

F107**Amylase Variant in *Drosophila melanogaster*: Genotype Polymorphism and Enzyme Activity in Different Diet**

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Genotype distribution and enzyme activity of amylase in a natural population of *Drosophila melanogaster* were analysed from 1988 to 1991. Nine different patterns of amylase genotype was detected by PAGE. Among these genotypes, *Amy*¹ seems to be the commonest and an ancestral allele, which frequencies observed as high as 69.67 percent from total 732 iso-female lines. In addition, *Amy*^{1.4} and *Amy*^{1.5} were firstly identified in this study. The four laboratory strains of amylase genotype (*Amy*¹, *Amy*^{1.3.6}, *Amy*^{1.2.3}, *Amy*^{1.6}) grown in the standard cornmeal-molasses-agar medium, were transferred to starch, sucrose and maltose medium. Enzyme activity were examined during 8 generations in each food components. Every strain revealed a different adaptation ability to carbon source. The amylase activity in starch medium was calculated lower than that in other two media. This probably means that starch gives less dietary stress to *D. melanogaster* than two other carbon source.

F108**Karyotype analysis of Cheju native horse (*Equus caballus*) by Giemsa staining Method**

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Chromosomal analysis in Cheju native horse genus *Equus* was performed by conventional Giemsa staining and air-drying method. The chromosomes were studied in cultured material from leucocytes. The normal diploid chromosome numbers of Cheju native horse were 64. The karyotype was consisted of 20 metacentric or submetacentric and 44 subtelo-centric or acrocentric chromosome. Therefore, Cheju native horse was determined to be *Equus caballus* in chromosomal level.