

## PZOV-363

**Molecular phylogenetic clades of Puumalavirus from the 2010 outbreak in Germany**

Ettinger J.<sup>1</sup>, Enders M.<sup>2</sup>, Ulrich R.<sup>3</sup>, Essbauer S.<sup>4</sup>, Klempa B.<sup>1</sup>, Krüger D.H.<sup>1</sup>, Hofmann J.<sup>1</sup>

<sup>1</sup>Institute of Medical Virology - Charité Medical School, Berlin, Germany

<sup>2</sup>Labor Prof. G. Enders & Partner and Institute of Virology, Infectious Diseases and Epidemiology e.V., Stuttgart, Germany

<sup>3</sup>Institute for Novel and Emerging Infectious Diseases, Riems/Greifswald, Germany

<sup>4</sup>Bundeswehr Institute of Microbiology, Munich, Germany

Hantavirus disease (hemorrhagic fever with renal syndrome, HFRS) is classified as a reportable infectious disease in Germany since 2001 with an average of about 220 cases per year. Most clinical cases are caused by Puumala virus (PUUV), mainly circulating in South- and Southwest-Germany. During the latest PUUV outbreak in 2010, approximately 2,000 laboratory confirmed cases have been reported to the Robert Koch Institute.

At the National Consultation Laboratory we received 583 human samples for more detailed hantavirus diagnostics. Out of them, 330 sera (56.7%) were tested positive not only for PUUV-IgG but also IgM. These acute sera were screened for Hantavirus-RNA in a RT-PCR assay targeting a conserved region within the polymerase gene. The 102 (30.9%) positive samples were tested in an additional PCR assay amplifying a 577 bp fragment within the nucleocapsid gene. Thirtyeight (37.3%) samples were tested positive by this approach; the nucleotide sequence was determined and used for molecular phylogenetic analysis. The dataset was completed by sequences obtained from murine and human samples collected in previous years.

The sequences acquired from the 38 patients form 7 different clades clearly depending on the geographical areas where the patients live. Besides *Swabian Jura*, *Northern Munsterland*, *Spessart* and *Bavarian Forest*, known since 2007, we identified 3 new clades, *Teutoburg Forest*, *Southern Munsterland* and *Northern Hesse*. Murine and human PUUV sequences within a clade show high similarity but are rather different from sequences obtained from other geographical regions. The data demonstrate a spatial diversification of clinically relevant PUUV strains in Germany.