

PZOV-373**Greifswald virus, representative of Dobrava-belgrade hantavirus causing hemorrhagic fever with renal syndrome in North-East Germany**

Popugaeva Elena¹, Schlegel Mathias², Ulrich Rainer G.², Ettinger Jakob¹, Rang Andreas¹, Hofmann Jörg¹, Krüger Detlev H.¹, Klempa Boris³

¹Institute of Virology Helmut-Ruska-Haus, Berlin, Germany

²Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany

³Institute of Virology, Bratislava, Slovakia

Dobrava-Belgrade virus (DOBV) is the most virulent hantavirus in Europe causing haemorrhagic fever with renal syndrome (HFRS) in humans with fatality rates of up to 12 %. There are three natural hosts of DOBV known so far: *Apodemus agrarius*, *A. flavicollis* and *A. ponticus*, carrying distinct virus lineages: DOBV-Aa, DOBV-Af and DOBV-*Ap*, respectively. In Germany, DOBV is endemic in the Northern part of the country.

Here we report on the generation of a cell culture isolate of DOBV from Germany and its first characterization. Lung tissue suspension of rodent samples, trapped in a region near Greifswald/ North-East Germany, was inoculated onto Vero E6 cells. After three blind passages, DOBV was detected by immunostaining and RT-PCR. The complete nucleotide sequence of the new isolate was then determined. Molecular phylogenetic analysis of all three genomic segments showed that the DOBV strain - although isolated from *A. flavicollis* - undoubtedly belongs to the DOBV-Aa lineage, indicating that the virus was obtained from a "spill-over" infected animal. Moreover, close clustering of virus sequences with nucleotide sequences amplified from North-East German HFRS patients demonstrate that this virus is the pathogen responsible for human infections.

Activation of selected innate immunity markers after viral infection of A549 and HuH7 cell lineages was investigated by Western blot and qRT-PCR analyses; induction patterns observed resemble the pattern of cell's immune responses after infection by pathogenic Hantaan virus.

The new DOBV isolate, called Greifswald virus, belongs to the DOBV-Aa lineage and can be regarded as the representative of DOBV causing HFRS in Northern Germany.