

Gene expression profiling of Bovine Ovarian Follicular Selection

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ABSTRACT

Lack of, or abnormal, ovarian follicular development is a major factor associated with impaired fertility in mammals. However, development of new treatments is limited by our poor understanding of ovarian follicular development. Understanding the mechanisms by which a cohort of follicles is recruited and a single follicle is selected for further development to a dominant follicle is the key to understanding pre-ovulatory follicular development. The objectives of this study are to identify changes in gene expression profiles during the selection stage of bovine follicular waves.

Follicles of different sizes (8 mm to 12 mm) were collected and intrafollicular concentrations of progesterone, estradiol and androstenedione were measured. Gene expression profiles were obtained using bovine cDNA microarrays.

Of the 17,692 probes on the arrays, 606 unique genes and 32 sequences not matching any known genes were identified as differentially expressed with a cut off false discovery rate (FDR) of 0.05. Seventeen gene expression profiles were confirmed using quantitative RT-PCR.

Five main expression profiles were discovered, in which gene expression patterns change according to follicle size. Genes involved in several biological processes were also identified as significantly over-represented, such as genes involved in immune function or regulation of cell cycle. Annotation of the cellular location of differentially expressed gene products identified the ribonucleoprotein complex and the extracellular matrix as over represented. More than one hundred genes were found to have a strong positive or negative association with LHR.

These data strongly support the essential role of LH/LHR pathway on follicular selection, the important function of the extracellular matrix and the associated cell receptors, and reveal a potentially important role for the immune system.