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Full genome sequencing of Ekpoma Virus 2 from human sera, Uganda

Inhalt

Ekpoma virus 2 (EKV-2) is a human-associated rhabdovirus first detected in a febrile case in Nigeria. Sero-prevalence studies from Nigeria and the Democratic Republic of Congo (DRC) reported EKV-2 reactivity rates ranging from 4 –94%. EKV-2 is closely related to Mundri virus (MUNV), identified in the cerebrospinal fluid of a girl with nodding syndrome in South Sudan, and to Bas-Congo virus (BASV), which has been linked to severe cases of haemorrhagic fever in the DRC.

In a cross-sectional study, we collected 2,062 human serum samples from 20 locations across the Albertine Rift region of Uganda and tested them for acute viral infections using next-generation sequencing.

We identified EKV-2 in two samples: a 39-year-old woman from an urban centre who reported febrile symptoms, and an asymptomatic 22-year-old man from a rural village 55 km away. Full genomes were obtained from both samples sharing 99% nucleotide (nt) with each other, and 89% nt identity with the Nigerian prototype strain. Phylogenetically, both strains clustered with EKV-2 and formed a clade with MUNV and BASV. To investigate human exposure to EKV-2 in the Albertine Rift region, we established a recombinant immunofluorescence assay as virus isolation in cell culture was not successful. The analyses are ongoing and will provide insights into the geographic distribution of EKV-2, potential regional differences and sociodemographic characteristics associated with EKV-2.

Keywords

Ekpoma virus 2, Rhabdovirus, Metagenomics, Emerging Infectious Diseases, Uganda

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PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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