

Molecular epidemiology of a large hantavirus outbreak in Germany, 2007

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More than 1,635 cases of hantavirus disease (mainly characterized by kidney failure) have been registered in 2007.

This outbreak enabled for the first time the molecular epidemiological analysis of the circulating virus. Out of 80 serum specimens found to be positive for Puumala virus (PUUV)-specific IgM antibodies, 42 samples (53%) revealed RT-PCR-positive. A subset of 14 RNA-positive samples were subjected to nucleotide sequence analysis of a 557 nt segment of the S gene. In the phylogenetic analysis the virus sequences unambiguously grouped within the PUUV species.

Nucleotide sequences formed distinct phylogenetic clades according to their geographical origin; Swabian Jura (the region with the highest morbidity rate of the outbreak), Munsterland, Spessart forest, and Bavarian forest. Sequence alignments within a clade revealed nucleotide sequence diversities of up to 5.5%. Between the different clades, a sequence variability of 12-18% was found.

Sequence comparisons revealed a tight correlation between human- and rodent-derived PUUV sequences obtained from the same regional provenance (nt identity >98%) but a high variability of sequences originating from different geographical regions (nt identity ~85%). The diversity of the different PUUV clusters suggests their separate evolutionary history in the different regions of Germany.

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