

Abstract

Deregulation of oxidative phosphorylation pathways in embryos derived *in vitro* from prepubertal and pubertal heifers based on whole-transcriptome sequencing

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Mitochondria are essential for the oocyte maturation and embryonic development by ATP production through oxidative phosphorylation. The transcriptomic profile of embryos could be used as a predictor for embryo's individual developmental competence. The aim of the study was to characterise and compare transcriptomic profile of blastocysts derived from prepubertal and pubertal heifers. Bovine cumulus-oocyte complexes were obtained by ovum pick-up method from prepubertal and pubertal heifers. After 24 hours, the mature cumulus-oocyte complexes (COCs) were fertilized *in vitro* using commercial bull semen. At 24 hours after fertilization, the embryos were transferred to culture medium and cultured for another 7 days to the blastocyst stage. Total RNA was isolated from two groups of blastocysts and RNA-seq was performed. Gene Ontology (GO) analysis was performed by DAVID (Database for Annotation, Visualization and Integrated Discovery).

A higher average blastocyst rate was obtained in the pubertal group than in the pre-pubertal group ($p < 0.05$). There were no differences in the quality of the obtained blastocysts between the two examined groups ($p > 0.05$). We identified 436 differentially expressed genes (DEGs) between embryos derived from prepubertal and pubertal heifers. Kyoto Encyclopedia of Genes (KEGG) pathway analysis suggested that the genes involved in mitochondrial function including oxidative phosphorylation were

different in two examined groups. Differences of the level of expression of genes associated with mitochondrial function were found: ATP synthases (ATP5MF-ATP synthase membrane subunit f, ATP5PD- ATP synthase peripheral stalk subunit d, ATP12A- ATPase H⁺/K⁺ transporting non-gastric alpha2 subunit), NADH dehydrogenases (NDUFS3- NADH:ubiquinone oxidoreductase subunit core subunit S3, NDUFA13- NADH:ubiquinone oxidoreductase subunit A13 , NDUFA3- NADH:ubiquinone oxidoreductase subunit A3), cytochrome c oxidase (COX17), cytochrome c somatic (CYCS) and ubiquinol cytochrome c reductase core protein 1 (UQCRC1).

This study indicated that genes involved in OXPHOS could be predictive indicators of embryo quality, developmental competence and implantation ability.