Z308 Localization and Process Pathway of Allatostatin in the Central Nervous System of lepidoteran moth, *Agrius Convolvuli*

Taekyun Kim[1], Dongkyung Sung[2], Hunhee Park[2], Jaesun Choi[2], and Bong Hee Lee[1,2]
[1]Department of Biology, [2]Department of Life Science Graduate School of Biotechnology, Korea University, Seoul, Korea

Over the last decade, a large number of insect neuropeptides have been identified. Allatostatin are a family of insect neuropeptides that inhibit juvenile hormone (JH) biosynthesis by the corpora allata. The rate of juvenile hormone biosythesis in different insect species can either be stimulated or inhibited by allatotropic and allatostatic neuropeptides. In this investigation, localization of allatostatin-producing neuron were observed in the central nervous system of 5th instar larva from lepidoteran moth, *Agrius convuli* using an immunocytochemical methods. The brain contains about 43 pairs of bilateral ATSs-immunoreactive cell bodies and they show bilateral localization of most of the cells in their ventral ganglia. The distribution pattern of neuronal cells of all the abdominal ganglia is very similar except for terminal abdominal ganglion.

Z309 Identification and characterization of a Ubiquitin C-terminal Hydrolase in C. elegans

Jungsoo Lee and Joohong Ahnn
Department of Life Science, Kwangju Institute of Science and Technology

Ubiquitin, a highly conserved protein composed of 76 amino acids, is important for many cellular processes including the regulation of intracellular protein breakdown, cell cycle regulation, and stress response.Ubiquitin C-terminal hydrolase (UCH) is a thiol protease that recognizes and hydrolyzes the peptide bond at the C- terminal glycine of ubiquitin. This enzyme is involved in the processing of poly-ubiquitin precursors as well as ubiquitinated proteins. UCHs have two homologous regions; the first region contains a conserved cysteine domain, the second contains two conserved residues. These two homologous regions are likely implicated in the catalytic mechanism. We searched the worm genome database and located a putative homologue of UCH in the cosmid ZK328 (LGIII). C. elegans UCH (ZK328.1) consists of 14 exons encoding 1178 amino acids and contains two functional domains that are well conserved in other organisms. Expression pattern was investigated using GFP and is shown to express in excretory cells, coelomocytes, hypodermal cells, pharynx, and neuronal cells. Northern blot experiments revealed an mRNA transcript of 3.7 kb. To better understand the function of UCH in C. elegans, RNA-mediated interference (RNAi) technology was conducted and resulted in high embryonic lethality suggesting that Ce-uch-1 has an essential role in the early embryo development of C. elegans. The RNAi phenotype was rescued by mating with wild type males. Furthermore, whole mount immunostaining showed that UCH stains the microtubule organizing center (MTOC) in fertilized embryo and in the sperm cytosol. Our data suggests that UCH is indispensable for the formation of a sperm-contributed functional MTOC and early cleavage during embryogenesis in C. elegans.