

Swine Flu Outbreak in Mexico

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What are the origins of the swine flu outbreak in Mexico?

Research workers at ICHAIR have been charting the genetic origins of the recent outbreak of influenza in Mexico, USA and elsewhere (including UK). The H1N1 swine influenza virus has been known since the 1930's. Over the years the virus has evolved through re-assortment of its genes to produce new viruses with pathological potential in pigs. Normally Swine influenza viruses are restricted to infection of pigs, occasionally giving rise to sporadic human infections. The ICHAIR group have been studying the genetic sequence of the 'Mexican' virus released by the US Centers for Disease Control and it is apparent that six subunits (the virus has eight subunits in its genome) are closely related to corresponding genes isolated from North American swine flu isolates and two segments originate from Eurasian isolates of swine influenza. This particular pattern has not been identified before, but may have existed in pigs for several years.

Why has the Virus "jumped" from pigs to humans?

RNA viruses change and recombine rapidly. It is for this reason that new vaccines are constantly needed to control flu. Why specifically the virus has "jumped" from one species to another has yet to be ascertained in this outbreak, but what is key is the fact that not only has this occurred, but also the virus has proved capable of human-to-human infection. It is for this reason that the WHO has raised its Pandemic Alert level to 5 (on a scale of 6). Outside Mexico, the infection to date has been relatively mild and responsive to treatment with the antiviral drugs Oseltamivir and Zanamivir.

Why is the Virus more pathogenic in Mexico than elsewhere, to date?

As yet, the answer to this question remains unknown. For example we do not know the extent of the infection within the population in Mexico. It may be that several thousand may have been infected of which the majority display only mild symptoms. In cases of high morbidity and mortality the swine 'flu infection may be complicated e.g. by co-infection with bacteria, a major cause of mortality in the 1918 Spanish influenza pandemic. We urgently need information from the Mexican public health authorities to enable epidemiologists to understand the point source of infection and from that the spread of the virus. We also need to understand the clinical picture of cases of influenza presenting at hospitals in Mexico

What age groups are most at risk?

Traditionally, respiratory infections, including flu strains that circulate mostly during the winter months, have generally been a threat to the young and elderly members of the population, causing several thousand deaths a year in the UK. The suggestion that this latest outbreak has been responsible for killing young adults is of great concern as this has also been true of flu pandemics in the past. However, in the absence of detailed knowledge from Mexico it is not possible to assess the specific risks.

Notes for the Editor

Interdisciplinary Centre for Human & Avian Influenza Research (ICHAIR)

ICHAIR is an initiative established in 2007 which brings together experts based at the Universities of Edinburgh, St Andrews and Glasgow in virology, inflammation biology, structural biology, epidemiology and evolutionary biology to work together in an interdisciplinary research programme on influenza. The initiative is supported by the Scottish Funding Council and the participating universities.