

F807 Genetic Polymorphism of the 9-bp Deletion in the Intergenic COII/tRNA^{Lys} Region in Korean and Several Asian Populations

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Length changes in mitochondrial DNA (mtDNA) offer a useful marker for the study of female aspects of human population history. One such length change is the intergenic COII/tRNA^{Lys} 9-bp deletion, which the region usually contains two tandemly arranged copies of a 9-bp sequence (ccccctcta) in human mtDNA. This deletion has been reported at varying frequencies in populations from Asia, Polynesia, the New World and sub-Saharan Africa. This genetic polymorphism of mtDNA was analyzed in samples from a total of 819 unrelated individuals from Mongolian, Chinese, Japanese, Korean, Indonesian and Vietnamese populations. The frequency of the 9-bp deletion was found to be relatively homogeneous in Chinese (13.7%), Japanese (14.3%) and Koreans (15.5%), with the exception of the low frequency (5.1%) of the 9-bp deletion in Mongolians among East Asian populations. On the other hand, Indonesian (25.0%) and Vietnamese (23.2%) of Southeast Asian populations appeared to have relatively high frequencies of the intergenic COII/tRNA^{Lys} 9-bp deletion. Uncommonly an insertion allele of approximately 6-bp in the COII/tRNA^{Lys} region was discovered particularly in Korean (2/349) and Japanese (2/147) populations. Therefore, the results of this study also supported that a large amount of the gene pool in mainland Japanese was derived from the continental gene flow after the Yayoi Age.

F808 Phylogenetic and genomic relationships in the genus *Allium* based on sequences from the NTS region of nuclear 5S rRNA gene

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Phylogenetic relationships among all 16 species of the genus *Allium* were inferred from nucleotide sequence variation in the non-transcribed spacer (NTS) region of nuclear ribosomal DNA. The NTS region from all 16 species of *Allium* were amplified by the polymerase chain reaction, cloned, estimated by fluorescence *in situ* hybridization (FISH) in metaphase chromosomes of corresponding *Allium* species, and sequenced. The sequences of NTS region were identified by comparison through multiple alignment among *Allium* species and by comparison on the basis of sequence similarity to each other eukaryotes using the BLAST network service of at the National Center for Biotechnology Information (NCBI). The length of the NTS sequences ranged from 196 to 485 nucleotides across all the species and spacer regions show little sequence homology among species. Parsimony analysis of the entire NTS region, using genus *Gentiana* as outgroup, resulted in narrow agreement with previous classifications of these species studied by FISH patterns of 5S rRNA gene.