

# Research sheds new light on how diseases jump across species

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Researchers at the University of Leeds have made a breakthrough in understanding a virus which poses one of the greatest global disease threats to wild carnivores including lions, African wild dogs and several types of seal.

The discovery of how canine distemper Virus (CDV) jumps across and infects different species of carnivores could lead to a more effective monitoring and control of the virus.

Whilst these ‘pathogen jumps’ across species are quite common, very little is known about the process of how viruses takes hold and become established in new host species.

CDV is passed through close contact from domestic and feral dogs causing epidemics that often result in mass mortalities – and is pushing some species to the brink of extinction.

“The virus needs to bind to a specific receptor on cells in the host in order to infect it,” explains lead researcher, PhD student Alex McCarthy, from the University’s Faculty of Biological Sciences. “But the sequences of receptors vary between species, so a virus from one species shouldn’t be able recognise and infect the cells of other species.”

By analysing the virus’ genetic sequence in both dog and wild carnivore species, the research team were able to prove that two key parts of a CDV protein specifically involved in receptor recognition had evolved

during the host jumps, whereas the rest of the protein showed very few changes among viruses from different species.

“It was a very satisfying moment when our ideas proved correct,” says McCarthy. “The results really screamed out at us. They were so clear-cut, we think it’s highly likely that pathogen evolution is a much more general mechanism in cross-species transmission of viruses than anyone imagined.”

The findings could lead on to new antiviral therapies that are targeted at the binding mechanism, to prevent the virus from taking hold, rather than trying to eradicate it once it’s in the host’s system.

Current conservation policies include vaccination of wild animal populations, but this is not appropriate for logistical or biological reasons for most species. Alternative strategies include vaccination of neighbouring domestic and feral dog populations, which prevents CDV circulating in dogs and therefore limits transmission to wildlife. Culling the surrounding domestic reservoir species, such as dogs, is also an option, but this is more controversial because its efficacy can be questionable and because of the impact this can have on support from local communities for wider conservation efforts.

The spread and incidences of CDV epidemics are increasing, due to globalisation and the rise in the domestic and feral dog populations associated with growing human populations, especially where these impinge on previously undisturbed habitats.

“CDV in wild carnivore populations is usually fatal” says McCarthy. “So as well as the possibility of developing new therapies, the techniques used in this research offer a way of predicting when local virus isolates may become capable of causing a full blown epidemic in species of conservation concern.”

The research could have similar implications for developing new therapies for pathogenic diseases that have successfully crossed species to humans. Additionally, the team believes that the phenomenon may be involved in the emergence of many new, previously species-specific diseases that have been able to infect new host species, such as SARS, Hendra and Nipah Virus.

Source: University of Leeds

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