

# Emerging viruses: past, present and future

A range of factors are converging to create opportunities for viral pathogens to dramatically expand the range of hosts they infect, making emerging viruses one of the great health challenges of the 21st century.

**Dr Eddie Holmes** discusses the factors that enable new viruses to emerge, and how to control them.



**E**MERGING viruses pose one of the great health challenges of the 21st century.

Environmental disruption, high population densities of humans, animals and crops, together with global climate change, migration and rapid transport to all parts of the world, are converging to create opportunities for viral pathogens to dramatically expand the range of hosts they infect. And as SARS, HIV/AIDS, and H1N1/09 influenza illustrate, the public health consequences of disease emergence can be profound.

Despite a strong health infrastructure, Australians are vulnerable to emerging viruses. This is, in part, a reflection of Australia's geographical proximity to Southeast Asia, where a combination of high biodiversity, close contact between humans and animals, and changes in agricultural systems, have made a fertile ground for viral emergence. These simple facets of natural ecology make it no surprise that viruses like Nipah, SARS and H5N1 influenza have emerged in Southeast Asia in the recent past, and ensure that more new viruses will emerge there in the future.

## Understanding the nature of emerging viruses

Not surprisingly, there is now a concerted effort to understand the factors that enable new viruses to appear and spread in our species. Disappointingly, we are currently only able to make a few broad scale conclusions on the mechanics of this process.

First, most emerging viruses are RNA viruses, with a genome composed entirely of RNA. Compared to DNA, RNA is highly error-prone, lacking any ability to correct the errors that frequently arise during replication. It is estimated that RNA viruses make roughly one genomic mutation each time they replicate, a rate that is several orders of magnitude higher than those of mammalian species.

Such an abundant source of mutations provides RNA viruses with the raw materials for life in the evolutionary fast-lane, allowing them to rapidly adapt to new environments, including treatment by drugs and vaccines, and of course new host species.

It is also well established that the vast majority of emerging viruses have 'jumped' into humans from other animal species. For example, non-human primates are the natural reservoirs of the AIDS viruses, while the ultimate source of all human influenza viruses are wild water birds. By increasing encroachment on animal habitats, such as through the expansion of the logging industry in Central-West Africa, humans expose themselves to this diverse array of viral pathogens. However, not every reservoir species has been identified for every human virus. A notable case in point is hepatitis C virus (HCV). Although HCV currently infects about 175 million people world-wide, so that it represents a major source of morbidity and mortality on a global scale, its ultimate species reservoir is unknown.

Despite the importance of emerging viruses for global health, most species jumps are unsuccessful; only a few individuals are infected and the infection quickly burns out, sometimes undetected. When a virus does successfully establish itself in humans, research has shown that it tends to come from a host species that is relatively closely related to us. For example, although we eat a plentiful supply of virally infected plants (and plant viruses are a common component of human fecal samples), plant viruses never cause disease in humans because human and plant cells are so dissimilar. The same applies to the viruses that infect fungi, fish, amphibians and reptiles.

Although viruses from birds can infect humans, with influenza and West Nile serving as good examples, avian and human cells are still sufficiently different to make this a relatively rare



event. For example, it is estimated that 13 mutations are required for an avian influenza virus to evolve human transmissibility. Even for genomes that evolve as rapidly as those from RNA viruses, acquiring this number of mutations represents a major challenge. The difficulty of this adaptive event may also explain why H5N1 influenza is still not able to routinely transmit among humans, despite repeated spill-over from poultry.

The largest source of human emerging viruses are therefore other mammalian species, either those that are very closely related to us (ie non-human primates), for which only a few mutations (if any) are usually required for the virus to adapt to human transmission, or those that live in close proximity to humans, and often in large aggregations, so that there is a greatly increased chance of exposure. Animals such as rodents and bats obviously fall into the latter category, as do those that we farm in large numbers.

## The future

The larger and denser the populations we live in, the more we travel, and the more we impinge on animal habitats through such processes as deforestation and intensive agriculture, then the more new viruses will appear in our species. ►

This is a certainty. It is therefore not surprising that predicting what virus will emerge next, in which geographical regions, and from which animal species, has become something of a holy grail in studies of disease emergence. Although predictions in this field are more akin to predicting earthquake zones than tomorrow's weather, they will at least allow the surveillance of emerging viruses to be undertaken in a more focused manner.

At present it seems safest to conclude that viral infections tend to emerge in geographic regions of high biodiversity, and that mammalian species with high density populations that live in close proximity to humans are the most likely reservoirs. Of course, the unique biota of Australia is also likely to provide a home for a myriad of unique viral infections, and every effort should be made to characterise them.

Given this knowledge, what can be done to counter the threat posed by emerging diseases? First, it is essential that we undertake large-scale surveys of viral biodiversity in potential reservoir species.

Thankfully, such surveys are already underway and are greatly assisted by improvements in the speed and scale of genome sequencing, including the advent of 'metagenomics' approaches in which all the different types of DNA/RNA in a sample can be sequenced. Indeed, it is now theoretically possible to identify all of the pathogens, RNA virus or otherwise, that circulate in a specific species.

In addition, recent advances in evolutionary and population biology make it possible to reveal key details about how viruses emerge – including how rapidly and in what directions a virus spreads – simply through computer-assisted gene sequence analysis. Such information is essential for the successful control of an emerging virus: the faster a virus spreads, the more people need to be vaccinated for its eradication, and knowing the directions of viral spread enables us to better identify at-risk populations.

Similarly, it is essential that we map the global genetic diversity of every major microbial pathogen that is currently circulating in human populations, sampling as many diverse geographical

locations as possible. Not only will information of this kind provide valuable insights into how any new emerging microbe may spread when it does enter the human species, but it will likely serve as a major stimulus package to studies of pathogenesis, drug resistance, and vaccine design.

Finally, it is crucial that we establish a global scientific infrastructure that combines active disease surveillance, particularly in those geographic regions and animal species that are most likely to harbour new viruses, with a rapid and coordinated response to any new emerging infection that should appear. To my mind, this is the most effective way to counter the threat posed by emerging viruses. It is also an area in which Australia can show strong leadership within the Asia-Pacific region.

*Dr Eddie Holmes is an evolutionary biologist who specialises in emerging viruses. He works at The Pennsylvania State University and Fogarty International Center, National Institutes of Health, USA, and spoke on this topic for the Sydney Science Forum earlier this year.*



## Enjoy Life!

There is more to medicine than hard work and long hours. You have chosen a career with the flexibility to select your own hours and lifestyle.

Established in the early 1980's, we have been placing doctors in hospitals and medical practices throughout metropolitan and rural Australia for nearly 30 years.

Australian Owned. Australian Operated.  
Australian Medical Placements.

Choose your lifestyle and change your life.

**1300 666 420**

Web: [www.australianmedicalplacements.com.au](http://www.australianmedicalplacements.com.au)

