

Z6 13 **Molecular Characterization of cDNA Encoding Allatostatin in German
Cockroach(*Blattella germanica*) Midgut**

JaeHyuck Yang*, Bong Hee Lee
고려대학교 생물학과

Allatostatins (ASTs, Tyr/Phe-Xaa-Phe-Gly-Leu/Ile-NH₂ family) were known to inhibit juvenile hormone (JH) biosynthesis *in vitro* by corpora allata (CA) in the cockroach, *Blattella germanica*. In order to determine the sequence of AST coding region, a cDNA library was constructed by RT-PCR with total RNA purified from midgut of *B. germanica*. To get the PCR product, PCR was conducted using the oligo d(T) primer and degenerated primers designed from the highly conserved region of *Diploptera punctata* and *Periplaneta americana*. The amplified fragments were subcloned into pGEM-T Easy vector, so three cDNA clones obtained were sequenced. They all were composed of 1,128bp and this can encode 375 amino acids for synthesis of ASTs in midgut of the adult cockroach. The nucleotide sequences of cDNA obtained are similar to those of *D. punctata* and *P. americana* reported previously. AST cDNA synthesizes thirteen subtypes of ASTs in midgut of adult cockroach, *B. germanica*.

Z6 14 **Fine Mapping of Lethal Mutants on Chromosome I of *Caenorhabditis
elegans***

Sunki Jung*, Jinsook Lee and Joohong Ahnn
광주과학기술원 생명과학과

We have isolated six independent mutants (*jh1* to *jh6*) out of approximately 5,200 ethyl methanesulfonate (EMS) treated haploids. Four of the six mutants demonstrated embryonic lethal phenotypes, while the other two showed embryonic and larval lethal phenotypes. Terminal phenotypes observed in two mutants (*jh1* and *jh2*) indicated developmental defects specific to the posterior part of the embryo which appeared similar to the phenotypes observed in *nob* (*no back end*) mutants. Another mutant (*jh4*) resulted in an interesting phenotype of body-wall muscle degeneration at larval stage. These mutants were mapped by using three-factor crosses and deficiency mutants in this region. We are currently characterizing two mutants, *jh2* and *jh4*, in order to map these genes by using several marker genes. Here, we report genetic analysis and fine mapping of these lethal mutants.