

# Lameness morbidity and association of locomotion score and diagnosis with case outcome in beef cattle in Great Plains feedlots

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## Introduction

This was a dynamic population longitudinal study to determine the association of lameness diagnosis and locomotion score at time of initial lameness diagnosis with case outcome in feedlot cattle, and provide beef cattle feedlot lameness morbidity, mortality, and realizer incidence due to different lameness etiologies.

## Materials and Methods

Cattle health records were maintained for analysis from 6 participating feedlots located in Kansas and Nebraska for a year by trained personnel. The initial study population was 245,494 head of feedlot cattle, with 524,780 animal arrivals and 527,220 animal departures recorded over the 12-month study. Additional treatments and outcome of each individual cattle lameness case were tracked until either the animal was transported for harvest with its entire original pen, realized, or the animal died.

## Results

Lameness morbidity incidence was 1.04 cases per 100 animal-years; lameness mortality was 0.397 cases per 100 animal-years. Cattle locomotion score (LMS; scale of 0 to 3 at time of initial diagnosis) were LMS1 (22% of lameness cases), LMS2 (31%), and LMS3 (22%). Twenty-four percent of the lameness cases were not assigned a locomotion score (NS). Mortality rates were greatest for LMS3 (33.0%) and NS (31.3%), and were least for LMS1 (10.0%) with LMS2 (19.1%) being intermediate ( $P<0.05$ ).

## Significance

This research has contributed to reported lameness morbidity, mortality, and realizer incidence for cattle in US feedyards. These data report the differences in observed case outcomes for lame cattle diagnosed by etiology of lameness and LMS.

# Are all bovine herpesvirus-1 reproductive disease events vaccine-induced?

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## Introduction

Modified-live virus (MLV) bovine herpesvirus 1 (BHV-1) vaccines have been a major part of the program to the prevention of reproductive disease in cattle. However, their use (or misuse) continues to result in major abortion storms. The results of 20 additional cases with reproductive losses are described where the single nucleotide polymorphism (SNP) analysis was done to identify the source.

## Materials and Methods

Case material from 12 BHV-1 reproductive cases from 2013-2015 submitted to the South Dakota State University Animal Disease Research and Diagnostic Laboratory was analyzed. Additionally, 3 BHV-1 cases from Colorado, 2 BHV-1 cases from North Dakota, 2 BHV-1 cases from Wyoming, and 1 BHV-1 case from Wisconsin were analyzed. PCR was performed on the tissues for BHV-1. The PCR products were