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Effect of CYP2C9*3 and CYP2C9*13 Alleles on the Pharmacokinetics of Lornoxicam in Healthy Koreans

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Background: Lornoxicam (LOX) is metabolized in the CYP2C9 to the 5'-hydroxylornoxicam. CYP2C9 is the principal enzyme responsible for the metabolism of numerous clinically important drugs. Genetic polymorphism of this enzyme shows high ethnic variations. To investigate the pharmacokinetics of lornoxicam and the relationship with CYP2C9 polymorphism in healthy Korean subjects.

Methods: A 8 mg oral dose of lornoxicam was given to 13 Korean volunteers with different CYP2C9 genotypes (5, 5 and 3 carriers of CYP2C9*1/*1, *1/*3 and *1/*13 genotypes, respectively). Lornoxicam and 5'-hydroxylornoxicam were analyzed by HPLC-UV in plasma samples collected up to 24 hours after drug intake.

Results: The Cmax of lornoxicam was greater in the CYP2C9*1/*3 and CYP2C9*1/*13 ($p<0.05$) subjects compared with the CYP2C9*1/*1 subjects. The t1/2 of lornoxicam was longer in the CYP2C9*1/*3 ($p<0.01$) and CYP2C9*1/*13 ($p<0.05$) groups than that in the CYP2C9*1/*1 group. The mean CL/F was increased in the CYP2C9*1/*3 ($p<0.01$) and CYP2C9*1/*13 ($p<0.01$) subjects compare with the CYP2C9*1/*1 subjects. The mean AUC0-∞ of lornoxicam was lower in the CYP2C9*1/*3 ($p<0.01$) and CYP2C9*1/*13 ($p<0.05$) subjects than that in the CYP2C9*1/*1 subjects. The plasma AUC ratio (AUCLOX/AUC5-OHLOX) was higher in the CYP2C9*1/*3 and CYP2C9*1/*13 groups than that in the CYP2C9*1/*1 group.

Conclusions: Lornoxicam pharmacokinetics differed significantly between subgroups with different CYP2C9 genotypes.