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Host range and genetic lineages of Tula virus in Central Europe

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European and Asian hantaviruses are rodent- or shrew-borne RNA viruses that can cause hemorrhagic fever with renal syndrome of different severity in humans. The Tula virus (TULV) is broadly distributed in Europe, is considered being non- or low pathogenic to humans and has been found in several rodent species (e.g. *Microtus arvalis*, *M. agrestis*).

(1) In this study we report the first molecular detection of TULV in the water vole *Arvicola amphibius*. The geographical clustering of the *Arvicola*-borne sequences with *Microtus*-derived TULV sequences from different parts of Germany and Europe may suggest TULV spillover infections of TULV from *M. arvalis* or *M. agrestis* to *A. amphibius*. Alternatively, *A. amphibius* may represent an additional reservoir host of TULV. To clarify this, future studies about the presence and frequency of TULV infections in water voles in different regions of Europe are needed.

(2) In 2009 rodents were trapped in a recultured landscape of the open cast coal mine "Welzow-Süd" near Cottbus, Eastern Germany. TULV was detected by RT-PCR in *M. arvalis* in the post-mining landscape. The phylogenetic analyses of these TULV sequences showed their close relationship to sequences from another site close to Cottbus and a clear separation from other TULV sequences originating from north Brandenburg, Lower Saxony and Baden-Wuerttemberg.

In conclusion, our studies demonstrate a broad geographical distribution, extensive host range and high genetic diversity of TULV in Central Europe. More investigations are needed to evaluate the risk of TULV infections for human health and to study molecular evolution and host adaptation processes on TULV in nature.