

Virus discovery helps scientists predict emerging diseases

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Fresh insight into how viruses such as SARS and flu can jump from one species to another may help scientists predict the emergence of diseases in future.

Researchers have shown that viruses are better able to infect species that are closely related to their typical target species than species that are distantly related.

Their results suggest that when diseases make the leap to a distant species – such as bird flu infecting humans – they may then spread easily in species closely related to the new victim, regardless of how closely related these are to the original target species.

Scientists from the Universities of Edinburgh and Cambridge looked at how relationships between species might determine the spread of an important group of emerging diseases, known as RNA viruses. This group of diseases includes HIV, [SARS](#) and flu.

By infecting more than 50 species of flies with three different viruses, the researchers showed that species closely related to a virus's usual target species were more susceptible than distantly related flies. They also showed that groups of flies that were closely related were similarly susceptible to the same [viruses](#).

The study, funded by the Biotechnology and Biological Sciences Research Council, Natural Environment Research Council, the

Wellcome Trust and the Royal Society, was published in the journal *PLoS Pathogens*.

Dr Ben Longdon of the University of Edinburgh's School of Biological Sciences, who led the study, said: "[Emerging diseases](#) such as SARS, HIV and some types of [flu](#) have all got into humans from other species. Understanding how diseases jump between different species is essential if we want to predict the appearance of new diseases in the future."

Provided by University of Edinburgh

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