

analysis revealed that the downstream *rfaZ* gene consists an operon with the *rfaY*. SoxS bound upstream of the -35 box and directly activated *rfaY* as judged by gel shift and in vitro transcription assay. To elucidate the function of *rfaYZ* genes in oxidative stress response, we disrupted *rfaYZ* operon. The *DrfaYZ* mutant was more sensitive to the oxidative stress. In addition, SoxR became more sensitized in the mutant to the quinone-type redox cycling agents, such as menadione and plumbagin. When *DrfaYZ* mutation was introduced into *rpoHp3-lacZ* single copy fusion strain, expression from *rpoHp3* promoter increased 5.4 fold, implying that *rfaYZ* mutation cause some extracytoplasmic stress. The phenotype of SoxR-sensitization in the mutant was complemented by overexpression of the *rfaYZ* genes. However, increase in *rpoH* expression was not rescued even with the overexpression of *rfaYZK* genes.

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(GT)*n* Repeats Polymorphism of the Third Intron of T Cell Receptor Delta (*TCRD*) among Koreans

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The gamma/delta T cells recognize unprocessed or native antigens independently of the MHC, rapidly enhancing the immunity defense mechanism. The gamma/delta T cells have cytotoxic effects and produce large amounts of Th1 cytokines. The *TCRD* is located on the chromosome 14q11.2 and consists of three variables, three diversities, and three joining and constant genes. We analyzed the (GT)*n* repeats polymorphism of the third intron of *TCRD* using 6% denaturing PAGE in two hundred thirty-one unrelated Korean subjects. The number of GT repeat was

estimated for repeat polymorphism by auto-sequencing. Six alleles ranged in size from *TCRD*13* (116 bp) to *TCRD*19* (128 bp). The allele frequencies, *TCRD*13*, *TCRD*15*, *TCRD*16*, *TCRD*17*, *TCRD*18*, and *TCRD*19* were 0.002, 0.424, 0.273, 0.026, 0.253, and, 0.022 respectively. No deviation from the expectations according to the Hardy-Weinberg equilibrium was found. The heterozygosity and polymorphism information content were 0.68 and 0.62. The highest allele frequency among Koreans was *TCRD*15* (0.424), while *TCRD*18* (0.308) among Caucasians.

F802

Single Nucleotide Polymorphisms in the Non-coding region of *CYP2E1* among Koreans

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Cytochrome P4502E1 (*CYP2E1*) is a major component of the microsomal ethanol-oxidizing system involved in the metabolism of a variety of foreign compounds including carcinogens. *CYP2E1* has been implicated in alcohol-related liver diseases and several forms of cancer because of its contribution to oxidative stress. From the genomic DNA of two hundred forty-eight Koreans who are not relatives, single nucleotide polymorphisms at -1293 and -1053 nucleotide of the 5' flanking region and at 7623 nucleotide of intron 6 of *CYP2E1*, which are contribute to regulation of *CYP2E1* expression, were screened using *Pst*I, *Rsa*I and *Dra*I RFLP. The genotype frequencies of *CYP2E1*c1*c1*, *CYP2E1*c1*c2* and *CYP2E1*c2*c2* of *Pst*I/*Rsa*I RFLP in the 5' flanking region were 69.8%, 25.8%, and 4.4% respectively; the allele frequency of *CYP2E1*c1* was 0.827; the genotype

frequencies of *CYP2E1**C/*C, *CYP2E1**C/*D and *CYP2E1**D/*D of *Dra*I RFLP in intron 6 were 3.2%, 25.8% and 71.0% respectively; the allele frequency of *CYP2E1**D was 0.839; and the heterozygosities of *Pst*I/*Rsa*I and the *Dra*I SNPs of *CYP2E1* were both at 0.258. The test for Hardy-Weingberg equilibrium showed no significant deviation from our expectations. The allele frequencies in the 5' flanking region and intron 6 of *CYP2E1* among Koreans were proven to be similar to those of other Orientals, and the allele frequency of *CYP2E1**c2 in the 5' flanking region in Caucasians is lower than that of Orientals including Koreans.

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Three Tetranucleotide Repeat Polymorphism at D16S539, D7S820 and D13S317 Loci in Korean Population

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The markers of microsatellite are polymorphic and are mostly based on loci with tetranucleotide repeats, each locus commonly having between 5 and 15 alleles. Allele and genotype frequencies of D16S539, D7S820 and D13S317 were analyzed using PCR and denaturing polyacrylamide gel electrophoresis followed by silver staining for visualization. DNA extracts were obtained from about 80 unrelated Koreans. The frequency of allele 11 at D16S539 locus in Korean was the lowest among some racial populations. The frequency of allele 11 at D13S317 in Korean was similar to that of Asian populations. Comparing the results of present study with other racial populations, allele frequencies of three loci were different according to the loci. This study confirms that the irregularity in distribution of microsatellite alleles in different populations

with the predominance of two or three alleles on these three investigated microsatellite loci.

F804

A Dinucleotide Repeat Polymorphism at the Calcium Sensing Receptor (CASR) Locus in Korean Population

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Calcium sensing receptor (CASR) in parathyroid gland regulates calcium homeostasis by sensing decreases in extracellular calcium levels and affecting an increase in secretion of parathyroid hormone and calcium reabsorption in the kidney. We analyzed a dinucleotide repeat polymorphism at CASR locus in normal individuals and osteoporosis patients by polymerase chain reaction and polyacrylamide gel electrophoresis. Eight alleles were detected and allele frequencies of A3 and A9 were 0.46 and 0.49 in the normal individuals. In osteoporosis patients, allele frequencies of A3 and A9 were 0.48 and 0.46, respectively. The observed heterozygosities were 0.552 in normal sample and 0.503 in osteoporosis one. Allele distribution and frequencies of normal group were similar to those of osteoporosis one in Koreans. Comparing this result with a Japanese population, some differences were found in the frequencies of main alleles, A3 (0.32) and A9 (0.57). It is concluded that there is significant difference in the allele frequency for normal groups between Korean and Japanese populations.

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Factor V Leiden (G1691A) and G20210A Prothrombin Variant by Multiplex PCR-RFLP