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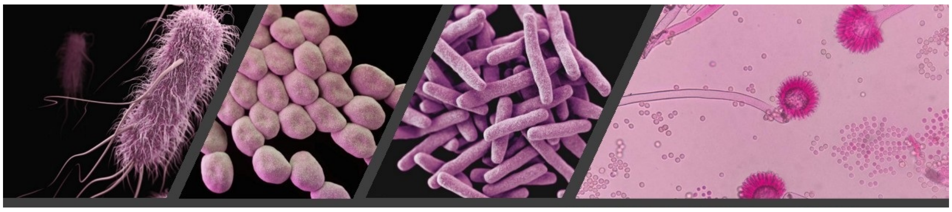

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Virome Diversity in Ticks Associated with Wild Boars: A Metagenomic Approach

Content

Tick-borne viruses (TBVs) include several emerging zoonotic agents with variable pathogenic potential ranging from asymptomatic to mild to severe symptoms, such as encephalitis, or meningitis. As part of the project “Ricerca Corrente 2022 –IZS ME 02/22 RC,”we investigated the virome of ticks collected from wild boars in Southern Italy, a species with potential epidemiological relevance for both domestic pigs and humans. A total of 36 *Dermacentor spp.* ticks were pooled (6 pools of 6 individuals) and analyzed using a metagenomic approach based on SISPA enrichment and Oxford Nanopore Technology sequencing. Viral reads corresponding to segments L and S of Tacheng tick virus 2 (TTV-2; Uukuvirus tachengense, family *Phenuiviridae*) were detected in 3 out of 6 pools. Nearly complete genomes of Tacheng tick virus 3 (*Rhabdoviridae*), Tacheng tick virus 5 (*Chuviridae*), Orthonairovirus sulainense, and Norwavirus grotenhoutense (*Nairoviridae*) were also recovered in other pools. TTV has been detected in human patients with TBV-like febrile disease in China, and it has since been detected in several tick genera/species across Asia and Europe. Its wide vector range suggests potential for ecological adaptation and cross-species transmission. These findings highlight the diversity of tick-associated virome in wildlife and the importance of surveillance.

Keywords

virome; ticks; wild boar; metagenomics

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