Whole blood RNA-Seq analysis of stocker calves reveals insights into BRD

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Introduction

Bovine respiratory disease (BRD) is the leading cause of morbidity and mortality in stocker cattle. It is difficult to predict which cattle will develop BRD. Improved prediction could facilitate more responsible and rational use of antimicrobials and vaccines to limit BRD. We hypothesize that altered transcriptional profiles in the blood of stocker calves on arrival represent regulatory pathways including biomarkers useful to improve prediction of BRD risk.

Materials and Methods

Blood was collected from bull and steer calves (n=80, mean=206 kg) into Tempus tubes at arrival. Animals were monitored for signs of BRD via the DART system. Cattle with BRD (n=6), and cattle without BRD over the 84-day study (n=5) were selected for blood RNA sequencing. Sequencing reads (80M PE/sample) were quality filtered and aligned to the bovine reference genome assembly ARS-UCD1.2. False discovery rate (FDR) adjusted p-values of 0.10 were applied to identify differentially expressed genes (DEGs), utilizing edgeR. WebGestalt and String v11.0 were used to identify biological functions, pathways, networks, and interactions represented by DEGs.

Results

Fifty-two DEGs were identified; thirty-six downregulated and sixteen upregulated in diseased calves, representing processes related to inflammatory mediation, metabolism, and stress regulation. Pathway analysis revealed upregulation of inflammatory resolution pathways in healthy calves and dysregulated metabolic pathways in diseased calves.

Significance

The identification of DEGs in whole blood at arrival revealed a clear distinction between calves diagnosed with BRD and those that remained healthy. Our analysis suggests that one or more of these genes could serve as biomarkers for improved BRD prediction.