

The CYP2D6 Pheno- and Genotypes in Korean Population

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Among 152 healthy Korean volunteers, we found no poor metaboliser (PM) of debrisoquine using the antimode 12.6 defined in Caucasians, confirming a low incidence of PM in Orientals. Polymerase chain reaction (PCR)-based amplification of genomic DNA with primers specific for the C¹⁸⁸→T mutation present in CYP2D5Ch allele revealed that 40 subjects (26%) were homozygous for the wild type allele, 69 subjects (45%) were heterozygous, and 43 subjects (28%) were homozygous for the CYP2D5Ch allele. All subjects except one in the homozygous wild type group had a metabolic ratio (MR) below 0.75 and all subjects homozygous for the mutated allele had an MR over 0.99. The MRs in the heterozygous group were in between these two genotype groups with some overlapping. The MR distributions of the three genotype groups were different ($p < 0.0001$, Kruskal-Wallis test). This indicates that genotyping for the CYP2D6Ch gene by allele specific PCR for the C¹⁸⁸→T mutation could be used to predict the metabolic capacity of CYP2D6 in Orientals. The proportion of subjects with MR > 1.0 among extensive metabolisers (EMs) of CYP2D6 was calculated and compared to previous studies in Oriental groups. Although the distribution of the debrisoquine MR in Koreans was shifted towards lower MR values than in Chinese, the allele frequency of the CYP2D6Ch gene was 51%, which is not significantly different from that found in other studies in Orientals.