Animal Reproduction

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Embriology, developmental biology and physiology of reproduction

Transcriptomic comparison between bovine sires with differing field fertility.

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Resumo

The objective of this study was to determine the differentially abundant genes between sires of known fertility, both in the conceptus and the uterus. The sires used have previously been reported to have drastically different levels of field fertility; however, they had passed all normal standards for frozen thawed semen. Bos indicus beef heifers (n=45) were subjected to estrous synchronization and embryo transfer on day 7 with IVP embryos from one of two sires (High Fertility and Low Fertility Sire) and pregnancies were later confirmed at slaughter. Samples were collected from the trophectoderm and uterus on day 25 and 36 of gestation to attain samples for RNA sequencing. Total RNA was isolated from tissue samples using the RNeasy kit (QIAGEN; Hilden, Germany) per manufacturer's instructions. The RNA sequencing was conducted using an Illumina platform. Sequences were aligned to the reference genome ARS-UCD 1.2. Differentially expressed genes (DEGs) between sires and by tissue were determined using edge-R package from R. The false discovery rate used was 0.05. On day 25 15,755 genes were identified in the trophectoderm between the two sires. Of those, 11 genes were downregulated in the Low Fertility Sire compared to the High Fertility Sire and an additional 6 genes were upregulated in the high fertility sire. Additionally, 16,044 genes were identified within the caruncle where the Low Fertility Sire resulted in 2 downregulated genes and the High Fertility Sire resulted in no upregulated genes. On day 36 17,080 genes were observed in the trophectoderm sample where the Low fertility Sire resulted in 23 downregulated genes in comparison with the High Fertility Sire that resulted in 4 upregulated genes, furthermore 17,843 genes were observed in the caruncle sample resulting in 8 downregulated genes for the Low Fertility Sire whereas 21 genes were upregulated for the High Fertility Sire. Gene ontology analysis reported differentially expressed genes in the High Fertility Sire compared to Low Fertility Sire were associated with hematology, immunology and reproduction. Of particular interest was the transferrin gene (TF) that is known to be responsible for the transport of iron from sites of absorption and heme degradation to those of storage and utilization, but it is also known for its role in stimulating cell proliferation. Additionally, the spermatogenesis associated 22 gene responsible for gamete generation, homologous chromosome pairing at meiosis, meiotic DNA repair synthesis was also found downregulated in between sires. These data suggests that other underlying factors are at work regarding conception rate and current methods are insufficient for sire selection and fertility testing. In conclusion, different paternal genome results in differences at both trophectoderm and uterus level in bos indicus beef cows. This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2019-67015-28998 from USDA NIFA.