

Epidemiology of Bovine Viral Diarrhea Virus and Bovine Enterovirus Infection in Yaks in Haibei Region of Qinghai Province, China

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Abstract

To investigate the epidemiology of bovine viral diarrhea virus (BVDV) and Bovine Enterovirus (BEV) in Haibei region and surrounding yak farms of Qinghai Province. 148 fecal samples were collected from yaks with diarrhea symptom during 2022 to 2024 and used for the detection of BVDV and BEV by real time fluorescence quantitative PCR. The homology and genetic evolution analysis were conducted on the 3D gene regions of BEV and 5'UTR of BVDV, respectively. The results showed that positive BVDV and BEV were detected in yak fecal samples from Menyuan, Qilian, Haiyan County, and nearby Huangyuan County in Haibei Prefecture, with infection rates ranging from 29.00% to 45.00% and 35.00% to 63.63%, respectively. The four yak BVDV 5'UTR genes have a close genetic evolutionary relationship with BVDV-1a strains from Iran, the United States, and the United Kingdom, and are clustered in the same evolutionary branch with BVDV-1/NADL and Oregon C24V strains, with a homology of 76.6% to 99.7%; After 3D gene regions sequencing of 10 strains of BEV virus, it was found that 8 strains along with Sichuan yak SWUN-AB001 strain, belong to the Yak enterovirus like evolutionary branch, with a homology of 83.0% to 88.4%. The other 2 strains along with Jilin goat SD-S67 strain and Japanese cattle BEV IS2/Bos taurus/JPN/1990 strain, belong to the F species enterovirus, with a homology of 91.3% to 93.4%. The research identified BVDV-1a virus and Type F Bovine Enterovirus as important pathogens causing diarrhea in yaks in Haibei area of Qinghai province, also provides a basis for understanding the characteristics of BVDV and BEV and contributes to the development of control measures against viral Diarrhea disease among yaks.

Keywords

Yak, Bovine Viral Diarrhea Virus, Bovine Enterovirus, Epidemiological Investigation, Genetic Evolution Analysis

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