The Pharmacokinetics of Omeprazole (A Substrate of CYP2C19) in The Genotypes of the *S*-mephenytoin hydroxylase

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The *S*-mephenytoin hydroxylase (CYP2C19) reveals two functionally defective alleles, *CYP2C19*$_{m1}$ and *CYP2C19*$_{m2}$. In the present study, we studied the pharmacokinetic profile of omeprazole (OMP) in 10 PMs (6 homozygotes for *CYP2C19*$_{m1}$ and 4 homozygotes for *CYP2C19*$_{m2}$) and 8 extensive metabolizers (EMs) determined by the genotyping study. There were statistically significant interphenotypic differences between the EMs and the PMs in the mean kinetic parameters of OMP and its metabolites.

However, we could not obtained any significant differences of those kinetic parameters in the two mutant subgroups.

	OMP			OH-OMP			OMP sulfone		
	EMs	PMs		EMs	PMs		EMs	PMs	
	Wt /wt	m1 /m1	m2 /m2	Wt /wt	m1 /m1	m2 /m2	Wt /wt	m1 /m1	m2 /m2
C_{max}	363	1049	1123	214	47.2	55	104	281	293
$T_{1/2}$	1.5	3.3	3.2	1.5	3.6	3.7	2.4	10.4	9.8
AUC_t	683	5325	5765	508	296	302	694	5691	6012
CL_0	476	59.3	58.3						

(C_{max}, ng/ml; $T_{1/2}$, hour; AUC_t, ng/ml · hr; CL_0, ml/hr/kg)

These results indicate that the genotypic subgroup of CYP2C19 is not the determinant of omeprazole pharmacokinetics.