D-19 Expression of Dopamine D_1 and D_2 Receptor mRNAs in the Peripheral Organs of the Rat Fetus

김명옥*, 최완성[1], 김경진
서울대학교 자연과학대학 분자생물학과, 경상대학교 의과대학 해부학교실[1]

Dopamine(DA), an endogenous catecholamine, has unique vasodilatory properties in certain vascular beds of adults. More specifically, evidence has accumulated favoring the presence of a vascular DA receptor that produces vasodilation when activated. However, little is known about the ontogenesis of DA receptor mRNAs in the vascular bed of peripheral organs. In the present study, we have examined the expression of DA D_1 and D_2 receptor mRNAs in the various peripheral organs during the rat fetal development. [^{35}S]UTP-labeled cRNA probes of rat DA D_1(500 bp) and D_2(309 bp) were used for our *in situ* hybridization. At the early developmental stages, signals for DA D_1 the D_2 mRNAs were observed only in the mid gut and the neural retina. A little later, DA D_1 mRNA was also detected in the mucosa of esophagus, in the transitional epithelium and submucosa of urinary bladder, and in the stroma of metanephros. However, DA D_2 mRNA was expressed in the tunica intima and media of coronary artery in the atrium of heart, in the blood vessels of metanephros and in the alveoli of the lung. In additiion, immunohistochemistry for tyrosine hydroxylase(TH) was performed in order to identify the dopamimergic cell bodies. TH immunoreactive cells were localized in the various peripheral organs which expressed DA D_1 and D_2 receptor mRNAs. Our results suggest that DA and its receptors exist from the early developmental stages and may have a role in the maturation of peripheral organs.

D-20 A Survey of Genes Expressed in Undifferentiated Mouse Embryonic Stem Cells to Isolate and Characterize New Developmental/Differentiation -Specific Regulatory Genes

김선홍*, 채지형, 박은정[1], 홍승환[1,2], 박상대[1], 김철근
한양대학교 자연과학대학 생물학과, 서울대학교 분자생물학과[1], 유전공학연구소[2]

ESTs (expressed sequence tags) provide complementary resources for structural and functional analyses of the genome. To identify the genes with functional roles in early development and differentiation, we have performed single-pass sequencing of randomely selected, directionally cloned cDNAs isolated from a mouse embryonic stem cell (129/v-originated CCE line) cDNA library constructed with oligo(dT) primers. Out of 111 clones, 83 clones which contained insert more than 400 base pairs were sequenced at their each ends. Computer-based GenBank analyses of these 5' -end and 3' -end sequences revealed that 71% of the clones (59 clones) were considered to be similar or identical to previously reported mammalian genes or ESTs, and 7 clones out of 24 unkown clones (8% of the total) were not matched at all to the public data bases; out of the 59 known genes, 25 clones (30%) were matched to already cloned mouse genes, 37 clones (45%) were not cloned in mouse but homologous to known mammalian genes, and 6 genes (7%) were originated from mitochondrial genome. Genes related to the transcription/translation machinery and metabolism were most abundant (49%) and 4 clones were cloned twice. Interestingly, at least 5 out of 24 unidentified genes looks like development-related and 2 out of 4 clones are unidentified transcription factors. To screen out the new clones that show temporal and spatial expression during development and differentiation, we are currently performing RT-PCR and the *in situ* hybridization assays to the above-mentioned candidates. Our approach may provide insights into the complex and ever-changing patterns throughout the developing mammalian embryos.