

## The Genetic Analysis of *CYP2C9* Polymorphism in a Korean Population

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Accumulation evidence indicates that *CYP2C9* ranks amongst the most important drug metabolizing enzymes in humans. Polymorphism in the coding region of the *CYP2C9* gene produce variants at amino acid residues. The distribution of *CYP2C9* allelic variants has been reported to be different among Asians, Caucasians and Africans. No information on the distribution of four known *CYP2C9* allelic variants has been available in a Korean population, except one report for base mutation of C416T (Arg<sup>144</sup>Cys) that has not been found in Asian (Ko et al., 1996). To assess the incidence of these allelic variants, genomic DNA was isolated from 276 healthy Korean subjects. The genotypes of *CYP2C9* genes were determined by PCR methods using synthetic oligonucleotide primers.

We found one subject of homozygous Leu<sup>359</sup>Leu variant and four subjects who have heterozygous Ile<sup>359</sup>Leu variant of *CYP2C9* among 276 Korean population.

No subject was found to have homozygous Cys<sup>144</sup>Cys, Cys<sup>358</sup>Cys, and Asp<sup>117</sup>Asp or heterozygous Arg<sup>144</sup>Cys, Try<sup>358</sup>Cys and Gly<sup>117</sup>Asp *CYP2C9* variants.

These findings suggest that the incidence of *CYP2C9* allelic variants of Korean population seems to be different with those of Caucasian and other Asian population. Further evaluations are under going to detect *CYP2C9* allelic variants in more Korean subjects.