viral agents lead to acute FRI, respiratory failure, and ARDS: seasonal influenza, avian influenza, coronavirus associated with severe ARDS, respiratory syncytial virus, adenovirus, varicella, human metapneumovirus, and hantavirus. A systematic approach to early isolation, testing for these agents, and public health involvement becomes important in dealing with acute FRI. Ultimately, this approach will lead to improved HCW protection, reduction of transmission to other patients, and prevention of transmission in the community.

Code(s) de classement : 002B11D; 002B12; 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Infection; Respiratory failure; Viral pneumonia; Acute; Fever; Respiratory tract; Disease; Transmission; Protection; Anesthesia; Circulatory system; Cardiology

Desc. génériques : Pneumology; Respiratory system; Medical sciences; Cardiovascular system; Medical sciences; Virology; Infectious diseases; Medical sciences; Respiratory disease; Lung disease

Descripteur(s) français

Descripteur(s) : Infection; Insuffisance respiratoire; Pneumonie virale; Aigu; Fievre; Voie respiratoire; Maladie; Transmission; Protection; Anesthésie; Appareil circulatoire; Cardiologie

Desc. génériques : Pneumologie; Appareil respiratoire; Sciences médicales; Systeme cardiovasculaire; Sciences médicales; Virologie; Maladies infectieuses; Sciences médicales; Pathologie de l' appareil respiratoire; Pathologie des poumons

Localisation : INIST, Shelf number 7627, INIST No. 354000183108710240

Origine de la notice : INIST

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RNase-Resistant Virus-Like Particles Containing Long Chimeric RNA Sequences Produced by Two-Plasmid Coexpression System

Titre : RNase-Resistant Virus-Like Particles Containing Long Chimeric RNA Sequences Produced by Two-Plasmid Coexpression System

Auteur(s) : YUXIANG WEI; CHANGMEI YANG; BAOJUN WEI; JIE HUANG; LUNAN WANG; SHUANG MENG; RUI ZHANG; JINMING LI

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Source : Journal of clinical microbiology Print. 2008; 46 (5) : 1734-1740

ISSN : 0095-1137

CODEN : JCMIDW

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 29 ref.

Résumé : RNase-resistant, noninfectious virus-like particles containing exogenous RNA sequences (armored RNA) are good candidates as RNA controls and standards in RNA virus detection. However, the length of RNA packaged in the virus-like particles with high efficiency is usually less than 500 bases. In this study, we describe a method for producing armored L-RNA. Armored L-RNA is a complex of MS2 bacteriophage coat protein and RNA produced in *Escherichia coli* by the induction of a two-plasmid coexpression system in which the coat protein and maturase are expressed from one plasmid and the target RNA sequence with modified MS2 stem-loop (pac site) is transcribed from another plasmid. A 3V armored L-RNA of 2,248 bases containing six gene fragments-hepatitis C virus, severe acute respiratory syndrome coronavirus (SARS-CoV1, SARS-CoV2, and SARS-CoV3), avian influenza virus matrix gene (M300), and H5N1 avian influenza virus (HA300)-was successfully expressed by the two-plasmid coexpression system and was demonstrated to have all of the characteristics of armored RNA. We evaluated the 3V armored L-RNA as a calibrator for multiple virus assays. We used the WHO International Standard for HCV RNA (NIBSC 96/790) to calibrate the chimeric armored L-RNA, which was diluted by 10-fold serial dilutions to obtain samples containing 10^{6-2} copies. In conclusion, the approach we used for armored L-RNA preparation is practical and could reduce the labor and cost of quality control in multiplex RNA virus assays. Furthermore, we can assign the chimeric armored RNA with an international unit for quantitative detection.

Code(s) de classement : 002A05

Descripteur(s) anglais

Descripteur(s) : Pancreatic ribonuclease; Resistance; Virus like particle; Plasmid; Gene expression; Microbiology; rnase

Desc. génériques : Microbiology; Biological sciences; Esterases; Hydrolases; Enzyme

Descripteur(s) français

Descripteur(s) : Pancreatic ribonuclease; Resistance; Particule type viral; Plasmide; Expression génique; Microbiologie; Pilege RNase

Desc. génériques : Microbiologie; Sciences biologiques; Esterases; Hydrolases; Enzyme

Localisation : INIST, Shelf number 17088, INIST No. 354000183109960250

Origine de la notice : INIST

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Development and Validation of a One-Step Real-Time PCR Assay for Simultaneous Detection of Subtype H5, H7, and H9 Avian Influenza Viruses

Titre : Development and Validation of a One-Step Real-Time PCR Assay for Simultaneous Detection of Subtype H5, H7, and H9 Avian Influenza Viruses

Auteur(s) : MONNE Isabella; ORMELLI Silvia; SALVIATO Annalisa; DE BATTISTI Cristian; BETTINI Francesca; SALOMONI Angela; DRAGO Alessandra; ZECCHIN Bianca; CAPUA Ilaria; CATTOLI Giovanni

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CODEN : JCMIDW

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 29 ref.

Résumé : Among the different hemagglutinin (HA) subtypes of avian influenza (AI) viruses, H5, H7, and H9 are of major interest because of the serious consequences for the poultry industry and the increasing frequency of direct transmission of these viruses to humans. The availability of new tools to rapidly detect and subtype the influenza viruses can enable the immediate application of measures to prevent the widespread transmission of the infection. In this study, a novel one-step real-time reverse transcription-PCR (RRT-PCR) was developed to detect simultaneously the H5, H7, and H9 subtypes of AI viruses from clinical samples of avian origin. The sensitivity of the RRT-PCR assay was determined by using in vitro-transcribed RNA and 10-fold serial dilutions of titrated AI viruses. High sensitivity levels were obtained, with limits of detection ranging from $10^{1.5}$ to $10^{3.5}$ RNA copies and from $10^{1.5}$ to $10^{2.5}$ 50% egg infectious dose (EID₅₀)/100 μ l to $10^{7.5}$ to $10^{4.5}$ EID₅₀/100 μ l with titrated viruses. Excellent results were achieved in the intra- and interassay variability tests. The comparison of the results with those obtained from the analysis of 725 avian samples by means of the reference method (virus isolation VI) showed a high level of agreement. To date, this is the first real-time PCR protocol available for the simultaneous detection of AI viruses belonging to subtypes H5, H7, and H9, and the results obtained indicate that this method is suitable as a routine laboratory test for the rapid detection and differentiation of the three most-important AI virus subtypes in samples of avian origin.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Descripteur(s) : Avian influenza virus; Real time; Polymerase chain reaction; Detection; Subtype; Microbiology

Desc. génériques : Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogen

Descripteur(s) français

Descripteur(s) : Influenzavirus aviaire; Temps réel; Reaction chaîne polymérase; Détection; Sous-type; Microbiologie

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Zoopathogène

Localisation : INIST, Shelf number 17088, INIST No. 354000183109960300

Origine de la notice : INIST

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Simultaneous Genotyping of All Hemagglutinin and Neuraminidase Subtypes of Avian Influenza Viruses by Use of Padlock Probes

Titre : Simultaneous Genotyping of All Hemagglutinin and Neuraminidase Subtypes of Avian Influenza Viruses by Use of Padlock Probes

Auteur(s) : GYARMATI Peter; CONZE Tim; ZOHARI Siamak; LEBLANC Neil; NILSSON Mats; LANDEGREN Ulf; BANER Johan; BELAK Sandor

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CODEN : JCMIDW

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 25 ref.

Résumé : A subtyping assay for both the hemagglutinin (HA) and neuraminidase (NA) surface antigens of the avian influenza virus (AIV) has been developed. The method uses padlock probe chemistry combined with a microarray output for detection. The outstanding feature of this assay is its capability to designate both the HA and the NA of an AIV sample from a single reaction mixture. A panel of 77 influenza virus strains was tested representing the entire assortment of the two antigens. One hundred percent (77/77) of the samples tested were identified as AIV, and 97% (75/77) were subtyped correctly in accordance with previous examinations performed by classical diagnostic methods. Testing of heterologous pathogens verified the specificity of the assay. This assay is a convenient and practical tool for the study of AIVs, providing important HA and NA data more rapidly than conventional methods.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Descripteur(s) : Avian influenza virus; Genotype; Typing; Hemagglutinin; Exo <alpha> sialidase; Subtype; Microbiology

Desc. génériques : Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Glycosidases; Glycosylases; Hydrolases; Enzyme; Zoopathogen

Descripteur(s) français

Descripteur(s) : Influenzavirus aviaire; Genotype; Typage; Hemagglutinine; Exo <alpha> sialidase; Soustype; Microbiologie

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Glycosidases; Glycosylases; Hydrolases; Enzyme; Zoopathogene

Localisation : INIST, Shelf number 17088, INIST No. 354000183109960270

Origine de la notice : INIST

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Inability of Real-Time Reverse Transcriptase PCR Assay To Detect Subtype H7 Avian Influenza Viruses Isolated from Wild Birds

Titre : Inability of Real-Time Reverse Transcriptase PCR Assay To Detect Subtype H7 Avian Influenza Viruses Isolated from Wild Birds

Auteur(s) : ZHENG XING; CARDONA Carol; DAO Phuong; CROSSLEY Beate; HIETALA Sharon; BOYCE Walter
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Source : Journal of clinical microbiology Print. 2008; 46 (5) : 1844-1846

ISSN : 0095-1137

CODEN : JCMIDW

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 17 ref.

Résumé : We report a failure of the real-time reverse transcriptase PCR H7 subtyping protocol currently used in national avian influenza surveillance programs. Significant substitutions in primer and probe target sequences were identified, especially in wild bird viruses. The protocol, originally designed for detecting H7 influenza viruses in poultry, is not reliable for wild bird surveillance.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Descripteur(s) : Avian influenza virus; Aves; Real time; RNA directed DNA polymerase; Polymerase chain reaction; Detection; Subtype; Microbiology

Desc. génériques : Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Vertebrata; Nucleotidyltransferases; Transferases; Enzyme; Zoopathogen

Descripteur(s) français

Descripteur(s) : Influenzavirus aviaire; Aves; Temps reel; RNA directed DNA polymerase; Reaction chaine polymerase; Detection; Soustype; Microbiologie

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Vertebrata; Nucleotidyltransferases; Transferases; Enzyme; Zoopathogene

Localisation : INIST, Shelf number 17088, INIST No. 354000183109960440

Origine de la notice : INIST

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Dhori Virus (Orthomyxoviridae: Thogotovirus) Infection of Mice Produces a Disease and Cytokine Response Pattern Similar to That of Highly Virulent Influenza A (H5N1) Virus Infection in Humans

Titre : Dhori Virus (Orthomyxoviridae: Thogotovirus) Infection of Mice Produces a Disease and Cytokine Response Pattern Similar to That of Highly Virulent Influenza A (H5N1) Virus Infection in Humans

Auteur(s) : GUANGYU LI; NAN WANG; GUZMAN Hilda; SBRANA Elena; YOSHIKAWA Tomoki; TSENG Chien Tek; TESH Robert B; XIAO Shu Yuan

Affiliation(s) : Department of Pathology and Center for Biodefense and Emerging Infectious Diseases, United States; Department of Microbiology and Immunology, University of Texas Medical Branch, Galveston, Texas, United States

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CODEN : AJTHAB

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Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 33 ref.

Résumé : Mice infected with Dhori virus (DHOV) develop a fulminant, systemic, and uniformly fatal illness that has many of the clinical and pathologic findings seen in H5N1 influenza A virus infection. However, the role of host's immune response in DHOV infection remains unclear. In this study, the concentrations of 23 inflammatory cytokines and chemokines were measured in the liver, lungs, and sera of mice during the course of DHOV infection. Liver function, level of viremia, and hematologic response were also monitored. Infected animals exhibited significant leucopenia and lymphopenia, which directly correlated with the disease progression. High yields of infectious virus along with strikingly elevated expression of various inflammatory mediators, including tumor necrosis factor (TNF)- α , interleukin (IL)-1, IL-6, IL-10, macrophage inflammatory protein (MIP)-1 α , monocyte chemoattractant protein (MCP)-1, and interferon (IFN)- α , indicate that these responses play an important role in the observed disease and pathology. The overall clinical, pathologic, and immunologic responses of ICR mice to DHOV infection closely resemble those described for highly virulent influenza A virus infection in humans, thereby offering a realistic, safe, and alternative animal model for studying the pathogenesis and treatment of highly pathogenic avian influenza virus.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Viral disease; Orthomyxoviridae; Animal; Mouse; Disease; Cytokine; Influenza A virus; Human; Tropical medicine; Experimental disease; Chemokine

Desc. génériques : Virology; Infectious diseases; Medical sciences; Infection; Virus; Rodentia; Mammalia; Vertebrata; Influenzavirus A

Descripteur(s) français

Descripteur(s) : Virose; Orthomyxoviridae; Animal; Souris; Maladie; Cytokine; Virus grippal A; Homme; Médecine tropicale; Pathologie expérimentale; Chimiokine; Virus Dhori

Desc. génériques : Virologie; Maladies infectieuses; Sciences médicales; Infection; Virus; Rodentia; Mammalia; Vertebrata; Influenzavirus A

Localisation : INIST, Shelf number 6817, INIST No. 354000172684270280

Origine de la notice : INIST

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Oseltamivir Prophylactic Regimens Prevent H5N1 Influenza Morbidity and Mortality in a Ferret Model

Titre : Oseltamivir Prophylactic Regimens Prevent H5N1 Influenza Morbidity and Mortality in a Ferret Model

Auteur(s) : BOLTZ David A; REHG Jerold E; MCCLAREN Jennifer; WEBSTER Robert G; GOVORKOVA Elena A
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Source : The Journal of infectious diseases. 2008; 197 (9) : 1315-1323

ISSN : 0022-1899

CODEN : JIDIAQ

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 33 ref.

Résumé : Background. Current oseltamivir prophylactic regimens may not be as effective against highly pathogenic H5N1 influenza viruses as they are against less pathogenic strains. An optimal regimen is urgently needed. Methods. Ferrets were given the neuraminidase inhibitor oseltamivir orally for 10 days (5 or 10 mg/kg once daily or 2.5 or 5 mg/kg twice daily). Prophylaxis was initiated 1 day before infection, and oseltamivir was given 4 h before the ferrets were inoculated with a lethal dose of A/Vietnam/1203/04 (H5N1) influenza virus. Results. At a dose of 5 mg/kg once daily, oseltamivir prevented death but not clinical signs of infection in ferrets; severe pathology was observed in the lungs, brain, and liver. At 10 mg/kg once daily, oseltamivir reduced clinical symptoms and systemic virus replication, but pathology was observed in the internal organs. The best results were obtained at a dose of 2.5 or 5 mg/kg given twice daily. Both regimens resulted in 100% survival and the absence of clinical symptoms, systemic virus spread, and organ pathology. Serum antibody titers were comparable across regimens and were sufficient to protect against rechallenge. Conclusions. An increased dose of oseltamivir or twice-daily administration effectively protects ferrets against morbidity and mortality caused by H5N1 infection and does not interfere with the development of protective antibodies against subsequent H5N1 infection.

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

Descripteur(s) anglais

Descripteur(s) : Prevention; Morbidity; Models; Microbiology; Infection; Oseltamivir; Influenza A; Antiviral

Desc. génériques : Microbiology; Biological sciences; Infectious diseases; Medical sciences; Exo <alpha> sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Viral disease; Enzyme inhibitor; Neuraminidase inhibitor

Descripteur(s) français

Descripteur(s) : Prévention; Morbidité; Modèle; Microbiologie; Infection; Oseltamivir; Grippe A; Antiviral

Desc. génériques : Microbiologie; Sciences biologiques; Maladies infectieuses; Sciences médicales; Exo <alpha> sialidase; Glycosidases; Glycosylases; Hydrolases; Enzyme; Virose; Inhibiteur enzyme; Inhibiteur neuraminidase

Localisation : INIST, Shelf number 2052, INIST No. 354000172798610110

Origine de la notice : INIST

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Trends in Recorded Influenza Mortality: United States, 1900-2004

Titre : Trends in Recorded Influenza Mortality: United States, 1900-2004

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Affiliation(s) : Massachusetts Institute of Technology, Cambridge, United States

Source : American journal of public health 1971. 2008; 98 (5) : 939-945

ISSN : 0090-0036

CODEN : AJPEAG

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 29 ref.

Résumé : Objectives. I sought to describe trends in historical influenza mortality data in the United States since 1900 and compare pandemic with nonpandemic influenza seasons. Methods. I compiled a database of monthly influenza-classed death rates from official US mortality tables for the years 1900 to 2004 (1905-1909 excluded), from which I calculated adjusted influenza season (July 1-June 30) mortality rates. Results. An overall and substantial decline in influenza-classed mortality was observed during the 20th century, from an average seasonal rate of 10.2 deaths per 100000 population in the 1940s to 0.56 per 100000 by the 1990s. The 1918-1919 pandemic stands out as an exceptional outlier. The 1957-1958 and 1968-1969 influenza pandemic seasons, by contrast, displayed substantial overlap in both degree of mortality and timing compared with nonpandemic seasons. Conclusions. The considerable similarity in mortality seen in pandemic and nonpandemic influenza seasons challenges common beliefs about the severity of pandemic influenza. The historical decline in influenza-classed mortality rates suggests that public health and ecological factors may play a role in influenza mortality risk. Nevertheless, the actual number of influenza-attributable deaths remains in doubt.

Code(s) de classement : 002B30A11; 002B05C02C; 002B30A01A

Descripteur(s) anglais

Descripteur(s) : Trend; United States; Influenza; Mortality; Epidemiology; Public health; Human

Desc. génériques : Public health; Medical sciences; Virology; Infectious diseases; Medical sciences; Public health; Medical sciences; North America; America; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Tendances; Etats Unis; Grippe; Mortalité; Epidemiologie; Sante publique; Homme; 1900 2004

Desc. génériques : Sante publique; Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Sante publique; Sciences medicales; Amerique du Nord; Amerique; Virose; Infection

Localisation : INIST, Shelf number 2009, INIST No. 354000195860650280

Origine de la notice : INIST

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Grippe aviaire

Titre : Grippe aviaire

Source : Revue des maladies respiratoires. 2008; 25 (4) : 488-506

Informations congrès : *Seminaire de formation medicale continue, *Paris France, *2007-12-07

ISSN : 0761-8425

CODEN : RMREEY

Date de publication : 2008

Pays de publication : France

Langue(s) : French

Type de document : Serial; *Conference-Meeting

Nombre de références : dissem.

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

Descripteur(s) anglais

Descripteur(s) : Avian influenza; Respiratory disease; Pneumology

Desc. génériques : Pneumology; Respiratory system; Medical sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Grippe aviaire; Pathologie de l' appareil respiratoire; Pneumologie

Desc. génériques : Pneumologie; Appareil respiratoire; Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection

Localisation : INIST, Shelf number 3501, INIST No. 354000172722620075

Origine de la notice : INIST

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Histoire des pandémies virales : Grippe aviaire

Titre : Histoire des pandémies virales : Grippe aviaire

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Source : Revue des maladies respiratoires. 2008; 25 (4) : 490-491

Informations congrès : *Séminaire de formation médicale continue, *Paris France, *2007-12-07

ISSN : 0761-8425

CODEN : RMREEY

Date de publication : 2008

Pays de publication : France

Langue(s) : French

Type de document : Serial; *Conférence-Meeting

Nombre de références : 5 ref.

Code(s) de classement : 002B11; 002B05C

Descripteur(s) anglais

Descripteur(s) : Respiratory disease; Viral disease; Case history; History; Pneumology

Desc. génériques : Pneumology; Respiratory system; Medical sciences; Virology; Infectious diseases; Medical sciences; Infection

Descripteur(s) français

Descripteur(s) : Pathologie de l'appareil respiratoire; Virose; Historique; Histoire; Pneumologie; Pandémie

Desc. génériques : Pneumologie; Appareil respiratoire; Sciences médicales; Virologie; Maladies infectieuses; Sciences médicales; Infection

Localisation : INIST, Shelf number 3501, INIST No. 354000172722620080

Origine de la notice : INIST

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Epidemiologie des pandemies grippales : Grippe aviaire

Titre : Epidemiologie des pandemies grippales : Grippe aviaire

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Source : Revue des maladies respiratoires. 2008; 25 (4) : 492-496

Informations congrès : *Seminaire de formation medicale continue, *Paris France, *2007-12-07

ISSN : 0761-8425

CODEN : RMREEY

Date de publication : 2008

Pays de publication : France

Langue(s) : French

Type de document : Serial; *Conference-Meeting

Nombre de références : 12 ref.

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

Descripteur(s) anglais

Descripteur(s) : Respiratory disease; Human; Public health; Influenza; Epidemiology; Pneumology

Desc. génériques : Pneumology; Respiratory system; Medical sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Pathologie de l' appareil respiratoire; Homme; Sante publique; Grippe; Epidemiologie; Pneumologie; Pandemie

Desc. génériques : Pneumologie; Appareil respiratoire; Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection

Localisation : INIST, Shelf number 3501, INIST No. 354000172722620090

Origine de la notice : INIST

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Conduite a tenir devant une suspicion de cas sporadique de grippe aviaire : Grippe aviaire

Titre : Conduite a tenir devant une suspicion de cas sporadique de grippe aviaire : Grippe aviaire

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Source : Revue des maladies respiratoires. 2008; 25 (4) : 497-499

Informations congrès : *Seminaire de formation medicale continue, *Paris France, *2007-12-07

ISSN : 0761-8425

CODEN : RMREEY

Date de publication : 2008

Pays de publication : France

Langue(s) : French

Type de document : Serial; *Conference-Meeting

Nombre de références : 3 ref.

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

Descripteur(s) anglais

Descripteur(s) : Avian influenza; Respiratory disease; Human; Clinical management; Pneumology

Desc. génériques : Pneumology; Respiratory system; Medical sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Grippe aviaire; Pathologie de l' appareil respiratoire; Homme; Conduite a tenir; Pneumologie

Desc. génériques : Pneumologie; Appareil respiratoire; Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection

Localisation : INIST, Shelf number 3501, INIST No. 354000172722620100

Origine de la notice : INIST

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Le diagnostic d' un cas de grippe aviaire en pratique : Grippe aviaire

Titre : Le diagnostic d' un cas de grippe aviaire en pratique : Grippe aviaire

Auteur(s) : FREYMUTH F; VABRET A

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Source : Revue des maladies respiratoires. 2008; 25 (4) : 500-501

Informations congrès : *Seminaire de formation medicale continue, *Paris France, *2007-12-07

ISSN : 0761-8425

CODEN : RMREEY

Date de publication : 2008

Pays de publication : France

Langue(s) : French

Type de document : Serial; *Conference-Meeting

Nombre de références : 3 ref.

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

Descripteur(s) anglais

Descripteur(s) : Avian influenza; Respiratory disease; Human; Diagnosis; Pneumology

Desc. génériques : Pneumology; Respiratory system; Medical sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Grippe aviaire; Pathologie de l' appareil respiratoire; Homme; Diagnostic; Pneumologie

Desc. génériques : Pneumologie; Appareil respiratoire; Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection

Localisation : INIST, Shelf number 3501, INIST No. 354000172722620110

Origine de la notice : INIST

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Grippe aviaire : vaccins et politique vaccinale : Grippe aviaire

Titre : Grippe aviaire : vaccins et politique vaccinale : Grippe aviaire

Auteur(s) : LAUNAY O

Affiliation(s) : CIC de vaccinologie Cochin Pasteur et AP-HP, Groupe Hospitalier Cochin Saint Vincent de Paul, Pole de medecine, Paris, France; INSERM, Universite Paris Descartes, Faculte de medecine, Paris, France

Source : Revue des maladies respiratoires. 2008; 25 (4) : 502-503

Informations congrès : *Seminaire de formation medicale continue, *Paris France, *2007-12-07

ISSN : 0761-8425

CODEN : RMREEY

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 : 002B11; 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Avian influenza; Respiratory disease; Health policy; Public health; Vaccine; Pneumology

Desc. génériques : Pneumology; Respiratory system; Medical sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Grippe aviaire; Pathologie de l' appareil respiratoire; Politique sanitaire; Sante publique; Vaccin; Pneumologie

Desc. génériques : Pneumologie; Appareil respiratoire; Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection

Localisation : INIST, Shelf number 3501, INIST No. 354000172722620120

Origine de la notice : INIST

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Plan national de prevention et de lutte " pandémie grippale " : Grippe aviaire

Titre : Plan national de prevention et de lutte " pandémie grippale " : Grippe aviaire

Auteur(s) : HOUSSET B

Affiliation(s) : Service de Pneumologie et de Pathologie Professionnelle, Creteil, France

Source : Revue des maladies respiratoires. 2008; 25 (4) : 504-506

Informations congrès : *Seminaire de formation medicale continue, *Paris France, *2007-12-07

ISSN : 0761-8425

CODEN : RMREEY

Date de publication : 2008

Pays de publication : France

Langue(s) : French

Type de document : Serial; *Conference-Meeting

Nombre de références : 3 ref.

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

Descripteur(s) anglais

Descripteur(s) : Respiratory disease; Human; Health policy; Influenza; Public health; Prevention; Pneumology

Desc. génériques : Pneumology; Respiratory system; Medical sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Pathologie de l' appareil respiratoire; Homme; Politique sanitaire; Grippe; Sante publique; Prevention; Pneumologie; Pandemie

Desc. génériques : Pneumologie; Appareil respiratoire; Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection

Localisation : INIST, Shelf number 3501, INIST No. 354000172722620130

Origine de la notice : INIST

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Predictable ecology and geography of avian influenza (H5N1) transmission in Nigeria and West Africa

Titre : Predictable ecology and geography of avian influenza (H5N1) transmission in Nigeria and West Africa

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Source : Transactions of the Royal Society of Tropical Medicine and Hygiene. 2008; 102 (5) : 471-479

ISSN : 0035-9203

CODEN : TRSTAZ

Date de publication : 2008

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Nombre de références : 1 p.1/2

Résumé : The emerging virus strain termed highly pathogenic H5N1 avian influenza (HP-H5N1) has spread widely in the past decade and is now the focus of considerable concern in several sectors. We tested the hypothesis that spatial distributions of veterinary and human HP-H5N1 cases are related to coarse-scale environmental features in West Africa. We used ecological niche models to associate Nigerian HP-H5N1 occurrences with 1 km resolution digital data layers summarizing parameters of surface reflectance and landform. Predictive challenges included anticipating the spatial distribution of (i) random subsamples and (ii) spatially and temporally stratified subsamples of Nigerian occurrence data, and (iii) more limited occurrence data from across West Africa. In almost all tests, we found that HP-H5N1 cases were occurring under predictable environmental conditions, suggesting that elements of the transmission cycle have some form of ecological determination, here measured as differences in land-surface reflectance and plant phenology through the year. Considerable additional work is needed to establish how these differences affect HP-H5N1 transmission.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Avian influenza; Ecology; Geography; Transmission; Nigeria; West Africa; Models; Tropical medicine; Public health; Epidemiology

Desc. génériques : Virology; Infectious diseases; Medical sciences; Viral disease; Infection; Africa

Descripteur(s) français

Descripteur(s) : Grippe aviaire; Ecologie; Géographie; Transmission; Nigeria; Afrique Ouest; Modele; Médecine tropicale; Santé publique; Épidémiologie

Desc. génériques : Virologie; Maladies infectieuses; Sciences médicales; Virose; Infection; Afrique

Localisation : INIST, Shelf number 3084, INIST No. 354000172778570130

Origine de la notice : INIST

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Cross-Recognition of Avian H5N1 Influenza Virus by Human Cytotoxic T-Lymphocyte Populations Directed to Human Influenza A Virus

Titre : Cross-Recognition of Avian H5N1 Influenza Virus by Human Cytotoxic T-Lymphocyte Populations Directed to Human Influenza A Virus

Auteur(s) : KREIJTZ J H C M; DE MUTSERT G; VAN BAALEN C A; FOUCHIER R A M; OSTERHAUS A D M E; RIMMELZWAAN G F

Affiliation(s) : Department of Virology, Erasmus Medical Center, P.O. Box 2040, Rotterdam, Netherlands

Source : Journal of virology. 2008; 82 (11) : 5161-5166

ISSN : 0022-538X

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 29 ref.

Résumé : Since the number of human cases of infection with avian H5N1 influenza viruses is ever increasing, a pandemic outbreak caused by these viruses is feared. Therefore, in addition to virus-specific antibodies, there is considerable interest in immune correlates of protection against these viruses, which could be a target for the development of more universal vaccines. After infection with seasonal influenza A viruses of the H3N2 and H1N1 subtypes, individuals develop virus-specific cytotoxic T-lymphocyte responses, which are mainly directed against the relatively conserved internal proteins of the virus, like the nucleoprotein (NP). Virus-specific cytotoxic T lymphocytes (CTL) are known to contribute to protective immunity against infection, but knowledge about the extent of cross-reactivity with avian H5N1 influenza viruses is sparse. In the present study, we evaluated the cross-reactivity with H5N1 influenza viruses of polyclonal CTL obtained from a group of well-defined HLA-typed study subjects. To this end, the recognition of synthetic peptides representing H5N1 analogues of known CTL epitopes was studied. In addition, the ability of CTL specific for seasonal H3N2 influenza virus to recognize the NP of H5N1 influenza virus or H5N1 virus-infected cells was tested. It was concluded that, apart from some individual epitopes that displayed amino acid variation between H3N2 and H5N1 influenza viruses, considerable cross-reactivity exists with H5N1 viruses. This preexisting cross-reactive T-cell immunity in the human population may dampen the impact of a next pandemic.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Descripteur(s) : Avian influenzavirus; Human; Influenza A virus; Recognition; Cytotoxic T lymphocyte; Virology

Desc. génériques : Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) français

Descripteur(s) : Influenzavirus aviaire; Homme; Virus grippal A; Reconnaissance; Lymphocyte T cytotoxique; Virologie

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST, Shelf number 13592, INIST No. 354000195920550060

Origine de la notice : INIST

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Multi-antigen vaccines based on complex adenovirus vectors induce protective immune responses against H5N1 avian influenza viruses

Titre : Multi-antigen vaccines based on complex adenovirus vectors induce protective immune responses against H5N1 avian influenza viruses

Auteur(s) : HOLMAN David H; WANG Danher; RAJA Nicholas U; MIN LUO; MOORE Kevin M; WORARATANADHARM Jan; MYTLE Nutan; DONG John Y

Affiliation(s) : Division of Biodefense Vaccines, GenPhar Inc., 600 Seacoast Parkway, Mount Pleasant, SC 29464, United States; Southern Research Institute, 2000 Ninth Avenue South, Birmingham, AL 35255, United States; Department of Microbiology and Immunology, Medical University of South Carolina, 173 Ashley Avenue, Charleston, SC 29403, United States

Source : Vaccine . 2008; 26 (21) : 2627-2639

ISSN : 0264-410X

CODEN : VACCDE

Date de publication : 2008

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Nombre de références : 39 ref.

Résumé : There are legitimate concerns that the highly pathogenic H5N1 avian influenza virus could adapt for human-to-human transmission and cause a pandemic similar to the 1918 "Spanish flu" that killed 50 million people worldwide. We have developed pandemic influenza vaccines by incorporating multiple antigens from both avian and Spanish influenza viruses into complex recombinant adenovirus vectors. In vaccinated mice, these vaccines induced strong humoral and cellular immune responses against pandemic influenza virus antigens, and protected vaccinated mice against lethal H5N1 virus challenge. These results indicate that this multi-antigen, broadly protective vaccine may serve as a safer and more effective approach than traditional methods for development of a pandemic influenza vaccine.

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

Descripteur(s) anglais

Descripteur(s) : Adenoviridae; Avian influenza virus; Antigen; Vaccine; Vector; Immunoprotection

Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Virus; Influenzavirus A; Orthomyxoviridae; Zoopathogen

Descripteur(s) français

Descripteur(s) : Adenoviridae; Influenzavirus aviaire; Antigène; Vaccin; Vecteur; Immunoprotection

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquée; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Virus; Influenzavirus A; Orthomyxoviridae; Zoopathogène

Localisation : INIST, Shelf number 20289, INIST No. 354000197733330090

Origine de la notice : INIST

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Protection of chickens against avian influenza with non-replicating adenovirus-vectored vaccine

Titre : Protection of chickens against avian influenza with non-replicating adenovirus-vectored vaccine

Auteur(s) : TORO Haroldo; TANG De Chu C; SUAREZ David L; JIANFENG ZHANG; ZHONGKAI SHI

Affiliation(s) : Department of Pathobiology, 264 Greene Hall, Auburn University, Auburn, AL 36849, United States; Vaxin Inc., 1500 First Avenue North, Birmingham, AL 35203, United States; Southeast Poultry Research Laboratory, Agricultural Research Service, United States Department of Agriculture, 934 College Station Road, Athens, GA 30605, United States

Source : Vaccine . 2008; 26 (21) : 2640-2646

ISSN : 0264-410X

CODEN : VACCDE

Date de publication : 2008

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Nombre de références : 21 ref.

Résumé : Protective immunity against avian influenza (AI) virus was elicited in chickens by single-dose vaccination with a replication competent adenovirus (RCA)-free human adenovirus (Ad) vector encoding an H7 AI hemagglutinin (AdChNY94.H7). Chickens vaccinated in ovo with an Ad vector encoding an AI H5 (AdTW68.H5) previously described, which were subsequently vaccinated intramuscularly with AdChNY94.H7 post-hatch, responded with robust antibody titers against both the H5 and H7 AI proteins. Antibody responses to Ad vector in ovo vaccination follow a dose-response kinetic. The use of a synthetic AI H5 gene codon optimized to match the chicken cell tRNA pool was more potent than the cognate H5 gene. The use of Ad-vectored vaccines to increase resistance of chicken populations against multiple AI strains could reduce the risk of an avian-originating influenza pandemic in humans.

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

Descripteur(s) anglais

Descripteur(s) : Chicken; Adenoviridae; Vector; Vaccine; Avian influenza

Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Aves; Vertebrata; Virus; Poultry; Viral disease; Infection; Veterinary; Farming animal

Descripteur(s) français

Descripteur(s) : Poulet; Adenoviridae; Vecteur; Vaccin; Grippe aviaire

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquée; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Aves; Vertebrata; Virus; Volaille; Virose; Infection; Vétérinaire; Animal élevage

Localisation : INIST, Shelf number 20289, INIST No. 354000197733330100

Origine de la notice : INIST

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Swine Influenza Virus : Zoonotic Potential and Vaccination Strategies for the Control of Avian and Swine Influenzas. Avian and Pandemic Influenza. A Biosocial Approach

Titre : Swine Influenza Virus : Zoonotic Potential and Vaccination Strategies for the Control of Avian and Swine Influenzas. Avian and Pandemic Influenza. A Biosocial Approach

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Source : The Journal of infectious diseases. 2008; 197 (SUP1) : S19-S24

Informations congrès : *The Harvard University Asian Flus and Avian Influenza Workshop, *USA, *2006-12

ISSN : 0022-1899

CODEN : JIDIAQ

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial; *Conference-Meeting

Nombre de références : 46 ref.

Résumé : Influenza viruses are able to infect humans, swine, and avian species, and swine have long been considered a potential source of new influenza viruses that can infect humans. Swine have receptors to which both avian and mammalian influenza viruses bind, which increases the potential for viruses to exchange genetic sequences and produce new reassortant viruses in swine. A number of genetically diverse viruses are circulating in swine herds throughout the world and are a major cause of concern to the swine industry. Control of swine influenza is primarily through the vaccination of sows, to protect young pigs through maternally derived antibodies. However, influenza viruses continue to circulate in pigs after the decay of maternal antibodies, providing a continuing source of virus on a herd basis. Measures to control avian influenza in commercial poultry operations are dictated by the virulence of the virus. Detection of a highly pathogenic avian influenza (HPAI) virus results in immediate elimination of the flock. Low-pathogenic avian influenza viruses are controlled through vaccination, which is done primarily in turkey flocks. Maintenance of the current HPAI virus-free status of poultry in the United States is through constant surveillance of poultry flocks. Although current influenza vaccines for poultry and swine are inactivated and adjuvanted, ongoing research into the development of newer vaccines, such as DNA, live-virus, or vectored vaccines, is being done. Control of influenza virus infection in poultry and swine is critical to the reduction of potential cross-species adaptation and spread of influenza viruses, which will minimize the risk of animals being the source of the next pandemic.

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

Descripteur(s) anglais

Descripteur(s) : Swine; Influenzavirus; Vaccination; Microbiology; Infection; Avian influenza

Desc. génériques : Virology; Microbiology; Biological sciences; Infectious diseases; Medical sciences; Artiodactyla; Ungulata; Mammalia; Vertebrata; Orthomyxoviridae; Virus; Veterinary; Viral disease

Descripteur(s) français

Descripteur(s) : Porcin; Influenzavirus; Vaccination; Microbiologie; Infection; Grippe aviaire

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Maladies infectieuses; Sciences médicales;

Artiodactyla; Ungulata; Mammalia; Vertebrata; Orthomyxoviridae; Virus; Veterinaire; Virose

Localisation : INIST, Shelf number 2052, INIST No. 354000183599690040

Origine de la notice : INIST

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Genetic Strategy to Prevent Influenza Virus Infections in Animals. Avian and Pandemic Influenza. A Biosocial Approach

Titre : Genetic Strategy to Prevent Influenza Virus Infections in Animals. Avian and Pandemic Influenza. A Biosocial Approach

Auteur(s) : JIANZHU CHEN; CHEN Steve C Y; STERN Patrick; SCOTT Benjamin B; LOIS Carlos; KLEINMAN Arthur M, ed; BLOOM Barry R, ed; SAICH Anthony, ed; MASON Katherine A, ed; AULINO Felicity, ed

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Source : The Journal of infectious diseases. 2008; 197 (SUP1) : S25-S28

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Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial; *Conference-Meeting

Nombre de références : 15 ref.

Résumé : The natural reservoirs of influenza viruses are aquatic birds. After adaptation, avian viruses can acquire the ability to infect humans and cause severe disease. Because domestic poultry serves as a key link between the natural reservoir of influenza viruses and epidemics and pandemics in human populations, an effective measure to control influenza would be to eliminate or reduce influenza virus infection in domestic poultry. The development and distribution of influenza-resistant poultry represents a proactive strategy for controlling the origin of influenza epidemics and pandemics in both poultry and human populations. Recent developments in RNA interference and transgenesis in birds should facilitate the development of influenza-resistant poultry.

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

Descripteur(s) anglais

Descripteur(s) : Influenzavirus; Genetics; Microbiology; Infection; Viral disease

Desc. génériques : Virology; Microbiology; Biological sciences; Infectious diseases; Medical sciences; Orthomyxoviridae; Virus

Descripteur(s) français

Descripteur(s) : Influenzavirus; Genetique; Microbiologie; Infection; Virose

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Maladies infectieuses; Sciences medicales; Orthomyxoviridae; Virus

Localisation : INIST, Shelf number 2052, INIST No. 354000183599690050

Origine de la notice : INIST

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Avian and Pandemic Influenza. A Biosocial Approach

Titre : Avian and Pandemic Influenza. A Biosocial Approach

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CODEN : JIDIAQ

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial; *Conference-Meeting

Nombre de références : dissem.

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

Descripteur(s) anglais

Descripteur(s) : Microbiology; Infection

Desc. génériques : Microbiology; Biological sciences; Infectious diseases; Medical sciences

Descripteur(s) français

Descripteur(s) : Microbiologie; Infection

Desc. génériques : Microbiologie; Sciences biologiques; Maladies infectieuses; Sciences médicales

Localisation : INIST, Shelf number 2052, INIST No. 354000183599690000

Origine de la notice : INIST

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Ecology of Avian Influenza Virus in Birds. Avian and Pandemic Influenza. A Biosocial Approach

Titre : Ecology of Avian Influenza Virus in Birds. Avian and Pandemic Influenza. A Biosocial Approach

Auteur(s) : CAUSEY Douglas; EDWARDS Scott V; KLEINMAN Arthur M, ed; BLOOM Barry R, ed; SAICH Anthony, ed; MASON Katherine A, ed; AULINO Felicity, ed

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Source : The Journal of infectious diseases. 2008; 197 (SUP1) : S29-S33

Informations congrès : *The Harvard University Asian Flus and Avian Influenza Workshop, *USA, *2006-12

ISSN : 0022-1899

CODEN : JIDIAQ

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial; *Conference-Meeting

Nombre de références : 48 ref.

Résumé : Avian influenza A virus (an orthomyxovirus) is a zoonotic pathogen with a natural reservoir entirely in birds. The influenza virus genome is an 8-segment single-stranded RNA with high potential for in situ recombination. Two segments code for the hemagglutinin (H) and neuraminidase (N) antigens used for host-cell entry. At present, 16 H and 9 N subtypes are known, for a total of 144 possible different influenza subtypes, each with potentially different host susceptibility. With >10,000 species of birds found in nearly every terrestrial and aquatic habitat, there are few places on earth where birds cannot be found. The avian immune system differs from that of humans in several important features, including asynchronous B and T lymphocyte systems and a polymorphic multigene immune complex, but little is known about the immunogenetics of pathogenic response. Postbreeding dispersal and migration and a naturally high degree of environmental vagility mean that wild birds have the potential to be vectors that transmit highly pathogenic variants great distances from the original sources of infection.

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

Descripteur(s) anglais

Descripteur(s) : Avian influenzavirus; Aves; Microbiology; Infection

Desc. génériques : Virology; Microbiology; Biological sciences; Infectious diseases; Medical sciences; Influenzavirus A; Orthomyxoviridae; Virus; Vertebrata; Zoopathogen

Descripteur(s) français

Descripteur(s) : Influenzavirus aviaire; Aves; Microbiologie; Infection

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Maladies infectieuses; Sciences médicales; Influenzavirus A; Orthomyxoviridae; Virus; Vertebrata; Zoopathogene

Localisation : INIST, Shelf number 2052, INIST No. 354000183599690060

Origine de la notice : INIST

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Siting Epidemic Disease: 3 Centuries of American History. Avian and Pandemic Influenza. A Biosocial Approach

Titre : Siting Epidemic Disease: 3 Centuries of American History. Avian and Pandemic Influenza. A Biosocial Approach

Auteur(s) : ROSENBERG Charles E; KLEINMAN Arthur M, ed; BLOOM Barry R, ed; SAICH Anthony, ed; MASON Katherine A, ed; AULINO Felicity, ed

Affiliation(s) : Department of the History of Science, Harvard University, Cambridge, Massachusetts, United States; Department of Anthropology, Harvard University, Cambridge, United States; John F. Kennedy School of Government, Harvard University, Cambridge, United States; Harvard Asia Center, Harvard University, Cambridge, United States; Department of Social Medicine, Harvard Medical School, Boston, Massachusetts, United States; Harvard School of Public Health, Boston, Massachusetts, United States

Source : The Journal of infectious diseases. 2008; 197 (SUP1) : S4-S6

Informations congrès : *The Harvard University Asian Flus and Avian Influenza Workshop, *USA, *2006-12

ISSN : 0022-1899

CODEN : JIDIAQ

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial; *Conference-Meeting

Nombre de références : 8 ref.

Résumé : Epidemics of infectious disease have always played a role in American history, and such epidemics are sited in time and place and configured in terms of ecology and demography, available medical knowledge, and cultural values and collective experience. The mix of these variables has changed dramatically since the theocratic world of 17th-century New England, but the relevance of each remains. Avian influenza already exists virtually in Western society in terms of planning, global networks, laboratory research, social expectations, media representations, and a specific shared history based on the memory of the 1918 influenza pandemic.

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

Descripteur(s) anglais

Descripteur(s) : Epidemic; American; Microbiology; Infection

Desc. génériques : Microbiology; Biological sciences; Infectious diseases; Medical sciences

Descripteur(s) français

Descripteur(s) : Epidemie; Americain; Microbiologie; Infection

Desc. génériques : Microbiologie; Sciences biologiques; Maladies infectieuses; Sciences médicales

Localisation : INIST, Shelf number 2052, INIST No. 354000183599690010

Origine de la notice : INIST

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China's Health Care System and Avian Influenza Preparedness. Avian and Pandemic Influenza. A Biosocial Approach

Titre : China's Health Care System and Avian Influenza Preparedness. Avian and Pandemic Influenza. A Biosocial Approach

Auteur(s) : KAUFMAN Joan A; KLEINMAN Arthur M, ed; BLOOM Barry R, ed; SAICH Anthony, ed; MASON Katherine A, ed; AULINO Felicity, ed

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Source : The Journal of infectious diseases. 2008; 197 (SUP1) : S7-S13

Informations congrès : *The Harvard University Asian Flu and Avian Influenza Workshop, *USA, *2006-12

ISSN : 0022-1899

CODEN : JIDIAQ

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial; *Conference-Meeting

Nombre de références : 18 ref.

Résumé : The severe acute respiratory syndrome crisis exposed serious deficiencies in China's public health system and willingness to report outbreaks of threats to public health. Consequently, China may be one of the weak links in global preparedness for avian influenza. China's rural health care system has been weakened by 20 years of privatization and fiscal decentralization. China plays a huge role in the global poultry industry, with a poultry population of 14 billion birds, 70%-80% of which are reared in backyard conditions. Although surveillance has been strengthened, obstacles to the timely reporting of disease outbreaks still exist. The weakened health care system prevents many sick people from seeking care at a health care facility, where reporting would originate. Inadequate compensation to farmers for culled birds leads to nonreporting, and local officials may be complicit if they suspect that reporting might lead to economic losses for their communities. At the local level, China's crisis-management ability and multisectoral coordination are weak. The poor quality of infection control in many rural facilities is a serious and well-documented problem. However, traditions of community political mobilization suggest that the potential for providing rural citizens with public health information is possible when mandated from the central government. Addressing these issues now and working on capacity issues, authority structures, accountability, and local reporting and control structures will benefit the control of a potential avian influenza outbreak, as well as inevitable outbreaks of other emerging infectious diseases in China's Pearl River Delta or in other densely populated locations of animal husbandry in China.

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

Descripteur(s) anglais

Descripteur(s) : China; Microbiology; Infection; Avian influenza

Desc. génériques : Microbiology; Biological sciences; Infectious diseases; Medical sciences; Asia; Viral disease

Descripteur(s) français

Descripteur(s) : Chine; Microbiologie; Infection; Grippe aviaire

Desc. génériques : Microbiologie; Sciences biologiques; Maladies infectieuses; Sciences médicales; Asie; Virose

Localisation : INIST, Shelf number 2052, INIST No. 354000183599690020

Origine de la notice : INIST

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Preparing for Avian Influenza : Lessons from the "Swine Flu Affair". Avian and Pandemic Influenza. A Biosocial Approach

Titre : Preparing for Avian Influenza : Lessons from the "Swine Flu Affair". Avian and Pandemic Influenza. A Biosocial Approach

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Source : The Journal of infectious diseases. 2008; 197 (SUP1) : S14-S18

Informations congrès : *The Harvard University Asian Flus and Avian Influenza Workshop, *USA, *2006-12

ISSN : 0022-1899

CODEN : JIDIAQ

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial; *Conference-Meeting

Nombre de références : 8 ref.

Résumé : As a low-likelihood, high-consequence event, the possibility of an influenza pandemic poses a difficult challenge to policymakers. Drawing from the ill-fated swine influenza immunization program of 1976, this article outlines 7 lessons that apply to preparations for avian influenza: (1) beware of overconfidence in models drawn from meager evidence, (2) invest in a balanced portfolio of research and contemporary preparedness, (3) clarify operational responsibilities in the federal government, (4) refrain from overstatement of objectives and mis-representation of risk, (5) strengthen local capacity for implementation, (6) communicate strategically, and (7) lay the basis for program review.

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

Descripteur(s) anglais

Descripteur(s) : Swine; Microbiology; Infection; Avian influenza

Desc. génériques : Microbiology; Biological sciences; Infectious diseases; Medical sciences; Artiodactyla; Ungulata; Mammalia; Vertebrata; Viral disease; Veterinary

Descripteur(s) français

Descripteur(s) : Porcin; Microbiologie; Infection; Grippe aviaire

Desc. génériques : Microbiologie; Sciences biologiques; Maladies infectieuses; Sciences médicales; Artiodactyla; Ungulata; Mammalia; Vertebrata; Virose; Veterinaire

Localisation : INIST, Shelf number 2052, INIST No. 354000183599690030

Origine de la notice : INIST

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Pathogenicity and transmission studies of H5N2 parrot avian influenza virus of Mexican lineage in different poultry species

Titre : Pathogenicity and transmission studies of H5N2 parrot avian influenza virus of Mexican lineage in different poultry species

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Source : Veterinary microbiology Amsterdam. 2008; 129 (1-2) : 48-57

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 : In 2004, a low pathogenic H5N2 influenza virus (A/parrot/CA/6032/04) was identified in a psittacine bird for the first time in the United States. Sequence and phylogenetic analysis of the hemagglutinin gene grouped the parrot isolate under the Mexican lineage H5N2 viruses (subgroup B) with highest similarity to recent chicken-origin isolates from Guatemala. Antigenic analysis further confirmed the close relatedness of the parrot isolate to Mexican lineage viruses, the highest cross-reactivity being demonstrated to Guatemala isolates. In vivo studies of the parrot isolate in chickens, ducks and turkeys showed that the virus, though did not cause any clinical signs, could replicate to high titers in these birds and efficiently transmit to contact control cage mates. The possibility that the parrot harboring the virus was introduced into the United States as a result of illegal trade across the border provides additional concern for the movement of foreign animal diseases from neighboring countries. Considering the potential threat of the virus to domestic poultry, efforts should be continued to prevent the entry and spread of influenza viruses by imposing effective surveillance and monitoring measures.

Code(s) de classement : 002A05C10

Descripteur(s) anglais

Descripteur(s) : Avian influenza virus; Pathogenicity; Transmission; Mexico; Poultry; Microbiology; Veterinary; Influenza

Desc. génériques : Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Central America; America; Zoopathogen; Viral disease; Infection; Farming animal

Descripteur(s) français

Descripteur(s) : Influenzavirus aviaire; Pouvoir pathogene; Transmission; Mexique; Volaille; Microbiologie; Veterinaire; Grippe

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Amerique Centrale; Amerique; Zoopathogene; Virose; Infection; Animal elevage

Localisation : INIST, Shelf number 16884, INIST No. 354000183076380050

Origine de la notice : INIST

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Development of a high-throughput Alamar blue assay for the determination of influenza virus infectious dose, serum antiviral neutralization titer and virus ca/ts phenotype

Titre : Development of a high-throughput Alamar blue assay for the determination of influenza virus infectious dose, serum antiviral neutralization titer and virus ca/ts phenotype

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Source : Journal of virological methods. 2008; 150 (1-2) : 63-69

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 : FluMist<Registered> is an intranasal influenza live vaccine containing two Influenza A strains (currently H1N1 and H3N2) and one B strain (Yamagata or Victoria lineage). Characterization of the vaccine requires determination of the median tissue culture infectious dose (TCID₅₀) titer, serum antiviral neutralization titer and vaccine cold adapted/temperature sensitive (ca/ts) phenotype. Visual cytopathic effect (CPE) readings are used widely in viral assays, but these are subjective and labor intensive. In response to the need for an efficient, inexpensive and high-throughput assay, a 96-well microplate assay was developed that uses Alamar blue dye staining as a replacement for CPE observation in the determination of influenza virus infectious dose, serum antiviral neutralization titer and virus ca/ts phenotype. Relative operating characteristic curves verified that there was a clear distinction between the fluorescence readings of the Alamar blue stained CPE positive and CPE negative wells. Virus titer was determined by use of both Alamar blue staining and CPE-based TCID₅₀ assays for wild-type and FluMist influenza vaccine strains as well as a plasmid-rescued influenza FluMist A strain containing a H5N1 derived hemmagglutinin and neuraminidase. Correlation of the two assays was measured by regression analysis and resulted in R^{sup}>2 values of 0.814 (Influenza A), 0.983 (Influenza B) and 1.000 (H5N1), respectively. Serum microneutralization as well as virus ca/ts phenotype assays also showed a high concordance between readings based on CPE observation and Alamar blue staining. The Alamar blue dye assay is user friendly, environmentally safe and sensitive. Also, it is adaptable to automation, which could provide a high-throughput platform for analysis of pre-clinical and clinical samples.

Code(s) de classement : 002A05C09

Descripteur(s) anglais

Descripteur(s) : Influenzavirus; High throughput screening; Serum; Neutralization; Phenotype; Microbiology; Method; Virology; Infection

Desc. génériques : Virology; Microbiology; Biological sciences; Orthomyxoviridae; Virus

Descripteur(s) français

Descripteur(s) : Influenzavirus; Criblage haut débit; Serum; Neutralisation; Phenotype; Microbiologie; Méthode; Virologie; Infection

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Orthomyxoviridae; Virus

Localisation : INIST, Shelf number 18295, INIST No. 354000195850830110

Origine de la notice : INIST

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Influenza viruses and the evolution of avian influenza virus H5N1

Titre : Influenza viruses and the evolution of avian influenza virus H5N1

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Affiliation(s) : St. Mary's Regional Medical Center, Sabattus Street Internal Medicine Clinic, 963 Sabattus Street, Lewiston, ME 04240, United States; Internal Medicine, Health Associates of Peace Harbor, Florence, Oregon, United States

Source : International journal of infectious diseases. 2008; 12 (3) : 233-238

ISSN : 1201-9712

Date de publication : 2008

Pays de publication : Netherlands

Langue(s) : English

Type de document : Serial

Nombre de références : 64 ref.

Résumé : Although small in size and simple in structure, influenza viruses are sophisticated organisms with highly mutagenic genomes and wide antigenic diversity. They are species-specific organisms. Mutation and reassortment have resulted in newer viruses such as H5N1, with new resistance against anti-viral medications, and this might lead to the emergence of a fully transmissible strain, as occurred in the 1957 and 1968 pandemics. Influenza viruses are no longer just a cause of self-limited upper respiratory tract infections; the H5N1 avian influenza virus can cause severe human infection with a mortality rate exceeding 50%. The case death rate of H5N1 avian influenza infection is 20 times higher than that of the 1918 infection (50% versus 2.5%), which killed 675 000 people in the USA and almost 40 million people worldwide. While the clock is still ticking towards what seems to be inevitable pandemic influenza, on April 17, 2007 the U.S. Food and Drug Administration (FDA) approved the first vaccine against the avian influenza virus H5N1 for humans at high risk. However, more research is needed to develop a more effective and affordable vaccine that can be given at lower doses.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Avian influenza; Immunoprophylaxis; Evolution; Transmission; Treatment; Human; Prevention; Vaccination; Influenzavirus AH5N1

Desc. génériques : Virology; Infectious diseases; Medical sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Grippe aviaire; Immunoprophylaxie; Evolution; Transmission; Traitement; Homme; Prevention; Vaccination; Influenzavirus AH5N1

Desc. génériques : Virologie; Maladies infectieuses; Sciences médicales; Virose; Infection

Localisation : INIST, Shelf number 26659, INIST No. 354000195851250010

Origine de la notice : INIST

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Evaluation of Gl11 and Gly8 of the H5N1 influenza hemagglutinin fusion peptide in membrane fusion using pseudotype virus and reverse genetics

Titre : Evaluation of Gl11 and Gly8 of the H5N1 influenza hemagglutinin fusion peptide in membrane fusion using pseudotype virus and reverse genetics

Auteur(s) : SU Y; ZHU X; WANG Y; WU M; TIEN P

Affiliation(s) : Center for Molecular Virology, Chinese Academy of Sciences, Institute of Microbiology, Beijing, China; Graduate School of the Chinese Academy of Sciences, Beijing, China

Source : Archives of virology. 2008; 153 (2) : 247-257

ISSN : 0304-8608

Date de publication : 2008

Pays de publication : Austria

Langue(s) : English

Type de document : Serial

Nombre de références : 30 ref.

Résumé : Influenza viruses gain entry into host cells by binding to cellular receptors and promoting the fusion of the viral envelope with the host cell membrane. The fusion peptide of influenza hemagglutinin (HA) is crucial for fusion. To examine the structural and functional roles of amino acids E11 and G8 of the H5 HA fusion peptide, a series of fusion mutants was generated. We determined the effect of each mutation on fusion activity and infection of rescued recombinant virus by polykaryon formation, cell-cell fusion assay, HA pseudovirus transduction and reverse genetics. Our findings indicate that E11 V and E11A mutants dramatically inhibit fusion and that at position 11 a polar residue such as glutamic acid or serine may be desirable for preserving the fusion activity. More interestingly, one mutation (G8E) raised the threshold pH of polykaryon formation. Our results suggest that G8 as well as E11 play an important functional and structural role in membrane fusion and that the polarity of E11 is crucial for fusion activity. Finally, we developed an assay based on a reporter gene plus pseudotyped virus that could sensitively detect fusion activity.

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

Descripteur(s) anglais

Descripteur(s) : Hemagglutinin; Peptides; Membrane fusion; Genetics; Influenza

Desc. génériques : Virology; Microbiology; Biological sciences; Genetics; Virology; Microbiology; Biological sciences; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Hemagglutinine; Peptide; Fusion membranaire; Genetique; Grippe

Desc. génériques : Virologie; Microbiologie; Sciences biologiques; Genetique; Virologie; Microbiologie; Sciences biologiques; Virose; Infection

Localisation : INIST, Shelf number 6355, INIST No. 354000173771030020

Origine de la notice : INIST

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Influenza vaccines and vaccination strategies in birds. Aspects of vaccine development

Titre : Influenza vaccines and vaccination strategies in birds. Aspects of vaccine development

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Source : Comparative immunology microbiology and infectious diseases. 2008; 31 (2-3) : 121-165

ISSN : 0147-9571

CODEN : CIMIDV

Date de publication : 2008

Pays de publication : United Kingdom

Langue(s) : English

Langue(s) du résumé : French

Type de document : Serial

Nombre de références : 356 ref.

Résumé : Bien qu'il soit à présent bien accepté que la panzootie au virus H5N1 asiatique soit avant tout un problème de santé animale, ses implications sur la santé publique et le risque de pandémie ont montré le besoin de plus d'information et de coordination entre le monde médical et le monde vétérinaire. Les virus du sous-type H5 et H7 ont l'unique propriété de devenir hautement pathogènes (IAHP) lors de leur circulation chez la volaille. Des lors, l'objectif final de la vaccination de la volaille est l'éradication de la maladie. En fait, il existe d'importantes différences entre le contrôle de l'influenza aviaire et celui de la grippe chez l'homme. Premièrement, contrairement aux vaccins humains qui doivent être ajustés aux souches circulantes pour procurer une bonne protection, les vaccins aviaires fournissent une plus large protection contre les souches IAHP. Deuxièmement, alors que le but premier des vaccins humains est la protection clinique, les vaccins aviaires doivent aussi réduire la transmission du virus de manière à permettre le contrôle de la maladie. Cet article tente d'aborder ces différences en passant en revue les vaccins actuels et futurs contre l'influenza et les différentes stratégies de vaccination chez la volaille.

Code(s) de classement : 002A05F04

Descripteur(s) anglais

Descripteur(s) : Aves; Vaccine; Vaccination; Vector; Microbiology; Immunology; Influenza

Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Vertebrata; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Aves; Vaccin; Vaccination; Vecteur; Microbiologie; Immunologie; Grippe

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquée; Microbiologie; Sciences biologiques; Vertebrata; Virose; Infection

Localisation : INIST, Shelf number 16817, INIST No. 354000183755360030

Origine de la notice : INIST

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A quantitative genotype algorithm reflecting H5N1 Avian influenza niches

Titre : A quantitative genotype algorithm reflecting H5N1 Avian influenza niches

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Source : Bioinformatics Oxford Print. 2007; 23 (18) : 2368-2375

ISSN : 1367-4803

Date de publication : 2007

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Nombre de références : 3/4 p.

Résumé : Motivation: Computational genotyping analyses are critical for characterizing molecular evolutionary footprints, thus providing important information for designing the strategies of influenza prevention and control. Most of the current methods that are available are based on multiple sequence alignment and phylogenetic tree construction, which are time consuming and limited by the number of taxa. Arbitrarily defining genotypes further complicates the interpretation of genotyping results. Methods: In this study, we describe a quantitative influenza genotyping algorithm based on the theory of quasispecies. First, the complete composition vector (CCV) was utilized to calculate the pairwise evolutionary distance between genotypes. Next, Hierarchical Bayesian Modeling using the Gibbs Sampling algorithm was applied to identify the segment genotype threshold, which is used to identify influenza segment genotype through a modularity calculation. The viral genotype was defined by combining eight segment genotypes based on the genetic reassortment feature of influenza A viruses. Results: We applied this method for H5N1 avian influenza viruses and identified 107 niches among 283 viruses with a complete genome set. The diversity of viral genotypes, and their correlation with geographic locations suggests that these viruses form local niches after being introduced to a new ecological environment through poultry trade or bird migration. This novel method allows us to define genotypes in a robust, quantitative as well as hierarchical manner.

Code(s) de classement : 002A01B

Descripteur(s) anglais

Descripteur(s) : Quantitative analysis; Genotype; Algorithm; Avian influenza; Molecular evolution; Quasispecies; Hierarchical classification; Gibbs sampling; Correlation; Ecological niche; Phylogeny; Original document

Desc. génériques : Biological sciences; Viral disease; Infection; Bioinformatics

Descripteur(s) français

Descripteur(s) : Analyse quantitative; Genotype; Algorithme; Grippe aviaire; Evolution moléculaire; Quasi espece; Classification hiérarchique; Echantillonnage Gibbs; Correlation; Niche écologique; Phylogénèse; Document original

Desc. génériques : Sciences biologiques; Virose; Infection; Bioinformatique

Localisation : INIST, Shelf number 21331, INIST No. 354000149812200030

Origine de la notice : LGMI

Generation and evaluation of the trivalent inactivated reassortant vaccine using human, avian, and swine influenza A viruses

Titre : Generation and evaluation of the trivalent inactivated reassortant vaccine using human, avian, and swine influenza A viruses

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Source : Vaccine . 2008; 26 (23) : 2912-2918

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 : Reassortant technology was used to obtain three interspecific reassortant influenza viruses using three influenza viruses of A/Puerto Rico/8/34(H1N1), A/swine/Hebei/1/2005(H3N2) and A/chicken/Guangdong/126/2002(H9N2). The high-growth reassortant strains were H9/PR8, H3/H9N2 and H1/H9N2 that contained hemagglutinin (HA) and neuraminidase (NA) genes from the inactivated parental viruses and the other 6 internal genes from the live parental viruses. The trivalent formalin-inactivated vaccine, containing H1, H3 and H9 subtype antigens from human, swine and avian influenza viruses respectively, was prepared using these reassortant viruses. Animal studies showed that the vaccine was safe and immunogenic. Two-dosing regimen of the influenza vaccine induced high titers of hemagglutination inhibiting (HI) antibodies and influenza-specific IgG antibodies without antigenic cross-interference. It protected 100% chickens from challenge of A/chicken/Guangdong/126/2002 virus and protected 100% mice against challenges with different combinations of the three infective parental viruses. These results indicated that the trivalent vaccine could offer multi-protection against multi-influenza viruses synchronously. This kind of multivalent inactivated reassortant influenza vaccine maybe enlightens the pandemic influenza preparedness as the emergency measure.

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

Descripteur(s) anglais

Descripteur(s) : Human; Avian influenza virus; Swine; Influenza A virus; Inactivated strain; Influenza; Genetic reassortment

Desc. génériques : Immunology; Pharmacology; Applied microbiology; Microbiology; Biological sciences; Virology; Microbiology; Biological sciences; Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Zoopathogen; Viral disease; Infection; Veterinary

Descripteur(s) français

Descripteur(s) : Homme; Influenzavirus aviaire; Porcin; Virus grippal A; Souche inactivee; Grippe; Reassortiment genetique

Desc. génériques : Immunologie; Pharmacologie; Microbiologie appliquee; Microbiologie; Sciences biologiques; Virologie; Microbiologie; Sciences biologiques; Influenzavirus A; Orthomyxoviridae; Virus; Artiodactyla; Ungulata; Mammalia; Vertebrata; Zoopathogene; Virose; Infection; Veterinaire

Localisation : INIST, Shelf number 20289, INIST No. 354000195954210150

Origine de la notice : INIST

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Les virus bougent : perils planétaires : Maladies infectieuses et l' Outre Mer; Global threats from emerging viral diseases

Titre : Les virus bougent : perils planétaires : Maladies infectieuses et l' Outre Mer; Global threats from emerging viral diseases

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Source : Bulletin de l'Academie nationale de medecine. 2007; 191 (8) : 1563-1577

ISSN : 0001-4079

CODEN : BANMAC

Date de publication : 2007

Pays de publication : France

Langue(s) : French

Langue(s) du résumé : English

Type de document : Serial

Nombre de références : 47 ref.

Résumé : L'histoire nous a appris que les émergences virales ne sont pas des phénomènes nouveaux. La variole, venue d'Asie, est probablement apparue en Europe dès le V^e siècle et la fièvre jaune a émergé en Amérique au XVI^e siècle, importée d'Afrique par la traite des Noirs. La dengue est apparue au XVIII^e siècle simultanément en Asie du Sud-est, en Afrique et en Amérique du Nord. Quant à la " grippe espagnole ", elle a tué, en 1918-1919, entre 25 et 40 millions de personnes dans le monde. La deuxième moitié du XV^e siècle a été marquée par de nombreuses émergences virales dont celle du Sida en 1981. Mais, ce qui caractérise l'évolution récente des émergences virales, c'est que non seulement de nouveaux virus émergent de façon répétée, mais qu'ils ont de plus en plus tendance à envahir de nouveaux pays, voire d'autres continents, et de s'y installer de façon plus ou moins durable. Des exemples de cette situation épidémique nouvelle sont donnés avec les infections à virus Nipah, West Nile, de la fièvre de la Vallée du Rift, du SRAS, du monkeypox, de la grippe aviaire H5N1 et Chikungunya. Les causes, multiples et complexes, de ces émergences et réémergences sont brièvement analysées.

Code(s) de classement : 002B01; 002B05C02I1E; 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Emerging disease; Danger; World; Rift valley fever; West Nile virus; Avian influenza; Variola virus; Monkey; Severe acute respiratory syndrome; Chikungunya virus; Medicine

Desc. génériques : Medical sciences; Virology; Infectious diseases; Medical sciences; Virology; Infectious diseases; Medical sciences; Arbovirus disease; Viral disease; Infection; Japanese encephalitis group virus; Flavivirus; Flaviviridae; Virus; Orthopoxvirus; Chordopoxvirinae; Poxviridae; Primates; Mammalia; Vertebrata; Alphavirus; Togaviridae; Respiratory disease; Lung disease

Descripteur(s) français

Descripteur(s) : Maladie émergente; Danger; Monde; Fièvre vallée Rift; Virus West Nile; Grippe aviaire; Virus variole; Singe; Syndrome respiratoire aigu sévère; Virus Chikungunya; Médecine; Virus Nipah; Menace; Virus H5N1

Desc. génériques : Sciences médicales; Virologie; Maladies infectieuses; Sciences médicales; Virologie; Maladies infectieuses; Sciences médicales; Arbovirose; Virose; Infection; Virus groupe encéphalite japonaise; Flavivirus; Flaviviridae; Virus; Orthopoxvirus; Chordopoxvirinae; Poxviridae; Primates; Mammalia; Vertebrata; Alphavirus; Togaviridae; Pathologie de l'appareil respiratoire; Pathologie des poumons

Localisation : INIST, Shelf number 740, INIST No. 354000183033710090

Origine de la notice : INIST

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Initial Test of Emergency Procedure Performance in Temporary Negative Pressure Isolation by Using Simulation Technologies

Titre : Initial Test of Emergency Procedure Performance in Temporary Negative Pressure Isolation by Using Simulation Technologies

Auteur(s) : DAVIS Mark A; LANDESMAN Roxanne; TADMOR Boaz; HOPMEIER Michael; SHENHAR Gili; BARKER Tobias; POZNER Charles N; BINSTADT Emily S; NELSON Stephen; LOOK Rodney; SHUBINA Maria; WALLS Ron M

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Source : Annals of emergency medicine. 2008; 51 (4) : 420-425

ISSN : 0196-0644

CODEN : AEMED3

Date de publication : 2008

Pays de publication : United States

Langue(s) : English

Type de document : Serial

Nombre de références : 17 ref.

Résumé : Study objective: The potential of infectious disease spread in diseases such as tuberculosis, infectious disease epidemic such as avian flu and the threat of terrorism with agents capable of airborne transmission have focused attention on the need for increased surge capacity for patient isolation. Total negative pressure isolation using portable bioisolation tents may provide a solution. The study assesses the ability of health care workers to perform emergency procedures in this environment. Methods: Physician performance in completing predetermined critical actions in 5 emergency care scenarios inside and outside of a bioisolation tent ("setting") was studied in an advanced medical simulation laboratory. By design, no pretraining of subjects about total negative pressure isolation use occurred. Impact of setting on time to completion of predetermined critical actions was the primary outcome measured. Secondary variables studied included impact of study groups, scenarios, and run order (inside or outside of the tent first). Subjective assessments were obtained through questionnaires. Results: Four teams of 3 physicians completed 5 emergency patient care scenarios during 2 4-hour sessions. Mean time to completion of critical actions was for tent/no tent 298 seconds/284 seconds ($P=.69$, one way ANOVA), respectively. Mean time to completion for first versus second performance of a scenario in the crossover design was 338 versus 243 ($P=.01$). The mean score for self-assessed performance did not differ according to setting. Conclusion: The ability of physicians naive to the total negative pressure isolation environment to perform emergency medical critical actions was not significantly degraded by a simulated bioisolation tent patient care environment.

Code(s) de classement : 002B27B; 002B27B14C

Descripteur(s) anglais

Descripteur(s) : Emergency procedure; Negative pressure; Simulation; Resuscitation; Intensive care

Desc. génériques : Resuscitation; Intensive care medicine; Medical sciences; Resuscitation; Intensive care medicine; Medical sciences

Descripteur(s) français

Descripteur(s) : Procedureurgence; Pression negative; Simulation; Reanimation; Soins intensif

Desc. génériques : Reanimation; Soins intensifs; Sciences médicales; Reanimation; Soins intensifs; Sciences

medicales

Localisation : INIST, Shelf number 19670, INIST No. 354000197773830130

Origine de la notice : INIST

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Display of avian influenza virus nucleoprotein on *Bacillus thuringiensis* cell surface using CTC as a fusion partner

Titre : Display of avian influenza virus nucleoprotein on *Bacillus thuringiensis* cell surface using CTC as a fusion partner

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Source : Applied microbiology and biotechnology. 2008; 78 (4) : 669-676

ISSN : 0175-7598

CODEN : AMBIDG

Date de publication : 2008

Pays de publication : Germany

Langue(s) : English

Type de document : Serial

Nombre de références : 1/2 p.

Résumé : The S-layer protein CTC surface display system of *Bacillus thuringiensis* was used to test the possibility of displaying avian influenza virus nucleoprotein (NP) on the cell surface of *B. thuringiensis*. By fusing np with the anchoring motif of ctc, four recombinant plasmids were constructed. They harbored fusion gene ctc-np, csa-ctc-np (csa representing csaAB operon, very important in anchoring S-layer protein on cell surface), ctc-npp (npp representing the part fragment of np), and csa-ctc-npp, respectively. Five recombinant strains were obtained by transferring recombinant plasmids to *B. thuringiensis* plasmid-free derivative strain BMB171. The vegetative cells of five strains were used as agglutinogens for slide agglutination assays. The assays showed recombinant NP proteins successfully displayed on the cell surface of five strains. After immunization of chickens with spores by oral route, all five strains elicited a humoral response to NP and exhibited immunogenicity as indicated by enzyme-linked immunosorbent assay (ELISA). ELISA also showed that one of five strains, CN (bearing csa-ctc-npp), exhibited the highest immunogenicity among five strains, which suggested that the best way of constructing ctc fusion gene was the csa-ctc-npp. The strategy developed in this study suggests the possibility of generating a heat-stable and oral veterinary vaccine with *B. thuringiensis* surface display system.

Code(s) de classement : 002A31D01C2; 215

Descripteur(s) anglais

Descripteur(s) : Nucleoprotein; *Bacillus thuringiensis*; Cell surface; S Layer; Genetically modified microorganism; Avian influenza virus; Fusion protein; Vaccine

Desc. génériques : Immunology; Pharmacology; Biotechnology; Biological sciences; Bacillaceae; Bacillales; Bacteria; Influenzavirus A; Orthomyxoviridae; Virus

Descripteur(s) français

Descripteur(s) : Nucleoproteine; *Bacillus thuringiensis*; Surface cellulaire; Couche S; Microorganisme génétiquement modifié; Influenzavirus aviaire; Protéine fusion; Vaccin

Desc. génériques : Immunologie; Pharmacologie; Biotechnologie; Sciences biologiques; Bacillaceae; Bacillales; Bactérie; Influenzavirus A; Orthomyxoviridae; Virus

Localisation : INIST, Shelf number 16771, INIST No. 354000175179140140

Origine de la notice : INIST

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The impact of contact structure on infectious disease control : influenza and antiviral agents

Titre : The impact of contact structure on infectious disease control : influenza and antiviral agents

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Source : Epidemiology and infection. 2007; 135 (7) : 1124-1132

ISSN : 0950-2688

CODEN : EPINEU

Date de publication : 2007

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Nombre de références : 28 ref.

Résumé : Planning adequate public health responses against emerging infectious diseases requires predictive tools to evaluate the impact of candidate intervention strategies. With current interest in pandemic influenza very high, modelling approaches have suggested antiviral treatment combined with targeted prophylaxis as an effective first-line intervention against an emerging influenza pandemic. To investigate how the effectiveness of such interventions depends on contact structure, we simulate the effects in networks with variable degree distributions. The infection attack rate can increase if the number of contacts per person is heterogeneous, implying the existence of high-degree individuals who are potential super-spreaders. The effectiveness of a socially targeted intervention suffers from heterogeneous contact patterns and depends on whether infection is predominantly transmitted to close or casual contacts. Our findings imply that the various contact networks' degree distributions as well as the allocation of contagiousness between close and casual contacts should be examined to identify appropriate strategies of disease control measures.

Code(s) de classement : 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Human; Antiviral; Epidemiology; Public health; Prevention; Infection; Influenza

Desc. génériques : Virology; Infectious diseases; Medical sciences; Viral disease

Descripteur(s) français

Descripteur(s) : Homme; Antiviral; Epidemiologie; Sante publique; Prevention; Infection; Grippe

Desc. génériques : Virologie; Maladies infectieuses; Sciences medicales; Virose

Localisation : INIST, Shelf number 6056, INIST No. 354000162017340080

Origine de la notice : INIST

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Children, avian influenza H5N1 and preparing for the next pandemic

Titre : Children, avian influenza H5N1 and preparing for the next pandemic

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Source : Archives of disease in childhood. 2008; 93 (5) : 433-438

ISSN : 0003-9888

CODEN : ADCHAK

Date de publication : 2008

Pays de publication : United Kingdom

Langue(s) : English

Type de document : Serial

Nombre de références : 54 ref.

Résumé : The emergence of avian influenza A/H5N1 viruses has driven pandemic preparations to become government priorities across Europe. To date these viruses have remained poorly adapted to humans and the risk of a pandemic based on H5N1 is unquantifiable. However, the risk of a future pandemic is 100%. Preparations are essential and without these many avoidable deaths will occur. Children will be affected at least as much as adults and may play an important role in amplifying transmission. Pharmacological and public health interventions focused on children will save lives through suggested community measures such as pre-emptive closures of schools, and need to be considered carefully, balancing benefits against negative consequences. Child health services will be hugely stressed by any pandemic but also have the potential to save many lives. The challenge will be to deliver core services in the face of major staff illnesses. Detailed local business continuity planning will be essential.

Code(s) de classement : 002B30A03C; 002B01; 002B05C02C

Descripteur(s) anglais

Descripteur(s) : Avian influenza; Child; Public health; World; Pediatrics; Influenzavirus AH5N1

Desc. génériques : Public health; Medical sciences; Medical sciences; Virology; Infectious diseases; Medical sciences; Viral disease; Infection; Human

Descripteur(s) français

Descripteur(s) : Grippe aviaire; Enfant; Sante publique; Monde; Pediatrie; Pandemie; Influenzavirus AH5N1

Desc. génériques : Sante publique; Sciences medicales; Sciences medicales; Virologie; Maladies infectieuses; Sciences medicales; Virose; Infection; Homme

Localisation : INIST, Shelf number 2035, INIST No. 354000172733690190

Origine de la notice : INIST

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CHIMIOThERAPIES ANTI-INFLUENZA. Le médicament vétérinaire; ANTI-INFLUENZA CHEMOTHERAPIES. Veterinary drugs

Titre : CHIMIOThERAPIES ANTI-INFLUENZA. Le médicament vétérinaire; ANTI-INFLUENZA CHEMOTHERAPIES. Veterinary drugs

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Source : Bulletin de l'Academie veterinaire de France. 2008; 161 (1) : 13-17

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CODEN : BAVFAV

Date de publication : 2008

Pays de publication : France

Langue(s) : French

Langue(s) du résumé : English

Type de document : Serial

Nombre de références : 3/4 p.

Résumé : L'actuelle epizootie de grippe A (H5N1) souligne la necessite de traitements antiviraux pour faire face a une eventuelle pandémie grippale. Les traitements anti-influenza ont aussi pour objectif de reduire les symptomes et complications survenant lors des epidemies saisonnieres. Deux classes d'antiviraux, les inhibiteurs du canal a protons M2 (amantadine, rimantadine), et les inhibiteurs de neuraminidase (zanamivir, oseltamivir), ont une efficacite prophylactique et therapeutique. L'emergence de virus resistants est particulierement frequente lors du traitement avec les inhibiteurs de M2, et limite leur utilisation. Le developpement d'une resistance a l'oseltamivir a ete decrit chez plusieurs patients infectes avec le virus H5N1. Une surveillance etroite de la resistance aux anti-viraux s'impose, ainsi que le developpement de nouveaux composes, pouvant cibler eventuellement d'autres proteines virales telles que l'hemagglutinine ou la polymerase, et pouvant etre utilises en polychimiotherapies.

Code(s) de classement : 002A05

Descripteur(s) anglais

Descripteur(s) : Veterinary; Chemotherapy; Exo <alpha> sialidase; Resistance; Microbiology; Influenza

Desc. génériques : Microbiology; Biological sciences; Treatment; Glycosidases; Glycosylases; Hydrolases; Enzyme; Viral disease; Infection

Descripteur(s) français

Descripteur(s) : Veterinaire; Chimiotherapie; Exo <alpha> sialidase; Resistance; Microbiologie; Grippe

Desc. génériques : Microbiologie; Sciences biologiques; Traitement; Glycosidases; Glycosylases; Hydrolases; Enzyme; Virose; Infection

Localisation : INIST, Shelf number 815, INIST No. 354000183638960020

Origine de la notice : INIST

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Proteomics analysis of differential expression of cellular proteins in response to avian H9N2 virus infection in human cells

Titre : Proteomics analysis of differential expression of cellular proteins in response to avian H9N2 virus infection in human cells

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Source : Proteomics Weinheim Print. 2008; 8 (9) : 1851-1858

ISSN : 1615-9853

Date de publication : 2008

Pays de publication : Germany

Langue(s) : English

Type de document : Serial

Nombre de références : 23 ref.

Résumé : We present the first proteomic analysis on the cellular responses to avian influenza virus (H9N2) infection in a human cell line in different time courses in order to search for target proteins for viral pathogenesis/adaptation studies. By using 2-DE coupled with MALDI-TOF MS and nanoESI-MS/MS, we identified a set of differentially expressed cellular proteins, including cytoplasmic actin, cytokeratin, prohibitin, enoyl-CoA hydratase, peptide-prolyl cis-trans isomerase A (PPIase A), chloride intracellular channel protein 1, pyruvate dehydrogenase E1 component subunit beta, adenine phosphoribosyltransferase, guanine nucleotide-binding protein subunit beta, nucleoside diphosphate kinase A, elongation factor 1-beta and splicing factor, arginine/serine rich 1. The most significant changes in different time courses were found in cytoplasmic actin and cytokeratin, both of which constituted the major components of cytoskeleton network in the cells. The obtained data suggested a possible role of the cytoskeleton during avian influenza virus infection of mammalian cells, which might help for better understanding of the dynamics of avian influenza virus and host interaction in mammalian cell setting.

Code(s) de classement : 002A02D10; 002B05C

Descripteur(s) anglais

Descripteur(s) : Aves; Human; Avian influenza virus; Proteomics; Protein; Cell line; Cytokeratin; Intermediate filament; Keratin; Cytoskeleton; Actin; Viral disease; Two dimensional electrophoresis

Desc. génériques : Proteins; Biochemistry; Biological sciences; Virology; Infectious diseases; Medical sciences; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Infection

Descripteur(s) français

Descripteur(s) : Aves; Homme; Influenzavirus aviaire; Proteomique; Protéine; Lignée cellulaire; Cytokeratine; Filament intermédiaire; Kératine; Cytosquelette; Actine; Virose; Electrophorese bidimensionnelle

Desc. génériques : Protéines; Biochimie; Sciences biologiques; Virologie; Maladies infectieuses; Sciences médicales; Vertebrata; Influenzavirus A; Orthomyxoviridae; Virus; Infection

Localisation : INIST, Shelf number 27206, INIST No. 354000183086770140

Origine de la notice : INIST

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Characterization of a trypsin-dependent avian influenza H5N1-pseudotyped HIV vector system for high throughput screening of inhibitory molecules

Titre : Characterization of a trypsin-dependent avian influenza H5N1-pseudotyped HIV vector system for high throughput screening of inhibitory molecules

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Source : Antiviral research. 2008; 79 (1) : 12-18

ISSN : 0166-3542

CODEN : ARSRDR

Date de publication : 2008

Pays de publication : Netherlands

Langue(s) : English

Type de document : Serial

Nombre de références : 1/2 p.

Résumé : In this study, we have generated and characterized an avian influenza H5N1 hemagglutinin (HA), neuraminidase (NA) and M2 ion channel pseudotyped HIV-based vector system (HaNaM-pseudotyped HIV vector). The cleavage site of the HA protein was modified to necessitate trypsin-dependent maturation of the glycoprotein. HA, NA and M2 were efficiently incorporated in HIV vector particles which could transduce different cell lines in a trypsin-dependent manner. Results also showed that the presence of avian influenza M2 and NA proteins maximized both vector production and transduction and that transduction was highly sensitive to the specific NA inhibitor oseltamivir (Tamiflu). H5N1 HaNaM-pseudotyped HIV vector system was also adapted for cell-based high throughput screening of drug candidates against influenza virus infection, and its high sensitivity to the specific oseltamivir validates its potential utility in the identification of new influenza inhibitors. Overall, the trypsin-dependent H5N1-pseudotyped HIV vector can mimic avian influenza virus infection processes with sufficient precision to allow for the identification of new antivirals and to study avian influenza virus biology in a lower biosafety level laboratory environment.

Code(s) de classement : 002B02S05

Descripteur(s) anglais

Descripteur(s) : Trypsin; Human immunodeficiency virus; Vector; High throughput screening; Avian influenza virus; Hemagglutinin; Exo <alpha> sialidase; Membrane protein; Influenzavirus AH5N1

Desc. génériques : Virology; Infectious diseases; Pharmacology; Medical sciences; Serine endopeptidases; Peptidases; Hydrolases; Enzyme; Lentivirus; Retroviridae; Virus; Influenzavirus A; Orthomyxoviridae; Glycosidases; Glycosylases

Descripteur(s) français

Descripteur(s) : Trypsin; Virus immunodéficience humaine; Vecteur; Crible haut débit; Influenzavirus aviaire; Hemagglutinine; Exo <alpha> sialidase; Protéine membranaire; Influenzavirus AH5N1

Desc. génériques : Virologie; Maladies infectieuses; Pharmacologie; Sciences médicales; Serine endopeptidases; Peptidases; Hydrolases; Enzyme; Lentivirus; Retroviridae; Virus; Influenzavirus A; Orthomyxoviridae; Glycosidases; Glycosylases

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Towards health security

Titre : Towards health security

Auteur(s) : Organisation Mondiale de la Sante OMS Bureau Regional de l' Europe Copenhague, International

Source : 2007; 77 p.

Éditeur : OMS, Copenhague

Date de publication : 2007

Pays de publication : International

Langue(s) : English

Type de document : Book

Nombre de références : 45 ref.

Résumé : The health security of Europe is increasingly threatened by communicable diseases, natural disasters and large-scale accidents, conflicts, complex emergencies and climate change. Recent health crises such as avian influenza and the threat of a human influenza pandemic, the heat-wave of 2003 and armed conflict in south-eastern Europe have brought these threats into focus. This publication reviews the lessons learned in tackling these threats. Although the health sector takes the lead in health security, health threats are multisectoral so it must also collaborate with and guide the responses of other sectors. As the lead agency of the United Nations health cluster, WHO's function is to promote effective partnerships with others, be they governments, international organizations, civil society or the private sector. Together they can help the Member States of the WHO European Region prepare to prevent and mitigate future health security crises. Targeted at policy-makers, this publication offers guidance on how the international community can apply the lessons learned to future threats, emphasizing the importance of preparing health systems for future challenges

Code(s) de classement : 002B30A01

Descripteur(s) anglais

Descripteur(s) : Europe; Crisis; Accident; Industry; Natural disaster; Epidemic; Epidemiology; Sanitary surveillance; Risk analysis; Risk management

Desc. génériques : Public health; Medical sciences

Descripteur(s) français

Descripteur(s) : Europe; Crise; Accident; Industrie; Cataclysme; Epidemie; Epidemiologie; Surveillance sanitaire; Analyse risque; Gestion risque

Desc. génériques : Sante publique; Sciences medicales

Localisation : BDSP/ENSP, Shelf number 163679, CA00/0405

Origine de la notice : BDSP

La société internationale et les grandes pandémies

Titre : La société internationale et les grandes pandémies

Auteur(s) : MALJEAN DUBOIS Sandrine; MEHDI Rostane

Auteur(s) : Institut d' Etudes Politiques IEP Aix en Provence, France

Source : 2007; 222 p.

Informations congrès : Quatorzième rencontre internationale d' Aix en Provence, France, 2006-12-08

Éditeur : Pedone, Paris

Date de publication : 2007

Pays de publication : France

Langue(s) : French

Type de document : Conference-Meeting

Nombre de références : dissem.

Résumé : Depuis la création de l' Organisation Mondiale de la Santé en 1948, les préoccupations sanitaires ont acquis une grande acuité : persistance de pandémies telles la tuberculose ou le paludisme, échec de certaines politiques et stratégies de développement, ravages du VIH/sida notamment en Afrique, apparition de nouveaux risques et grandes peurs (SRAS, grippe aviaire, attaques terroristes chimiques et bactériologiques). La lutte contre les grandes pandémies s'intensifie et est devenue un objectif majeur pour les Nations Unies. La santé est l'un des Objectifs du Millénaire pour le Développement, notamment le combat contre le VIH/sida, le paludisme et d'autres maladies. Le 10 janvier 2000, le Conseil de sécurité des Nations Unies a identifié la pandémie du sida comme une menace pour la paix et la sécurité mondiales. Toutes les organisations internationales sont concernées. Les programmes se multiplient, de même que les initiatives locales ou internationales. Sur de telles questions, la nécessité d'un partenariat entre les institutions internationales et les autres acteurs de la société internationale (gouvernements, entreprises, société civile) se fait particulièrement sentir. Mais la communauté internationale avance encore en ordre dispersé, et les résultats de ces multiples stratégies sont assez modestes. De récentes crises ont mis en lumière l'inadaptation d'un cadre institutionnel et normatif international en pleine recomposition. Les quatorzièmes rencontres internationales d'Aix-en-Provence ont réuni les 8-9 décembre 2006 des enseignants-chercheurs d'horizons disciplinaires différents et des praticiens (hauts fonctionnaires internationaux et nationaux, diplomates, représentants d'ONG et de grandes entreprises, médecins) pour en débattre.

Code(s) de classement : 002B30A01

Descripteur(s) anglais

Descripteur(s) : Epidemic; World; Prevention; Health; WHO; Human immunodeficiency virus; AIDS; Crisis; Accessibility; Care; Congress; Terrorism; Public health; Globalization; Antiviral; Chemotherapy

Desc. génériques : Public health; Medical sciences; Lentivirus; Retroviridae; Virus; Viral disease; Infection; Treatment

Descripteur(s) français

Descripteur(s) : Epidémie; Monde; Prévention; Santé; OMS; Virus immunodéficience humaine; SIDA; Crise; Accessibilité; Soins; Congrès; Terrorisme; Santé publique; Mondialisation; Antiviral; Chimiothérapie

Desc. génériques : Santé publique; Sciences médicales; Lentivirus; Retroviridae; Virus; Virose; Infection; Traitement

Localisation : BDSP/ENSP, Shelf number 162203, ED00/0079

Origine de la notice : BDSP