

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

Hye Jin Oh, Dong Jik Shin and Wook Kim
Department of biology, Dankook University, Cheonan 330-714, Korea

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

Seon Ah Kang and In Soon Choi
Department of Biology, Silla University

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.