

Alteration of Substrate Specificity by Mutations on Flavin-Containing Monooxygenase 3 (*FMO3*) Gene in Man

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In previous studies, we found a significant correlation between the activities of ranitidine *N*-oxidation catalyzed by flavin-containing monooxygenase (FMO) and the presence of mutations in exon 4 (Glu158Lys) and exon 7 (Glu308Gly) of *FMO3* gene in Korean volunteers. However, the caffeine *N*-1 demethylase activities catalyzed also by *FMO3* were not significantly correlated with these *FMO3* mutations. Results of present study show that another mutation in exon 6 of *FMO3* (Val257Met), which occurs commonly in our Korean population, is significantly correlated with the *N*-1 demethylation of caffeine but not with the *N*-oxidation of ranitidine.

The exon 6 mutation in *FMO3* was caused by a point mutation (G769A) and was observed commonly (17.1% allele frequency) in our Korean population (n=197). This point mutation in *FMO3* brings about a substitution of Val²⁵⁷ to Met²⁵⁷ and transforms the secondary structure of *FMO3* from a sheet to a helix structure. Presence of this mutant allele was correlated significantly with the reduced FMO activity catalyzing the *N*-1 demethylation of caffeine producing the bromine but was not correlated with the FMO activity catalyzing the *N*-oxidation of ranitidine producing ranitidine *N*-oxide. The low FMO activity (*N*-1 demethylation of caffeine) observed in a family of a person showing heterozygous nonsense mutation in exon 4 (Gly148Stop) and heterozygous missense mutation in exon 6 (Val257Met) of *FMO3* could be explained by the inheritance of exon 6 mutation but not by the inheritance of exon 4 and/or exon 7 mutations. Results of these human studies suggest that different point mutations in the coding regions of *FMO3* could alter the secondary structure of *FMO3* and this, in turn, may alter the substrate specificity. Result further suggest that phenotyping people for their *FMO3* activity need to be conducted with several probe compounds of varying chemical structure that correlate with each mutation on the *FMO3* gene.