RESEARCH SNIPPETS FROM THE MEDICAL WORLD

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A total of 12,515 cases and 91 deaths of influenza A (H1N1) infection have officially been reported to the World Health Organization (WHO), from 46 countries, (http://www.who.int/csr/don/2009_05_25/en/index.html), as of 25th May, 2009. As a neighbor of China, India has serious cause for concern. Between 11 to 25 May, 2009, 12 human A (H1N1) Influenza cases were reported in mainland China. Data from China CDC (http://www.chinacdc.net.cn) shows that the cases had epidemiological features suggesting they were all imported through international flights. These flights arrived from USA (seven cases), Canada (four cases), and Australia (one case). Seven of the 12 cases had moved to other provinces/ municipalities in China before they were identified.

Since its identification in April 2009, an influenza A (H1N1) virus containing a unique combination of gene segments from both North American and Eurasian swine lineages has continued to circulate in humans. The lack of similarity, between the 2009 A (H1N1) virus and its nearest relatives, indicates that its gene segments have been circulating undetected for an extended period. Its low genetic diversity suggests that the introduction into humans was a single event or multiple events of similar virus. Molecular markers predictive of adaptation to humans are not currently present in 2009 A(H1N1) virus, suggesting previously unrecognized molecular determinants could be responsible for transmission among humans (Science. 2009 May 22.Epub ahead of print, PMID: 19465683). Antigenically, the virus is homogeneous and similar to North American swine A (H1N1) virus but distinct from seasonal human A (H1N1) virus.

Given the worldwide increase of adamantane-resistant influenza A(H3N2) and oseltamivir-resistant influenza A(H1N1) viruses, a study was carried out to analyze the prevalence of anti-viral drug-resistant influenza A in northern Spain (Euro Surveill. 2009 May 21;14(20). pii: 19215). Resistance to adamantanes was detected in 45.3% (68/150) of influenza AH3 virus analyzed for the period from 2000/1 to 2008/9. No resistance to adamantanes was detected among the 65 influenza AH1 viruses analyzed throughout the study period. Among the 172 influenza A (76 AH1 and 96 AH3) virus analyzed, five strains (AH1 with mutation H274Y) showed oseltamivir resistance.

A study mapping the sequence mutations of the 2009 H1N1 influenza A virus neuraminidase (Biol Direct. 2009 May 20:4(1):18) found that it is phylogenetically more closely related to European H1N1 swine flu and H5N1 avian flu than to the H1N1 counterparts in America. A homology-based 3D structure modeling revealed that the novel mutations are preferentially located at the protein surface and do not interfere with the active site. Since the active site is the binding cavity for oseltamivir (Tamiflu(R)), zanamivir (Relenza(R)) and peramivir, the drugs should remain effective for treatment. However, the antigenic regions of neuraminidase relevant for vaccine development, serological typing and passive antibody treatment, were found to differ from those of previous strains and vary among current strains.

Pandemic influenza remains a potential major threat to global public health. It is essential for emergency departments plan for the management of such a major event. Suggestions for preparedness of emergency departments (Emergency Medicine Journal 22/4/09 10:42:52) for staff include - discussing pandemic flu, procuring personal protection equipment (PPE), organizing training programs in use of (PPE) and establishing a method of communication during a pandemic.

A perspective on H1N1 (Virol J. 2009 May 7;6(1):51) states that actions concerning Influenza H1N1 2009 need to be based on fact and science, following recommendations of public health officials, and not fuelled by political, legal or other interests. It also states that the outbreak does not appear to be severe either in terms of the attack rate in communities or in the virulence of the virus itself. However, there are significant changes in both the hemaglutinin and neuraminidase proteins of the new virus (27.2% and 18.2% respectively), of the amino acid sequence, from prior H1N1 isolates in 2008. The author feels that such a degree of change qualifies as an “antigenic shift,” while the virus remains in the H1N1 family of influenza viruses. However, it may give influenza H1N1 2009 significant pandemic potential. On the other hand, the virus retains more of the core influenza proteins from animal strains than successful human influenza virus. Therefore, it may be inhibited from its maximum potential until further re-assortment or
mutation helps it adapt more to multiplication in humans.

The Salmonella species lives in a diverse range of hosts and environments, transferring readily between them. As a result of grabbing mobile elements called pathogenicity islands from other bacterial species it has evolved, stepwise, into multiple strains of pathogens. A sensor kinase and response regulator pair of components on one of the islands acts as an antenna for environmental changes. Depending on the signals it receives, this antenna orchestrates expression across virulence genes by binding to their respective cis-regulatory elements, wherever they are in the genome. Thus, environmental cues can be matched to niche-specific gene expression. A study (Proc. Natl. Acad. Sci. U.S.A. 106, 10.1073/pnas.0811669106, 2009) confirmed the evolutionary significance of cis regulation for Salmonella enterica by a series of in vivo competition experiments between mutants allowed to infect mice. This shows that mutations in regulatory elements enable a bacterium to thrive in multiple and contrasting niches without suffering from conflicting selection pressure on its genome.

Congenital infection with cytomegalovirus (CMV) is an important cause of hearing, cognitive, and motor impairment in newborns. A phase 2, placebo-controlled, randomized, double-blind trial evaluated a vaccine consisting of recombinant CMV envelope glycoprotein B with MF59 adjuvant, as compared with placebo (N Engl J Med. 2009 Mar 19; 360(12):1191-9). Three doses of the CMV vaccine or placebo were given at zero, one and six months, to CMV-seronegative women within one year after they had given birth. It was found that CMV glycoprotein B vaccine has the potential to decrease incident cases of maternal and congenital CMV infection.

Risk factors for mother-to-child transmission (MTCT) of human immunodeficiency virus (HIV) via breast-feeding were evaluated in a randomized trial (J Infect Dis. 2009 Feb 1;199(3):414-8). HIV-infected women and their infants received zidovudine as well as single-dose nevirapine or placebo. Infants were randomized to formula-feed (FF) or breast-feed (BF) in combination with zidovudine prophylaxis. The findings of the trial support the safety of one month of breast-feeding in combination with maternal and infant antiretroviral prophylaxis.

To end with, a refreshing bath might be positively dangerous. A study (Jpn J Infect Dis. 2009 May;62(3):182-6) tested 29 bathrooms, and isolated strains of Mycobacterium avium intracellulare (MAC) from 14 bathtub inlets and three showerheads. Seven bathrooms contained MAC strains that were identical/similar to their respective clinical isolates, in five, polyclonal colonization was revealed by pulsed-field gel electrophoresis. The results imply that colonization of MAC organisms in the bathrooms of MAC patients occurs predominantly in the bathtub inlets and there is, thus, a risk of infection and/or re-infection with MAC when people have a bath.