

THE VIROME OF RHIPICEPHALUS, DERMACENTOR AND HAEMAPHYSALIS TICKS FROM EASTERN ROMANIA INCLUDES NOVEL VIRUSES WITH POTENTIAL RELEVANCE FOR PUBLIC HEALTH

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Abstract

Ticks are involved in the transmission of various pathogens and some tick-borne diseases cause significant problems for the health of humans and livestock. Despite their obvious importance, the composition of viral communities in ticks, and their interactions with pathogens, is poorly understood, particularly in Eastern Europe that constitutes (via bird migrations for example) a major hub for animal-arthropod vectors exchanges. The aim of this study was first to describe the virome of *Dermacentor* sp., *Rhipicephalus* sp. and *Haemaphysalis* sp. ticks collected from poorly investigated regions of Romania (Iasi and Tulcea counties) located at the intersection of various biotopes, countries and routes of migrations. We then focused the study on viruses that could have potential relevance for human and animal health. More than 500 ticks were collected in 2019 from the environment and from small ruminants and analyzed by high-throughput transcriptome sequencing. Among the viral communities infecting Romanian ticks, viruses belonging to the Flaviviridae, Phenuiviridae and Nairoviridae families were identified and full genomes were derived. Phylogenetic analyses placed them in clades where mammalian isolates are found, suggesting that these viruses could constitute novel arboviruses. We also assessed the bacterial microbiome of the collected ticks. The characterization of these microbial communities increases the knowledge of the diversity of viruses in Eastern Europe and provide a basis for further studies on the relationship between ticks and tick-borne viruses.

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