



Contribution ID: 317

Type: Oral presentation

Screening of shrews for Borna disease virus 1 (BoDV-1) and its implications for public health management

Wednesday, October 15, 2025 10:30 AM (15 minutes)

Borna disease virus 1 (BoDV-1) causes mostly fatal encephalitis in humans and other mammals. Its distribution area is restricted to parts of Southern and Eastern Germany, Austria, Switzerland and Liechtenstein. Spillover to dead-end hosts results from direct and/or indirect contact to bicolored white-toothed shrews (*Crocidura leucodon*), the natural BoDV-1 reservoir, which shed the virus via urine, feces, saliva and skin, but remain unaffected by the disease.

As part of this project, 263 shrews, predominately from Bavaria, were tested for BoDV-1 and their species was determined by a newly established RT-qPCR assay targeting the cytochrome b gene. Twenty-four (26.4%) of 91 *C. leucodon* as well as one out of 11 (9.1%) Mediterranean water shrews (*Neomys anomalus*) tested positive for BoDV-1, all of which originated from Bavaria. Phylogenetic analyses demonstrated the BoDV-1 sequences to belong to the same local clusters as found in Borna disease cases in the respective regions.

Several BoDV-1-positive shrews were found in human dwellings. Environmental samples were collected in five instances two to four weeks later, revealing low levels of BoDV-1 RNA but no infectious virus. In two cases, submitters had experienced close contact to excretions of BoDV-1-positive shrews, initiating post-exposure prophylaxis and 12-months of monitoring.

This One Health approach refines BoDV-1 risk areas and provides valuable insights into the poorly defined human-animal interface of BoDV-1 infection.

Keywords

BoDV-1, public health management, screening,

Registration ID

OHS25-141

Professional Status of the Speaker

Postdoc

Junior Scientist Status

Yes, I am a Junior Scientist.

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Session Classification: Session 9: One Health in Public Health II

Track Classification: One Health in Public Health