

Abstract

The antral follicle provides a specialized microenvironment or niche, which is necessary for production of high quality oocyte. The developmental competence of bovine oocyte is influenced by the follicle size. Oocytes originated from medium or larger follicles (≥ 6 mm) have greater developmental competence (ability to develop to the blastocyst stage). The changes in cytoplasmic factors, for example mRNAs, could explain differences in oocyte developmental potential. Using Bovine Oligonucleotide microarrays the differences in gene expression profiles of oocytes at germinal vesicle and MII stages from medium (MF, 6-10 mm) or small (SF, 2-5 mm) follicles were characterized. The aim was to find differences between oocytes diverse developmental competence. The expression fold change between the two experimental groups was in 61 genes. Subsets of 15 differentially expressed genes were validated by quantitative RT-PCR. Before maturation, significant differences were confirmed at the level of *ATP5C1*, *MAP3K13*, *MTRF1L*, *TAF1A* and *UBL5*. Subpopulations of oocytes were classified according to atresia of cumulus cells and follicle size. We determined the level of 12 individual transcripts after maturation. *ATP5F1* remained stable in all experimental groups of oocytes. The level of *BRD7* transcript remained stable in SF oocyte independent of atresia in the cumulus cells. The level of *TAF1A* transcript decreased in MF oocytes independent sign of atresia in the cumulus. Other analyzed genes show substantial drop in the level of individual transcripts in MF and SF oocytes after maturation. Next, we characterized expression profile of 6 selected genes throughout early embryonic development. The relative abundance of *MLF1IP* was the highest in MII and progressively decreased during further early embryonic development. The level of transcript is gradually degraded or deadenylated and we hypothesized that maternal transcript is essential for development to late 8-cell embryo. Expression pattern of *ATP5C1*, *ATP5F1*, *GATA3*, *PRPF18* and *MTRF1L* from embryonic genome was confirmed at late 8-cell stage. Our results suggest that small changes in the RNA transcription profiles of many genes are necessary for production of high quality oocyte.

Keywords

bovine oocyte, maturation, quantitative reverse transcription polymerase chain reaction, size of antral follicle, developmental competence