



### Abstract 1817

#### Epidemiological investigation of newly detected highly lethal Borna disease virus 1 cases reinforcing indirect shrew contact as possible source of infection: results from in-depth interviews, Germany, 2019

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**Background:** In 2018, Borna disease virus 1 (BoDV-1) was first confirmed as a zoonotic pathogen causing severe human encephalopathy in Germany with an extremely high case fatality (15/16). Bicoloured white-toothed shrews (*Crocidura leucodon*) have been identified as reservoir hosts shedding virus in urine, saliva and faeces in endemic areas. Clinical presentation, risk factors and transmission routes for human infection are unknown. We aimed to generate hypotheses about transmission routes and provide evidence to guide prevention.

**Materials/methods:** We defined cases as BoDV-1-confirmed by pro- or retrospective nucleic acid detection. Viruses were sequenced. We conducted interviews with family members at patients' homes in 2019 using a standardized semiquantitative questionnaire covering a broad spectrum of clinical presentation and pre-existing conditions. Queried exposures included housing environment, profession, animal contacts, outdoor activities, travel, and nutrition.

**Results:** We identified family members of five patients deceased 1996 through 2019 (4/5 female, median age 25 years, range 13-56). Immunosuppression was known for none. Four had presented with fulminant encephalitis starting with headache and fever, the fifth had initially shown signs of Guillain-Barré-syndrome. All had developed confusion, deep coma and had died within a median of 2.5 (range 1-11) months after symptom onset. All had lived their whole life in rural areas of Germany. Other than private gardening no communalities were identified. Three families kept domestic or farm animals (cat, dog, hare, duck, chicken). Family members did not know of any direct contact to shrews, but all had observed irregular peridomestic presence of shrews. Three families reported domestic cats bringing home shrews. All human BoDV-1 sequences clustered with animal BoDV-1 sequences from the respective regions.

**Conclusions:** Rural residence is a common denominator of all five patients but transmission routes remain poorly understood. Phylogenetic analysis and shrew presence suggest peridomestic infection from the local reservoir. In the absence of direct shrew contact, most likely transmission may be via indirect contact. Interviews with other patients' families are ongoing. To prevent cases of this fatal zoonosis, we recommend against avoidable contact to shrews and their secretions and published an online-handout on prevention measures targeting the public in endemic areas.

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