The Correlation Between enotyping and Phenotyping with Omeprazole for S-Mephenytoin 4-Hydroxylase

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The S-mephenytoin 4-hydroxylase (CYP2C19) metabolizes a number of clinically used drugs and shows a marked interethnic difference in the incidence of the poor metabolize (PM). In the present study, we genotyped 144 healthy unrelated Koreans (54 females, aged 20-41 yr, residing in Chungcheong province) for functionally defective alleles, *CYP2C19*$_{m1}$ and *CYP2C19*$_{m2}$. The S-mephenytoin hydroxylation capacity was also measured using the ratio of omeprazole to 5-hydroxyomeprazole in postdose 2-hr plasma after taking a p.o. dose of 20mg of omeprazole in 70 subjects recruited from the subjects involved in genotype study. Detection of the normal(*CYP2C19*$_{wt}$) and defective alleles was performed by polymerase chain reaction/restriction enzyme analysis. The genomic DNA was isolated from peripheral blood. The frequencies of the wild type (*CYP2C19*$_{wt}$) and *CYP2C19*$_{m1}$ were 74.3% and 25.7%, and the wild type(*CYP2C19*$_{wt}$) and *CYP2C19*$_{m2}$ were 83.7% and 16.3%, respectively. The frequencies of homozygotes for *CYP2C19*$_{m1}$, *CYP2C19*$_{m2}$ and compound heterozygotes were 10.4%, 3.4% and 4.9%, respectively. The mutants of CYP2C19 were identified in 27 subjects (18.8%). Thirteen of 72 phenotyped subjects were classified as PMs and were homozygous for the *CYP2C19*$_{m1}$ and *CYP2C19*$_{m2}$. These results suggest that the genotype for the CYP2C19 is well correlated with the phenotype status and genotyping is the useful determinant of S-mephenytoin hydroxylation in Korean population.