Relationship of rectal temperature at first treatment for bovine respiratory disease complex in feedlot calves to probability of not finishing the production cycle normally

M.E. Theurer, *BS*[1]; **B.J. White**, *DVM, MS*[2]; **R.L. Larson**, *DVM, PhD*[2]; **K. Holstein**, *DVM*[2]; **D.E. Amrine**, *DVM, PhD*[1]

[1]*Department of Diagnostic Medicine and Pathobiology, Kansas State University, Manhattan, KS 66502*
[2]*Department of Clinical Sciences, Kansas State University, Manhattan, KS 66502*

Introduction

Monitoring rectal temperature is a common component of health protocols, and treatment decision may be influenced by rectal temperature at time of initial diagnosis of bovine respiratory disease (BRD). The objective of this project was to determine potential associations between rectal temperature at first-time identification of BRD and the probability of not finishing the production cycle normally.

Materials and Methods

Individual animal health data from 19 US feedlots were collected from 2000 to 2009. Data from the initial BRD episode for individual cattle were included in the study population. A binary variable was created to identify calves that did not finish (DNF) the production cycle normally (died or culled prior to harvest of cohort). A generalized mixed linear model was created to evaluate potential associations of common cohort factors with the probability of DNF and a receiver-operating characteristic curve was used to determine model predictive accuracy.

Results

Data consisted of 344,982 individual calves at first time identification of BRD and 7.97% of these calves DNF. Rectal temperatures were normally distributed with a mean and median of 104°F. Calves exhibited a greater probability of DNF at greater rectal temperatures, although this relationship was influenced by quarter of arrival, gender, and days-on-feed at BRD diagnosis. The area under the curve for the receiving-operating characteristic curve was 0.6460.

Significance

Producers and consulting veterinarians can utilize these results to improve understanding of how to use rectal temperature at first BRD identification to more accurately predict cohort outcomes.

A meta-analysis of vaccine effectiveness against bovine herpesvirus, bovine viral diarrhea virus, bovine respiratory syncytial virus, and parainfluenza-type 3 virus in cattle for bovine respiratory disease complex

M.E. Theurer, *BS*[1]; **R.L. Larson**, *DVM, PhD*[2]; **B.J. White**, *DVM, MS*[2]

[1]*Department of Diagnostic Medicine and Pathobiology, Kansas State University, Manhattan, KS 66502*
[2]*Department of Clinical Sciences, Kansas State University, Manhattan, KS 66502*

Introduction

Multiple commercial vaccines are available with the goal of decreasing risk and severity of bovine respiratory disease complex (BRDC). The objective was to perform a systematic review of published literature and meta-analysis to evaluate the efficacy of vaccinating cattle with available viral vaccine antigens to mitigate the effects of BRDC compared to unvaccinated controls.

Materials and Methods

A literature search was performed to identify studies evaluating the effectiveness of bovine herpesvirus-1 (BHV-1), bovine respiratory syncytial virus (BRSV), bovine viral diarrhea virus (BVDV), and parainfluenza-type 3 (PI3) vaccination in cattle. Literature inclusion criteria included appropriate allocation of experimental units to treatment groups and blinding of evaluators. Studies were categorized as natural exposure or challenge studies, and the challenge studies were further divided by the viral antigen evaluated, and whether the product was a modified-live (MLV) or inactivated vaccine.

Results

Thirty-one studies with 88 trials were included; however, few trials (n = 9) were natural exposure in beef calves. The natural exposure trials showed reduced risk of BRDC in vaccinated calves. Evaluation of commercially available BHV-1 and MLV BVDV vaccines using challenge models demonstrated reduced morbidity risk; however, trials evaluating MLV BRSV and PI3 vaccines in challenge settings failed to demonstrate evidence of reduced morbidity and mortality risk in vaccinated calves.

Significance

Published literature regarding viral vaccine efficacy in the face of natural challenge was sparse, but provided some information that vaccination mitigated disease risk. The literature did not provide evidence for determining which viral components are necessary to include in a vaccination program to reduce BRDC risk.

Characterization of the 13 cytopathic BVDV strains from mucosal disease cases from a single herd

M.F. Darweesh, *PhD*[1]; **M.K.S. Rajput**, *PhD*[1]; **L.J. Braun**, *MS*[1]; **J.D. Neill**, *PhD*[2]; **J.F. Ridpath**, *PhD*[2]; **C.C.L. Chase**, *DVM, PhD, DACVM*[1]
[1]*Department of Veterinary and Biomedical Sciences, South Dakota State University, Brookings, SD 57007*
[2]*National Animal Disease Center, Agricultural Research Service, United States Department of Agriculture, Ames, IA 50010*

Introduction

Bovine viral diarrhea virus (BVDV) is a positive single-stranded RNA virus belonging to the Pestivirus genus of the Flaviviridae family. BVDV has a wide host range that includes most ruminants. Noncytopathic (ncp) BVDV may establish lifelong persistent infections in calves following infection of the fetus between 40 and 120 days of gestation. Cytopathic (cp) BVDV strains arise from ncp strains via mutations. The most common cp mutations are insertions of RNA derived from either host or a duplication of viral sequences into the region of the genome coding for the NS2/3 protein. Superinfection of a persistently infected animal with a cp virus can give rise to mucosal disease (MD), a condition that is invariably fatal.

Materials and Methods

A herd of 136 bred first-calf heifers was studied. These heifers gave birth to 36 PI animals of which 13 succumbed to mucosal disease. We characterized the ncp and cp viruses isolated from these 13 animals. The viruses were isolated and the polymerase chain reaction was used to characterize the type of insertions in the cp viruses. We then sequenced the virus and compared the sequences of the 13 ncp and cp both to the pair isolated from the calf but also to the isolates from the other calves.

Results

All viruses belonged to the BVDV-2a genotype and were highly similar. All the cp viruses contained an insertion in the NS2/3 coding region consisting of the sequences derived from the transcript encoding a DnaJ protein named Jiv90. Comparison of the inserted DnaJ regions along with the flanking viral sequences in the insertion 3' end of the 13 cp isolates revealed sequence identities ranging from 96% to 99% with common borders. This suggested that 1 animal likely developed a cp virus that then progressively spread to the other 12 animals.