

Genetic comparison of Florida beef cows with and without ovarian follicular dysplasia

J. Gard, DVM, PhD, DACT¹; **J. Roberts**, DVM, DACVP²; **F. Biase**, PhD³; **M. Mansour**, DVM, PhD²; **J. Wenzel**, DVM, PhD, DACT, DACVPM¹; **M. Edmondson**, DVM, MS, DACT¹; **O. Rae**, DVM, MPVM⁴; **T. Braden**, PhD²

¹Department of Veterinary Clinical Services, Auburn University, College of Veterinary Medicine (AUCVM), Auburn, AL 36849

²Department of Anatomy, Physiology and Pharmacology, AUCVM, Auburn, AL 36849

³Department of Animal Science, College of Agriculture, Auburn University, Auburn AL 36849

⁴Department of Large Animal Clinical Sciences, College of Veterinary Medicine, University of Florida, Gainesville, FL 32611

Introduction

Beef operations in Florida and other areas of the southeastern United States have a yearly calving percentage of less than 80%. Studies commissioned by the Florida Cattleman's Association in 2007 and 2016 found ovarian follicular dysplasia (OFD) as a primary cause of infertility in Florida beef cows. The later stages of OFD can be detected via ultrasound examination of the ovaries but earlier stages cannot be reliably detected utilizing ultrasound. The objective of this study was to examine the variation in ovarian gene expression between OFD cows and non-OFD cows. Identification of specific genetic profiles could aid in the development of an ante-mortem molecular test for early detection of OFD.

Materials and Methods

The ovaries from 66 cows were harvested at slaughter from four herds that were located in south central Florida. These herds were determined to have a high incidence of OFD. The ovaries were histologically examined to determine their OFD status and five OFD cows and five non-OFD cows were selected for ovarian cortex transcriptome analysis. RNA-Seq was performed at Center for Comparative Genomics and Translational Research at the Hudson Alpha Institute for Biotechnology.

Results

Of the cows sampled, 57.5% (38/66) had OFD identified via histological examination. Infertility from other disease was diagnosed in 12% (8/66) and 15.2% (10/66) were

determined to be normal. The distribution of OFD for the 38 affected females was 44.7% (17/38) Grade I, 39.5% (15/38) Grade II, 10.5% (4/38) Grade III, and 5.3% (2/38) Grade IV. Approximately 13,100 genes were commonly expressed in ten ovaries. Forty-four genes had significant variable expression between the OFD and non-OFD cows. Of these genes, 38 were characterized in at least one species of animal but six genes were non-annotated. Ten genes were over expressed and 34 were under expressed. One of the up-regulated genes (FAM189A2) is also reported to be over expressed in gonadal dysgenesis of humans. One of the down-regulated genes (TCF4) is associated with polycystic ovary syndrome in humans. Of the annotated genes, 34.2% (13/38) have been implicated in cancer pathogenesis (ATP4B, CCL21, CDH5, CHGA, CLMN, ECEL, FAM43A, FLI1, FLT, KAT2A, MECAM, NISCH, TCF4), 23.7% (9/38) were found to be associated with vascular endothelial function (ASB5, CD300LG, CDH5, ECE2, FLT4, PECAM, CDC42EP1, CLEC14A, KDR), and 10.5% (4/38) were involved in testicular function (BCL6B, CLGN, PECAM, and SOX18). Expression profiles of 2/6 non-annotated genes showed good potential as markers for OFD.

Significance

The OFD cows had significant variations in ovarian gene expression that showed promise for investigation into the pathogenesis of OFD. These findings may aid in the discovery a genetic marker for early detection of sub-fertile OFD females.