# MEFLOQUINE METABOLISM BY HUMAN LIVER MICROSOMES

#### EFFECT OF OTHER ANTIMALARIAL DRUGS

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Abstract—A number of drugs have been studied for their effect on the metabolism of the antimalarial drug mefloquine by human liver microsomes (N = 6) in vitro. The only metabolite generated was identified as carboxymefloquine by co-chromatography with the authentic standard. Ketoconazole caused marked inhibition of carboxymefloquine formation with  $IC_{50}$  and  $K_i$  values of 7.5 and 11.2  $\mu$ M, respectively. The inhibition by ketoconazole, a known inhibitor of cytochrome P450 isozymes, and the dependency of metabolite formation on the presence of NADPH indicated that cytochrome P450 isozyme(s) catalysed metabolite production. Of compounds actually or likely to be coadministered with mefloquine to malaria patients only primaquine and quinine produced marked inhibition ( $IC_{50}$ , 17.5 and 122  $\mu$ M;  $K_i$ , 8.6 and 28.5  $\mu$ M, respectively). However, despite these in vitro data with primaquine, clinical studies have failed to show any significant effect of single dose primaquine on the pharmacokinetics of mefloquine. With quinine, because peak plasma concentrations are very close to the  $K_i$  value, there is likely to be inhibition of mefloquine metabolism in patients receiving both drugs. Sulfadoxine, artemether, artesunate and tetracycline did not significantly inhibit carboxymefloquine formation.

A single oral dose of mefloquine (WR 142,490, (+)erythro-(2-piperidyl)-2,8-bis(trifluoromethyl)-4-quinolinemethanol) has proved to be a relatively effective treatment against multi-drug resistant falciparum malaria in recent years. However, resistance to mefloquine is emerging [1, 2] particularly in parts of Thailand. There is therefore considerable interest in using mefloquine with other antimalarial drugs both concurrently and sequentially. Multiple drug administration raises the question of potential pharmacokinetic/metabolic drug interactions with consequent implications for clinical usage.

Despite numerous pharmacokinetic studies of mefloquine [3] there is comparatively little information available on the metabolism of mefloquine in humans. The main circulating metabolite is carboxymefloquine with concentrations exceeding those of the parent compound by more than 3-fold [4-6]. This metabolite appears to be devoid of any significant antimalarial activity [7]. Most metabolic data have been obtained from rodents [8-11] with the carboxylic acid metabolite being identified in rat faeces. It is not known if cytochrome P450 isozyme(s) are responsible for removal of the piperidine ring and formation of carboxymefloquine.

In the present work we have screened a number of antimalarial and other drugs for their propensity to inhibit the metabolism of mefloquine by human liver microsomes in vitro. Previous studies have shown that primaquine inhibits hepatic microsomal cytochrome P450-dependent enzymes both in vitro and in vivo [12-19] and therefore inhibition of mefloquine metabolism would be one pointer

towards P450 involvement in the formation of the carboxy metabolite. The other drugs studied were quinine, sulfadoxine, tetracycline, artemether and artesunate, all actually or potentially used in combination with mefloquine. For comparative purposes, the antifungal agent, ketoconazole, which is well established as a potent inhibitor of cytochrome P450 enzymes was also studied.

# MATERIALS AND METHODS

Drugs and chemicals. Drugs and chemicals used were: mefloquine hydrochloride, [14C]mefloquine (sp. act. 138  $\mu$ Ci/mg; radiochemical purity > 97%) and carboxymefloquine which were gifts from the Walter Reed Army Medical Research Centre (Washington, DC, U.S.A.). NADPH (B-nicodinucleotide-3'-phosphate, tinamide adenine reduced form), tetracycline, primaquine diphosphate, quinine hydrochloride and sulfadoxine were obtained from the Sigma Chemical Co. (Poole, U.K). Ketoconazole was a gift from Janssen (Beerse, Belgium). Solvents were of HPLC-grade and obtained from the Fison Co. (Loughborough, U.K.). All other reagents were of analytical grade and supplied by BDH (Poole, U.K.).

Human liver samples. Histologically normal livers were obtained from kidney transplant donors soon after clinical death (four males, two females; aged 21–66 years). Ethical approval for the study was granted and consent to removal of the liver samples was obtained from the donors' relatives. Livers were stored as 10–20-g portions at -80° until required.

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Preparation of liver microsomes. Washed microsomes were prepared by the classical differential

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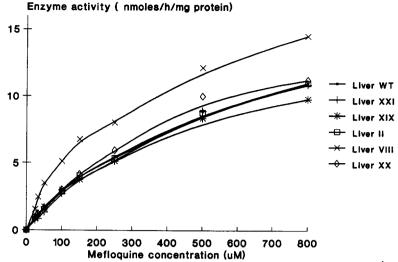


Fig. 1. Plot of velocity (nmol/hr/mg protein) vs mefloquine concentration for the formation of carboxymefloquine in microsomes from six human livers.

centrifugation technique [20]. Microsomal protein content was determined by the method of Lowry et al. [21].

Kinetic and inhibition studies. Incubations containing [ $^{14}$ C]mefloquine (0.1  $\mu$ Ci), mefloquine (100  $\mu$ M), microsomal protein (2 mg) and 0.067 M phosphate buffer (pH 7.4) to a final volume of 2.5 mL were performed in Sovirel tubes (15 mL capacity) at 37° with agitation. Microsomal reactions were started by the addition of 1 mM NADPH. Mefloquine and the putative inhibitors were dissolved in methanol which was evaporated to dryness before addition of the other reaction constituents. The range of inhibitor concentrations used for calculation of IC50 values was 2.5–500  $\mu$ M. The reaction was terminated after 3 hr by the addition of 2 mL 0.1 M glycine buffer (pH 3.4).

Radiolabelled unmetabolized mefloquine and its metabolite, carboxymefloquine were extracted into 6 mL of ethylacetate by mechanical tumbling for 20 min. The organic layer was separated by centrifugation (2500 g for 10 min) and evaporated to dryness in a Buchler vortex evaporator. Extraction of total radioactivity was greater than 95%. The residue was reconstituted in methanol (50  $\mu$ L) and an aliquot (20  $\mu$ l) was analysed by radiometric HPLC (slight modifications from previously published method of Riviere et al. [22]).

Carboxymefloquine was identified according to the retention time of the authentic standard (retention time of carboxymefloquine, 2.2 min; retention time of mefloquine, 8.5 min). Separation was performed on a Techopak 10 C-18  $(30\,\mathrm{cm}\times0.39\,\mathrm{cm})$  column protected by an inline guard column. The system was operated at room temperature in an isocratic mode with the mobile phase of 68% methanol and 32% water containing 0.01 M octanesulfonic acid (adjusted to pH 3.4 with phosphoric acid) at a flow rate of 2.2 mL/min.

Initial velocity conditions for enzyme activity were

established employing a mefloquine concentration of  $100 \,\mu\text{M}$  which was linear over 3 hr and up to 5 mg microsomal protein. The coefficient of variation of the rate of metabolite formation between different incubations (N = 6) of the same liver was < 8%.

The kinetic parameters ( $V_{\text{max}}$  and  $K_m$ ) of formation of carboxymefloquine (mefloquine concentration of 25–800  $\mu$ M) were determined in the absence and presence of some of the inhibitors using an iterative programme (ENZPACK) based on non-linear least squares regression analysis to fit the experimental data to the Michaelis-Menten equation. The apparent  $K_i$  was determined by substituting  $K_m$  and  $V_{\text{max}}$  values in the appropriate equation [23] and by the graphical method of Dixon [24].

## RESULTS

Microsomal protein content was  $16.2 \pm 2.4$  mg/g of liver (mean  $\pm$  SD, N = 6), and the enzyme activity for carboxymefloquine formation at a substrate concentration of  $100 \,\mu\text{M}$  was  $2.85 \pm 0.74 \,\text{nmol/hr/mg}$  protein. This metabolite was the only one evident in the *in vitro* incubations and was not seen in the absence of NADPH. Enzyme activity was highest in microsomes prepared from a liver obtained from a donor who had been receiving phenobarbitone for more than 20 years (Liver VIII, Fig. 1).

Table 1 shows mean IC<sub>50</sub> values and enzyme kinetic parameters determined in the absence and presence of alleged inhibitors. Graphical plots for determination of IC<sub>50</sub> values are presented in Fig. 2. The most potent inhibition was evident with the 1-substituted imidazole antimycotic compound, ketoconazole, and the antimalarial primaquine with IC<sub>50</sub> values of 7.5 and 17.5  $\mu$ M, respectively; while for quinine it was 122  $\mu$ M. Other compounds showed little or no inhibition of the enzyme activity as judged by IC<sub>50</sub> values of more than 500  $\mu$ M.

The  $K_m$  value for carboxymefloquine formation

Inhibitors	$K_m$ $(\mu M)$	V <sub>max</sub> (nmol/hr/mg protein)	IC <sub>50</sub> (μ <b>M</b> )	<i>K<sub>i</sub></i> (μΜ)	Nature of inhibition
Control	236 ± 46	9.9 ± 1.2		_	<b>—</b>
Ketoconazole	$243 \pm 27*$	$3.0 \pm 0.9*$	7.5	11.2	Non-competitive
Primaquine	$268 \pm 49*$	$3.3 \pm 1.1^*$	17.5	8.6	Non-competitive
Quinine	$331 \pm 73 \dagger$	$7.5 \pm 2.2 \dagger$	122	28.5	Mixed
Sulfadoxine	_	_ `	>500	_	_
Artemether		_	>500	_	_
Artesunate		_	>500	_	_
Tetracycline	_	_	>500		_

Table 1. Characteristics of inhibition of carboxymefloquine formation by various drugs

Results are expressed as means  $\pm$  SD (N = 6).

<sup>†</sup> At the inhibitor concentration of 25  $\mu$ M.

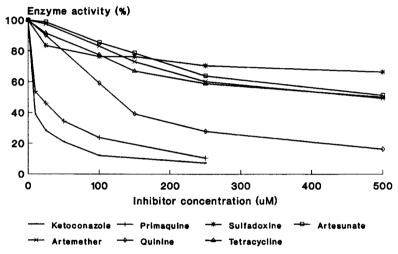


Fig. 2. Effect of ketoconazole, primaquine, sulfadoxine, artesunate, arthemether, quinine and tetracycline on the formation of carboxymefloquine by human liver microsomes. Results are expressed as percentage enzyme activity with the formation of carboxymefloquine in control incubation taken as 100%. Each point represents the mean data from six livers.

determined by regression analysis from Lineweaver-Burk plots with mean data from six livers was  $236 \pm 46 \,\mu\text{M}$  and the  $V_{\text{max}}$  value was  $9.9 \pm 1.2 \,\text{nmol/hr/mg}$  microsomal protein. Ketoconazole and primaquine produced non-competitive inhibition (decrease in  $V_{\text{max}}$ , no change in  $K_m$ ) with the respective  $K_i$  values being 11.2 and 8.6  $\mu$ M, while quinine produced mixed inhibition (a greater than 5% change in  $V_{\text{max}}$  and  $K_m$ ) with a  $K_i$  value of 28.5  $\mu$ M (Fig. 3).

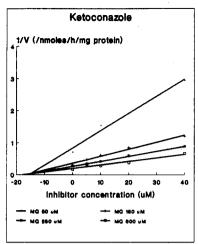
## DISCUSSION

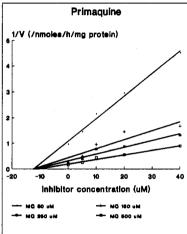
This study has provided some evidence for the involvement of isozyme(s) of cytochrome P450 in the formation of carboxymefloquine, i.e. no metabolite formation when NADPH was omitted from the incubation and marked inhibition of metabolism in the presence of ketoconazole. The antimycotic drug ketoconazole gave non-competitive inhibition ( $K_i = 11.2 \mu M$ ) and this is consistent with

previous findings of inhibition of the oxidation of many other substrates both *in vitro* and *in vivo* [14, 25–31].

Primaquine was also a potent inhibitor of mefloquine metabolism in vitro ( $K_i = 8.6 \,\mu\text{M}$ ) and again this is consistent with previous work showing that primaquine as a nitrogen heterocycle binds to the heme site of cytochrome P450. However, despite the in vitro inhibition, clinical studies have failed to show any significant effect of coadministered primaquine on the pharmacokinetics of mefloquine [32]. An in vivo interaction is very much dependent on plasma (or more importantly, hepatic) concentration of drug. After oral administration of 750 mg mefloquine, peak plasma concentrations are approximately 1500-2000 ng/mL (5  $\mu$ M) at 4-18 hr [33]. After oral administration of 45 mg primaquine, peak plasma levels of 150-200 ng/mL (0.4 µM) are reached within 2 to 3 hr [3]. The concentration of primaquine attained is thus lower than the  $K_i$  value for inhibition of mefloquine metabolism. Resetar et

<sup>\*</sup> At the inhibitor concentration of  $10 \mu M$ .





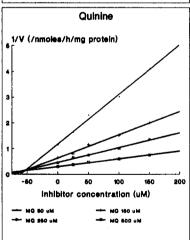


Fig. 3. Dixon plots (reciprocal of velocity, 1/v, vs inhibitor concentration) showing inhibition of mefloquine metabolism by ketoconazole, primaquine and quinine.

al. [34] have calculated the theoretical percentage inhibition obtainable in vivo at physiological (peak plasma) concentrations of a putative inhibitor and substrate using the equation

$$i = 100 \times [I]/(K_i(1 + [S]/K_m) + [I]).$$

Using the same equation (where i = per cent inhibition), primaquine will produce less than 5% inhibition. Another important in vivo consideration is that the half-life of primaquine is very much shorter (6–8 hr) than that of mefloquine (15–20 days). In contrast to primaquine, at a peak concentration of  $6 \mu M$  ketoconazole [35], the calculated inhibition in vivo will be 35%.

Quinine inhibited carboxymefloquine formation, while sulfadoxine, artemether, artesunate and tetracycline were found to be very weak inhibitors. Peak concentration of quinine after oral administration of 600 mg quinine sulphate is approximately 20 μM [36] and this translates into a calculated inhibition in vivo of approximately 40%. The inference is that in patients receiving both mefloquine and quinine higher blood concentrations of mefloquine will be seen. Sulfadoxine is a drug of particular interest because it is used in combination with mefloquine and pyrimethamine in the preparation MSP (Fansimef®). In a previous clinical study [37], it was shown that when mefloquine was administered as the combination of MSP (mefloquine + sulfadoxine + pyrimethamine) the half-life of mefloquine was slightly prolonged. We suggested the possibility of inhibition of mefloquine metabolism by sulfadoxine. This now seems unlikely.

Clinically important pharmacokinetic interactions have also been shown when tetracycline was coadministered with quinine and mefloquine (Karbwang, unpublished observations). In both studies, plasma levels of quinine or mefloquine were elevated significantly. However, the results from the present study again do not support the role of inhibition of drug-metabolizing enzymes by tetracycline. As tetracycline is excreted into bile and faeces in significant amounts, it may be of interest to investigate further whether there is competition for biliary excretion.

In conclusion, the results of the present study have indicated that some drugs can inhibit the biotransformation of mefloquine by human liver. The concurrent administration of quinine and ketoconazole with mefloquine could lead to clinically important pharmacokinetic interactions.

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