

Identification of Differentially Expressed Genes in Human Fetal Astrocytes

**Hye-Myung Yoo, Hyun-Sook Park, Hyun-Chul Cho,
Choon-Myung Koh and Joo-Young Park**

Department of Microbiology, Wonju College of Medicine, Yonsei University, Wonju, Korea

Astrocytes are ubiquitous in the brain and have multiple functions. It is becoming clear that they play an important role in monitoring the neuro-microenvironment, information processing, and signaling in the CNS in normal conditions and respond to CNS injuries.

To identify genes which could participate in neurogenesis, we used the differential display RT-PCR (DDRT-PCR) method. Human fetal astrocytes were cultured and total RNA was isolated at intervals of 5 days for 50 days. Using 24 primer combinations, we have identified a set of 19 candidate cDNAs

deriving from 29 excised DDRT bands. DNA sequencing revealed that 17 genes are described genes (*SPARC*, thyroid receptor interactor gene etc.). We found 6 of 17 genes were expressed increasingly and 11 genes were expressed decreasingly according to their culture stages. Temporal expression of sequenced genes in this study suggests that the proteins may play different roles during brain development. In the future study, we are focusing to investigate the role of differentially expressed gene in human fetal astrocytes.