

F811 · Analysis of Genetic Variance for Body Weight in Korean Natural Population of *Drosophila melanogaster*.

Mee-Jeoung Shim¹, Yong-Sung Kim², Young-Min¹ Park, Ki-Chang Sung¹, Seung-Hyun Sung³, Dong-Sang Suh³

Department of Biology¹ and Genetic Engineering³, SungKyun Kwan Univeristy,
²Genome Center, Korea Research Institute of Bioscience and Biotechnology

We estimated genetic variance components for body weight in *D.melanogaster*. Ninety second chromosomes were extracted from the Suwon natural population. Analyses of heritability and genetic variance were performed by partial diallele cross. The correlation coefficient (r) of body weight between female and male was estimated to be 0.9969. The heritability (H^2) was estimated to be 0.317 for female and 0.308 for male and the additive genetic variance ($\hat{\sigma}_a^2$) was 0.00136 ± 0.00096 and 0.00127 ± 0.00047 and the dominance variance ($\hat{\sigma}_d^2$) was -0.00014 ± 0.00031 and -0.00052 ± 0.00026 , respectively. The analysis of these data indicates that, in this population, mutation-selection balance is the mechanism for the maintenance of genetic variability of body weight.

F812 Sequence Analysis of the *Bombyx* Fibroin Gene Promoters

Hyung Wook Jeon^{*}, Seung Hyun Sung, Seung il Kim,
Dong Young Lim, Ji Yoeun Suh, Dong Sang Suh
Dept. of Genetic Engineering, SungKyunKwan University

Silk proteins spun from the posterior silk gland are composed of two types of proteins, fibroin and sericin. The fibroin is made of two polypeptides, H- and L-chain. Each chain is produced by different genes. It has been known that H-chain and L-chain are expressed simultaneously when they are needed. The promoter region of these two genes (H- and L-chain) were cloned from *Bombyx mori*, *Bombyx mandarina*, three mutants (Nd , $Nd-t$, Nd^H) and named pFLP, pFHP, pNd, pNdt and pNdh, respectively. We sequenced 1,030 nucleotides from *Fib-L* of *Bombyx mori*, *Bombyx mandarina* and three mutants (Nd , $Nd-t$, Nd^H). It has been found that 14 bases in *B. mandarina*, 14 bases in Nd , 16 bases in $Nd-t$ and 18 bases in Nd^H showed different sequences from the wild, *B. mori*. It implies that mutation ratio marks 1.36% in *Bombyx mandarina*, 1.36% in Nd , 1.55% in $Nd-t$, 1.65% in Nd^H . As a result, we identified that the major promoter regions including TATA box and CAAT sequence was conservative.