Bovine Viral Diarrhea Viruses(BVDV) in Beef Breeding Herds and Feedlots: Diversity of BVDV Subtypes in Persistently Infected Cattle

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Introduction

Bovine viral diarrhea viruses (BVDV) represent significant pathogens in cattle affecting several organ systems, particularly involving the respiratory tract and fetal infections. The principal reservoir of BVDV is the persistently infected (PI) animal. The PI cattle are born to susceptible heifers/cows exposed during pregnancy, carried to term, and are lifetime shedders of the virus. Current control programs focus on biosecurity using testing of new additions including calves born to negative dams, isolation of new animals until testing completed, and vaccination. Identification by testing and removal of PI cattle are critical to control programs. PI cattle may expose susceptible breeding females resulting in more PI calves; and/or cause primary infections in acute/transient infections and predispose the BVDV exposed animal to other pathogens. The purpose of this study was: (1) detect PI cattle in beef breeding herds and cattle entering feedlots; and (2) determine distribution of BVDV subtypes in PI cattle.

Materials and Methods

Cattle entering a southwest Kansas feedlot in 2005-2006 were tested for BVDV using fresh ear notches and tested by an antigen capture ELISA test. Repeat samples were collected for ACE and formalin notches for immunohistochemistry (IHC). Cattle entering the OSU Department of Animal Sciences Sparks Facility in 2005-2006 and 2006-2007 were tested for BVDV using ACE and IHC. Also in 2006 there were beef breeding herds for testing the calves using notches for IHC and ACE.Animals positive in these studies had serums collected with the viruses grown, and subtyped by sequencing of a region of the 5'-UTR.

Results

From the commercial feedlot in 2005-2006 there were 318 PI cattle. The distribution of BVDV subtypes was: BVDV1b, 241 (75.8%); BVDV1a, 37 (11.6%); and BVDV2a, 40 (12.6%). During 2005-2006 at the OSU Sparks Facility there were 9/1021 incoming cattle that were PI (0.88%). There were 8 BVDV1b PI cattle and 1 BVDV1a PI cattle. In 2006-2007 there were 3/1016 cattle PI (0.2%). All three PI cattle were BVDV1b. From the cattle in the beef breeding herds tested in the Spring 2006, there were 25/4530 calves that were PI (0.55%). All the PI strains in these calves were BVDV1b. Only one of the 25 PI calves had a dam that was PI.

Significance

The results of these studies indicate that the ACE and IHC tests can be utilized on fresh and formalin notches to detect PI BVDV cattle. The distribution of BVDV subtypes indicates that the predominant BVDV subtype in this region is BVDV1b. However the two subtypes in US vaccines are BVDV1a and BVDV2a which represent the minority of the BVDV subtypes identified in these studies. The critical point underscored in this study is that BVDV PI begins in the breeding herd. Effective control programs eliminating BVDV in breeding herds should minimize risks due to BVDV later in stocker and feedlot operations. Also, vaccinations to prevent BVDV fetal infections preventing PI cattle are critical to control programs.