



tags, ESTs) with colorimetric detection system was used to identify differentially expressed genes between pre-hatched and hatched blastocyst. According to cDNA microarray analysis, we have identified 1193 genes were detectable during blastocyst stage, 13 genes whose expression was higher in pre-hatched blastocyst, and 85 genes were higher at hatching stage. The differentially expressed genes were further grouped into categories by their putative functions, including: cell adhesion molecules, hormones/cytokines, immuno-response related factors, cytoskeleton/extracellular matrix proteins and related enzymes, and some expressed sequence tags (ESTs). This work adds to our understanding in the mechanisms of blastocyst hatching and provides the information for studying the cross-talk of blastocyst and endometrium by reporting the global gene expression profiles of blastocyst hatching process.