

Gene Expression Profile of Oocytes Using Microarray and Single Nucleotide Polymorphisms of Stat3 and Odc1 Genes in Sperms Linked With Their Quality in Holstein-Friesian

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Abstract

Identification of molecular fingerprints of gametes quality could be used as a foundation for finding markers associated with fertility of dairy cattle. Therefore, the current investigation aimed to identify differential gene expression profile in oocytes collected from cyclic healthy heifers (n = 16) of Holstein breed with estimated breeding value of fertility. The animals were slaughtered at day 0 or day 12 of the oestrous cycle. The recovered oocytes from high-fertile animals (H-EBV-F >100; n=8) were compared with low-fertile group (L-EBV-F <100; n=8) using cDNA microarray. Additionally, SNPs were analysed for two candidate genes (STAT3 and ODC1) in relation with sperm quality traits. The results of this study clearly showed link of candidate genes with fertility and progesterone profile during oestrous cycle. For example, gene expression profile of STAT3 was increased in oocytes collected from H-EBV-F animals at day 0 and 12 of oestrous cycle. While ODC1 gene was up-regulated at day 12 and down-regulated at day 0 in H-EBV-F compared to L-EBV-F oocytes. Moreover, association study showed that SNP polymorphisms of STAT3 and ODC1 were linked ($p < 0.05$) with sperm quality traits. Therefore, it could be concluded that ODC1 and STAT3 could be considered candidate genes that are connected with Holstein cows fertility genetic merit of the associated with semen quality of sires.

Key words: Developmental potential, transcriptome profile, SNP, oocyte, sperm.