

F103 Genetic variation for the *SRY* gene of the Y chromosome
in the Korean and several Asian populations

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We examined a polymorphism in the coding sequence of the sex-determining region Y (*SRY*) in samples from a total of 1,280 unrelated males in the eight Asian ethnic groups using allele-specific PCR amplification and DNA sequencing. We found a new C to T transition at nucleotide 465 of the *SRY* gene (denoted *SRY465*), which is raised by silent mutation in the 155th amino acid sequence [serine (AGC) → serine (AGT)]. The frequency of the *SRY*-T allele was found to be relatively high in Indonesians (33.3%), Japanese (31.5%) and Koreans (28.5%), respectively. On the other hand, Vietnamese (10.3%), Chinese (7.2%), Thai (6.8%), Mongolians (2.6%), and Philippines (0.9%) appeared to have relatively low frequencies. Cavalli-Sforza's Chord genetic distance ($4\bar{D}$) based on the frequencies of the *SRY465* alleles showed that Koreans and Japanese are likely to have a relatively similar genetic structure ($4\bar{D} = 0.0021$) than to the other surveyed East Asian populations. It was also reported that most Caucasian and Negroid males examined so far completely lack the *SRY465*-T allele. Finally, the result of the allelic variation at the *SRY465* locus in this study provides an evidence for a recent gene flow among Asian populations and may contribute to the study of the origin of Koreans.

F104 Characterization of DNA Repair Genes from Fission Yeast
Schizosaccharomyces pombe

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The *RAD3* gene of *Saccharomyces cerevisiae* is required for excision repair and is essential for cell viability. *RAD3* encoded protein possesses a single stranded DNA-dependent ATPase and DNA-RNA helicase activities. To examine the extent of conservation of structure and function of *RAD3* during eukaryotic evolution, we have cloned the *RAD3* homolog, *HRD3*, from the distantly related yeast *Schizosaccharomyces pombe*. Here, we report the partial cloning and characterization of *HRD3* gene (Homologous of *RAD3* gene) which was isolated by PCR amplification using conserved domain of *Saccharomyces cerevisiae* *RAD3* gene. Chromosomal DNA isolated from *S. pombe* had similar restriction patterns to those from *S. cerevisiae*, as determined by Southern blot analysis. The 2.8 kb transcript of mRNA was identified by Northern hybridization. The level of transcript did not increase upon UV-irradiation, suggesting that the *HRD3* gene in *S. pombe* is not UV-inducible.