

# Agents of haemorrhagic fevers often change host

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(Phys.org) -- Biologists at the University of York have helped to discover that one of the world's most infectious classes of disease – viral haemorrhagic fevers – can spread much more easily than previously thought.

Nancy Irwin and Dr Oliver Missa, of the Department of Biology at York, played a key role in new research into viruses hosted by rodents.

Working with Michaela Bayerlová and Natália Martínková from the Masaryk University and Academy of Sciences in the Czech Republic, they studied the evolutionary host associations of the Tacaribe virus complex – the New World Arenaviruses – responsible for South American haemorrhagic fevers.

The research, published in the latest issue of *Molecular Ecology*, revealed that viruses can switch hosts more easily than previously understood. The findings conflict with an earlier hypothesis that the viruses co-evolved with their rodent hosts.

New World Arenaviruses consist of 23 viral species split into four groups and known to infect 32 mammal species, mainly rodents. Five of these viruses are known to cause human disease, which up to one third of patients die. The disease is spread principally by inhalation of aerosolized droplets of saliva, respiratory secretions, urine, or blood from infected rodents. There are no vaccines, or prophylactic treatment. It is therefore important to know which rodent species are capable of

hosting and spreading the viruses.

Dr Missa said: “This project brought scientists together from different disciplines which enabled us to look at the virus-host relationship from a new perspective.”

The researchers demonstrated with co-phylogenetic analysis that with the exception of the viruses of North America there was no pattern of co-divergence. Using statistical techniques used more frequently in ecology, they found that the four groups of viruses were associated differently with their hosts, and that the pathogenic group of viruses were randomly distributed across the rodent hosts available to them.

The researchers found that the occurrence of hosts in the same locality was a better predictor for the pathogenic viruses to jump to a different host than the need to find closely related hosts with similar characteristics and defensive capabilities.

Nancy Irwin added: “No longer can it be thought that these [viruses](#) evolved with their hosts but are instead opportunistically host switching which has important bearings on understanding the potential for the pathogenic strains to affect many types of animal and to expand their range.”

**More information:** The paper ‘Complex patterns of host switching in New World Arenaviruses’ is published in *Molecular Ecology* and is available online at [onlinelibrary.wiley.com/doi/10 ... 4X.2012.05663.x/full](http://onlinelibrary.wiley.com/doi/10.1111/j.1365-3113.2012.05663.x/full)

Provided by University of York

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