

Effects of transportation to and commingling at an auction market on the upper and lower respiratory tract bacterial communities of recently weaned calves

Christina Stroebe¹, DVM; Trevor Alexander,² PhD; Edouard Timsit,¹ DVM, PhD, DECBHM

¹Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, T2N 4N1, Canada

²Agriculture and Agri-Food Canada, Lethbridge, AB, T1J 4B1, Canada

Introduction

Commingling at auction markets is considered a major predisposing factor for bovine respiratory disease (BRD) in beef cattle. However, the extent to which commingling may affect the bacterial communities of the respiratory airways is largely unknown. The objective of this study was to evaluate the effects of transportation to and commingling at an auction market on the upper and lower respiratory tract microbiotas of recently weaned beef calves.

Materials and Methods

Two replicates of 30 angus-cross beef calves were studied (n=60). Calves originated from 2 ranches and were placed at 2 different feedlots. At ranches, calves were randomly allocated to 2 groups and were either transported to and commingled at an auction market for 24 hrs before being placed in the feedlot (AUCT, n=30) or were transported directly to the feedlot (RANC, n=30). Twelve hrs after arrival of AUCT calves at the feedlot (d2), calves from both groups were vaccinated against major respiratory viruses and treated with an injectable antimicrobial (tildipirosin, 1.8 mg/lb [4 mg/kg]). Deep nasopharyngeal swab (DNS) and transtracheal aspiration were collected before leaving the ranch (d0) and 12 hrs after arrival at the feedlot (d2). DNS sampling only was then repeated on d9 and d30. DNA was extracted from each sample and the V4 region of the 16S rRNA gene was sequenced using a MiSeq. α -diversity (intra-sample diversity) was calculated using Chao1 and Shannon diversity index; α -diversity between groups and among time points was compared using a Wilcoxon Rank Sum test. Effects of time (d0, d2,

d9, and d30), treatment (AUCT vs RANC) and replicate on the bacterial communities were investigated using permutational multivariate analyses of variance (PERMANOVA).

Results

α -diversity analysis did not reveal differences between AUCT and RANC ($P>0.05$) at any time points or at both the upper and lower respiratory tract level. However, a significant decrease in richness (Chao1 $P<0.01$) and evenness (Shannon; $P<0.01$) was observed at d9 (i.e. after antimicrobial treatment) in both replicates. Concerning beta diversity, no differences were observed between AUCT and RANC based on PERMANOVA ($P=0.26$). However, time ($R^2 = 0.12$; $P<0.01$) and replicate ($R^2 = 0.06$; $P<0.01$) had a significant effect on the structure of the bacterial communities. A significant increase in the relative abundance of *Mycoplasma bovis* was observed at d9 and d30 in replicate 1 whereas an increase in the relative abundance of *Mycoplasma dispar* and *Moraxella bovis* was observed at d9 and d30, respectively, in replicate 2.

Significance

Transportation to and commingling at an auction market for 24 hrs did not influence the diversity and composition of the upper and lower respiratory tract bacterial communities. However, time and replicate had a major impact on the airways bacterial communities, with a significant decrease in bacterial diversity after entrance at the feedlot and treatment with a parenteral antibiotic (i.e. d9).