Large-Scale Transcriptional Analysis of Bovine Oocytes Derived from Growth and Dominance Phases of Follicular Development

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Introduction

Blastocyst rate of oocytes derived from growth/stagnation (G/S) stage was reported to be higher than from dominance/regression (D/R) stage. However, so far the intrinsic properties of these oocytes in relation to the gene expression patterns have not been investigated.

Therefore, the objective of this study was to compare the transcriptional activity of bovine oocytes derived from small follicles (3-5 mm) at growth and dominance phases of first follicular wave using custom cDNA microarray.

Materials and Methods
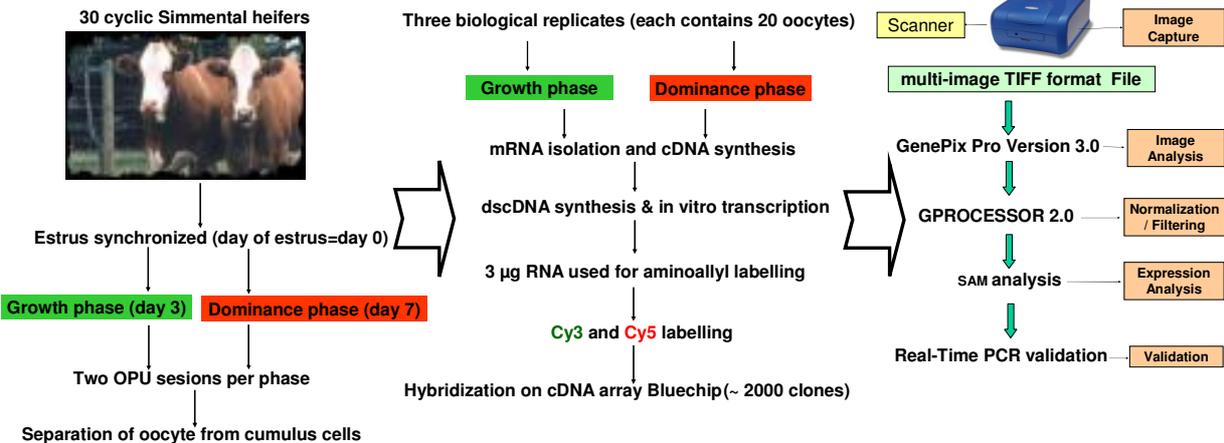
Results

Microarray data analysis (SAM) revealed a total of 51 differentially regulated transcripts, which were functionally classified according to the Gene Ontology Consortium classifications (Fig. 1). A heat map (Fig. 2A) was drawn to show the overall expression pattern and the hierarchical clustering (Fig. 2B) was used to predict the functional category of the novel transcripts. Five genes were validated by real-time PCR (Fig. 3)
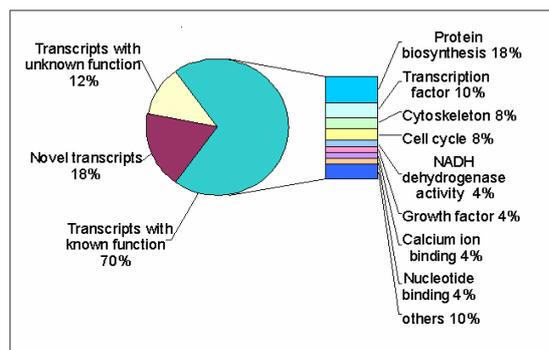
Fig. 1. Oocyte differentially expressed genes were classified based on the Gene Ontology Consortium classifications (http://www.geneontology.org).
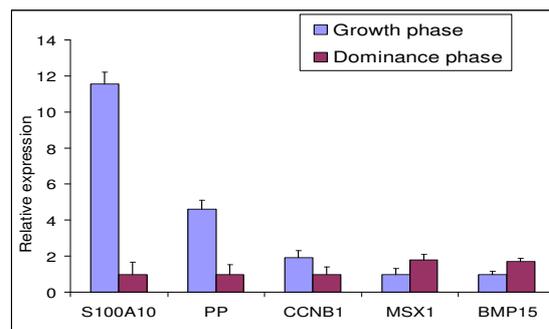
Fig. 3. Quantitative real-time PCR validation of 5 differentially expressed genes in bovine oocytes recovered at growth phase (day 3) vs. dominance phase (day 7).
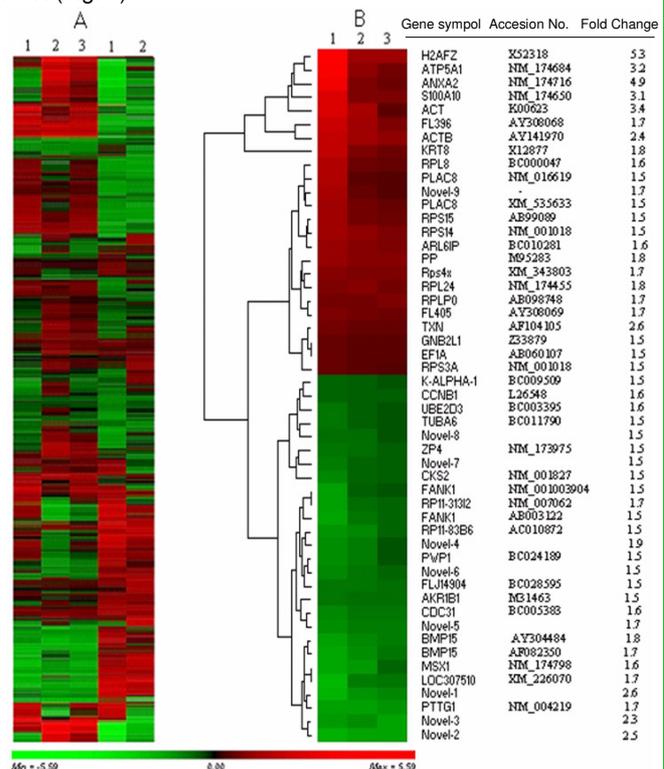
Fig. 2. Heat map of 700 normalized $\log_2$ transformed ratios (A) and hierarchical clustering of 51 differentially regulated genes (B). The red blocks represent up-regulated and green ones represent down-regulated genes.

Conclusion

Our results showed differences in transcriptional activity of oocytes derived from different stages of follicular development, which may explain their reported differences in developmental competence.