Application of integrative genomics and systems biology to conventional and in vitro reproductive traits in cattle

Assisted reproductive technologies (ARTs) have a strong impact on breeding especially when coupled with genomic selection (GS). The routine implementation of in vitro production (IVP) and GS of embryos before embryo transfer (ET) in breeding companies is not yet possible. Improvement of oocyte donor and embryo recipient quality is needed to make realistic a commercialization of these procedures in the near future. A better understanding of both biological mechanisms and molecular markers associated to IVPET related traits is necessary to improve the prediction of donor and recipient cow quality for IVP procedures. The huge amount of data generated from high throughput technologies has a tremendous impact in the search for biomarkers of complex traits. This paper reviews integrative genomics and systems biology approaches as applied to both Bos indicus and Bos taurus cattle reproduction by both conventional and ARTs such as OPU-IVP. The integration of systems biology information across different biological layers generates a complete view of the different molecular networks that control complex traits and can provide a strong contribution to the understanding of traits related to ARTs.
better understand complex traits and improve genetic gains. In this study, we performed a genomewide association study (GWAS) to identify genetic variants associated with reproductive traits in Nelore beef cattle. Heifer pregnancy (HP) was recorded for 1,267 genotyped animals distributed in 12 contemporary groups (CG) with an average pregnancy rate of 0.35 (+/- 0.01). Disregarding one of these CG, the number of antral follicles (NF) was also collected for 937 of these animals, with an average of 11.53 (+/- 4.43). The animals were organized in CG: 12 and 11 for HP and NF, respectively. Genes in linkage disequilibrium (LD) with the associated variants can be considered in a functional enrichment analysis to identify biological mechanisms involved in fertility. Medical Subject Headings (MeSH) were detected using the MESHR package, allowing the extraction of broad meanings from the gene lists provided by the GWAS. The estimated heritability for HP was 0.28 +/- 0.07 and for NF was 0.49 +/- 0.09, with the genomic correlation being -0.21 +/- 0.29. The average LD between adjacent markers was 0.23 +/- 0.01, and GWAS identified genomic windows that accounted for > 1% of total genetic variance on chromosomes 5, 14, and 18 for HP and on chromosomes 2, 8, 11, 14, 15, 16, and 22 for NF. The MeSH enrichment analyses revealed significant (P <0.05) terms associated with HP-"Munc18 Proteins," "Fucose," and "Hemoglobins"-and with NF-"Cathepsin B," "Receptors, Neuropeptide," and "Palmitic Acid." This is the first study in Nelore cattle introducing the concept of MeSH analysis. The genomic analyses contributed to a better understanding of the genetic control of the reproductive traits HP and NF and provide new selection strategies to improve beef production.

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In vitro production of bovine embryos: cumulus/granulosa cell gene expression patterns point to early atresia as beneficial for oocyte competence

In vitro production (IW) of bovine embryos has become widespread technology implemented in cattle breeding and production. Here, we review novel data on cumulus/granulosa cell gene expression, as determined by RNAseq on cellular material from pooled follicular fluids at the single animal level, and relate these finding to previous data on oocyte developmental competence and ultrastructure. The cumulus/granulosa cell gene expression patterns indicate that early follicular atresia is associated with increased blastocyst yield and this hypothesis is supported by previous data on oocyte competence and ultrastructure.

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