

Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses

Journal Information
Journal ID (nlm-ta): elife
Journal ID (hwp): eLife
Journal ID (publisher-id): eLife
Title: eLife
ISSN: 2050-084X
Publisher: eLife Sciences Publications, Ltd

Article/Issue Information
Date received: 29 October 2014
Date accepted: 27 January 2015
Publication date: 29 January 2015
Volume: 4
Electronic Location Identifier: e05378
Publisher ID: 05378
DOI: 10.7554/eLife.05378

Categories

Subject: Research Article

Categories

Subject: Microbiology and Infectious Disease

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Research organism

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Virus

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Abstract

Although arthropods are important viral vectors, the biodiversity of arthropod viruses, as well as the role that arthropods have played in viral origins and evolution, is unclear. Through RNA sequencing of 70 arthropod species we discovered 112 novel viruses that appear to be ancestral to much of the documented genetic diversity of negative-sense RNA viruses, a number of which are also present as endogenous genomic copies. With this greatly enriched diversity we revealed that arthropods contain viruses that fall basal to major virus groups, including the vertebrate-specific arenaviruses, filoviruses, hantaviruses,

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influenza viruses, lyssaviruses, and paramyxoviruses. We similarly documented a remarkable diversity of genome structures in arthropod viruses, including a putative circular form, that sheds new light on the evolution of genome organization. Hence, arthropods are a major reservoir of viral genetic diversity and have likely been central to viral evolution.

Competing interest

The authors declare that no competing interests exist.

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