Comparative Analysis of Gene Expression Profiling of Mouse Morula and Blastocyst stage Embryos Revealed Several Candidate Genes Associated with Early Embryogenesis

Young Jin Lee[*], Ju Hyun Kim[*], Se-Ra Kim[*], Bo Mee Chung[*], Beom Sue Kim[*],
Seok Ho Hong[**], Ji Hyung Chae[*], Chul Geun Kim[*]
[*]Department of Life Science, Hanyang University,
[**]Department of Obstetrics and Gynecology, Asan Medical Center

There are many changes at the molecular level during the morula-to-blastocyst transition, in which one of the first cellular differentiation events occurs. As an effort to understand the fundamental mechanisms for the pluripotency and differentiation of early mouse embryos, large-scale gene expression profiling was performed on morula and blastocyst stage embryos of mouse. The combination of nylon arrays (containing 5,354 mouse EST clones, Research Genetics) and P33 probes made it possible to produce expression profiles with tiny amounts of RNA. We have carried out four hybridization experiments with radio-labeled cDNAs for ~300 blastocysts and morulas, respectively. When genes with more than 2-fold expression difference between morula and blastocyst were counted to be significant, Student's t-test identified 17 and 127 genes as ones up-regulated in morula and blastocyst, respectively, at 5% confidence level. To remove false-positive clones, we performed further study using mouse reference total RNA (Clontech) as well as various data mining algorisms. Four and twenty clones were identified as preferentially expressed in morula and blastocyst, respectively, when the signal intensity was normalized by subtracting the background signal, whereas 21 and 34 clones were identified when clones showing higher intensity over reference RNA were compared between morula and blastocyst stage embryos. Interestingly, 7 clones among them were commonly detected in both methods. It is suggested that they are associated with early embryogenesis, although none of them expressed solely in morula or blastocyst stage embryos as revealed by RT-PCR.