



# Minnesota Dairy Health Conference

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UNIVERSITY OF MINNESOTA

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College of Veterinary Medicine

VETERINARY CONTINUING EDUCATION

May 19-20, 2010  
St. Paul, Minnesota



# ***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:

Cattle persistently infected (PI) with BVDV are an important reservoir for the virus and BVDV control and eradication strategies focus on the detection and removal of PI cattle. PI cattle occur when a fetus is infected with noncytopathic BVDV during the first trimester of pregnancy.<sup>1,4,5</sup> Fetuses that survive a noncytopathic BVDV infection during the first trimester are immunotolerant to, and persistently infected with, BVDV. If a PI calf is detected and confirmed, the dam of the calf should be tested for persistent infection. If the dam of a PI calf is not herself PI, researching the signalment of the dam can provide additional information about BVDV infections within the herd. Determining the location of the dam of the PI calf during the first trimester of pregnancy will reveal the time and location of fetal infection. When a PI calf is detected, the time and location of BVDV infection of the dam can be retrospectively calculated to a time approximately 5 to 9 months prior to the birth date of the PI calf. The “point-in-time” infection that results in the birth of a PI animal provides information that cannot always be obtained when documenting acute infections by seroconversion in non-PI cattle.

Dairy cattle persistently infected with BVDV are rare. In one study, 8 of 961 (0.8%) dairy calves born on four large dairy farms in Minnesota and California were PI.<sup>6</sup> In addition to determining the location of the PI calf’s dam during the first trimester, the virus shed by the PI animal can be sequenced and compared to other PI cattle and acute infections to further describe the epidemiology of virus transmission.

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 Midwest.

## 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 3 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.

Once an animal was determined BVDV PI, the farm records were examined to determine the dam of the PI. When available, the dam was tested for BVDV PI. The dam’s lactation number (1<sup>st</sup> calf heifer, 2<sup>nd</sup> lactation cow, etc.) when she bore the PI calf was obtained from farm records. To further characterize the virus detected in BVDV PI cattle, a 270 base pair segment of the 5’ untranslated region (5’ UTR) was sequenced and analyzed.

## Results:

Almost all of the PI calves (36/40, 90%) included in this study were shedding a virus similar to the BVDV 1b subgenotype and all 36 1b sequences were greater than 95% similar to each other.

Across all dairies, a majority (23/37, 62%) of the BVDV PI dairy calves were offspring of first calf heifers exposed to other growing heifers, and presumably one or more PI cattle, within the non-lactating youngstock population. A minority of PI calves (14/37 38%) were calves from lactating dairy cows in a second or greater lactation where the fetal infection would have occurred in the herd of lactating cows.

## Discussion:

Genetic sequencing data showed that most PI cattle (36/40, 90%) from these dairies are infected with BVDV strains similar to the 1b subgenotype. This is consistent with previous reports on PI beef cattle in central plains feedlots.<sup>2,3</sup> Virus 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.

The dams of most of the PI calves (23/37, 62%) were heifers and four dairies used one or more custom heifer raisers to raise and breed heifers. In addition to using heifer raisers, all four dairies had reported buying pregnant heifers from suppliers. Commingling animals from multiple sources is not an unusual practice for heifer raisers. One publication reported that off-site heifer facilities rarely separated heifers according to farm of origin during the rearing period.<sup>7</sup> This information suggests that the risk of exposure to BVDV, presumably from another PI animal, is greater in a youngstock heifer population than in a lactating cow population.

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