IN VITRO METABOLISM OF FERROQUINE (SSR97193) IN ANIMAL AND HUMAN HEPATIC MODELS AND ANTIMALARIAL ACTIVITY OF MAJOR METABOLITES ON PLASMODIUM FALCIPARUM

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ABSTRACT:
Ferroquine (SSR97193) has been shown to be a promising antimalarial, both on laboratory clones and on field isolates. So far, no resistance was documented in Plasmodium falciparum. In the present work, the metabolic pathway of ferroquine, based on experiments using animal and human hepatic models, is proposed. Ferroquine is metabolized mainly via an oxidative pathway into the major metabolite mono-N-demethyl ferroquine and then into di-N,N-demethyl ferroquine. Some other minor metabolic pathways were also identified. Cytochrome P450 isoforms 2C9, 2C19, and 3A4 and, possibly in some patients, isoform 2D6, are mainly involved in ferroquine oxidation. The metabolites were synthesized and tested against the 3D7 (chloroquine-sensitive) and W2 (chloroquine-resistant) P. falciparum strains. According to the results, the activity of the two main metabolites decreased compared with that of ferroquine; however, the activity of the mono-N-demethyl derivative is significantly higher than that of chloroquine on both strains, and the di-N-demethyl derivative remains more active than chloroquine on the chloroquine-resistant strain. These results further support the potential use of ferroquine against human malaria.

The generalization of Plasmodium falciparum resistance to chloroquine and to some other antimalarials represents an urgent problem to cure malaria in endemic areas. Some drugs are currently available, alone or in association with other antimalarials (Wiesner et al., 2003; Baird, 2005), but the development of new molecules remains a priority in the absence of an efficient vaccine strategy.

Ferroquine (SSR97193), resulting from the incorporation of a metallocenic moiety to chloroquine (Fig. 1), was demonstrated to be a new drug with a powerful antimalarial activity in vitro and in vivo (Biot et al., 1997, 1999a,b; Delhaës et al., 2001, 2002). Tests on field isolates confirmed the susceptibility of all resistant parasites to ferroquine and the absence of a significant cross-resistance with major strains, and the di-N-demethyl derivative is significantly higher than that of chloroquine on both strains, and the di-N-demethyl derivative remains more active than chloroquine on the chloroquine-resistant strain. These results further support the potential use of ferroquine against human malaria.

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ABBREVIATIONS: P450, cytochrome P450; HPLC-UV, high-performance liquid chromatography coupled with UV detection; TOF-MS/MS, quadrupole-time-of-flight/tandem mass spectrometry; FMO, flavin-containing mono-oxygenase; Q-TOF, quadrupole-time of flight; DMFQ, mono-N-demethyl-ferroquine; HPLC-MS/MS, high-performance liquid chromatography/tandem mass spectrometry; DMSO, dimethyl sulfoxide; FQ, ferroquine; DMFQ, mono-N-demethyl ferroquine; HH, human hepatocyte metabolite.
Flow rate was 250 μl/min over a 2.1-mm column (J
cbor, H) at 37°C. The mixture was UV detected at λ = 254 nm, total run time was 75 min, and column temperature was set at +38°C.

Synthesis of Ferroquine and Ferroquine Metabolites. General. The 1H NMR spectra were recorded on a Bruker AC300 spectrometer using tetramethylsilane as the internal standard and deuterated chloroform (CDCl3) and deuterated dimethylsulfoxide (DMSO-d6) as the solvent. MS matrix-assisted laser desorption ionization TOF spectra were obtained using a Vision 2000 time-of-flight instrument (Finnigan MAT, Bremen, Germany) equipped with a nitrogen laser operating at wavelength of 337 nm. The matrix used was 1,4,6-trihydroxyacetophenone. SDS gel (35–70 mesh) was used for chromatography. Ferroquine and mono-N-demethyl-ferroquine (DMFQ or Met C) were synthesized as previously reported (Biot et al., 1997, 1999a,b). The 4-amino-7-chloroquinoline (named Met A) was obtained starting from 4,7-dichloroquinoline as already described (Vippagunta et al., 1999).

Synthesis of Metabolite 7-Chloro-4-(2-(Hydroxymethyl)Ferrocylenylmethylanino) Quinoline (Corresponding to Met G). 7-Chloro-4-(2-(acetoxymethyl)ferrocylenylmethylanino)quinoline. A mixture of ferroquine (530 mg, 1.22 mmol) and acetic anhydride (4 ml, 42 mmol) were heated at 85°C for 5 min. After cooling, water (50 ml) was added. The mixture was made alkaline with addition of K2CO3. The organic compounds were extracted by CH2Cl2 (3 × 20 ml). The organic layers were combined, dried over Na2SO4, and evaporated. The oil was purified by column chromatography (eluent: methyl acetate; then methyl acetate/triethylamine, 90:10), giving the ester as a red oil (507 mg, 92%). 1H NMR (CDCl3) δ 8.53 (1H, d, J = 5.1 Hz, H2), 7.92 (1H, s, H8), 7.65 (1H, d, J = 9.3 Hz, H5), 7.29 (1H, d, J = 9.1 Hz, H6), 6.50 (1H, d, J = 5.4 Hz, H3), 5.54 (1H, s, NH), 5.09 (1H, d, J = 12.2 Hz, CH2OAc), 4.92 (1H, d, J = 12.2 Hz, CH2OAc), 4.03 (2H, m, Cp), 4.27 (2H, m, NHCH3), 4.18 (5H, s, Cp). 4.09 (1H, m, Cp), 1.94 (3H, s, COCH3).

7-Chloro-4-(2-(hydroxymethyl)ferrocylenylmethylanino)quinoline (Met G). An aqueous solution of K2CO3 (5 g, 25 ml) was added to a solution of 7-chloro-4-(2-(acetoxymethyl)ferrocylenylmethylanino)quinoline (507 mg, 1.13 mmol) in MeOH (50 ml).

The mixture was stirred at 20°C for 4 h. The advancement of the reaction was followed by TLC. The mixture was extracted by CH2Cl2 (3 × 20 ml). The combined organic layers were dried over Na2SO4 and evaporated. The resulting oil was purified by column chromatography (eluent: CH2Cl2/triethylamine, 90:10), giving 7-chloro-4-(2-(hydroxymethyl)ferrocylenylmethylanino)quinoline as yellow...
crystals (120 mg, 26%). $^1$H NMR (DMSO-d$_6$) $\delta$ 8.39 (1H, d, $J = 5.3$ Hz, H2), 8.18 (1H, d, $J = 9.0$ Hz, H5), 7.77 (1H, s, H8), 7.43 (1H, d, $J = 8.4$ Hz, H6), 7.31 (1H, s, NH), 6.63 (1H, d, $J = 5.1$ Hz, H3), 4.92 (1H, d, $J = 8.5$ Hz, CH$_2$N), 4.46 (1H, d, $J = 8.5$ Hz, CH$_2$N), 4.32–4.03 (5H, m, Cp). MS 406 (M$^{35}$Cl), 407 (M$^{37}$Cl), 408 (M$^{35}$Cl), 409 (M$^{37}$Cl).

Synthesis of 7-Chloro-4-(2-(N,N-Dimethylaminomethyl)Ferrocenylmethylamino) Quinoline Oxide (Met D). A solution of 7-chloro-4-(2-(acetoxymethyl)ferrocenylmethylamino)quinoline (100 mg, 0.22 mmol) and NH$_4$OH (4 ml, 25%) in acetonitrile was stirring at 60°C. After 5 h, the solution was extracted by CH$_2$Cl$_2$ (3 ml). The aqueous layer was neutralized by a potassium carbonate solution and extracted for 1 h, the solvent was evaporated, and the resulting oil was purified by column chromatography (eluent, methyl acetate; methyl acetate/triethylamine, 50:45:5), giving Met D as brown crystals (397 mg, 88%). m.p., decomposed before fusion. $^1$H NMR (DMSO-d$_6$) $\delta$ 8.58 (1H, d, $J = 5.3$ Hz, H2), 7.91 (1H, d, $J = 5.1$ Hz, H3), 7.81 (1H, d, $J = 8.96$ Hz, H5), 7.25 (1H, m, H6), 6.47 (1H, d, $J =$ 5.4 Hz, H3), 4.35 (1H, d, $J = 13.1$ Hz, CHNDQ), 4.28 (1H, m, Cp), 4.21 (1H, m, Cp), 4.13 (1H, m, CHNDQ), 4.12 (5H, s, Cp'), 4.10 (1H, m, Cp), 3.74 (2H, 2s, CHNDQ). SM 428 (M$^{35}$Cl + sodium), 408 (M$^{37}$Cl), 406 (M$^{35}$Cl).

Antimalarial Tests. Parasites. Plasmodium falciparum clones 3D7 (provided by Paris Pasteur Institute Genopole, Paris, France) and W2 (provided by Dr. B. Pradines, Institut de Médecine Tropicale du Service de Santé des Armées, Marseille, France) were routinely maintained in cultures (Trager and Jensen, 1976) in complete RPMI 1640 medium (25 mM HEPES and 300 mg/l L-glutamine; Invitrogen), enriched with 10% decomplemented human serum (O$^+$, 5% CO$_2$/90% N$_2$; Air Liquide, Paris, France). Serum and red blood cells were supplied by Centre Régional de Transfusion Sanguine, Lille, France. Cultures were controlled by thin smears stained with Giemsa (Merck, Darmstadt, Germany). Parasitemia were monitored on 1000 red blood cells.

In Vitro Antimalarial Assay on Plasmodium falciparum. The assays were conducted in vitro on asynchronous P. falciparum cultures using a modification of the semiautomated microdilution technique of Desjardin et al. (1979) based on radiolabeled hypoxanthine incorporation in nucleic acids of parasites. Chloroquine (provided by Sigma, Saint Quentin Fallavier, France) stock solutions were prepared in 70% methanol and ferroquine, and its synthesized metabolites in DMSO. The final concentrations ranged from 4.5 to 581.5 nM. Tests starting conditions were 0.5% initial parasitemia and 0.5% hematocrit. After addition of 0.5 $\mu$Ci/well of [H]$^3$hypoxanthine (Amersham Biosciences), microplates were incubated at 37°C under controlled atmosphere (O$_2$ 5%/CO$_2$ 5%/N$_2$ 90%; Air Liquide, Paris, France) for 48 h. Well contents were then harvested on a Skatron system and dried. Incorporation of radiolabeled [H]$^3$hypoxanthine into parasites' nucleic acids was monitored in a fluorescence spec-trometer (PerkinElmer microplate scintillation and luminescence counter; PerkinElmer Life and Analytical Sciences). Fifty and 90% inhibitory concent-
tions (IC_{50} and IC_{90}) refer to molar concentrations of drug causing 50 and 90% reduction, respectively, in [3H]hypoxanthine incorporation compared with drug-free control wells. They were estimated by linear interpolation from dose-response curves.

Results

Metabolism of Ferroquine in Hepatic Microsomal Systems. Ferroquine was incubated with liver microsomal preparations obtained from various species, and both the disappearance of the drug and formation of mono-N-demethyl ferroquine (DMFQ, Met C, HH-3) were monitored (Fig. 2). Strong interspecies differences were observed, and consumption appeared to be much more rapid in rodent and monkey hepatic microsomes than in dog or human hepatic microsomes (Fig. 2A). The extent of formation of DMFQ (Fig. 2B) was well correlated with ferroquine consumption, and it certainly represents the major pathway involved in ferroquine metabolism in all species studied.

Metabolism of Ferroquine in Recombinant Human Cytochromes P450 and FMO Isoforms. To identify the main enzymes involved in ferroquine oxidative biotransformation in human liver, different recombinant human P450 and FMO isoforms were used (Fig. 3). P450 isoforms 2C9, 2C19, 2D6, and 3A4 were all able to oxidize ferroquine (Fig. 3A). The formation of DMFQ was mainly associated with P450 isoforms 2C9, 2C19, and 3A4 (Fig. 3B).

Metabolism of Ferroquine in Freshly Isolated Human Hepatocytes in Primary Culture. The fate of ferroquine was also studied in vitro in freshly isolated human hepatocytes (Fig. 4). The in vitro intrinsic metabolic clearance (Cl_{int}) of ferroquine ranged between 0.032 and 0.067 ml h^{-1} (10^{6} hepatocytes^{-1}) with a mean value of 0.053 ml h^{-1} (10^{6} hepatocytes^{-1}) (n = 4 preparations), which, in our experimental conditions, can be considered as a low to intermediary value. When tested simultaneously, chloroquine exhibited a low metabolic clearance value of 0.029 ml h^{-1} (10^{6} hepatocytes^{-1}) (n = 1 preparation). With two of the human hepatocyte preparations studied, ferroquine was also incubated in the presence of specific and potent P450 inhibitors. In the presence of 10 μM ketoconazole, a potent and specific inhibitor (under these experimental conditions) of CYP3A4, the amount of DMFQ (HH-3) formed appeared to decrease in both hepatocyte preparations studied (Fig. 5), thus confirming the implication of CYP3A4 in the N-demethylation process suggested by the use of recombinant enzymes. A similar inhibitory effect was observed in both donors 1 and 2 in the presence of 10 μM sulfaphenazole, a potent and specific inhibitor of CYP2C9, also suggesting a role of CYP2C9 in contributing to this pathway. In addition, and in donor 2 only, quinidine also exhibited a certain inhibitory effect on ferroquine disappearance kinetics. However, in agreement with the results obtained with recombinant human P450 isoforms, this inhibition by quinidine did not produce any significant decrease in DMFQ (HH-3) formation kinetics, thus confirming that CYP2D6 does not support this particular metabolic route. This result, observed in only one human hepatocyte preparation of two, suggests a possible partial role.
of CYP2D6 in ferroquine biotransformation in certain individuals (Fig. 5).

Metabolic Pathways of Ferroquine in Human Hepatic Models.

The use of human hepatic in vitro models enabled us to establish the major metabolic pathways of ferroquine. The HPLC-UV chromatograms and MS and MS/MS spectra of available synthetic standards (i.e., FQ, Met B, DMFQ or Met C, Met D, and Met G) are shown in Fig. 6. Although it was only present as its glucuronide derivative in human hepatocyte incubates, metabolite G [i.e., 7-chloro-4-(2-(hydroxymethyl)ferrocenylmethylamino) quinoline] was included in these analyses.

All metabolites formed in vitro were separated by HPLC-UV and identified using on-line triple Q-TOF MS/MS detection (Figs. 7a and 8a). They were named according to their HPLC retention time (i.e., A to F in microsomal incubates and HH-1 to HH-4 in hepatocyte incubates). The structures of the metabolites were proposed based on the MS/MS spectra, on fragmentation patterns deducted from these spectra, and on the basis of coelution with available reference com-
Fig. 6. Continued.
Fig. 6. Continued.
FIG. 7. a, HPLC-UV chromatograms (254 nm) of incubation of FQ with animal and human liver microsomal fractions. Metabolites of ferroquine are named A, B, C, D, E, F, and G according to their chromatographic retention time. The control incubation in the absence of NADPH cofactor is shown for mouse only; it did not produce any metabolites in any of the species tested. b, LC-ESI−MS and MS/MS spectral data of metabolites observed in animal and human liver microsomal incubates; data shown were obtained with mouse liver microsomes. Left, LC-ESI−MS spectra of ferroquine (SSR97193, FQ), Met A, Met B, DMFQ (Met C), Met D, Met E, and Met F showing the parent ion fragmented during the subsequent MS/MS analysis. Right, LC-ESI−MS/MS spectra and proposed fragmentation schemes and structures of ferroquine (SSR97193, FQ), Met A, Met B, DMFQ (Met C), Met D, Met E, and Met F. These MS/MS spectra correspond to the fragmentation of the precursor ion detected after single MS analysis.
Fig. 7. Continued.
Fig. 7. Continued.
FIG. 8. A, HPLC-UV chromatograms of incubation of FQ with fresh human primary culture human hepatocytes. Metabolites of ferroquine are named HH-1, HH-2, HH-3, and HH-4 according to their chromatographic retention time (only the peaks related to ferroquine or its metabolites are named). B, LC-MS/MS spectral data of metabolites observed in primary human hepatocytes incubated with ferroquine—structural identification studies.
FIG. 8. Continued.
ANTIMALARIAL PROPERTIES OF FERROQUINE METABOLITES

Fig. 8. Continued.
pounds (i.e., FQ, Met B, DMFQ or Met C, and Met D). Figure 7b and Fig. 8b represent the chemical structure and the ESI/MS and ESI/MS/MS spectra of the different metabolites of ferroquine produced in animal (mouse data shown in Fig. 7) and human liver microsomal fractions (Fig. 7b) or human hepatocytes (Fig. 8b) as well as their fragmentation schemes and proposed structures. To further confirm the structures of the main metabolites, a sample of mouse liver microsomal incubate was spiked with the mixture of available metabolites B, C, D, and G (Fig. 9). This spiking experiment confirmed that metabolites named B and C were the di- and mono-N-demethylated derivatives because they coeluted with the corresponding synthetic references and showed identical MS and MS/MS spectra to those of these two references. Metabolite D coeluted with the mono-N-oxide synthesized reference and it showed identical MS and MS/MS spectra. On the other hand, as expected, the synthetic reference corresponding to metabolite “G” (only observed as its glucuronide derivative in human hepatocyte incubates) did not coelute with any chromatographic peak and exhibited a retention time slightly longer ($T_R = 33.02$ min) than that of the carboxylic acidic derivative named metabolite “F” ($T_R = 32.22$ min).

The analysis of mouse liver microsomal incubates allowed to identify several metabolites related to an oxidative process (oxidation and/or N-dealkylation). In humans, the metabolism was moderate. The main metabolism route (accounting for at least 50% of total ferroquine disappearance in all species studied) consisted in an oxidative N-demethylation of ferroquine on the terminal tertiary amine group, yielding mono-N-demethyl ferroquine (DMFQ, Met C), and, subsequently, di-N-demethyl ferroquine (Met B). A second pathway, N-dealkylation on the amino-quinoline secondary amine, was quantitatively less important and led to the loss of the lateral chain carrying the ferrocene ring and the formation of 7-chloro-4-aminooquinoline (Met A). A third pathway resulted in the elimination of the terminal nitrogen from the lateral chain, thus leading in turn to the formation of 7-chloro-4-(2-hydroxymethylferrocenymethylaminooquinoline (Met G) and the corresponding carboxylic acid (Met F). This pathway represented a minor part of the original amount of ferroquine added.

Two other minor pathways resulted in the formation of two ferroquine N-oxides or hydroxylated derivatives (Met D and E, also named “FQ + O”; see Fig. 10). For metabolite D, the N-oxide on the tertiary amine structure was further confirmed by cochromatography with the synthesized reference, whereas for metabolite E, the precise oxidation position could not be elucidated further in view of the mass spectrometry data available. Table 1 summarizes the relative abundance of the metabolites identified in liver microsomal fractions from animal spe-

![Fig. 9. Mouse microsomal incubate spiked with a mixture of synthetic references B, C, D, and G.](image1)

![Fig. 10. Metabolic pathways of ferroquine in human hepatic models. The analytical HPLC conditions were detailed under Materials and Methods. Samples were analyzed by HPLC-MS/MS using a Micromass Q-TOF fitted with an electrospray source in positive ion mode.](image2)
one major metabolite, active as chloroquine on the W2 strain. Met B and Met G were less active than chloroquine on a chloroquine-sensitive strain, but the product remains as the major metabolite observed in all six species investigated. Finally, in human hepatocytes (Fig. 8b), two glucuronic acid derivatives were also identified, namely HH-1 and HH-4, both formed from either the single oxidized derivative (Met E) or from the deaminated derivative, i.e., 7-chloro-4-(2-hydroxymethylferrocenylmethyl) aminoquinoline (Met G), respectively.

The analysis of intra- and extracellular pooled mixtures shows the presence of a major mono-demethylated derivative (HH-3; DMFQ). The search for chlorinated compounds allowed to identify three additional minor metabolites either under their free form (HH-2, Met B, di-N-demethyl-ferroquine) or glucuronon conjugated (HH-1, glucuronide of a monohydroxylated derivative of ferroquine; HH-4, glucuronide of a ferrocene-methanol derivative most likely resulting from the oxidative deamination of the primary amine HH-2).

**Antimalarial Activity of Main Ferroquine Metabolites.** According to the metabolism pathways identified for ferroquine, the metabolites B, C, D, and G were synthesized and their antimalarial activities were tested on two strains of *P. falciparum* (strain 3D7 chloroquine-sensitive and W2 chloroquine-resistant). Results are shown in Table 2.

The activity of DMFQ on 3D7 strain is very close to that of ferroquine itself and similar to that of chloroquine. The IC_{90}/IC_{50} index of DMFQ is similar to that of ferroquine and significantly lower than that of chloroquine. Concerning the chloroquine-resistant strain W2, DMFQ is less active than ferroquine (3.4-fold) but remains much more active than chloroquine with a lower IC_{90}/IC_{50} index. Activity of Met D appeared much lower than that of ferroquine and chloroquine on a chloroquine-sensitive strain, but the product remains as active as chloroquine on the W2 strain. Met B and Met G were less active than chloroquine on both *P. falciparum* strains tested.

**Discussion**

In humans, the antimalarial drug chloroquine is metabolized into one major metabolite, N-desethylchloroquine, and then into N-didesethylchloroquine. The formation of N-desethylchloroquine was reported to be catalyzed mainly by CYP3A4, CYP2C8, and CYP2D6 (Projan et al., 2003). In this study, we examined the metabolism of ferroquine in different in vitro hepatic models. Our results clearly show that the drug is metabolized more slowly by human liver microsomes than by rodent liver microsomes. This strongly suggests a lower clearance of ferroquine in humans compared with rodents and a longer persistence of efficient concentrations in patients. However, this hypothesis has to be confirmed in clinical pharmacokinetic studies.

In vitro studies using human liver microsomes as well as human recombinant enzymes demonstrated that several P450 isozymes were mainly involved in ferroquine metabolism (i.e., isozymes 2C9, 2C19, 2D6, and 3A4). More extensive inhibition studies using freshly isolated human hepatocytes in primary culture have also demonstrated that CYP3A4 and, to a lesser extent, CYP2C9 both play a major role in the overall hepatic metabolic clearance of ferroquine and more particularly in the major metabolic pathway identified, i.e., the N-demethylation of the terminal tertiary amine. In one preparation of hepatocytes, a noticeable inhibitory effect was exerted by quinidine thus suggesting some partial contribution by CYP2D6 also in some subjects. Thus, the effect of genetic polymorphisms would not be a limiting factor on ferroquine metabolism and on its effectiveness.

The metabolic pathways determined during our study (Fig. 10) confirm, at least in part, the hypothesis previously proposed concerning ferroquine metabolism (Biot et al., 1999b). The main degradation pathway is an oxidative route resulting in the formation of mono-N-demethyl ferroquine (DMFQ, Met C, or HH-3) and di-N-demethyl ferroquine (Met B or HH-2). Another pathway results in the formation of 4-amino-7 chloroquinoline (Met A). These two main metabolic pathways are very similar to those reported previously for chloroquine (Aderounmu, 1983; Verdier et al., 1984; Brown et al., 1985; Karbwang and Wermster, 1993).

Examination of antimalarial activities of major ferroquine metabolites showed that DMFQ remains as active as ferroquine on the chloroquine-sensitive strain 3D7 and less active than ferroquine but much more active than chloroquine on chloroquine-resistant strain W2. The other metabolites (Met B, Met D, and Met G) were less effective than ferroquine (8- to 10-fold according to their IC_{50} values), and their IC_{90} (>100 nM) values show that they would not be efficient in parasite elimination. In a previous study (Biot et al., 1999b), DMFQ was found as active as ferroquine on chloroquine-sensitive strain (HB3) and on a moderate chloroquine-resistant strain (Dd2). Met C was found only 2-fold less active than ferroquine on Dd2.

Thus, DMFQ is significantly involved in the global antimalarial activity of ferroquine previously observed on rodent *Plasmodium* species (Biot et al., 1997, 1999a; Delhaës et al., 2001, 2002). Con-

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**TABLE 1**

<table>
<thead>
<tr>
<th>Metabolite</th>
<th>Mouse</th>
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**TABLE 2**

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<tr>
<th>Product</th>
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<th>Strain W2 IC_{50}</th>
<th>IC_{90}/IC_{50}</th>
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<tr>
<td>Chloroquine</td>
<td>11.6 ± 5.2 (29)</td>
<td>37.5 ± 16.3 (25)</td>
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<td>Ferroquine</td>
<td>8.0 ± 2.5 (29)</td>
<td>15.1 ± 25 (25)</td>
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<tr>
<td>Met C</td>
<td>12.0 ± 7.7 (3)</td>
<td>23.0 ± 13.3 (3)</td>
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<td>Met D</td>
<td>77.2 ± 25.3 (6)</td>
<td>301.8 ± 121.5 (6)</td>
<td>3.8</td>
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<tr>
<td>Met B</td>
<td>73.8 ± 8.5 (3)</td>
<td>259.1 ± 80.2 (3)</td>
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<tr>
<td>Met G</td>
<td>226.1 ± 31.1 (6)</td>
<td>&gt;100 (6)</td>
<td>&gt;4.4</td>
</tr>
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</table>

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IC_{50} and IC_{90} are given as values ± standard deviations. Number of experiences in parentheses.
cerning potential ferroquine therapy in human malaria, the present results obtained with human hepatic in vitro systems indicate that DMFQ may also be involved. This point remains to be further documented by clinical pharmacokinetic studies.

**Conclusion**

Our study allowed us to determine the probable metabolic pathways of ferroquine and the antimalarial properties of the main identified metabolites. Based on 1) the relatively low metabolism rate of ferroquine in various human hepatic in vitro systems compared with rodent systems, 2) the genetic stability and the plurality of the main P450 isoforms involved in ferroquine biotransformation in humans, and 3) the significant antimalarial activity of DMFQ, we expect strong efficacy of ferroquine (SSR97193) in human malaria therapy.

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**References**


Karbwang J and Wernsdorfer W (1993) *Clinical Pharmacology of Antimalarials*. p 107, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand.


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