Evaluation of diagnostics for ante-mortem testing of ovarian follicular dysplasia (OFD) in cattle

Julie Gard, a John F Roberts, b Mahmoud Mansour, b Misty Edmondson, a Humberto Nobre, a Timothy Braden b

aDepartment of Clinical Sciences and bDepartment of Anatomy, Physiology and Pharmacology, College of Veterinary Medicine, Auburn University, Auburn, AL

The objectives of this study were to more thoroughly evaluate the presence of ovarian follicular dysplasia (OFD) in Florida herds, assess characteristics of OFD positive cattle through ultrasound examination, endocrine profiles, and RNA analysis in order to develop an ante-mortem test for reliable identification of OFD in cattle. The RNA sequencing and gene analysis was performed by Hudson-Alpha Institute for Biotechnology. Four hundred and fifty cull cows selected by private veterinarians representing five Florida ranches received reproductive tract palpation, ultrasound examination and blood collection. Based on the ultrasound findings, 66 total cows (10-16 per ranch) were followed to slaughter the following day for collection of reproductive tracts, and ovarian sampling. Five non-OFD and five OFD were selected for RNA sequencing. Ovaries with OFD were graded histologically I to IV and follicular morphometrics were recorded. Circulating serum levels of progesterone (P4) and anti-Mullerian hormone (AMH) were quantified in 200 cows. Ovarian follicular dysplasia was diagnosed in 57.6% of cows followed to slaughter. Infertility from other diseases was diagnosed in 12.1% of these cows and 30.3% were determined to be normal. The distribution of OFD grades was; Grade I: 44.7%, Grade II: 39.5%, Grade III: 10.5% and Grade IV: 5.3% of affected females, respectively. Increased hyperechogenicity and decreased number of fluid filled follicles were present on ultrasound in higher grades of OFD. There was no defined relationship between circulating levels of AMH and P4 and OFD. Genomic analysis indicated that 1085 genes are differentially expressed in ovarian tissue of OFD versus non-OFD animals with increased expression of 628 genes and decreased expression of 457 genes, respectively. Cluster analyses of these differentially expressed genes identified relationships with processes such as cell-cell adhesion, collagen regulation, steroid hormone regulation, and vascular support. Additional genomic analyses indicated that, of 706 microRNAs (small RNAs), 28 were differentially regulated in Non-OFD and OFD cattle with 23 increased in expression and five decreased in expression. Additionally, initial analyses of these microRNAs show relationships to various cancers. Single analysis of P4 and AMH in serum did not serve for ante-mortem diagnosis of OFD. However, variation in genetics between OFD positive and OFD negative cattle has led to multiple targets for continued bioinformatics studies.

Keywords: Ovarian follicular dysplasia, infertility, bovine