

Background

Influenza virus is a major viral respiratory pathogen that can cause severe illness. It belongs to the family *Orthomyxoviridae*, which is characterized by a segmented, negative-stranded RNA genome. There are two types of influenza that cause disease of clinical significance, type A and B. Unlike influenza B viruses which occur in humans only, influenza A viruses have an animal reservoir and can cause global pandemics in humans. The influenza A viruses can be subdivided into different subtypes based on the antigenicity of the two surface proteins, the haemagglutinin (HA) and neuraminidase (NA). Sixteen different HAs and nine different NAs have been identified in various combinations in wild aquatic birds, the reservoir host.

Both influenza A and B viruses cause influenza epidemics almost annually in many parts of the world with high mortality and morbidity. The epidemics are the result of frequently occurring point mutations that occur in the viral surface haemagglutinin (HA) and neuraminidase (NA) proteins, which allow these viruses to escape existing immunity to previously circulating influenza viruses in an individual and in the population. Through this process of antigenic drift, new variants evolve in humans throughout the world, causing epidemics almost every year.

In addition to the annual outbreaks of disease, influenza A viruses have been responsible for several human pandemics in recent history. The Spanish H1N1 influenza pandemic in 1918, for example, killed an estimated 40 -50 million people globally. Pandemics occur due to an abrupt major change in the viruses, resulting in new HA and/or new HA and NA proteins not present in the previously circulating human influenza viruses. This antigenic shift results in a novel influenza A subtype with most people having little or no protection, and subsequent high morbidity in millions of individuals and a high level of mortality worldwide.

The principal way to reduce the illness burden during seasonal influenza is by vaccination. Monitoring the antigenicity of viruses circulating each year is

necessary to ensure the best possible match between the prevailing viruses and the vaccine strains.

2005 Influenza season in South Africa

The WHO recommended strains for use in the 2005 Southern Hemisphere vaccine were:

- an A/New Caledonia/20/99-like strain (H1N1)
- an A/Wellington/1/04-like strain (H3N2)
- B/Shanghai/361/02-like strain (B)

Influenza activity during the South African 2005 winter season was monitored mainly in Johannesburg and surrounding areas where the active viral watch system has been strengthened this year to include over sixty participating centres. Five influenza B virus isolates were also sent from the NIC in Cape Town for further characterisation. Both subtypes of influenza A and B viruses circulated during the season but the predominant virus subtype isolated was A H1N1.

Antigenic analysis of the South African 2005 isolates

A total of 582 influenza isolates were made i.e. 468 influenza A virus and 114 influenza B. Of the influenza A isolates, 319 were identified as Caledonia/20/99-like (H1N1), 127 as A/California/7/04-like (H3N2) and 22 were untyped. The majority of the influenza B isolates were identified as B/Hong Kong/333/01-like while a low percentage were B/Shanghai/361/02-like.

Influenza A H1 viruses

Three hundred and nineteen of the influenza A positive specimens reacted well with the A/New Caledonia/20/99 antiserum supplied in the WHO kit.

Influenza A H3N2 viruses

The South African viruses were subtyped by HI using the kit supplied by the WHO Collaborating Centre for Reference and Research on Influenza, Melbourne. The antiserum used for identifying subtype H3N2 influenza specimens was the H3N2 A/Wellington/1/04 strain. Many of the Johannesburg H3N2 isolates sent to the WHO CCs in Melbourne and London showed low reactivity in HI tests with ferret antiserum to the A/California/7/04-like viruses.

Influenza B viruses

Ninety one of the influenza B viruses reacted with the B/Hong Kong/330/01 antiserum in the HI tests, 20 B isolates reacted to high titres with the B/Shanghai/361/02 antiserum while the remaining 3 viruses could not be further characterized due to low titres. All 5 influenza B isolates from Cape Town reacted well with the B/Shanghai/361/02 antiserum.

Molecular analysis of the South African 2005 isolates

Influenza A H1N1

Sequence analysis of the HA1 subunit revealed the H1 viruses isolated during the season showed some genetic drift from the A/New Caledonia/20/99 vaccine strain.

Influenza A H3N2 viruses

The molecular characterisation of representative influenza H3N2 isolates revealed that the viruses circulating in Johannesburg had drifted extensively from the A/Wellington/1/04 vaccine strain. Genetic drift was also observed compared to A/California/7/04 reference strain.

Influenza B viruses

Sequence analysis of the HA1 subunit of representative South African 2005 influenza B viruses showed that the B/Hong Kong-like viruses had seven changes in the amino acid residues relative to the B/Hong Kong/330/01 strain. In the B/Shanghai-like viruses, substitutions were seen at five residues.

Pandemic influenza

In the recent avian H5N1 outbreaks in Asia, there has to date been no evidence of sustained person-to-person transmission A probable instance of limited person-

to-person transmission in a family cluster was however identified in Thailand earlier in 2004. The concern nevertheless exists that the H5N1 viruses have the potential to reassort with existing human influenza viruses to produce a strain with high virulence and efficient transmissibility, thereby initiating a new influenza pandemic. The NICD influenza laboratories have been involved in drawing up pandemic plans and putting into place new methods to be able to detect a new subtype influenza infection in humans.