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Characterization of Enhancer Trap Lines AH70, F263, J29 and P101 Regulating Glial Cells Formation in *Drosophila* Nervous System

Jae-Kyoung Kim[P], Sang-Hak Jeon[C], Sang Hee Kim[1], Kyoung Ja Jeon[2], Sung-Jin Kim[3]

[PC3]Department of Biology education, Seoul National University, Seoul 151-748; [1]Department of Chemistry, Konkuk University, Seoul 143-701; [2]Department of Biological Sciences, Konkuk University, Seoul 143-701

Glial cells play many central roles in the development and function of nervous system. These roles include structural support, wrapping and insulating neurons, and regulating them with cytokines and growth factors. The development of a functional glial cell requires the correct specification, precise organization and interaction of a large number of neural cell types. Therefore, influence of cellular intrinsic and extrinsic factors on glial cells formation were characterized. We used *spitz (spi)/Egfr* signaling genes as external factors because an important step in *Drosophila* neurogenesis is to establish the neural dorsoventral (DV) patterning. The loss-of-function mutation of *spi* and *Egfr*repressed expression of enhancer trap lines AH70, J29 and P101 that were found as glial cell-specific markers. And we also investigated the expression of AH70, F263, J29 and P101 in the loss-of-mutation of *reverse polarity (repo)* and *pointed (pnt)*, which are downstream of *glial cell missing (gcm)* as internal factors. The expression of AH70, F263, J29 and P101 in the loss-of-mutation of *repo* and *pnt* partially or severely disappeared. These results suggest that AH70, F263, J29 and P101 enhancer trap lines involved in differentiation and maintenance of glial cells.

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Genetic Variation in *Arisaema robustum* (Araceae) Using SSCP Analysis

Yong-Hwan Jung[P], Eun-Young Song[1], Ki-Chang Jang[1], Kong-Ho Kim[1], Misun Kim[1], Seung-Jong Chun[1], Seong-Cheol Kim[C]

National Jeju Agricultural Experiment Station, R.D.A., Jeju 690-150

The genetic variation among nine taxa of *Arisaema robustum* distributed in Korea was analyzed using single stranded conformation polymorphism (SSCP) analysis. The *trn*L(UAA)-*trn*F(GAA) intergenic spacer of the chloroplast DNA (cpDNA) of *A. robustum* was amplified directly by polymerase chain reaction (PCR) using the universal primers, trnLF and trnFR. SSCP analysis of denatured amplification products was carried out by polyacrylamide (10%) gel electrophoresis followed by ethidium bromide staining. The SSCP analysis identified two different band patterns and comparison of these two nucleotide sequences identified five sites of point mutation (nucleotide substitutions). We cloned two SSCP variants in order to determine the *trn*L-*trn*F intergenic spacer sequences. There were 372 base pairs in the *trn*L-*trn*F intergenic spacers. The different cleavage patterns of four restriction endonucleases, *Dra*I, *Mae*III, *Sch*I and *Tfi*I, were found. These results show that SSCP analysis of the *trn*L-*trn*F intergenic spacer region is a useful technique for inferring genetic variation among members of the *A. robustum* distributed in Korea.

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Molecular Cloning and Expression of *DMRT* Gene in Wrasse, *Halichoeres tenuispinis*

Hyung-Bok Jeong[P], Ji-Gweon Park[2], Jin-Young Choi[1], Young-Jun Jin[1], Gi-Ok Kim[2], Se-Jae Kim[C]

[PC1]Department of Life Science, Cheju National University, Jeju 690-756; [2]Technology Innovation Center, Cheju National University, Jeju 690-756

The sex differentiation of fishes occurs under the control of geneticand various environmental factors. *DMRT* is novel zinc finger transcription factor and plays key role in sex determination. In order to isolate the *DMRT* cDNA from the protogynous wrasse (*Halichoeres tenuispinnis*), the wrasse testis cDNA library was screened using the 32P-labeled PCR products, which were amplified with degenerate primers from conserved DM-domain regions of several *DMRT*genes. Among a few positives obtained through screening, the full length *wDMRT* cDNA of 2.9kb size encoding a predicted 300 amino acid residues was isolated. The sequence analysis exhibited 60%, 43% sequence identity with rainbow trout and tilapia *DMRT*1, respectively. RT-PCR assay showed that *wDMRT* was expressed specifically in male testis. Also, it was strongly expressed in May, a season when the reproductivity of wrasse is most active. This results suggested that *wDMRT*gene function in testis differentiation. Additionally, the conserved DM-domain regions were amplified using PCR from *DMRT* genes of several species among Labridae, and their sequences were determined.

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Expression of Cytochrome C Oxidase Subunit IV Isoform 2 in Human Lung Tissues

Min A Hong[P], Kyo-Young Lee[1], Eunsook Song[C]

[PC]Department of Biology, Sookmyung Women University, Seoul 140-742; [1]Department of Pathology, St. Mary Hospitol, Seoul 150-713

Cytochrome c oxidase (COX) is the last enzyme in electron transport chain and composed of 13 subunits. The 3 large subunits are encoded on mitochondrial DNA whereas 10 are on nuclear genome. Among the nuclear encoded subunits, subunit IV is the largest having contact sites with the catalytic subunits I and II. So it is an attractive candidate for regulating COX activity. Subunit IV has been shown to bind ATP at both matrix side and intermembrane space, leading to an allosteric inhibition of enzyme activity at high intramitochondrial ATP/ADP ratio. Lung is under high oxygen pressure. Recently COX subunit IV isoform (COX IV-1 and COX IV-2) has been found only in lung tissue (Httemannet al, 2001). As it seems COX IV-2 play an important role in regulation of COX activity and related respiratory function, we examined the transcription of cytochrome c oxidase(COX) subunit IV isoform in human lung cancer. COX IV-2 expression greatly increased compared to COX IV-1 in situ hybridized lung cancer. In addition, D-loop and COX III region were increased in parallel with COX IV-2 suggesting enhanced mitochondria (DNA). It seems that mitochondria are increased in human lung cancer and COX IV-2 is related with lung mitochondrial biogenesis during carcinogenesis.