# Transcriptome analysis in blastocyst hatching by cDNA microarray

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摘要

**Abstract**

BACKGROUND: Hatching is an important process for early embryo development, differentiation and implantation. However, little is known about its regulatory mechanisms. By integrating the technologies of RNA amplification and cDNA microarrays, it has become possible to study the gene expression profile at this critical stage. METHODS: Pre-hatched and hatched ICR mouse embryos (25 blastocysts in each group were used in the triplicate experiments) were collected for RNA extraction, amplification, and microarray analysis (the mouse cDNA microarray, 6144 genes, including expressed sequence tags). RESULTS: According to cDNA microarray data, we have identified 85 genes that were expressed at a higher level in hatched blastocyst than in pre-hatched blastocysts. In this study, 47 hatching-related candidate genes were verified via re-sequencing. Some of these genes have been selected and confirmed by real-time quantitative RT－PCR. These hatching-specific genes were also expressed at a lower level in the delayed growth embryos (morula or blastocyst without hatching at day 6 post hCG). These genes included: cell adhesion and migration molecules [E-cadherin, neuronal cell adhesion molecule (NCAM), lectin, galactose binding, soluble 7 (Lgals7), vanin 3 and biglycan], epigenetic regulators (Dnmt1, and SIN3 yeast homolog A), stress response regulators (heme oxygenase 1) and immunoresponse regulators [interleukin (IL)-2-inducible T-cell kinase, IL-4R, interferon- receptor 2, and neurotrophin]. The immunostaining of E-cadherin and NCAM showed strong and specific localization in hatched blastocyst. CONCLUSIONS: This work provides important information for studying the mechanisms of blastocyst hatching and implantation. These hatching-specific genes may have potential as new drug targets for controlling fertility