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Maternal mRNA profile analysis in the mouse ova by cDNA microarray

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Maternal gene expression is important biological process for the oocyte maturation and early cleavage. To gain insights into oocyte maturation and early embryo development, we used microarray to compare gene expression profiles in germinal vesicle (GV), metaphase II (MII) stage oocytes, zygotes, 2-cell and 4-cell stage embryos. Oocytes and fertilized embryos were collected from superovulated C57BL/6J female mice. Messenger RNAs from 50 ova at each stages were extracted by means of the Dynabeads mRNA Direct Kit (Dynal, Oslo, Norway), and then linearly amplified for two rounds using the RiboAmp HS RNA Amplification Kit (Arcturus Bioscience, Inc., Mountain View, CA, USA). A set of cRNA targets from the embryos was assembled into a hybridization reaction on the Applied Biosystems 1700 chemiluminescent microarray analyzer (Jung Hwa Scientific Co., Ltd., Seoul, Korea). Each set was repeated four times. All of the correlation coefficients were above 0.95 for experiment replications. Differences in microarray intensities were normalized and grouped by using the Avadis Prophetic 3.3 version, and categories are based on the PANTHER classification system. According to the cDNA microarray data, we additionally categorized genes into metabolism, electron transport, intracellular protein traffic, protein metabolism and modification, and signal transduction and compared them in each stage. Further, genes that increased their expression levels in GV compared to MII stage were grouped in Cluster 1, and genes that increased MII compared to GV stage were grouped in Cluster 2. The transcription of Cluster 2 were continuously decreased from the 4-cell to 8-cell stage. In addition we identified 187 signal transduction genes which were increased in MII stage oocytes. The results indicate that identification of large number of maternal genes is a first step toward analysis of the complex gene regulatory networks during oocyte maturation and early cleavage in mammals.

Keywords: **Maternal mRNA,. oocyte maturation, Microarray**