

**F803** Y chromosomal DNA variation and its potential for inferring the genetic relationship between Korean and Vietnamese populations

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We have analyzed Y chromosomal haplotypes using four polymorphic loci to estimate genetic distance between Korean (n=340) and Vietnamese (n=75) populations. Variation at these loci was also examined in 27 individuals from a naturalized Korean sample of Hwasan Lee families. These families are known to be descendent from one or very few male Vietnamese ancestor about 750 years ago. The Y-specific polymorphic markers included the Y *Alu* polymorphic element designated YAP (*DYS287*), two point mutations (*DXYS5Y* and *SRY465*) and a tetranucleotide microsatellite (*DYS19*). Combing the allelic variation at these four loci resulted in a total of 10 combination haplotypes, which is shared in the 18 combination haplotypes of the Korean population. The mean combination haplotype diversity found to be 0.848 and 0.806 in Korean and Vietnamese populations, respectively. Cavalli-Sforza's Chord genetic distance ( $4\bar{D}$ ) based on the frequencies for these Y-specific markers showed that Koreans and Vietnamese are likely to have a relatively similar genetic structure ( $4\bar{D}=0.0312$ ) among several South and East Asian populations. Only subset of four haplotypes were found in the Hwasan Lee families, which are shared with the haplotypes in the Vietnamese population, with the exception of one haplotype. This result suggests that the Hwasan Lee families might be somewhat admixed with Korean males through a system of adopted sons in Korea. Finally, the results of Y chromosomal haplotypes in this study provide an evidence for a recent gene flow and some amount of admixture of Y chromosomes between Koreans and Vietnamese.

**F804** Cloning and expression of the *HOM2* and *HOM6* genes in *Saccharomyces cerevisiae*

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Synthesis of threonine and methionine in yeast, *Saccharomyces cerevisiae* shares a common pathway from aspartate via homoserine. *HOM2* gene encodes aspartate semi-aldehyde dehydrogenase(ASADH) which catalyzes the second step and *HOM6* gene encodes homoserine dehydrogenase(HSDH) which catalyzes the inter-conversion of  $\beta$ -aspartate semi-aldehyde and homoserine. According to the previous enzymatic data, the level of ASADH and HSDH were under methionine specific control. In the present study, *HOM2* and *HOM6* were isolated from *S. cerevisiae* genomic DNA by polymerase chain reaction amplification and each recombinant plasmid was cloned into *E. coli* and sequenced. Fragments of the cloned genes were used as a probe to measure each mRNA level in a wild-type strain grown under repressing or derepressing conditions. The regulation at the translational level were analyzed through  $\beta$ -galactosidase activities encoded by *lacZ* fusions. In addition, deletion mapping of the regulatory regions of both genes is now in progress.