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Genome discovery of novel RNA viruses infecting Formica exsecta

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Only a few viruses are currently known to infect ants. Metagenomic and transcriptomic approaches have accelerated the rate of discovery of viruses and other infectious agents, allowing for new studies into biological interactions between a species and its pathogens. Here, we report on two putative new viruses that infect the ant *Formica exsecta*. We used a metatranscriptomic approach to detect sequences with homology to viral pathogens. The viruses, provisionally named *Formica exsecta* virus 1 (FEX-1) and *Formica exsecta* virus 2 (FEX-2), belong to the insect specific viruses family Dicistroviridae and Iflaviridae (respectively). A phylogenomic analysis of these and 17 other Dicistroviruses and seven other Iflaviruses showed that these viruses were phylogenetically distinct from other known viruses in these groups. Domains such as RNA-dependent RNA polymerase (RDRP) and Helicase, responsible for viral replication and genome organization were highly conserved and observing very slow evolution rate with purifying selection. Helicase and RDRP used to know taxonomy of these viruses and for inferring their evolutionary relationships. In contrast structural proteins, which function to build capsid structure of virus were evolving faster. We also predicted the protein structure and performed homology modeling of the apavavirus proteins. These methods showed that helicase domain position shifting gives indication of parallel evolution between *Solenopsis invicta* virus-1 and FEX1, where as other apavavirus showed structural homology with FEX-1 polyprotein. Overall, our study shows the usefulness of metatranscriptomic approaches for virus discovery and also great resources for specific information regarding genome organization, molecular characteristics, virion structure, phylogenetics, host immune response elicited by social insect viruses.