일반연제

Effect of CYP2D6 Genetic Polymorphism and Metabolic Inhibition on the Pharmacokinetics and QTc Intervals after Single Oral Administration of Flecainide in Healthy Subjects

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Background: Drug-induced QT/QTc prolongation may lead to development of cardiac arrhythmias. Flecainide is a class Ic antiarrhythmic agent and is metabolized by CYP2D6. Our objective was to evaluate the effect of CYP2D6 genetic polymorphism, and also drug interaction with paroxetine as a CYP2D6 inhibitor, on flecainide pharmacokinetics and QTc intervals after single oral administration in healthy subjects.

Methods: An open label, two period cross-over study was performed in ten healthy male volunteers (two for CYP2D6*1/*1, two for *1/*10, and six for *10/*10). Subjects were administered 200 mg of flecainide on day 1. After a seven-day washout period, subjects were administered 20 mg of paroxetine from day 8 to 14, and 200 mg of flecainide on day 15. Blood sampling and 12-lead electrocardiograms were performed up to 72 hrs after flecainide administration. QT intervals were corrected by individual QT-RR regression.

Results: There were significant differences of QTc change between genotype groups $(-9.0\pm3.4, 11.3\pm3.4, 11.3\pm2.0 \text{ msec})$ for *1/*1, *1/*10, and *10/*10, respectively). QTc change also differed between periods, but this change was statistically significant in only the *1/*1 (extensive metabolizer; EM) group.

Conclusions: The CYP2D6*10 allele was characterized to have a substantially greater increasing effect on QT/QTc than the wild-type (*1) allele after single administration of flecainide to healthy subjects. The paroxetine-flecainide interaction augmented QT/QTc changes in the EM group.