

F804 Y chromosomal DNA variation in east Asian populations and its potential for inferring the peopling of Korea

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Y chromosomal DNA markers of five polymorphic loci (*DYS287*, *DXYS5Y*, *SRY465*, *DYS19* and *DXYS156Y*) were examined in samples from a total of 1,260 males in eight east Asian populations to study genetic structure of Koreans and the relationship between east Asian populations. We found four unique haplotypes constructed from three biallelic markers (*DYS287*, *DXYS5Y* and *SRY465*) and significant geographic differences in the distribution of the haplotypes. All four combination haplotypes were only found in the Korean and Japanese populations among the eight east Asian populations in this survey. The haplotype II-1 (+/Y1/C) was only found in four northeast Asian populations (Chinese, Japanese, Koreans and Mongolians) with the exception of one subject of Thai samples (1.4%) in four southeast Asian populations (Indonesians, Philippines, Thai and Vietnamese). The Japanese were revealed to have the highest frequency (27.5%), followed by Koreans (2.9%), Mongolians (2.6%), and mainland Chinese (2.2%). Whereas haplotype I-2b (-/Y2/T) was mainly distributed in Japanese (17.1%), Indonesians (9.5%), Koreans (6.3%), Vietnamese (3.8%), and Thai samples (2.7%). Combining multiallelic variation at two microsatellite markers (*DYS19* and *DXYS156Y*) resulted in a total of 72 combination haplotypes. We used the Neighbor-joining (NJ) tree to analyze the Cavalli-Sforza's Chord genetic distance based on the frequencies of the combination haplotypes. Phylogenetic analysis using the NJ tree revealed a considerable distinction between southern and northern east Asian populations. A notable exception to this pattern was the finding of the Vietnamese which was more likely clustered with northeast Asians (e.g. Koreans). Based on our results, the Japanese population appeared to have a closer genetic relationship to Koreans than to the other surveyed Asian populations. Moreover, we found the Korean population to have dual origins of Y chromosome variation by population expansions from northeast and southeast Asians. Therefore, it is more likely that the population structure of Koreans is not just monophyletic derived from northeast Asians, but somewhat large infusion of Y chromosomes entered to Korea from southeast Asia.

F805 Control of the expression of the Aspartokinase gene(*HOM3*) in yeast, *Saccharomyces cerevisiae*

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The yeast gene *HOM3* encodes Aspartokinase (EC 2.7.2.4) which catalyses the first step (aspartate to β -aspartyl-phosphate) of common pathway to threonine and methionine. The *HOM3* was previously cloned independently in our laboratory and also in other's. According to the previous enzymatic data, the *HOM3* gene expression is known to be regulated by threonine and methionine specific control, and also by general control of amino acid biosynthesis. We have analyzed the regulation at the translational level and the effect of deletions in the promoter region of this gene on the expression of the enzyme using a fusion of the *HOM3* gene promoter to the bacterial *lacZ* gene. Recombinant fusion plasmids were cloned into *E.coli* and sequenced. Using a fragments of the cloned genes as probes in Northern blot hybridizations, we investigated their transcriptional regulation. The levels of mRNA were examined in a cells grown under repressing or derepressing conditions according to the different metabolic signals.