

Abstract

# Detection of Known and Novel Viral Pathogens in Belgian *Ixodes ricinus* Ticks †

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**Abstract:** Recent metagenomics studies have revealed several arthropod species to be major reservoirs for RNA viruses. One of these reservoirs is *Ixodes ricinus*, the most prevalent tick species in Europe, which is known to be a vector for many viral and bacterial pathogens. For this study, we decided to investigate the virosphere of Belgian *Ixodes ricinus* ticks. High-throughput sequencing of tick pools collected from six different sampling sites revealed the presence of viruses belonging to many different viral orders and families, including *Mononegavirales*, *Bunyavirales*, *Partitiviridae*, and *Reoviridae*. Of particular interest was the detection of several putative human pathogens, including members of the families *Nairoviridae* and *Phenuiviridae* as well as three new reoviruses, two of which cluster together with members of the genus *Coltivirus*. One of these two viruses represents a new strain of Eyach virus, a known causative agent of tick-borne encephalitis. All genome segments of this new strain are highly similar to those of previously published Eyach virus genomes, except for the fourth segment, encoding VP4, which is markedly more dissimilar, potentially indicating the occurrence of an antigenic shift. Further PCR-based screening of over 200 tick pools for 11 selected viruses showed that most viruses could be found in all six sampling sites, indicating the wide spread of these viruses throughout the Belgian tick population. Taken together, these results illustrate the role of ticks as important virus reservoirs, highlighting the need for adequate tick control measures.

**Keywords:** Ticks; *Ixodes ricinus*; Coltivirus



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