The calcium channel blocker diltiazem (DTZ) is used in treatment of hypertension and angina pectoris. It has recently been shown that long-term use of DTZ reduces cardio- and cerebrovascular morbidity and mortality (Hansson et al., 2000). The first-line metabolite desacetyl-DTZ (M1) exhibits approximately 50% of the vasodilating properties of DTZ (Yabana et al., 1985; Schoemaker et al., 1987; Li et al., 1992). In addition, M1 has been shown to exert an inhibitory effect on thrombocyte aggregation about 3-fold that of DTZ (Kiymoto et al., 1982). Therefore, the overall clinical effect of DTZ might, in part, be mediated by M1.

Biotransformation of DTZ is substantial and complex and involves deacetylation, N-demethylation, and O-demethylation (Fig. 1). The former process is mediated by esterases, whereas the two latter reactions are catalyzed by cytochrome P450 (P450) isoenzymes. More than 10 years ago, Pichard et al. (1990) revealed that the P450 subfamily 3A, which is primarily represented by the isoenzyme CYP3A4 in humans, played an important role in N-demethylation of DTZ. In a recent in vitro investigation we showed that the isoenzyme CYP3A4 in humans, played an important role in the overall metabolism of DTZ. However, previous observations indicate that the opposite might be true for the pharmacologically active metabolite desacetyl-DTZ (M1). Thus, the aim of the present in vitro investigation was to study the relative affinity of M1 to CYP2D6 and CYP3A4. Immortalized human liver epithelial cells transfected with either CYP2D6 or CYP3A4 were used as a model system, and the presence of M1 and its metabolites in the cell culture medium was analyzed by high-performance liquid chromatography/UV detection both before and following 90 min of incubation. The estimated $K_m$ value for the CYP2D6-mediated O-demethylation of M1 was approximately 5 \( \mu \)M. In comparison, the affinity of M1 to CYP3A4 (N-demethylation) was about 100 times lower ($K_m \approx 540 \, \mu \text{M}$) than to CYP2D6. These in vitro data suggest that M1 metabolism via CYP2D6, in contrast to the parent drug, probably is the preferred pathway in vivo. Metabolism mediated through CYP2D6 is associated with a substantial interindividual variability, and since M1 expresses pharmacological activity, individual CYP2D6 metabolic capacity might be an aspect to consider when using DTZ.

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data (DeltaGraph Pro 3.5; Deltapoint, Inc., Monterey, CA). Calculation of enzyme-kinetic parameters was based on separate estimations of four experiments. In experiments with inhibitors, paroxetine was coincubated in concentrations ranging from 1 to 20 \( \mu \)M, whereas erythromycin was administered in the concentration interval from 12.5 to 400 \( \mu \)M (M1 concentration 100 \( \mu \)M).

Approximate IC\textsubscript{50} values were visually defined from the graphical presentation of the relative metabolite production in the presence of increasing inhibitor concentrations. In a control experiment, M1 (100 \( \mu \)M) was incubated with non-P450-transfected THLE cells.

**Results**

The metabolite M4 (\( O \)-demethylation) was only detected in incubations with T5-2D6 cells, whereas the metabolite M2 (\( N \)-demethylation) was exclusively produced by T5-3A4 cells. Formation rates of both M4 and M2 could be described by a nonlinear, single-enzyme Michaelis-Menten model in the studied concentration ranges of M1 (Fig. 2, A and B). The average estimated \( K_m \) values (±S.D.) from formation rates of M4 (CYP2D6) and M2 (CYP3A4) were 5 ± 2 and 540 ± 188 \( \mu \)M, respectively. Estimated \( V_{\text{max}} \) values were almost equal for both metabolites, 0.46 ± 0.09 nmol/min/mg of protein for M4 and 0.56 ± 0.13 nmol/min/mg of protein for M2 (extrapolated).

Due to development of cell toxicity when incubating M1 concentrations higher than 500 \( \mu \)M, it was not possible to obtain formation rates of M2 close to \( V_{\text{max}} \).

In agreement with CYP2D6-catalyzing \( O \)-demethylation of M1, a dose-dependent reduction in the production of M4 was observed when coincubating M1 and paroxetine (a CYP2D6 inhibitor) in T5-2D6 cells (Fig. 3A). The IC\textsubscript{50} value of paroxetine was approximately 3 \( \mu \)M. Erythromycin (a CYP3A4 inhibitor) inhibited the conversion of M1 to M2 in incubations with T5-3A4 cells (Fig. 3B), and the IC\textsubscript{50} value was approximately 50 \( \mu \)M. Neither paroxetine nor erythromycin interfered with the detection of any of the analytes.

Based on the cumulative concentration of M1 and its metabolites in the cell culture medium, average (±S.D.) recoveries were 91 ± 7 and 83 ± 8% in experiments with T5-2D6 and T5-3A4 cells, respectively.

**Discussion**

The present in vitro experiments show that the primary deacetylated DTZ metabolite (M1) exhibits approximately 100-fold higher affinity to CYP2D6 compared with CYP3A4. Although the expression of CYP3A4 has been estimated to be approximately 15 times higher than CYP2D6 in human liver (Shimada et al., 1994), it is still likely that the relative contribution of CYP2D6 to the hepatic clearance of M1 is greater than that of CYP3A4. In contrast, since the affinity of DTZ to CYP2D6 is much lower compared with CYP3A4 (Jones et al., 1999; Molden et al., 2000; Sutton et al., 1997), CYP2D6 most probably is of limited importance in the metabolism of DTZ.

In an earlier study with renal transplant recipients treated with DTZ, we reported that a subgroup of the patients showed severalfold higher plasma concentrations of deacetylated DTZ metabolites (i.e., M1 and M2), but not the parent drug, compared with the rest of the study population (Åsberg et al., 1999). Others have also made similar observations (Andren et al., 1988), and in light of the data obtained in the present in vitro study, it could be speculated that patients showing such extensive accumulation of M1 and M2 might be representatives of the population with a deficient CYP2D6 phenotype (approximately

![Chemical structure of diltiazem with the sites of biotransformation and the enzymes catalyzing each reaction indicated by arrows.](image1)

![Formation rates of the CYP2D6-mediated metabolite M4 in T5-2D6 cells (A) and of the CYP3A4-mediated metabolite M2 in T5-3A4 cells (B) as a function of the initial measured M1 concentration in four separate experiments.](image2)

Formation rates were measured as the accumulation of metabolites in the cell culture medium after 90 min of incubation related to the protein (prot) content in the cells. The data were described by a nonlinear, single-enzyme Michaelis-Menten model (regression coefficients, \( r^2 \), are indicated). Average (±S.D.) \( K_m \) values obtained were 5 ± 2 \( \mu \)M for CYP2D6 and 540 ± 188 \( \mu \)M for CYP3A4.
Concentration of the substrate M1 was 100 μM. Formation rates were measured as the accumulation of metabolites in the cell culture medium after 90 min of incubation related to the protein content in the cells (n = 1).

7% of Caucasians). Coadministration of quinidine, known as a potent inhibitor of CYP2D6, did not significantly increase plasma concentration of DTZ in healthy volunteers (Laganiere et al., 1996). Although the participants in the study with quinidine were not CYP2D6-genotyped, the results support that CYP2D6 plays a secondary role in the biotransformation of DTZ.

In conclusion, the present in vitro results suggest a major involvement of CYP2D6 in the in vivo metabolism of the deacetylated DTZ metabolite M1. Since M1 exhibits pharmacological activity, it might be advisable to consider individual CYP2D6 metabolic capacity when using DTZ, although this needs to be evaluated in controlled clinical studies.

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References


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Fig. 3. Formation of M4 by T5-2D6 cells in the presence of increasing concentrations of paroxetine (a CYP2D6 inhibitor) (A) and of M2 in T5-3A4 cells at different concentrations of erythromycin (a CYP3A4 inhibitor) (B) relative to the metabolite production in the absence of inhibitors (control).