Outbreaks of Severe Acute BVDV in Quebec, Ontario and New York State, Occurring Between 1993 and 1995, Linked to the Same Strain of Type 2 BVDV

Julia F. Ridpath, PhD; John D. Neill, PhD National Animal Disease Center/ARS/USDA, Ames, IA

Introduction

When first described by Cornell University researchers in 1946, bovine viral diarrhea (BVD) was characterized as an acute transmissible viral infection marked by severe leukopenia, high fever, depression, diarrhea, gastrointestinal erosions and hemorrhages. While the first report of BVD in the literature described a severe acute disease, the most commonly observed form of acute BVDV in ensuing years was clinically mild. Acute BVD infections came to be regarded as clinically unimportant, and the transmission of the virus between healthy immunocompetent cattle was considered insignificant. However this mindset began to change in the late 1980s when severe acute BVD cases were reported with increasing frequency in North America. These outbreaks were particularly devastating in the Canadian provinces of Quebec and Ontario. In the province of Quebec, a BVD epidemic starting in early 1993 resulted in the death of 32,000 out of 143,000 (22.4%) animals in the 1993 veal calf crop. A virus, called IAF 103, was isolated from an outbreak of severe acute BVDV in Quebec by the Institut Armand-Frappier in Quebec, Canada. An epidemic of severe acute BVDV, beginning in 1993 and waning in 1995, was reported In Ontario. It was estimated that 150 dairy, 660 beef and 100 veal calf herds were affected in this epidemic, with death seen in all age groups and economic losses reaching \$100,000 in severely affected herds. Two viruses, called 1373 and 24515, were isolated from animals housed on two different farms involved in the Ontario epidemic, by the Animal Health Laboratory, University of Guelph, Guelph, Ontario. The spread of BVDV during these outbreaks was described as explosive and was not linked to the presence of persistently infected animals.

Concurrently, a BVDV2 strain called NY 93 was isolated in 1993 from an outbreak of severe acute BVD observed in one dairy herd following the importation of an apparently acutely infected heifer from Canada. This strain was isolated at the Diagnostic Laboratory, New York State College of Veterinary Medicine, Cornell University Ithaca, New York. All four viruses isolated from these outbreaks were typed as BVDV2 genotype strains, but no comparison was made between these strains. In this study we compared the virulence and genetic sequence of these four strains to each other,

and to strains isolated in North America from 1989 to 1996.

Materials and Methods

The complete sequence of the virus 1373 was derived by direct sequencing of RT-PCR amplification products. Amplicons averaged 500 base pairs, and successive amplicons overlapped by approximately 200 bases. All sequencing reactions were done in duplicate and all sequences were confirmed by sequencing both strands. Primers were designed that amplified a portion of the 5' UTR, the region coding for the E2 and a sequence motif observed in the 1373 that had not been previously reported in BVDV reference strains. These primer sets were used to screen BVDV genotype 2 viruses in the collection. In vivo studies were performed using viruses selected based on this screening. In vivo studies used one to three month old colostrum-deprived calves, tested free of BVDV and antibodies to BVDV. Five calves were infected per BVDV strain by the oral nasal route. Basal temperature was measured for 17 days following infection and lymphocyte, platelet counts and serum antibody titers determined on days 3, 6, 9, 11 and 13 post-infection.

Results

Comparison of the complete sequence of the noncytopathic BVDV strain 1373 to standard laboratory strains of BVDV revealed an 18 amino acid residue insertion in the portion of the genome coding for the NS2/3 nonstructural protein. The location of the insertion was the same as that of inserted sequences reported in cytopathic BVDV. Subsequently this same insertion was found in viruses 24515, IAF 103 and NY 93, which had been isolated following outbreaks of severe acute BVDV occurring between 1993 and 1995. Further sequencing revealed that these four strains (1373, 24515, IAF 103 and NY 93) had sequence identities greater than 99%. The virulence of these four strains was compared to two BVDV2 strains that had been used in earlier studies of virulence, 890 and CD 87. These two strains did not have the 18 amino acid insertion found in 1373. Infection with all six strains resulted in severe clinical disease (temperature exceeding 105°F [40.6°C], lymphopenia >50%, thrombocytopenia >50% and mortalities >10%).

Significance

Conventional wisdom holds that BVDV outbreaks are subclinical in healthy animals, can nearly always be traced to contact with a persistently infected animal, and that transmission of the virus following acute infection is insignificant to the spread of virus. Thus the observation that outbreaks of severe acute BVDV observed in Quebec, Ontario and New York State were due to a single strain of BVDV that spread explosively following acute infection requires a paradigm shift in our concepts of BVDV transmission. The spread of low virulence within a population is most likely the result of contact with a persistently infected (PI) animal, and thus the number of contacts available to the PI animal limits spread. The spread of highly virulent BVDV strains

within cattle populations is more similar to that of classical swine fever viruses. Transmission by acutely infected animals is significant and the sources of virus increase as the number of infected animals increases. Thus management to control outbreaks of severe acute BVD requires a different approach than that used for subclinical BVD. A number of studies have been undertaken to search for virulence markers. Failure to recognize that 1373, 24515, IAF 103 and NY 93 are all the same strain may lead to misinterpretation of results. There are virulent viruses, such as 890 and CD 87, that are not related to 1373. When looking for commonalities among virulent strains that may be related to virulence it is important to compare divergent rather than identical strains.

Effect of Cow Comfort on Herd Health and Milk Production on a Large Commercial Dairy

R.M. Stockler, DVM; L.M. Neuder, DVM; P.M. Sears, DVM, PhD
Department of Large Animal Clinical Science, Michigan State University, East Lansing, MI

Introduction

Lameness at calving can have a lasting effect on heifers and cows as they begin their lactation. If they are reluctant to lie down in the stall or get up, it can affect their normal daily activity and reduce feed intake, milk production and possible health of the animal. The objective of this study was to access the differences in milk production and fresh cow health between two groups of cows. Half of the cows were fitted with rubber boots before calving, and their performance was compared to control cows as they walked on a normal freestall barn hard floor surface.

Materials and Methods

Cows were paired five to seven days before calving and rubber boots were fitted on all four feet of 20 cows in a 40-cow trial. These cows were paired by lactation and 305 ME with no history or signs of lameness. All cows went through the maternity and fresh pens without any special care, and boots were kept on the cows for 60 days after calving. Using the farm Dairy Comp 305 database, milk production was analyzed at 14, 28, 42 and 56 days-in-milk and by the first DHIA 305 ME

test day using Chi square, t-test and ANOVA in Microsoft Excel and SAS programs. Fresh cow heath was evaluated for the first month after calving. Cows were evaluated for lameness, displaced abomasums (DA), ketosis, metritis or retained placenta.

Results

In the 30 cows (15 with boots and 15 without boots) that had complete health records for the trial period, there were no differences in any of the health parameters, although three of the 15 controls had a DA as compared to only one of the 15 cows with boots. This difference was not significant, and there were no differences in any other health category. However, production did differ. Cows fitted with boots produced an average of 10 lb (4.5 kg) more milk in the first 45 days after calving than cows without boots (89.1 lb [40.5 kg] of milk to 79.0 lb [35.9 kg] of milk, respectively). Cows with boots had the greatest increase in production in the first 28 days, reaching 100 lb (45 kg) of milk in that period. The control group took 42 days to reach 100 lb (45 kg) of milk. The two groups' differences were not as great after 42 days, but the first 305 ME was 2005 lb (911 kg) greater for cows with boots, with a ME of 23,408

SEPTEMBER, 2005 289