

Qualification and Quantification of Bacterial Pathogen Load in Acute Bovine Respiratory Disease Cases

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Introduction

In December 2009 a total 194 steers, bulls, and heifers weighing 400-700 lb (180-320 kg) were purchased at an Arkansas sale barn on a Friday and shipped 12 hours to a northern Kansas feedlot on Saturday. There was no previous history of treatment. The objectives of the study were to evaluate (1) bacterial pathogen isolates in different locations in the respiratory tract, (2) pathogen load in lung tissue as it corresponds to histology scores, and (3) total pathogen load in clinically ill and clinically normal calves.

Materials and Methods

Fifteen calves were identified with signs of acute bovine respiratory disease (BRD) based on a required clinical score of 1-3 on a 0-4 scale and a minimum rectal temperature of 104°F (40°C). An additional five calves with clinical scores of 0 and rectal temperatures < 104°F (40°C) were selected as controls. Cattle were humanely euthanized following collection of antemortem clinical observations and a postmortem examination was conducted. At postmortem, samples for bacteriology and histology were collected from grossly normal and/or consolidated tissue in each lung lobe. Weights were recorded for each type of tissue in each lung lobe. Samples

for bacteriology were also collected from the tonsils and trachea. Quantification of the BRD pathogens per gram in lung were conducted and then converted to total counts based on weight of the tissue from which each quantified sample was collected.

Results

Total colony forming units (CFU) of pathogens in the entire lung for cattle with identified pathogens ranged from 2×10^7 – 2×10^8 CFU for *Pasturella multocida* and 9×10^6 – 9×10^8 CFU for *Mannheimia haemolytica*. Total visual estimated percent consolidation ranged from 0.0% to 45.0% of the total lung. Histopathological observations were scored (0-4) for each tissue sample, and then correlated to bacterial counts.

Significance

The pathogen load in acute bovine respiratory disease has not been previously determined. The total pathogen CFU in the lung is worth consideration when discussing whether encountered resistance in clinical cases is due to a spontaneous mutation in that animal during therapy or due to selection of a resistant pathogen clone already in the animal as a subpopulation, or the entire pathogen population.