differential PCR and sequencing of a 5'-UTR with phylogenetic analysis, BVDV1a, BVDV1b and BVDV2a strains were identified. Controls included reference BVDV strains, including vaccinal strains in the US plus BVDV2b. A BVDV2b had been isolated from a feedlot in Oklahoma pneumonia case, thus surveillance for that BVDV subgenotype continues. There were 67/86 (77.9%) BVDV1b; 10/86 (11.6%) BVDV1a; and 9/86 (10.5%) BVDV2a. The BVDV1b was more common than BVDV1a or BVDV2a ($P<0.05$). None of the 86 isolates were genetically identical to the BVDV subgenotypes in US vaccines.

Significance

These results indicate that an antigen capture ELISA test on fresh PBS notches identifies a very high percentage (97.7%) of cattle defined as PI. While a small number in this study (2/88) were considered only acute/transiently infected, the feedlot veterinarian is presented extremely important information for BVDV control/management based on positive or negative results. At least all the positive animals could be segregated and/or tested again to confirm PI status. By testing the animals individually, as in the initial ACE, solid evidence is obtained for each animal rather than retesting individual animals a second time as expected with a positive-pooled number of samples (PCR). The distribution of the BVDV in cattle entering the feedlot into subgenotypes confirms our prior findings of BVDV positive diagnostic laboratory accessions, with BVDV1b being the predominant BVDV strain. Equally important is the issue that effective vaccines must be developed/used to control this predominant BVDV strain in the US.

Characterization of Bovine Viral Diarrhea Virus (BVDV) Genetics, Antibody Response and Viremia from a Group of BVDV Persistently Infected Calves

CCL Chase, *DVM, PhD*[1]; **LJ Braun,** *MS*[1]; **L Holler,** *DVM, PhD*[1]; **J Neill,** *PhD*[2]; **J Ridpath,** *PhD*[2]
[1] *Dept Vet Sci, South Dakota State University, Brookings, SD*
[2] *NADC, Ames, IA*

Introduction

Bovine viral diarrhea virus (BVDV) infections cause major problems in the US cattle industry. BVDV persistent infections are the result of fetal infections in the first trimester of pregnancy. Persistently infected animals are a major reservoir of the virus in nature and are extremely efficient at spreading the virus among cattle populations. Understanding the nature of persistent infections and developing diagnostics and surveillance schemes that eliminate PI animals is vital to the control of BVDV. In this study we look at variations in clinical presentation, viral spread, immune response and viral stability in a large group of calves infected with the same BVDV strain.

Materials and Methods

One hundred twenty-eight bred cows were obtained from a private ranch and moved to a university field station. The vaccination history of the herd indicated that a BVDV type 1 vaccine had been used. Following weaning the calves were screened in September 2004 and 44 were found to be immunohistochemistry (IHC) positive for BVDV antigen. Polymerase chain reaction (PCR) analysis indicated that the animals were infected with a BVDV type 2a isolate. Five of these animals died prior to being moved to a university research facility. Three months later in December 2004, the remaining 39 calves were tested via PCR and IHC, and 36 of the 39 were positive for BVDV by both tests.

Results

Sequence comparison of the 5'UTR of the 36 isolates showed a > 99% sequence homology. Comparison of the highly variable region coding for the E2 polypeptide showed a greater than 96% sequence conservation among strains. Three of the PI animals had titers against BVDV. Studies are ongoing to see if the presence of titers will affect viral sequence over time. Viral titers are being assessed. The animals are being tested monthly for viral and antibody titers. Additional lymphocyte marker and neutrophil studies are also ongoing.

Significance

This study indicates that three of the animals initially thought to be persistently infected were instead acutely infected and IHC positive. Although sequence homology was high between isolates from the animals, a subgroup of animals have a slightly different E2 profile. These PI animals provide an excellent opportunity to monitor virus evolution and immune response in animals infected with the same isolate.

Effect of Two Commercially Available Multivalent Modified-Live Viral Vaccines on Milk Production of Holstein Dairy Cows

E.F. Garrett, *DVM*
Novartis Animal Health US, 1447 140th Street, Larchwood, IA

Introduction

Vaccination of lactating dairy cows is a common practice among US dairy herds. The objective of vaccination during lactation is to bolster immunity against common agents that may cause failure to conceive, fetal loss, or respiratory disease. The viruses commonly included in these vaccines are bovine viral diarrhea virus (BVDV), bovine herpes virus 1 (BHV-1), bovine respiratory syncytial virus (BRSV) and parainfluenza-3 virus (PI-3). The vaccines may contain inactivated virus or modified-live virus (*Compendium of Veterinary Products* 2004). In addition to the cost of vaccine and labor to administer the vaccine, producers should consider the cost of lost production when evaluating the economic benefits of vaccinating a lactating cow. Vaccination with an inactivated viral vaccine in combination with leptospiral bacterin produced a significant decrease in production compared to controls (Scott 2001). The effect of modified-live viral vaccines on milk production has not been reported. The objective of this study was to determine the effect of two commercially available multivalent modified-live viral vaccines on milk production of Holstein dairy cows.

Materials and Methods

The study was conducted on a commercial dairy farm in the United States milking approximately 2,100 Holstein cows milked three times per day and producing approximately 70.4 lb (32 kg) milk/cow/day with 3.6% fat and 3.0% protein. The farm utilized a Westfalia parlor system with milk meters and electronic identification of animals in the milking stall, which allowed capture of daily milk weights. Cows were housed in sand-bedded freestalls and divided among 17 pens based on a combination of age, stage of lactation and pregnancy status. Three hundred and two non-pregnant animals were enrolled over a 45 day period. Animals eligible to be enrolled were either less than 50 days-in-milk (DIM) and therefore not eligible to have been inseminated at the time of enrollment, or were diagnosed open by rectal palpation on the day of enrollment. At enrollment, cows were randomly assigned to one of three treatment groups using a prepared, randomly ordered treatment list. The treatment groups were control (C) which received 2 ml sterile saline intramuscularly, Arsenal (A) which received 2 ml of Arsenal 4.1 (Novartis) subcutaneously, and Bovishield (B) which received 2 ml of Bovishield Gold 5 (Pfizer) intramuscularly. A new needle was used for each injection and all injections were given in the neck. Vaccine was administered following the morning milking while cows were restrained in feed lane headlocks for routine herd management procedures. Ambient temperature at the time of vaccination ranged from 33.8 to 55.4°F (1 to 13°C). Vaccine was reconstituted just prior to use and any excess was discarded at the completion of the day's enrollment. Daily milk production was recorded for each cow from five days prior to vaccination until 14 days after vaccination. Of the 302 animals enrolled, 43 were eliminated from the data set prior to analysis. Health events or meter errors resulted in the removal of 14 animals (A, n=8; B, n=5; C n=1). All animals for week 6 (n=27) and two animals from week 7 were removed due to a failure to record pen location at the time of vaccination (A, n=9; B, n=10; C, n=10). Pre-vaccination (day -5 to 0) milk production results were analyzed by repeated measures analysis of variance. The model included the fixed effects of treatment group, day relative to vaccination, the interaction