포스터 23

Meloxicam Pharmacokinetics in Relation to CYP2C9*3 and CYP2C9*13 Allele

Jung-Woo Bae

Sungkyunkwan University School of Medicine

Background: Meloxicam is a member of the oxicam group of nonsteroidal anti-inflammatory drug which decreases prostaglandin synthesis via inhibiting cyclo-oxygenase, exhibiting analgesic, antipyretic, and anti-inflammatory effects. Meloxicam is metabolized in the CYP2C9 to the 5'-hydroxymeloxicam. CYP2C9 is the principal enzyme responsible for the metabolism of numerous clinically important drugs. Genetic polymorphism of this enzyme shows high ethnic variations. The effects of major polymorphism of the CYP2C9 on the pharmacokinetics of meloxicam were studied in healthy Korean subjects.

Methods: A 15 mg oral dose of meloxicam was given to 20 Korean volunteers with different CYP2C9 genotypes (9, 9 and 2 carriers of CYP2C9*1/*1, *1/*3 and *1/*13 genotypes, respectively). Meloxicam was analyzed by HPLC-UV in plasma samples collected up to 72 hours after drug intake.

Results: In subjects heterozygous for the CYP2C9*3 and CYP2C9*13 allele, AUC0-∞ of meloxicam was significantly greater (both $p<0.001$), the half-life of meloxicam was significantly longer (both $p<0.001$), and oral clearance was significantly lower ($p<0.001$and $p<0.05$, respectively) than those in homozygous CYP2C9*1 subjects.

Conclusions: The CYP2C9*3 and CYP2C9*13 alleles were associated with the decreased metabolism of meoloxicam.