

# Bovine Viral Diarrhea Virus: Genetic Analysis and Signalment of Persistently Infected Dairy Calves Detected in the Upper Midwestern United States

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## Introduction

The purpose of this study was to detect and confirm PI dairy cattle, research the dam's location during the first trimester of gestation, and genetically sequence a portion of the 5' untranslated (UTR) region of viral RNA to determine the prevalence of different genotypes of BVDV PI dairy cattle in the upper midwestern United States.

## Materials and Methods

Only dairy cattle that were confirmed BVDV PI were included in this study. Persistently infected cattle reported in this study had at least two positive test results, at least three weeks apart, and were tested with either antigen-capture enzyme-linked immunosorbent assay (AC-ELISA) on skin or reverse transcription-polymerase chain reaction (RT-PCR) on skin or serum. To further characterize the virus detected in BVDV PI cattle, a 270 base pair segment of the 5' untranslated region (5' UTR) was analyzed. Once an animal was de-

termined BVDV PI, the farm records were examined to determine the dam of the PI. When available, the dam was tested for BVDV PI.

## Results

Genetic sequence indicated that 90% (37/40) of the PI calves were shedding a virus similar to the Draper 1b reference strain. Most (23/37, 62%) of the PI calves were from first-lactation heifers and the remaining (14/37, 38%) were from lactating cows. None of the dams of the PI calves available for testing were themselves PI.

## Significance

Strains most similar to BVDV genotype 1b appear to persist despite the widespread use of vaccines and few, if any, commercially available vaccines contain viruses similar to the 1b subgenotype. Exposure to BVDV and the development of PI calves, presumably from other PI cattle, is greater in a youngstock heifer population than in a lactating cow population.