P40

Characterization of the murine dopamine receptor regulating factor (DRRF) promoter

Sang-Hyeon Lee*, Jae-Hwa Lee, Jong Myung Ha and Bae-Jin Ha

Department of Bioscience and Biotechnology, Silla University, San 1-1, Kwaebop-dong, Sasang-gu, Pusan, 617-736.

To study the transcriptional mechanisms by which expression of the Dopamine Receptor Regulating Factor (DRRF) gene is regulated, a murine genomic clone was isolated using a DRRF cDNA as probe. A 24-kb genomic fragment, which comprises 13-kb upstream of the transcription initiation site was sequenced. The promoter region lacks a TATA box and CAAT box, is rich in G+C content, and has multiple putative binding sites for the transcription factor Sp1. The DRRF gene also has consensus sequences for AP1 and AP2 binding sites. The transcriptional activity of five deletion mutants of a 1.5-kb fragment was analyzed by modulating transcription of the heterologous chloramphenicol acetyltransferase (CAT) gene in the promoterless plasmid pCAT-Basic. All mutants showed significant transcriptional activity in the murine neuroblastoma cell line NB41A3. Transient expression assays suggested the presence of positive regulators between 1153 and 901 and between 118 and 93 while a negative regulator was found in the region between 901 and 118. Strong transcriptional activity was observed in neuronal NB41A3 cells and moderate activity in hepatic HepG2 and renal OK cells, but none in skeletal muscle C2C12 or glial C6 cells. These findings confirm the tissue-specific activity of the DRRF promoter and suggest that this gene shares structural and functional similarities with the dopamine receptor genes that it regulates.