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Prevalence and genetic diversity of Puumala virus(*Orthohantavirus puumalaense*) in bank voles (*Clethrionomys glareolus*) from northern boreal forest Sweden

Inhalt

Puumala virus (PUUV, *Orthohantavirus puumalaense*), the causative agent of human nephropathia epidemica, is an important zoonotic pathogen in Europe. Our study investigated PUUV RNA occurrence, genetic diversity, and environmental associations in bank voles (*Clethrionomys glareolus*) from two boreal forest areas in northern Sweden across a vole population cycle from 2020–2023. Lung-derived RNA from 519 bank voles was screened for a partial PUUV S-segment by RT-PCR and Sanger sequencing, and infection probability was analysed using logistic regression. Overall, 83/519 voles tested PUUV RNA-positive. Seasonality was the main factor influencing PUUV RNA occurrence, with study-area differences most evident in spring and body weight positively associated with infection probability particularly in autumn. Predicted prevalences were higher in males than females, 23.7% (95% CI: 17.0–32.0) vs. 8.3% (95% CI: 4.6–14.8), and increased from 8.6% in 2020 (95% CI: 3.6–19.2) to 25.6% in 2022 (95% CI: 17.6–35.6). All detected PUUV RNA sequences belong to the North-Scandinavian lineage, with limited spatial or temporal structuring. Land-use analyses at multiple spatial scales identified no significant habitat predictors. Overall, PUUV dynamics appeared to be shaped mainly by seasonality, reservoir demography, and vole population cycles rather than broad-scale landscape composition, emphasizing the importance of these factors for predicting periods of elevated human infection risk.

Keywords

Puumala virus, Orthohantavirus, Zoonotic, bank vole

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