

Comprehensive phylogeographic analysis of zoonotic Borna disease virus 1 (BoDV-1) infections in domestic mammals and humans

Arnt Ebinger; Pauline Santos; Ralf Dürrwald; Timo Homeier-Bachmann; Jolanta Kolodziejek; Kore Schlottau; Viktoria Ruf; Friederike Liesche-Starnecker; Jenny Fürstenau; Florian Hansmann; Torsten Seuberlich; Daniel Nobach; Viola Haring; Matthias Müller; Antonie Neubauer-Juric; Marcel Suchowski; Markus Bauswein; Hans-Helmut Niller; Barbara Schmidt; Dennis Tappe; Kirsten Pörtlner; Christina Frank; Lars Mundhenk; Bernd Hoffmann; Wolfgang Baumgärtner; Norbert Nowotny; Jürgen Schlegel; Rainer G. Ulrich; Martin Beer; Dirk Höper; [Dennis Rubbenstroth](#)¹

¹ Friedrich-Loeffler-Institut

Keywords: Bornaviridae, encephalitis, Borna disease, BoDV-1

Borna disease virus 1 (BoDV-1) causes fatal encephalomyelitis in domestic mammals and humans following spill-over transmission from shrews of the genus *Crocidura*, the known natural reservoir host. The known endemic areas of BoDV-1 are restricted to parts of Germany, Austria, Switzerland and Liechtenstein, whereas specific transmission routes remain elusive.

In this study, we performed a comprehensive phylogeographic analysis of BoDV-1 to assess potential sources of human BoDV-1 infections. We collected material and metadata of 152 domestic mammals, 19 human patients, and seven shrews with confirmed BoDV-1 infection from Germany and Switzerland. Complete or partial BoDV-1 genome sequences were generated from 59 domestic mammals, 17 humans and all seven shrews and analysed together with 127 previously published BoDV-1 sequences.

Most cases originated from the previously known endemic areas with few exceptions, some of which may indicate previously unknown risk areas for BoDV-1 transmission. In line with the strongly territorial reservoir host, the sequences showed a remarkable geographic association with distinct phylogenetic clades occupying barely overlapping dispersal areas.

Our work raised the number of confirmed human BoDV-1 infections to 34. The closest genetic relatives of most available human BoDV-1 sequences were located at distances below 50 km (median 27 km), indicating that the majority of zoonotic spill-over transmissions occur close to the patient's residence.