F818 Genetic analysis of Inversions in the duplicated *Amy* locus of *Drosophila melanogaster*

Hye-Young Nam*, Seung-Hyun Sung, Hyung-Wook Jeon and Dong-Sang Suh
Department of Genetic Engineering, Sungkyunkwan Univesity

The *Amy* locus(*Amy*, 2-80; 54A1-B1) of *D.melanogaster* is duplicated (*Amy-p*, *Amy-d*). The members of duplicated genes are ~4 kb apart, consisting of 1482bp ORF without introns. They do not evolve independently but exhibit an evolutionary process called concerted evolution. To infer the concerted evolution, we analysed inversions of the *Amy* locus using PCR. In order to detect intergenic inversions, PCR primers were selected from highly divergent regions flanking *Amy-p* and *Amy-d*. The frequency of inversions in Suwon natural population was $(7.018 \pm 0.001) \times 10^{-3}$. For genetic analysis, 6 homozygous lines of inversion mutants were made by mating with Cy/Pm. Homozygous inversion mutants were analysed by PAGE and Southern blotting. For detailed molecular analysis of *Amy* region in homozygous inversion mutants, we have constructed genomic DNA library from one mutant line and isolated two genomic clones for the *Amy* gene. The cloned genes were sequenced by dideoxy chain termination method. From the detection of the inversions in the *Amy* locus, we obtained some evidences of interchromosomal recombination or gene conversion.

F819 Studies on the Regulation of the Expression for *Ultrabithorax* Gene in *Drosophila melanogaster* Using Microinjection.

Soon-Jeung Kim*, Seung-Min Shin, Man-Wook Hur† and Dong-Sang Suh

Department of Genetic Engineering, Sungkyunkwan University
†Department of Biochemistry, Medical College of Yonsei University

Homeotic genes are important for the regulation of the developmental processes. We have examined the regulation of the expression for *ultrabithorax* gene, which is a kind of homeotic genes of *Drosophila melanogaster* in the embryogenesis at anterior part of the embryo. We have already known through the transgenic *Drosophila melanogaster* that transcription factor GAGA, which binds to proximal promoter from -200bp to -31bp, cross-talks with upstream *cis*-regulatory elements. We will map the upstream regulatory elements of the *ultrabithorax* gene which cross-talk with GAGA transcription factor. To study this, we have made the plasmid constructs which bind to proximal promoter containing GAGA binding site, and various deletions in 22kb upstream sequence; pCpWβ- Xkb - GAGA -ubx- LacZ- P-element plasmids (GAGA 1.2kb, GAGA 6.1kb, GAGA XhoI-XhoI religated). Microinjecting them into embryos of *Drosophila melanogaster*, we have analysed the anterior part of embryos with β-gal assay. The results were: GAGA 1.2kb and GAGA 6.1kb didn't show the suppression of the expression for *ultrabithorax* gene at the anterior part of the embryo , but GAGA Xho I -Xho I religated site did. Therefore we supposed that the regulatory site may be in the GAGA XhoI-XhoI religated site which lacks -19kb to -12kb of total 22kb upstream sequence.