F812 PCR-based polymorphisms for the Y-linked microsatellite locus DYS19 and the 47z (DXYS5Y) RFLP in the Korean population

Wook Kim, Dong-Jik Shin and Jung-Min Kim Department of Biology, Dankook University, Cheonan-Si 330-714, Korea

The Y-linked tetranucleotide repeat (GATA)n of microsatellite locus DYS19 and RFLPs detected by the probe 47z (DXYS5Y) have been examined from a total of unrelated 480 male samples in Korean population. The frequency of Y1 and Y2 alleles in DXYS5Y locus found to be 95.4% (458/480) and 4.6% (22/480), respectively. Although the frequency of the Y2 allele in this study is not as high as published previously, the presence of both Y1 and Y2 alleles in this population is consistent with other survey that the Y2 allele revealed to have restricted geographic distribution in Korean and Japanese group. We identified all five common alleles at the DYS19 locus. The C allele is the most frequent (212/480), followed by the D (136/480), B (75/480), E (36/480) and A (21/480) allele. This predominance of the C allele is similar to the majority of the results previously reported from Asian populations. Nine haplotypes are identified with respect to the DYS19/DXYS5Y combination, and the mean combination haplotype diversity is 0.72. On the basis of results for the DYS19/DXYS5Y haplotypes, Korean population appears to share a common genetic structure of some magnitude with Japanese, in agreement with the hypothesis that Korea was the origin of migration routes of Yayoi immigrants of Japan.

F813 Amylase Variation in a Korean *Drosophila melanogaster*: Genotype Polymorphism, Enzyme Activity, Competetion

Jong Kil Choo, Hyung Chan Son, Chi Hyun Ahn, and Min Kyung Kim Department of Biology, College of Natural Science, Chungang University

Among four natural populations of *Drosophila melanogaster*, the genotype distribution and specific enzyme activity of amylase(Amy) were analysed from total 588 isofemale lines from 1996 to 1997. Total patterns of Amy variants have been found as Amy^1 , $1\cdot 2$, $1\cdot 3$, $1\cdot 4$, $1\cdot 5$, $4\cdot 5$, and $1\cdot 2\cdot 3$. At these genotypes it revealed that Amy^1 seems to be the commonest and an ancestral allele and that all population has to be like the distribution. The protein concentration and enzyme activity of amylase variants were detected by Lowry assay and starch-iodine assay. The average of protein content was shown similarly as $13.1226\mu g$ Protein. Specific amylase activity of the Amy^1 was used standard enzyme activity. Each enzyme activities in adult single fly of Amy variants were revealed as similar as $1.9695\mu g$ Maltose/ μg Protein of Crude extract/min. Also, of competetion among Amy variants were analysed the distribution and the frequency after cage flies were underwent the competetion of the survival. We have the same result as that of natural population, Amv^1 and $Amv^{1\cdot 3}$ were the commonest.