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Selection of Neural Differentiation-Specific Genes from Gene Expression Profiles

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Neural differentiation of embryonic stem (ES) cells requires a high level of transcriptional regulation. To understand the transcriptional regulation in neural differentiation, we examined the gene expressions of the guided differentiation (GD) model for dopaminergic (DA) neurons from mouse ES cells using oligonucleotide microarray. In parallel, we determined the gene expression profiles of the random differentiation (RD) model of mouse ES cells into embryoid bodies (EBs). From K-means clustering analysis using the expression patterns of the two models, 1282 from 1884 genes overlapped in their expressions. In random variance *F*-test for GD model, 622 differentially expressed genes (DEGs) were selected and classified by their critical molecular functions in neurogenesis and DNA replication. However, 400 genes among 622 GD-DEGs (64.3%) showed a high correlation with RD in Spearman's correlation analysis (Spearman's coefficient $\rho_s \geq 0.6$). Some genes showed marginal correlation ($-0.4 < \rho_s < 0.6$) at the early stages of differentiation of both GD and RD. Finally we distinguished 66 GD-specific genes based on $\rho_s \leq -0.4$, whose molecular functions were mainly related to vesicle formation, neurogenesis and transcription. Among these GD-specific genes, we confirmed the expression of Serpini1 and Rab 33a in mouse brain and P19 differentiation model. We identified the neural differentiation-specific genes that are required for neural differentiation by comparing gene expressions of GD with RD, which would potentially be the highly specific candidate genes necessary for differentiation of neurons.