

F805Cloning and characterization of *YDR1*
of the yeast *Saccharomyces cerevisiae*

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Human Dr1 interacts with the TATA-binding protein, TBP and functions as a transcriptional repressor. The association of Dr1 with TBP results in repression of both basal and activated levels of transcription. Dr1 activity is phosphorylated in vivo and phosphorylation of Dr1 affected its interaction with TBP (Inostroza et al., 1992; *Cell* **70**: 447-489). The potential counterpart of the human Dr1 gene in *Saccharomyces cerevisiae* was found from the yeast data bank based on the amino acid similarity. The gene designated *YDR1* was amplified using PCR and cloned into a yeast vector. The *YDR1* gene is an essential gene and overexpression of *YDR1* confers deleterious effect. The human Dr1 gene can functionally replace *YDR1*. To study structure-function of Ydr1 protein mutagenesis is in progress and the *K. lactis* Dr1 gene is being cloned.

F806Y-Specific Polymorphisms of the Alu (*YAP*) Element and the Microsatellite Locus *DYS19* in Korean PopulationsKyoung Hwa Ryu, Dong Jik Shin, Jung Min Kim, Wook Kim* and Yung Jin Kim[†]

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The Y *Alu* polymorphic (*YAP*) element and the Y-linked tetranucleotide repeat (GATA)_n of microsatellite locus *DYS19* have been examined in Korean populations to raise the possibility of tracing paternal lineages and male-mediated gene flow between Korea and Japan. The frequency of *YAP* element was found to be 1% (3/301). This result is consistent with previous reports that showed the *YAP* element to be absent in most Asian populations and the high frequency of the *YAP* element in Japanese. The *YAP*⁺ chromosomes detected in this study appeared to be *YAP* haplotype 3, which is frequently found in the Japanese population. On the basis of the result for the locus *DYS19* (n=252), Korean populations appear to have the most similar allelic frequency (C>D>B>E>A) to Mongolian populations among Asian populations. Although the *DYS19* locus distinguishes the Japanese population (C>D>E>A>B) from most Asian populations, they tend to be somewhat closer to the result of the Korean population, with regard to the frequency of D allele. Finally, all of these results support the hybridization theory that modern Japanese populations have resulted from the ancient Jomon people (*YAP*⁺) and Yayoi immigrants (*YAP*⁻) from Korea.