The first evidence of shaking mink syndrome (SMS)-astrovirus infection in farmed minks, China

Xue Bai¹, rongguang lu¹, Shuang-Shuang Li¹, Bo Hu¹, Hong-Ye Li¹, Hong Tian², Weiquan Liu³, Xi-Jun Yan¹, and Hao Liu⁴

¹Chinese Academy of Agricultural Sciences Institute of Special Animal and Plant Sciences ²Lanzhou Veterinary Research Institute ³China Agricultural University State Key Laboratory of Agrobiotechnology ⁴Foshan University

May 22, 2022

Abstract

A novel neurological disorder disease, shaking mink syndrome (SMS), emerged in Denmark and Sweden since 2000. The SMS has seldom been reported in China, and the causative agent is uncertain. SMS outbreaks occurred in multiple provinces in 2020, A total of 44 brain samples from minks associated with SMS were collected from Heilongjiang, Liaoning, and Shandong provinces, of which 28 samples (63.3%) were SMS-Astrovirus (SMS-AstV) positive by reverse transcription PCR. Moreover, the complete coding region sequences (CDS) of a sample collected from a two-month-old mink (termed SMS-Astv-H1) were amplified by PCR. The complete CDS and ORF2 sequences of SMS-AstV-H1 were 94.3% and 96.4% identical to an SMS-AstV strain (GenBank accession number: GU985458). Phylogenetically, SMS-Astv-H1 was closely related to an SMS-AstV strain (GU985458). Based on the above results, we describe the SMS-AstV infections related to SMS among farmed minks in China. Future studies need to focus on epidemiology, virus isolation, and potential interspecies transmission of SMS-AstV.

Hosted file

2. First evidence of SMS-astrovirus infection in farmed mink, China 20220517 Lu revised For TED.docx available at https://authorea.com/users/484208/articles/570119-the-first-evidence-of-shaking-mink-syndrome-sms-astrovirus-infection-in-farmed-minks-china

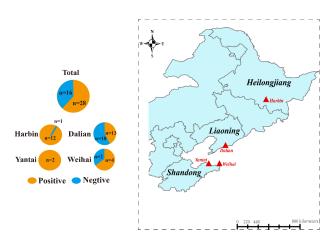


Fig 1. Map of the northern part of China containing the sample collection areas indicated by red triangles. The positive samples are shown in orange, and the negative samples are shown in blue.

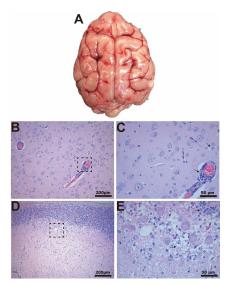


Fig 2. Neuropathology of SMS-AstV associated encephalitis in the cerebrum and epencephalon of a mink kit (one-month-old; Strain SMS-AstV-H1). (A) Gross observation of the whole brain exhibited mild congestion and hydrocephalus. (B) Histopathological lesion of the cerebrum (H&E), showing neuronal necrosis, gliosis, and mononuclear perivascular cuffing. (C) High magnification of the marked area in panel B. (D) Histopathological lesion of the epencephalon (H&E) showing gliosis, Purkinje cell necrosis, and histiocytosis. (E) High magnification of the marked area in panel D. The arrows point to the major pathological lesions such as perivascular cuffis, gliosis, and neuronal necrosis. The scale bars are shown at the bottom right of panel B to panel E.

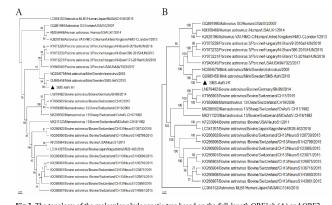


Fig 3. The topology of the molecular phylogenetic tree based on the full-length ORF1ab (A) and ORF2 (B) sequences of representative astrovirus species. The sequences from SMS-AstV-H1 are indicated as black triangle and SMS-AstV (GU985458). GenBank accession numbers and strain details are listed in Table S3. The scale bar indicates the estimated nucleotide sequence phylogenetic distance.