

PZOV-378**Detection of a shrew-borne hantavirus in Germany**

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Hantaviruses are negative stranded RNA viruses that can cause hemorrhagic fever with renal syndrome in Eurasia and hantavirus cardiopulmonary syndrome in America. In general, each hantavirus species is associated to a single rodent species or closely related species of the same genus. The recent detection of different shrew- and mole-borne hantaviruses has opened novel challenges for the understanding of hantavirus evolution. As the shrew-borne Seewis virus has been detected in the common shrew (*Sorex araneus*) from Switzerland, the objective of our study was to prove the presence, prevalence and genetic diversity of shrew-borne hantaviruses in Germany.

Embedded in the network "Rodent-borne pathogens" a total of 197 insectivores were trapped during 2005-2009 in 10 different federal states of Germany. The animals were necropsied in a BSL3 containment laboratory. For hantavirus detection total RNA was extracted from lungs, reverse transcribed and amplified using primers targeting the polymerase encoding L genome segment.

We found four novel hantavirus L segment sequences from 59 initially investigated small mammals. These sequences originating from *Sorex araneus* trapped in three federal states of Germany, i.e. Thuringia, Hesse and Bavaria, are closely related to a Seewis virus sequence from Switzerland and another sequence from Saxony-Anhalt. The phylogenetic analysis suggests a geographical clustering of the German Seewis virus sequences. Further investigations are dedicated to characterize the molecular nature and evolution of this novel Seewis virus lineages in more detail and to prove its relevance as a human pathogen.