

# Emerging viruses set to soar

Stacy Fitzsimons, BMN News

The emergence rate of novel viruses – such as the coronavirus that sparked severe acute respiratory syndrome (SARS) – could well be on the rise, warn researchers.

## Coronavirus

There are three distinct groups of coronavirus known to exist. Some of these RNA viruses are known to cause illnesses such as the common cold in humans. When SARS first emerged, scientists thought the SARS virus was a fourth distinct type of coronavirus.

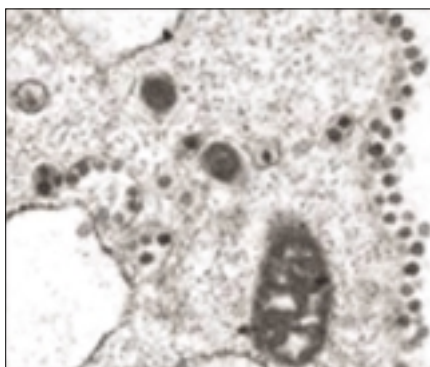
But researchers now think that the SARS virus actually split from group 2 coronaviruses, and that this happened relatively recently on the scale of coronavirus evolution. Evidence of this was recently reported by Alexander Gorbalenya, from the Department of Medical Microbiology at the Leiden University Medical Center in the Netherlands (<http://www.lumc.nl>), and colleagues [1].

Several groups have independently recognized the clustering of the SARS virus with group 2 coronaviruses, says Gorbalenya. Although, he cautioned, 'It would be premature to say a consensus has been reached.'

## Unique genetic features

The group has identified unique genetic features of the SARS virus that have not previously been identified in other coronaviruses. Thus, the virus may have a significant potential for macro-evolution – it might be able to evolve rapidly by incorporating or deleting large pieces of RNA, as well as by the common point mutations that cause most viruses to mutate. 'This should not be overlooked in the current anti-SARS effort,' said Gorbalenya.

Gorbalenya's team have also provisionally identified several enzyme activities in the part of the SARS virus responsible for replication. Together with other known enzymes, these activities make sense when speculating how the virus might replicate itself and multiply. 'This analysis identifies new potential targets for anti-SARS drugs,' he said.



Research into SARS is both helping and being helped by work with other viruses. Although it has only been a few months since the SARS virus was identified, it has already been extensively characterized. Research has turned up much about the genetics and structure of the virus. 'The knowledge that had been accumulated on many viruses, coronaviruses in the first place, for years was projected on and, in some cases, verified for the SARS virus,' said Gorbalenya. 'This has resulted in the enormous speed of the advancement of our knowledge on SARS.'

## The jump to man

Kathryn Holmes, in the Department of Microbiology at the University of Colorado Health Science Center (<http://www.uchsc.edu>), has also been looking at the molecular biology of coronaviruses for many years. Her

laboratory is working out how the SARS virus jumped from an animal host into humans, and to identify ways to block its entry into human cells.

Coronaviruses are unusual in that they are known to cross the animal-human barrier.

Holmes welcomes Gorbalenya's findings. 'The analysis is very well done. It will be very interesting to learn the biological implications,' she said. The work provides insight into how long ago the virus diverged from other coronaviruses, she notes, and shows that it has had plenty of time to evolve in its natural animal host before it jumped to humans.

'Viruses are always jumping around, but usually fail to find a host,' said Holmes. 'When a virus does cross to a new host, it is usually by chance.' Many such pathogens will find a human host, infect and possibly kill the person, but not be passed on, she says. 'New viruses that are transmissible between humans are rarer – those are the scariest,' she said.

Human activity, including increased international travel and improved methods of virus identification, are behind much of the reported increase in viral emergence, says Holmes.

Gorbalenya agrees. 'It is widely recognized that humans may drive virus evolution through activities associated with the modern society – frequent travel, densely populated cities, frequent intrusion in the endemic habitats and so on.'

## Reference

- 1 Snijder, E.J. et al. (2003) Unique and conserved features of genome and proteome of SARS-coronavirus, an early split-off from the coronavirus group 2 lineage. *J. Mol. Biol.* 331, 991–1004