

Impact of the host transcriptome on bovine respiratory disease treatment during backgrounding

M. M. Green,¹ BS; A. R. Woolums,² DVM, PhD, DACVIM, DACVM; B. B. Karisch,³ PhD; K. M. Harvey,⁴ PhD; M. A. Scott,⁵ DVM, PhD; S. F. Capik,⁶ DVM, PhD

¹Department of Agricultural Sciences, West Texas A&M University, Canyon, TX 79016

²Department of Pathobiology and Population Medicine, Mississippi State University, Mississippi State, MS 39762

³Department of Animal and Dairy Sciences, Mississippi State University, Mississippi State, MS 39762

⁴Prairie Research Unit, Mississippi State University, Prairie, MS 39756

⁵Veterinary Education, Research, and Outreach Center, Texas A&M University and West Texas A&M University, Canyon, TX 79015

⁶Texas A&M AgriLife Research, Texas A&M University System, Amarillo, TX 79106 and Department of Veterinary Pathobiology, TAMU CVMBS, College Station, TX 77843

Introduction

Bovine respiratory disease (BRD) continues to be problematic across the beef cattle industry. Marketing strategies made prior to backgrounding may shift the initial treatment for BRD into a different phase of production, and the importance of host gene expression on BRD incidence is poorly understood. Whole blood transcriptomes measured on arrival could inform our ability to better manage these cattle and predict BRD risk. Our objective was to compare host transcriptomes as measured on arrival at a backgrounding facility on the probability of being treated for BRD during the following 45 days on feed.

Materials and methods

Whole blood was collected on arrival from 81 beef cross steers (mean: 519 lbs) observed for signs of clinical BRD over a 45-day backgrounding period. Samples from cattle treated for clinical BRD after arrival (n = 32) and randomly selected clinically healthy animals (n = 12) were utilized. Cattle were further categorized if they were weaned at the farm in Mississippi for 3 days prior to shipment directly to the backgrounding operation in Texas (Direct; BRD n = 20, Healthy n = 6) or were weaned and shipped to an auction market, then an order-buyer for 3 days prior to shipment to Texas (Auction; BRD n = 12, Healthy n = 6). Isolated mRNA from cattle was sequenced (NovaSeq 6000; ~35M reads/sample), and reads were processed through ARS-UCD1.2 reference-guided assembly (HISAT2/Stringtie). Differentially expressed genes (DEGs) were identified with edgeR glmLRT (FDR < 0.05). Functional enrichment analyses for biological functions were performed with WebGestalt (FDR < 0.05).

Results

A profound difference in DEGs (n = 2,961) was identified between Auction cattle compared to Direct cattle, regardless of BRD development; DEGs encoded for antiviral defense (increased in Auction), cell growth regulation (decreased in Auction), and inflammatory mediation (decreased in Auction). Nine and 4 DEGs were identified between BRD and Healthy cohorts in the Auction and Direct groups, respectively; DEGs between disease cohorts in the Auction group encoded for collagen synthesis, platelet aggregation, and lymphoid-nonlymphoid immunoregulation (all increased in Healthy).

Conclusions

Our work demonstrates the clear influence marketing has on host expression and identified increased platelet activation and collagen formation is associated in Auction cattle that remain clinically healthy. These findings define and corroborate genes and mechanisms which may predict BRD risk at arrival.

