

## Bank vole evolutionary lineage association of Puumala virus in Germany

*Drewes, Stephan*<sup>1</sup>; *Ali, Hanan Sheikh*<sup>1,2</sup>; *Saxenhofer, Moritz*<sup>3,5</sup>; *Rosenfeld, Ulrike M.*<sup>1</sup>; *Binder, Florian*<sup>1</sup>; *Cuypers, Fabian*<sup>1</sup>; *Schlegel, Mathias*<sup>1,6</sup>; *Röhrs, Susanne*<sup>4</sup>; *Heckel, Gerald*<sup>3,5</sup>; *Ulrich, Rainer G.*<sup>1</sup>

<sup>1</sup> *Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Institute of Novel and Emerging Infectious Diseases, Greifswald - Insel Riems, Germany*

<sup>2</sup> *College of Veterinary Medicine, Sudan University of Science and Technology, Khartoum, Sudan*

<sup>3</sup> *University of Bern, Institute of Ecology and Evolution, Bern, Switzerland*

<sup>4</sup> *Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Institute of Diagnostic Virology, Greifswald - Insel Riems, Germany*

<sup>5</sup> *Swiss Institute of Bioinformatics, Genopode, Lausanne, Switzerland*

<sup>6</sup> *Seramun Diagnostica GmbH, Heidensee, Germany*

Bank voles, *Myodes glareolus*, serve as natural reservoir for the hantavirus species Puumala virus (PUUV). This virus is responsible for the majority of human hantavirus infections in Germany mostly occurring in western and southern regions. During outbreak years more than 2,000 cases can be recorded, while in the northeastern part of the country human infections are only rarely detected. Therefore, this study aimed to identify possible reasons for the heterogeneous distribution of human PUUV cases in Germany.

For this purpose, 1,758 bank voles from Germany were investigated by serologic and molecular assays. A moderate to high PUUV prevalence was detected in bank voles from the endemic western and southern part of the country. In contrast, in northernmost and eastern parts of Germany no PUUV-positive bank voles were found. Further, *cytochrome b* gene sequence analysis indicated a geographic association of the PUUV occurrence in Germany and the Western evolutionary lineage of the bank vole. PUUV infections were detected also in voles of the Eastern and Carpathian lineages, but only when the Western lineage was present at the particular locations too.

In conclusion, our findings support the hypothesis that during or after the bank vole recolonization process after the last glacial period PUUV spread to Germany through the Western evolutionary lineage. Future analyses will have to investigate the susceptibility of the different bank vole lineages for infection by PUUV of different clades.