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Hantavirus screening of insectivores from Germany

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Background and objectives: Recently many novel hantaviruses have been discovered in shrews, moles and bats. Shrew-borne Seewis virus (SWSV) and Asikkala virus (ASIV) were detected in several European countries. This pilot study was focusing on the molecular detection of insectivore-associated hantaviruses in Germany.

Materials and methods: A total of 700 shrews of three species were collected during a monitoring study at four regions in Germany. Additional 213 shrews of three species were collected at further sites by collaborators. Lung tissue RNA was used for hantavirus RT-PCR analysis targeting the S, M and L segments.

Results: SWSV RNA was detected in 42 of 700 (6.0 %) shrews from monitoring areas and in 5 of 213 shrews (2.3 %) from non-monitoring sites. The majority of affected shrews were *Sorex araneus*, but also a few *S. minutus*, and *S. coronatus* were found to be SWSV RNA-positive. Phylogenetic analysis indicated a clustering of the novel sequences with the previously published SWSV sequences. ASIV RNA was detected in 2 out of 54 (3.7%) pygmy shrews. No RNA was detected in any of the 27 greater white-toothed shrews.

Conclusion: This study confirms the continuing abundance of SWSV in common shrews and rare spillover infections to other shrew species. Future studies will be dedicated to understand the potential influence of changes in shrew populations on the prevalence and molecular evolution of insectivore-associated hantaviruses and to evaluate their zoonotic potential.