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Alphamesonivirus-1 in Culex pipiens: Genomic Insights and Diagnostic Tool Design

Inhalt

Mesoniviruses (Order: *Nidovirales*) are generally considered insect-specific viruses that do not infect vertebrates. However, this assumption was recently challenged by the detection of Alphamesonivirus-1 (AMV1) in two horses that died of acute respiratory syndrome in Italy (Jurisic et al.; J. Virol. 2025). Genetic analysis revealed a close relationship between the viral sequences isolated from the horses and those identified in local *Culex* mosquitoes, suggesting active local transmission. As part of metagenomic surveillance aimed at characterizing the virome of arthropod vectors, AMV1 RNA was detected in pools of *Culex pipiens*. These positive samples and the corresponding sequences were used to develop and validate a novel real-time RT-PCR assay for AMV1 detection, which was then compared to an existing pan-Mesonivirus qRT-PCR assay (Diagne et al.; Virus Res. 2020). The new assay was applied to hundreds of *Culex* mosquito pools collected across Italy to assess viral circulation. Additionally, AMV1 genomic variability was investigated. Three amino acid substitutions—located in ORF1a/ORF1b (RdRp), and ORF2a (Spike)—were uniquely identified in the horse-derived AMV1 sequence, potentially explaining the observed host switch. These findings underscore the importance of metagenomic surveillance in syndromic animals and highlight the need to monitor AMV1 circulation and evolution in *Culex* mosquito populations.

Keywords

Alphamesonivirus-1; Genomic heterogeneity: Real-time RT-PCR validation

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Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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Typ des Beitrags: Both options possible