

Zoonoses**0511****Shrew-borne Seewis hantavirus in Central Europe: high genetic diversity and putative spillover infections**

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For decades hantaviruses were considered to be exclusively rodent-borne pathogens. Recent findings of numerous shrew- and mole-borne hantaviruses raise important questions on the phylogenetic origin of current hantaviruses.

The objective of our study was to prove the presence and distribution of *Sorex*-associated hantaviruses in their reservoir hosts in Central Europe. Therefore, during 2004 - 2011 a total of 359 *Sorex araneus*, 61 *S. minutus*, 27 *S. coronatus* and one *S. alpinus* were collected at 86 different trapping sites in Germany, Czechia and Slovakia. Analyses by hantavirus-specific L- and S-segment RT-PCR revealed specific amplification products in tissues of 49 *S. araneus* and 4 *S. minutus*.

Phylogenetic analyses of the obtained sequences revealed that the animals were infected by Seewis virus (SWSV). High genetic diversity (up to 34% differences in nucleotide sequences) and phylogenetic clustering of the strains from Germany, Czechia and Slovakia according to the geographic origin was observed indicating long-term independent evolution of the viruses in local shrew populations. In addition, the multiple detection of SWSV in *S. minutus* might be explained by spillover infections from the *S. araneus* as the natural host.

This is the first comprehensive sequence analysis of SWSV strains from Germany, Czechia, and Slovakia indicating its broad geographical distribution in Central Europe.

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