

Beef Day 2021

Prevalence of Bovine Viral Diarrhea Virus subspecies among persistently infected samples from cattle in the United States

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Objective

The focus of this survey was to determine the prevalence of BVDV subspecies in the United States.

Study Description

Ear notch samples from confirmed or suspected PI animals were submitted by veterinary clinics and producers between November 1, 2018 through December 20, 2019. One thousand and ninety-three samples (1,093) were submitted for processing to the Animal Disease Research and Diagnostics Laboratory of South Dakota State University. The initial screening PCR used by ADRDL detected 1,000 samples as BVDV PI positive. Positive submissions were supplied from 21 states with sample size ranging 1-288 samples/state. Samples from 4 states: Kansas (n=258), Kentucky (n=288), Oklahoma (n=237), and Texas (n=81) accounted for 86.4% of total accessions. Samples were predominately obtained from beef operations, with 17 samples sourced from dairies in California, New York, Connecticut and Wisconsin. Of the PCR confirmed samples, the prevalence of subspecies was BVDV1b 702/1,000 (70.2%), BVDV1a 44/1000 (4.4%), and BVDV2a 178/1000 (17.8%) with 76/1000 (7.6%) of samples unable to be translated successfully. The 76 samples unavailable for subtyping was attributed to either low concentration of BVD nucleic acid or noisy multiple peak sequence data, preventing sequencing of 5' UTR.

Take Home Points

A pool of 1,000 samples were diagnosed positive for persistent infection of bovine viral diarrhea virus via PCR. Results of sequencing the 5' UTR of the viral genome showed that BVDV 1b was by 3.5 X (70%) more prevalent than BVDV2a (17.8%) and BVDV1a was the least at 4.4%. These findings support previous research suggesting BVDV 1b is the predominant strain circulating in the United States.

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