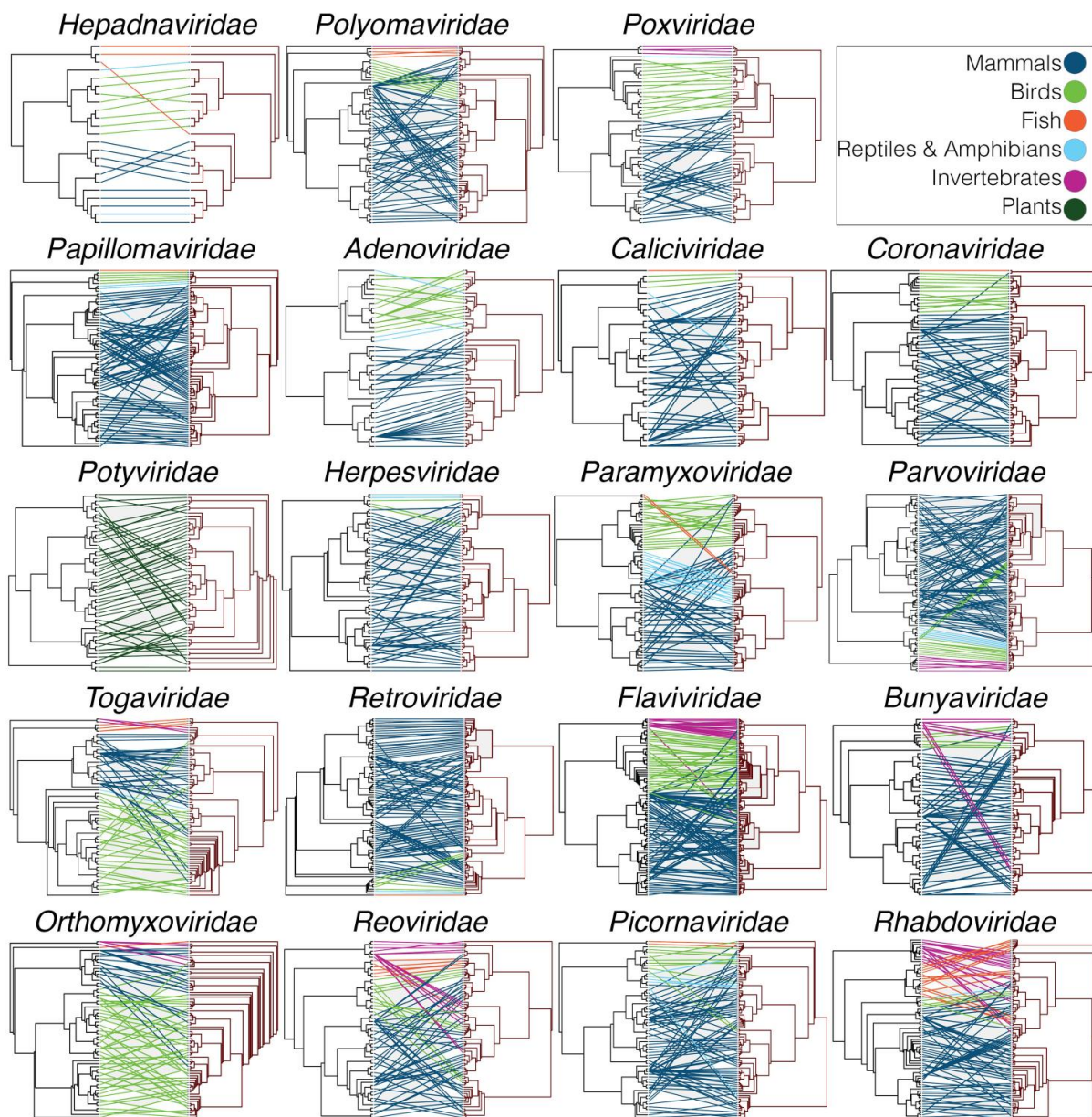


Cross-species jumps may play unexpectedly big role in virus evolution

March 9 2017



Tanglegrams of rooted phylogenetic trees for each virus family. Credit: Geoghegan JL, et al. (2017)

On occasion, a virus may jump from one host species to another and adapt to the new host. Such cross-species transmission happens more often than expected, according to new research published in *PLOS Pathogens*, and it may play a much bigger role in virus evolution than previously thought.

Understanding how viruses evolve and how often they jump to new hosts is important for studying emerging viral diseases. Scientists have hypothesized that viruses usually co-diverge with their hosts, forming new viral species as their hosts evolve into new species. It has been assumed that cross-species jumps are relatively rare and contribute less to [virus evolution](#).

To better understand how viruses evolve, Jemma Geoghegan of the University of Sydney, Australia, and colleagues compared the evolutionary histories of viruses and [host species](#). Previous studies had focused on narrow groups of viruses; for a broader picture, Geoghegan's team studied 19 virus families that infect a variety of hosts, including mammals, birds, reptiles, amphibians, fish, plants, and insects.

The researchers began with branching "tree" diagrams that illustrated the evolutionary history of each virus family and its host species. Like family trees, these evolutionary trees trace the lineage of species back through common ancestors that later evolved into new species.

The scientists then used a previously developed method to compare the evolutionary trees of viruses and hosts. The method measures similarity

between trees; co-divergence results in host and virus trees with similar branching patterns, as the virus evolves alongside the host. Meanwhile, cross-species jumps result in dissimilar host and virus trees, as new viruses evolve and jump from host to host.

The scientists found that cross-species transmission has played a central role in evolution for all 19 virus families, while co-divergence is relatively rare. Cross-species jumps were especially frequent in virus families whose genetic material is encoded in RNA rather than DNA. The findings also revealed which virus families may be more likely to jump hosts and evolve to infect new species.

'An important implication from our work is that the more new viruses we discover, then the more examples of species jumping we are likely to see' said project leader Professor Edward Holmes from the University of Sydney. 'Jumping hosts is the way many RNA [viruses](#) live their life' he continued.

This research was performed at the level of virus families, and not for individual viral [species](#). Further studies with larger datasets could help confirm the findings and provide further insight into virus evolution.

More information: Jemma L. Geoghegan et al, Comparative analysis estimates the relative frequencies of co-divergence and cross-species transmission within viral families, *PLOS Pathogens* (2017). [DOI: 10.1371/journal.ppat.1006215](https://doi.org/10.1371/journal.ppat.1006215)

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Citation: Cross-species jumps may play unexpectedly big role in virus evolution (2017, March 9) retrieved 27 April 2024 from

<https://phys.org/news/2017-03-cross-species-unexpectedly-big-role-virus.html>

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