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Differences in gene expression profiles in mouse embryos developing in vitro following fertilization and parthenogenetic activation

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Following parthenogenetic activation, in the absence of a male contribution, oocytes progress into early gestation. To gain insight into the role of the paternal genome during pre-implantation development, we used microarray to compare gene expression profiles in pre-implantation embryos following fertilization and parthenogenetic activation. Fertilized embryos and oocytes were collected from superovulated C57BL/6J female mice. The oocytes were activated with 50μM calcium ionophore A23187 for 5 min. After 5 h of culture in M16 medium with 7.5 μg/ml cytochalasin B, oocytes with one polar body and two pronuclei were used in this experiment. The activated oocytes and zygotes were cultured in M16 to the blatocyst stage. Messenger RNAs from 50 embryos 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 three times. All of the correlation coefficients were above 0.9 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 transcription- and developmental process-related genes and compared them in both fertilized and parthenogenetically activated blastocysts. The results indicate that parthenotes during early may lack or over express genes related to transcription and development processes which possibly result in fetal lethality. Further studies are required to determine whether aberrant gene expression in parthenotes is due to lack of paternal contribution.

Keywords: ***Parthenogenesis, Gene expression, Microarray***