The shifting travel coats of influenza

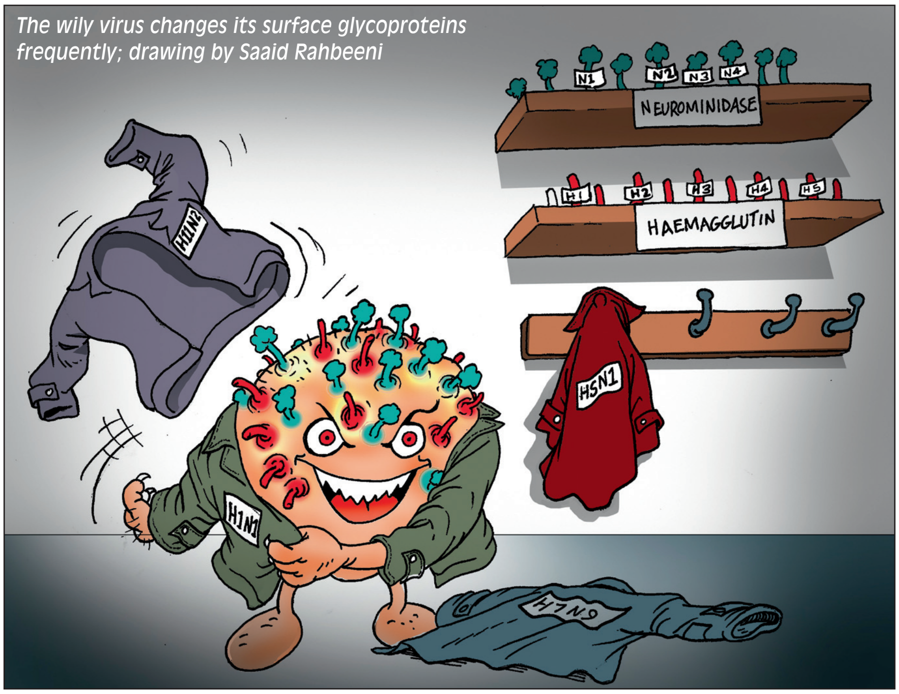
The only constant predictable factor about influenza is its unpredictability. Whilst mankind has advanced remarkably with antiviral treatments and vaccines; the virus has been outfoxing all attempts to tame it. Smallpox has been eliminated; polio would have followed the same fate were it not for politics and mistrust, and some common but potentially serious childhood diseases such as measles can be controlled with well managed vaccination programmes as well as the roping in of the anti-vaccination lobby.

The three viruses mentioned above differ significantly from influenza however. Firstly humans are the only objects of their desires whilst influenza seeds in several species and can cross specie barriers in unpredictable manners. Secondly they do not change their structure significantly whilst influenza undergoes genetic rearrangements; subtle drifts over a period of a few years; or more pronounced, radical, and at times pandemic causing shifts. Thirdly the spread of the three viruses depends on humans and human behaviour, whilst influenza hitches rides on a variety of species able to cross vast distances.

Influenza has always confounded scientists. The first recorded pandemic was in 1578, and enough documentation exists showing episodic recurrences thereafter. Nothing can compare with The Spanish Flu of 1918 however. This horror episode is estimated to have caused more than 50 million deaths, with 10 million being in India alone. Soldiers returning from Northern France at the end of World War One introduced it to the USA causing over 600 000 deaths, as well as to Britain resulting in close to 300 000 fatalities. It is one of the great ironies that soldiers who did not succumb to the ravages of the war transported back a much more lethal weapon. It is commonly held that this pandemic was caused by the virus crossing the species barrier from birds to vulnerable humans having no resistance to it.

Scientists have since then been predicting the next pandemic with various degrees of success. The one of 1957 originated in China and spread worldwide within six months. The 1968 pandemic originated in Hong Kong and rapidly spread via international air travel and other modes of travel. The last plague epidemic occurred in China. A potentially nightmarish scenario reared its head with the 2002 Severe Acute Respiratory Syndrome (SARS) outbreak taxing scientists and governments alike. It spread from mainland China to infect citizens of 37 different countries within weeks. It is known that influenza thrives in the vast avian and porcine reservoirs. Avian influenza is well recognised, and just recently led to the culling of hundreds of thousands of poultry in Singapore. Indochina has the highest concentration of humans with significant interaction with our feathered and fattened feasts, so surely the next pandemic would have to originate in that region?

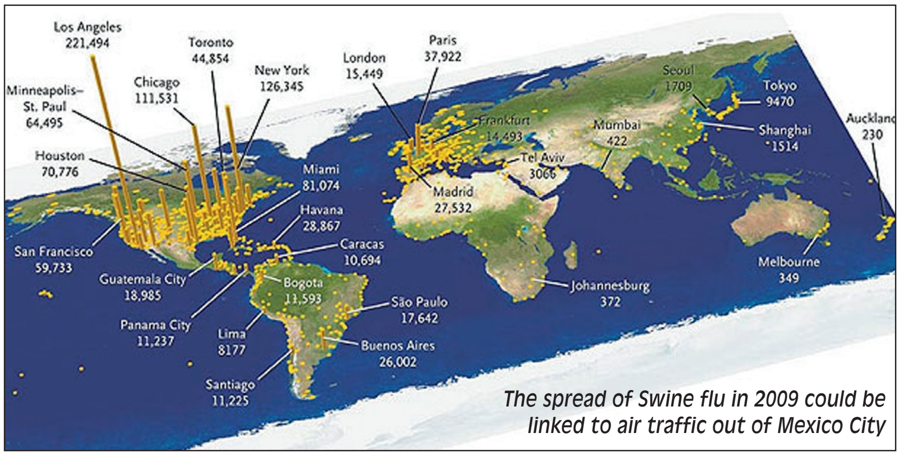
Again the virus outwitted us and simply carried on doing what it was designed to do; replicating, mutating and re-assorting genetic material. A snip of a porcine sequence, a dash of avian input, a pinch of human genes and hey presto! A triple re-assortment was the end product resulting in a potpourri novel to mankind. A mankind with a younger population completely naive to the supposedly primitive invader commonly called swine flu, which was later genetically linked to the 1918 Spanish Flu. And this manifested itself in Mexico! On 22 April 2009 the first few cases were identified in Mexico and the USA. By the 28th April Mexico reported


The wily virus changes its surface glycoproteins frequently; drawing by Saaid Rahbeeni

TRAVEL MEDICINE

By Dr Salim Parker
President-elect
SASTM

SOUTH AFRICAN SOCIETY OF TRAVEL MEDICINE
SASTM
Guiding the Profession
Protecting the Public



The spread of Swine flu in 2009 could be linked to air traffic out of Mexico City

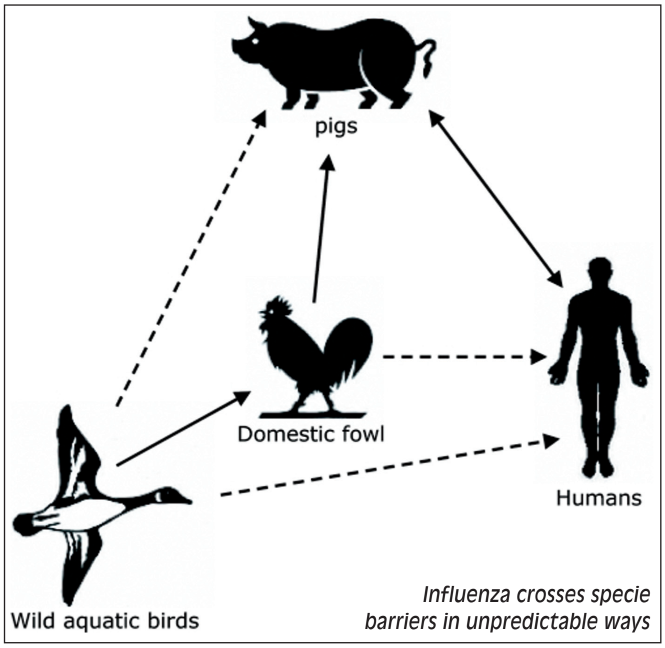
1600 suspected cases with at least seven deaths. The spread of swine flu could be clearly linked to air travel out of Mexico City. Countries such as the USA, Britain, Canada, Spain and Germany were the first to report cases of the new influenza strain before the end of April, reflecting the densities of air travel between them and Mexico. By the 30th April the World Health Organisation sent out a warning of an imminent pandemic.

On the 1st May European countries, the USA and Britain reported cases of secondary transmission, where the disease was spread locally. By the 3rd of May, at least 18 countries had confirmed cases of the disease. By the 13th May, only the African continent did not report cases of the disease, reflecting the paucity of travel between it and Mexico. By the 10th June 141 countries, including Egypt as the first African country, had confirmed cases and the next day the WHO officially declared the presence of the pandemic. By the end of July 2009 there were over 170 000 confirmed cases with more than 1100 deaths. The swine flu in effect 'crowded out' other strains of the influenza virus and dominated the landscape for the following three years.

Three types of influenza viruses are found, namely A, B and C. Influenza A viruses are further sub typed according to surface glycoproteins called haemagglutinin (H) and neuraminidase (N). Swine flu is thus known as H1N1, bird flu currently has two worrying strains. The one that has been lurking around for the last decade is H5N1. Though it does not easily cross from birds to mankind, it causes the demise of 50% of infected humans. H7N9 is another strain that again, though not easily crossing the specie barrier, is lethal in close to a third of humans who are infected by it. The concern is that a small mutation in either species would make it far more transmissible to us with potentially devastating effects.

A few months ago, a novel avian influenza virus causing disease in penguins was discovered. Again not in Eurasia where the bulk of mankind populates the land masses but in fact it was found in Antarctica! Termed H11N2, it is not considered very infectious to humans as it is unable to cause disease in ferrets, a marker of its potential pathogenicity in humans. What was intriguing in the gene sequences of this penguin flu virus was that some genetic sequences were from North American influenza virus origin, some from South American origin, and some from a flu virus that is known to cause disease in dogs, horses and birds.

It is speculated that migratory birds that fly from land masses to Antarctica, such as giant petrels and skuas, could be introducing the viruses into the penguin and other populations there. Genetic reassortment and a sudden ability to easily infect humans......how far away is the next pandemic?



Influenza crosses specie barriers in unpredictable ways

Giant Petrels cover vast distances between the southern continents and Antartica

Spanish Flu struck down thousands of returning World War One soldiers