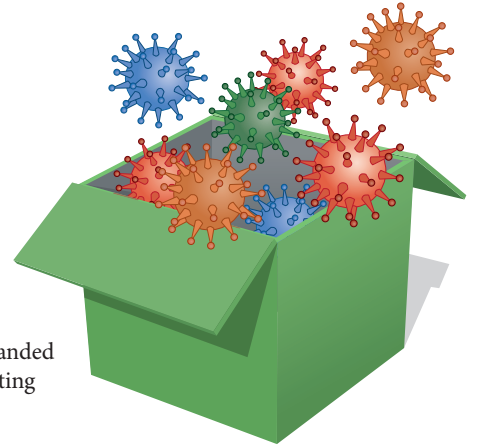


 VIRAL EVOLUTION

Uncovering the secrets of the RNA virosphere



Our current view of the biodiversity of RNA viruses has been biased towards understanding the causes of human, veterinary and plant diseases. In a large transcriptomics study, Shi *et al.* now provide insights into the biodiversity and evolution of RNA viruses in invertebrates.

The authors sequenced the transcriptomes of more than 220 invertebrates spanning nine animal phyla, including arthropods, nematodes and molluscs. They identified, based on the presence of the RNA-dependent RNA polymerase (RdRp), which is required for the replication of RNA viruses, 1,445 phylogenetically distinct RNA viruses. Many of the newly identified viruses were unable to be classified into existing taxa, which led the authors to propose five new

virus families and greatly expanded the diversity of viruses in existing families.

Furthermore, the authors observed little concordance between viral and host phylogenetic lineages and found evidence of frequent cross-species transmissions. For example, viruses that were previously found only to infect fungi, plants and protists were also found to infect diverse invertebrates. Indeed, the host range has been expanded markedly for each major virus group, and will keep on expanding. Viral lineages that originated from arthropod-associated viruses were particularly diverse and were found in many other hosts. Most hosts contained several distinct RNA viruses and in some hosts, the majority of

the transcripts, after the removal of ribosomal RNA, may be of viral origin. The invertebrate virome was also characterized by substantial genomic flexibility, including genetic exchange between RNA viruses and hosts, gene gain and loss, and complex structural rearrangements.

This study reveals unprecedented insight into the expanding virosphere, which is more phylogenetically and genomically diverse than previously anticipated.

Ashley York

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