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Identification and Characterization of the *Drosophila* Short Neuropeptide F

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Functional properties of neuropeptides in animals include the regulation of homeostasis and physiological behavior such as feeding and circadian rhythm. Neuropeptide-receptor signaling pathways are remarkably conserved through evolution from mammals to fruit flies (*Drosophila melanogaster*). Therefore, the *Drosophila* model system is extremely valuable to understand the role of these neuropeptides in physiological process and for unraveling genetic pathways in which these neuropeptides participated. Neuropeptide Y (NPY) signaling pathway has been strongly related to the stimulation of food uptake in mammals. With PCR based cloning, we have obtained the gene encoding short neuropeptide F (sNPF) precursor, which is the mammalian NPY counterpart. Here, we report cloning and characterization of the Drosophila sNPF. Using in situ hybridization and immunohistochemistry, we have analyzed the expression pattern of the Drosophila sNPF in embryos and larvae. Interestingly, sNPF is mainly expressed in the embryonic and larval central nervous systems. Using RT-PCR, we found that sNPF mRNA is expressed in all developmental stages. However, the presumed functional sNPF peptide is strongly expressed in pupae and adults conformed by the Western blot. Our results suggest that *Drosophila* neuropeptide F may possess functional properties for controlling eating behavior like a mammalian counterpart, NPY.

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Localization of Neuropeptide F Receptor in the *Drosophila* Central Nerve System

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Neuropeptide Y (NPY) is one of stimulatory neuropeptides on feeding behavior. They are synthesized and secreted by discrete populations of neurons in the CNS. Short neuropeptide F (sNPF), which is the invertebrate counterpart of the mammalian NPY, was expected having a variety of neurobiological functions in Drosophila CNS. These diverse effects of sNPF are mediated through the sNPF receptor (sNPFR), which is a seven transmembrane G-protein coupled receptor. Previous study also suggested that sNPFR mediated physiological responses was activated by sNPFs. In this study, we haveinvestigated the distribution of the sNPFR protein in the Drosophila embryos by the immunohistochemistry analysis using the chromogenic signal amplification method. Synthetic peptides (sNPFR1-4) from four regions of sNPF amino acid sequences were used to generate antibodies against sNPFR. We tested these four antibodies is working in the western blot experiment. In immunohistochemistry analysis with the sNPRF1 antibody, we found that sNPFR was predominantly expressed in Drosophila embryonic CNS. These data suggest that sNPFR may participate in neurophysiological behavior.

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Identification and Characterization of *Eamar*, *mariner*-like Elements in the Earthworm *Eisenia andrei*

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mariner-like transposable elements (MLEs) are widely distributed from prokaryotes to eukaryotes including vertebrates. MLEs from earthworm were first identified and named *Eamar* for *mariner*-like elements from *Eisenia andrei*. Molecular characteristics of *Eamar* were analyzed by PCR, DNA sequencing and multiple sequence alignments. We obtained two positive clones, *Eamar*1 and *Eamar*2 which were 1424 bps and 1434 bps in length, respectively. *Eamar*consists of one open reading frame (ORF) and incomplete inverted terminal repeats 68 bps of flanking by a transposase gene. It appears that ORF harbors a D,D(37)D motif, which is known as a catalytic domain and a conserved amino acid block that shows similarities to MLEs from other animal species. It is likely that *Eamar*1 and *Eamar*2 were nonautonomous bacause of many mutations that could disrupt functional domain in ORF. It was revealed by southern hybridization that they would be rich in the genomic DNA of *Eisenia andrei*. Phylogenetic analysis of amino acid sequence of *Eamar*1 with *Tc1-mariner*like elements isolated from the animal species indicates that the element from *Eisenia andrei* comprises a new subfamily of MLEs and that *Eamar* would be invaded by horizontal transfer in the genome of the earthworm.

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Detection of the Recessive Lethal Gene Linked with the Allozymeand Microsatellite Markers in the Pacific Abalone

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"Inbreeding depression" should be one of the most avoidable phenomena for abalone culture as well as other aquatic animals. Recessive lethal gene is one of the most important factors for inbreeding depression, but no report has published yet in abalone, because of its difficulty of detection. It would be necessary for detection of the recessive lethal gene to make an effective mating system and to use the effective marker genes.In the present study, using two families producing in 1994, factorial mating system including 10 inbreeding and 6 outbreeding was conceived in order to demonstrate genetic factors of inbreeding depression at the Pacific abalone, and parentage analyses were performed by four allozyme makers and newly developed four microsatellite marker genes (Park et al.2003). As the results, crosses of segregation distortion indicates the homozygotes of recessive lethal genes linked to *B* allele of the *Hdh145* locus and to n allele of the *Hdh57* locus in family A and B, and at the *Pgm-2* locus, *C* allele was detected to be a lethal gene related with the *Pgm-2* isozyme gene.