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Malaria Infection Alters the Expression of Hepatobiliary and Placental Drug Transporters in Pregnant Mice

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ABSTRACT

Preventing and treating malaria in pregnancy is a global health priority. However, little is known regarding the impact of malaria infection on the maternal and fetal disposition of pharmaceuticals and xenobiotics. Our objective was to characterize the expression of key determinants of drug disposition in maternal and fetal tissues in a validated murine model of experimental placental malaria. Balb/c mice were infected with Plasmodium berghei at mid gestation (gestational day [GD] 13) and maternal, placental, and fetal tissues were collected at GD19. Expression of key ABC drug transporters and Cyp3a11 was examined by quantitative polymerase chain reaction. Western blotting was used to examine the protein expression of multidrug resistance protein 1 (MDR1, Abcb1a), ABC transporter B1b (Abcb1b), OCT1 (Abcc1), OCT2 (Abcc2), ABCG2, and Cyp3a11. Compared with controls, placental mRNA expression of Abcb1a, Abcb1b, Abcc1, Abcc2, Abcc3, and Abcg2 were significantly downregulated in the malaria-infected group (P < 0.05), as was placental MDR1 protein (P < 0.05). Significantly decreased hepatic expression of Abcc2, Abcg2, and Abcg11 and significantly increased expression of Abcb1b, Abcc1, and Abcc3 were seen in malaria-infected dams (P < 0.05) in comparison with uninfected controls. The expression of Abcb1a and Abcg2 was significantly decreased in fetal liver of infected dams, whereas levels of Abcb1b were increased (P < 0.05). Maternal and fetal hepatic expression of Cyp3a11 was significantly downregulated in the malaria group (P < 0.05). Together, malaria-induced alterations in the expression of transporters and drug-metabolizing enzymes in maternal and fetal tissues may alter the disposition of endogenous and therapeutic substrates, potentially impacting maternal and fetal outcomes.

Introduction

Each year over 125 million women are at risk of malaria infection during pregnancy. In Sub-Saharan Africa an estimated 25% of all pregnancies are complicated by placental malaria (PM) infection (Dellicour et al., 2010). PM is associated with increased risk of adverse outcomes for both mother and fetus, including an increased risk of anemia, preterm birth, stillbirth, and delivery of low birth weight infants. During pregnancy, malaria-infected red blood cells accumulate in the placental intervillous blood spaces, resulting in altered placental angiogenesis and vascular flow, reduced nutrient and waste transfer, placental insufficiency, and a chronic localized proinflammatory environment (Fried and Duffy, 1996; Matteelli et al., 1997; Miller et al., 2002; Conroy et al., 2013). As such, optimization of pharmacological treatment of malaria in pregnancy is a global health priority. However, little research has been conducted to investigate the determinants of drug-disposition in malaria-infected pregnant populations.

Studies in humans and experimental rodent models have reported malaria-induced alterations in the hepatic metabolism and clearance of numerous drugs, including many that are used in the treatment of malaria (Mihaly et al., 1987; Mansor et al., 1990; Murdoch et al., 1991; Pukrittayakamee et al., 1997). In mice, malaria infection is associated with decreases in the hepatic expression of CYP3A11 and other drug-metabolizing enzymes (DMEs) (De-Oliveira et al., 2006; Carvalho et al., 2009). CYP3A11 is the murine ortholog of human CYP3A4, which is involved in the metabolism of many antimalarials including quinine (Zhang et al., 1997), chloroquine (Kim et al., 2003), halofantrine (Baune et al., 1999), mefloquine (Fontaine et al., 2000), piperaquine (Lee et al., 2012), artemisinin, and artemisinin derivatives (Svensson and Ashton, 1999). Although many of these drugs are used to treat malaria in pregnant populations, little is known about the impact of malaria infection on CYP3A expression in maternal and fetal tissues.

ABBREVIATIONS: ABC, ATP-binding cassette; BCRP, breast cancer resistance protein; DME, drug metabolizing enzymes; GD, gestational day; HO-1, heme oxygenase-1; MDR, multidrug resistance; MRP, multidrug resistance-associated protein; iNOS, inducible nitric oxide synthase; PM, placental malaria; qPCR, quantitative polymerase chain reaction; TNF, tumor necrosis factor.
In addition to DMEs, the ATP-binding cassette (ABC) drug transporters act as major determinants of maternal and fetal exposure to endogenous and exogenous compounds during pregnancy. The multidrug resistance protein (MDR) 1 (P-glycoprotein; encoded by ABCC1 in humans and Abcb1a and Abcb1b in the mouse), multidrug resistance-associated proteins (MRP; encoded by ABCC genes), and the breast cancer resistance protein (BCRP; encoded by ABCG2) are transporters that mediate the ATP-driven efflux of substrates from liver and kidney and limit drug exposure of highly sensitive sites such as the brain and fetal compartment. Within the placenta, these transporters reduce the maternofetal transfer of their substrates via ATP-driven efflux from the fetal-to-maternal circulation (Fig. 1). Their importance in determining fetal xenobiotic exposure has been well established in vivo in knockout mouse and ex vivo in human placental perfusion models (Vahakangas and Myllynen, 2009; Aye and Keelan, 2013). With regards to therapeutics, MDR1 (P-glycoprotein, ABCB1) plays an important role in the pharmacokinetics of quinine (Pussard et al., 2007; Mukonzo et al., 2010) and could transport other antimalarials, because the Mdr homolog of *Plasmodium falciparum*, PfMDR1, has been shown to extrude a wide variety of antimalarials including amodiaquine, mefloquine, lumefantrine, and artemisinin, thereby contributing to drug resistance (Foote et al., 1989; Wilson et al., 1989; Price et al., 2004; Sisowath et al., 2007; Sa et al., 2009; Chavchich et al., 2010).

The expression of several drug transporters as well as CYP3A are altered in both pregnant and nonpregnant rodent models of bacterial and viral infection, and these changes have been associated with altered disposition of their substrates (Cressman et al., 2012). Administration of bacterial endotoxin also impacts the expression of Cyp3a11 in fetal liver (Xu et al., 2005). Whether these findings extend to malaria infection is unknown. Inasmuch as many clinically important drugs are substrates of the ABC transporters and DMEs, disease-induced changes could have important implications on drug efficacy and toxicity, thereby impacting maternal and fetal outcomes. Hence further investigation on the impact of malaria infection on drug transporters and metabolic enzymes is warranted.

We hypothesized that malaria infection would induce changes in the maternal and fetal expression of drug transporters and Cyp3a11. The impact of malaria was examined in a *Plasmodium berghei* ANKA (PbA) murine model of PM that mimics the pathophysiology and clinical features of human PM (Hviid et al., 2010). To our knowledge, this is the first study to examine the impact of malaria on drug transporters in maternal and fetal tissue.

**Materials and Methods**

**Plasmodium berghei ANKA Placental Malaria Model.** Animal protocols were approved by the Toronto University Health Network Animal Care Committee and performed in accordance with the Canadian Council on Animal Care Guidelines. We used a previously validated mouse model of PM that replicates key pathogenic features of human PM, including placental parasite sequestration, placental inflammation, spontaneous abortion, and fetal growth restriction (Silver et al., 2010). Eight- to ten-week-old Balb/c female mice were obtained from The Jackson Laboratories Inc. (Bar Harbor, ME) and maintained on a 12-hour light/dark cycle with ad libitum access to standard rodent chow and water. Females were mated and checked for the presence of a vaginal plug (GD1). Cryopreserved PbA strain malaria (MR4; American Type Culture Collection, Manassas, VA) was passaged through a male Balb/c mouse as previously described (Silver et al., 2010). On GD13, dams were inoculated with 10⁶ PbA-infected erythrocytes in RPMI (Sigma-Aldrich, Oakville, ON, Canada) via tail vein injection. Control dams were injected with an equivalent volume of RPMI alone. Maternal peripheral parasitemia was monitored daily over the course of infection (GD13–GD19) by thin blood smear with modified Giemsa stain (Protocol Hema3 Stain Set; Sigma-Aldrich) and is reported as percentage of infected red blood cells. Dams were euthanized by CO₂ on GD19. Maternal blood was collected by cardiac puncture, centrifuged at 13,000 rpm for 5 minutes, and plasma was stored at −80°C until further use. Maternal tissues were removed immediately after death and snap frozen in liquid nitrogen. Uteri were removed and examined for evidence of reabsorptions. Yolk sacs were dissected from uteri, and fetuses were removed and weighed. Fetal viability was determined by the pedal withdrawal reflex and placentae and fetal tissues from viable fetuses were removed immediately and snap frozen in liquid nitrogen. Placentae and fetuses were obtained from 5 or 6 dams per group. Samples were subsequently stored at −80°C until further use.

**Total RNA Extraction and Quantitative Polymerase Chain Reaction.** Methods for RNA isolation, cDNA synthesis, and quantitative polymerase chain reaction (qPCR) have been described previously (Anger et al., 2012). Briefly, RNA was extracted from −75 mg of snap-frozen tissue using TriZol reagent (Invitrogen, Carlsbad, CA) and cDNA was synthesized from 2 μg of DNase I treated RNA using the High-Capacity cDNA Reverse Transcription Kit. Total RNA was quantified by UV spectrophotometry. PCR primers and qPCR methods have been described previously (Cressman et al., 2007). Following cDNA synthesis, real-time PCR analysis was performed using Applied Biosystems 7500 Real-Time PCR System and SYBR Green PCR Master Mix (Applied Biosystems, Foster City, CA). Relative expression levels of target genes were normalized to Gapdh and calculated using the 2⁻ΔΔCT method (Livak and Schmittgen, 2001). 

![Fig. 1.](https://example.com)
Kit (Applied Biosystems, Burlington, ON, Canada) according to manufacturer’s instructions. mRNA expression of drug transporters and Cyp3a11 were determined by qPCR using LightCycler technology with SYBR detection (Roche Diagnostics, Montreal, QC, Canada). qPCR oligonucleotides were synthesized at The Hospital for Sick Children (DNA Synthesis Centre, Toronto, ON, Canada) and reconstituted in nuclease-free DEPC H₂O (Table 1). Amplicon sequences were amplified as described elsewhere (Anger et al., 2012). Melt-curve analysis was used to ensure primer specificity. Expression levels of each gene were determined using the Roche LightCycler II software (Ver. 3.5) configured with the Roche LightCycler II Real-time qPCR instrument (Roche Diagnostics GmbH, Hamburg, Germany). Gene-of-interest expression in each sample was normalized to cyclophilin A mRNA expression. Data are presented as percentage of expression compared with control ± S.E.M.

Detection of MDR1 Protein Expression by Western Blot. Given the dissimilar changes seen in the expression of Aabchla and Aabchlb mRNA in several tissues and the fact that both of these mRNA encode for the MDR1 protein in mice, we further investigated the impact of malaria on the protein expression of MDR1. Methods for protein isolation and Western blotting have been described previously (Anger et al., 2012). Briefly, protein samples were isolated from 300 mg of snap-frozen tissue homogenized in lysis buffer containing dithiothrieto (1 mM; Sigma-Aldrich), phenylmethylsulfonyl fluoride (0.5 mM; BioShop Canada Inc., Burlington, ON, Canada), and 1× protease-inhibitor cocktail (Sigma-Aldrich) at 4°C. Homogenates were centrifuged at 18,000 g for 15 minutes at 4°C, and the supernatant was isolated. Protein concentrations were measured using the Bradford assay. Protein samples containing 50 μg of isolated protein were separated via 10% SDS polyacrylamide gel electrophoresis and transferred to polyvinylidene difluoride membranes (Bio-Rad Laboratories Canada, Ltd., Mississauga, ON, Canada). Polyvinylidene difluoride membranes were then blocked in 5% nonfat dry milk in Tris-buffered saline + 0.1% Tween 20, membranes were incubated with an anti-mouse horseradish peroxidase-labeled secondary antibody (1:500, 1 mg/ml mC219 clone; IDEXX Laboratories Biotechnology, Inc., London, ON, Canada) overnight at 4°C, followed by Aabchla (C219) mouse monoclonal antibody (1:500, 1 mg/ml mC219 clone; ID Laboratories Biotechnology, Inc., London, ON, Canada). Polyvinylidene difluoride membranes were then blocked in 5% nonfat dry milk in Tris-buffered saline + 0.1% Tween 20, membranes were incubated with an anti-mouse horseradish peroxidase-labeled secondary antibody (1:5000; goat-anti mouse; Jackson ImmunoResearch Laboratories, Inc., West Grove, PA) for 1 hour in 2% nonfat milk TBST. Bound immunoreactive proteins were detected using an ECL Plus chemiluminescence kit (Amersham Biosciences, Baie d’Urfé, QC, Canada) and visualized using the Alpha Innotech FluorChem imaging system (San Leandro, CA). To confirm equivalent protein loading, each blot was stained with Avidol Black (0.03% Napthol Blue Black in 3% acetic acid) (BioShop Canada Inc.) and allowed to air-dry before scanning at 600 dpi using an HP Scanjet 7400C. The optical density of each lane was determined using ImageJ (Software version 1.44o) for Macintosh. Unfortunately, because of low expression and limited quantity of fetal tissues, we were unable to assess MDR1 protein expression in fetal liver.

Total Cellular Antioxidant Assay. Total cellular antioxidant capacity of hepatic lysates from infected and control dams were measured using the Cayman antioxidant assay kit (Cayman Chemical Company, Ann Arbor, MI), which evaluates the combined effect of all antioxidants present in tissue. The colorimetric antioxidant assay was conducted according to the manufacturer’s protocol. Briefly, ~150 mg of maternal liver was homogenized on ice in 1 ml of homogenization buffer (5 mM potassium phosphate, pH 7.4, containing 0.9% NaCl and 0.1% glucose) and centrifuged at 12,000g for 15 minutes at 4°C, and supernatant was collected and stored on ice until use. Protein concentrations were measured using the Bradford assay. Whole cell lysate samples (5–10 mg/ml) and kit reagents were added to a 96-well plate, and absorbance of sample was determined using an ultraviolet-visible spectrophotometer at 750 nm following manufacturer’s protocol. Results were then calculated and reported as micromoles of total antioxidant levels relative to the Trolox standard, normalized to total hepatic protein content.

Serum Chemistry Analysis. Total bile acid concentrations were analyzed in plasma samples obtained from infected and control dams at a certified GLP laboratory (IDEXX Laboratories, Inc., Markham, ON, Canada) using current standard methods of the International Federation of Clinical Chemistry. Total bile acid levels were also compared in 100 mg liver homogenate samples of infected and control dams using the Mouse Total Bile Acids Assay Kit (Crystal Chem Inc., Downers Grove, IL) following manufacturer’s protocol.

Statistical Analysis. All data were analyzed with GraphPad Prism 5.0 for Macintosh (GraphPad Software, Inc., San Diego, CA). Tests on maternal and fetal physiologic parameters were completed using Student’s unpaired two-tailed t test. To assess for differences in gene and protein expression between the infected and control groups, Student’s unpaired two-tailed t tests were conducted. Levels of significance for all statistical analyses were set at or below α = 0.05, with the following symbols denoting statistical significance: *P < 0.05, **P < 0.01, and ***P < 0.001. Performing the nonparametric Mann–Whitney U test yielded comparable results to Student’s unpaired two-tailed t test. Gene and protein expression results are presented as mean percentage of control ± S.E.M.

Results

Maternal and Fetal Parameters. Given the established impact of malaria infection on maternal and fetal weight and splenomegaly in humans, we confirmed whether these changes were present in this study. Increasing peripheral parasitemia was seen from GD16 to GD19 from 2.37 ± 0.38 to 49.88 ± 2.67% at GD16 and GD19, respectively. A corresponding decrease in maternal body weight was observed with Pbs-infected dams weighing 7.53 ± 1.21 g less at GD19, relative to uninfected dams (P < 0.05). No significant

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TABLE 1
Sequences of oligonucleotide primers used for qRT-PCR analysis.
differences were seen on GD13 or GD16. Spleen weight was significantly higher in PbA-infected dams relative to uninfected control dams (208.1 ± 13.0 versus 102.2 ± 8.9 mg; P < 0.001). Fetal weight was also significantly lower in fetuses obtained from PbA-infected dams relative to those from uninfected control dams (748.50 ± 40.38 versus 1082.00 ± 44.71 mg, respectively; P < 0.001).

Increased Hepatic Inflammation and Oxidative Stress. We examined mRNA expression of hepatic inducible nitric oxide synthase (iNOS) and heme oxygenase-1 (HO-1) as these enzymes are both induced by hepatic inflammation and have been shown to play a protective role in host response to malaria infection (Taylor et al., 1998; Seixas et al., 2009; Sass et al., 2012). As depicted in Fig. 2A, we identified pronounced increases in the hepatic expression of both iNOS and HO-1 in the maternal liver of PbA-infected dams, relative to uninfected control dams (P < 0.001). We also observed a significant decrease in the total cellular antioxidant capacity of the livers of infected dams relative to uninfected control dams (P < 0.001) (Fig. 2B).

Hepatic Cyp3a11 and Drug Transporters in Maternal Liver. Given that hepatic metabolism and transport processes influence the pharmacokinetics of xenobiotics and their metabolites within the maternal circulation and that these processes are known to be modulated by infection and inflammation, we examined whether malaria infection would alter their expression. Expression of Cyp3a11 was significantly decreased (P < 0.001) in the livers of infected dams relative to uninfected control dams (Fig. 3A). Significant decreases in the expression of the canalicular transporters Abcc2, Abcg2, Abcb11 were seen in the livers of infected dams, where expression levels ranged from 11 to 54% compared with controls (Fig. 3A). A dramatic increase in mRNA expression of Abcb1b (P < 0.001) was seen in the infected group, whereas Abcb1a was unaffected. Hepatic protein expression of the gene product of Abcb1a and Abcb1b, multidrug resistance protein 1 (MDR1), was not significantly different between infected and control dams (Fig. 4). Dramatic increases in the expression of the basolateral transporters Abcc1 and Abcc3 were observed in the livers of infected dams (P < 0.001) (Fig. 3A). We also found a significant decrease in the expression of the organic anion transporter Slo2b1 (40 ± 33%; P < 0.01), whereas the expression of Slo10a1 (also known as the Na+-dependent taurocholate transporter, Ntcp), an important transporter involved in hepatic bile salt uptake was not significantly changed relative to control dams (80 ± 30%; P > 0.05).

Malaria Infection Alters Total Plasma Bile Acid Levels. Because jaundice, hyperbilirubinemia, and hepatic cholestasis are seen in severe malaria and because bilirubin and bile acids are substrates for many of the same transporters (Treerasertsuk et al., 2010), we investigated the functional consequence of the observed PbA-induced changes in the maternal hepatic expression of the bile transporters by examining the levels of endogenous serum bile acids. The bile salt export transporter (ABCB11) is a critical determinant of bile acid homeostasis in liver and facilitating hepatobiliary clearance of lipophilic substrates. We hypothesized that the decreased expression of canalicular Abcb11 would result in decreased efflux of bile salts into bile, resulting in a compensatory increased transport into the maternal circulation by Abcc1 and Abcc3 at the basolateral domain (Fig. 3A). These processes in turn would result in significantly increased serum bile acids. As illustrated in Fig. 3B, we observed a significant and dramatic increase of ~80-fold in total serum bile acid concentrations in PbA-infected dams relative to uninfected control dams (382.0 ± 152.3 versus 4.833 ± 0.1667 μmol/l, respectively). Relative total bile acid levels were significantly increased in the livers of PbA infected dams (195 ± 32% of control values, P < 0.05).

Drug Transporter Expression Changes in Maternal Brain. The expression of Abcb1a, Abcb1b, and Abcg2 was assessed in whole brain homogenates of pregnant dams because of the important protective role they play in the blood-brain barrier. A significant increase in Abcb1b was observed in infected dams relative to control dams (158 ± 22%; P < 0.01). We observed a corresponding significant increase in the protein expression of MDR1 in brain isolated from PbA-infected dams compared with controls (P < 0.05; Fig. 4). No significant differences were observed in the expression of Abcb1a or Abcg2.

Gene Expression in the Maternal Kidney. The expression of Abcb1a and Abcb1b was assessed in whole kidney homogenate due to their role in the extrusion of drugs and other xenobiotics from the kidney proximal tubule into the tubule lumen. We observed significant 2- to 3.5-fold increases in the expression of Abcb1a (350 ± 101%; P < 0.05) and Abcb1b (226 ± 99%; P < 0.05) in infected compared
with control dams. Likewise, malaria infection was associated with a significantly higher renal protein expression of MDR1 ($P < 0.05$, Fig. 4).

**Drug Transporter Expression in the Placenta.** Given the critical role of placental drug transporters in fetal drug accumulation and their function as a protective barrier limiting fetal exposure to toxic xenobiotics, we investigated the impact of malaria infection on the placental expression of several ABC efflux drug transporters. Compared with controls, we observed significant decreases in the placental mRNA expression of *Abcb1a, Abcb1b, Abcc1, Abcc2, Abcc3, and Abcg2* in malaria-infected dams ($P < 0.05$) (Fig. 5). A significant decrease in the protein expression of MDR1 was seen in placenta isolated from infected dams compared with uninfected controls ($P < 0.05$; Fig. 4).

**Expression of Hepatic Cyp3a11 and Drug Transporter Expression in Fetal Liver.** Given that fetal hepatic metabolism and transport processes may influence levels of xenobiotics and their metabolites within the fetal compartment, we examined whether malaria infection would alter their expression. As depicted in Fig. 6, we observed significant changes in the expression of *Cyp3a11* and drug transporters in the fetal liver. Significant 40–70% decreases in expression of fetal hepatic *Cyp3a11, Abcb1a, Abcg2, and Abcb11* was seen in pups isolated from infected dams compared with uninfected controls, whereas the expression of *Abcb1b* was significantly increased ($P < 0.01$). Contrary to changes observed in the maternal liver, the expression of fetal liver *Abcc1* (151.94 ± 62.00% of control; $P = 0.097$) was not significantly altered.

**Discussion**

In this study we demonstrated that malaria imposes significant changes in the expression of *Cyp3a11* and transporters including *Abcb1a, Abcc1, Abcc3, Abcb11*, and *Abcg2* in maternal and fetal tissue of pregnant mice. This was associated with functional changes in the transport of bile acid substrates because plasma bile acid concentrations were dramatically increased in the infected dams. Evidence of inflammation and oxidative stress was also seen in maternal liver. A substantial decrease in the expression of *Cyp3a11* was seen in livers obtained from malaria infected dams. The downregulation we observed likely stems from inflammation associated with parasitic infection. Our data demonstrating increases in *HO-1* and *iNOS* mRNA as well as decreased antioxidant levels support this. This is in agreement with a body of literature illustrating infection and inflammation-mediated downregulation of hepatic CYP3A in rodents and humans (Cressman et al., 2012). Previous reports also indicate reduced expression of *Cyp3a11* in nonpregnant rodent models of malaria (De-Oliveira et al., 2006; Carvalho et al., 2009). Inflammation-mediated suppression of CYP3A4 activity has been shown to impart clinically important changes in patients (Morgan et al., 2008).

*Cyp3a11* was also downregulated in fetal livers of pups from malaria-infected dams. Although little is known about the impact of maternal disease on fetal gene expression, it was previously reported that endotoxin administration elicited a reduction in expression of *Cyp3a11* in maternal and fetal livers on GD17 (Xu et al., 2005). Although expression of *Cyp3a11* in fetal liver is much lower than that of adults, levels increase rapidly from GD16 to postgestation,
therefore infection-mediated downregulation of gene expression could impact ontogenic changes and hepatic function in the fetus and neonate. Inasmuch as so many of the antimalarial drugs are metabolized by CYP3A, inflammation-mediated changes could have important implications for metabolic capacity of both mother and developing offspring.

In the malaria-infected dams we also observed pronounced changes in the hepatic expression of several transporters that are involved in the transport of bile and bilirubin, and this was associated with a dramatic 80-fold increase in serum levels of bile acids. This could have important consequences on fetal outcomes because increased levels of bilirubin and bile acids within maternal plasma are clinical features associated with poor pregnancy outcomes including premature birth, fetal distress, and stillbirths (Uneke, 2007; Lammert et al., 2000). Expression of Abcb11, the key transporter responsible for secretion of bile salts into bile, was decreased by nearly 10-fold in the infected animals, resulting in increased hepatic accumulation of bile acids. Observed increases in basolateral expression of Abcc3 and Abcc1 likely served to shuttle excess bile acids from hepatocytes into maternal blood. The changes in expression of these transporters and increased serum bile acids are consistent with other animal models of inflammation-induced cholestasis (Vos et al., 1998; McGillicuddy et al., 2009; Yang et al., 2009; Kosters and Karpen, 2010). It is believed that increased expression of basolateral efflux transporters is a homeostatic mechanism evoked to protect hepatocytes (Wagner et al., 2009; Keppler, 2011). Decreases in Abcb11 are also frequently associated with downregulation of uptake transporters such as Slco10a1 (Ntcp) in cholestasis. Although we did not detect significant changes in Slco10a1, expression of Slco2b1, which is involved in sodium-independent bile acid uptake was significantly downregulated.

ABCB1/MDR1 is involved in absorption, distribution, and clearance of many clinically important drugs. This transporter has been shown to transport quinine (Pussard et al., 2007; Mukonzo et al., 2010) and may play a role in transport of other antimalarial drugs as discussed earlier. In maternal liver, mRNA levels of Abcb1b but not Abcb1a were increased; however, protein levels of MDR1 were unchanged. Previous studies in rodent models of infection and inflammation have also shown an induction of Abcb1b mRNA.
However, the contribution of \textit{Abcb1b}, relative to \textit{Abcb1a}, to hepatic MDR1 protein expression is currently debated. To this point, decreased hepatic MDR1 protein expression, corresponding to decreased \textit{Abcb1a} mRNA levels, has been shown in endotoxin-treated rats, despite an observed 10-fold increase in mRNA levels of \textit{Abcb1b} (Wang et al., 2005). We observed decreased \textit{Abcb1a} expression and increased \textit{Abcb1b} expression in fetal livers from infected dams. This suggests that drug transporter regulatory mechanisms occur in fetal tissues and that these tissues are also subject to inflammation-mediated changes in gene expression. Although expression of \textit{Abcb1a} and \textit{Abcb1b} is much lower in fetal liver than that of adult levels (Sharma et al., 2013), levels are thought to increase rapidly postgestation (Lee et al., 2011); therefore inflammation-mediated alterations in gene expression could impact ontogenic changes and potential function in fetal and neonatal livers.

Interestingly, we found increased expression of \textit{Abcb1b} in brains of infected dams, which was associated with increased protein expression of MDR1. Changes in MDR1 expression at the blood-brain barrier impact the central nervous system exposure and effects of its substrates. Therefore, malaria may be associated with a reduced accumulation of MDR1 substrates in brain. Our findings may provide a mechanism to a previous study investigating mefloquine brain permeation in malaria-infected rodents. Farinotti (de Lagerie et al., 2009) observed a 2-fold decrease in concentrations of mefloquine (a MDR1 substrate) in the brains of mice infected with malaria compared with controls. It is plausible that malaria-induced changes in expression of MDR1 in brain contributed to these altered brain concentrations. Conversely, a decreased expression of \textit{Abcb1a} and MDR1 has been reported in the brains of endotoxin-treated rats. These divergent results may stem from potential differences in models and chronicity of infection. Inflammatory stimuli such as endotoxin, viruses, and malaria exert effects on the immune system through unique mechanisms. Endotoxin is a characteristic TLR4 ligand (Koga and Mor, 2010) and may downregulate gene expression via the activation of nuclear factor-κB downstream. The viral mimetic poly I:C activates the immune system through TLR2 and TLR3 pathways. In contrast, \textit{P. falciparum} glycosylphosphatidylinositol and the malaria pigment hemoglobin have been shown to activate TLR2, TLR4, and TLR9 (Coban et al., 2005; Trinchieri and Sher, 2007; Erdman et al., 2008), and this broad TLR activation may result in a unique effect on gene regulation and consequent protein expression.

Drug transporters in kidney are known to impact the pharmacokinetics and renal clearance of numerous drugs, and the expression of these transporters can be altered by disease states (Cressman et al., 2012). Indeed, within our study, we found a significant increase in expression of \textit{Abcb1a} and \textit{Abcb1b} in infected compared with control dams. Likewise, malaria infection was associated with a significantly higher renal protein expression of MDR1. Others have also reported infection or inflammation-mediated increases in the mRNA and protein expression of MDR1 in kidney (Hartmann et al., 2005; Heemskerk et al., 2010). Increased renal expression of MDR1 in endotoxin-treated mice was associated with increased renal elimination of the MDR1 substrate doxorubicin (Hartmann et al., 2005). It is plausible that malaria-imposed changes could impact renal clearance of antimalarials and other substrates.

One of our key objectives was to examine expression of transporters in placenta because these proteins are important in fetal protection. In addition to the decreased expression of \textit{Abcb1a} and \textit{Abcb1b} resulting in a corresponding reduction in immunodetectable levels of MDR1, we observed decreased expression of several other transporters including \textit{Abcc1-3} and \textit{Abcg2}. These proteins are also important in transport of drugs, conjugated-drug metabolites, and endogenous substrates (e.g., bile acids) (Cressman et al., 2012). Previous studies in models of bacterial and viral infection have also reported similar changes (Petrovic et al., 2008; Petrovic and Piquette-Miller, 2010). In endotoxin-treated rats, decreased placental expression of \textit{Abcg2} and \textit{Abcb1} was associated with increases in fetal accumulation of the ABCG2 and ABCB1 substrates glyburide and sestamibi (Wang et al., 2005; Petrovic et al., 2008). The implications of our findings suggest that comparable changes in drug disposition may occur in malaria infection and may contribute to increased fetal exposure to endogenous and exogenous compounds.

Changes in fetal expression of transporters were similar to the changes seen in the maternal liver. This may suggest that comparable regulatory mechanisms are occurring in fetal and maternal liver and also suggests that transporter regulatory pathways are intact in the fetal liver. Therefore fetal exposure to potentially toxic substances, such as the elevated concentrations of bile acids observed in the malaria-infected dams, may be further altered because of infection-mediated changes to transporters and metabolizing enzymes in placental and fetal tissues. Very little is known about the expression of transporters and DMEs in fetal tissues and even less about how disease states impact the expression of these proteins. Nevertheless, this field is currently evolving, and it will be important to investigate how these alterations impact the in vivo disposition of their substrates. Whether these changes persist in the developing fetus and offspring and the consequences is an important question and currently being examined in ongoing studies.

Herein, we demonstrate that malaria infection alters expression of a number of drug transporters and Cyp3a11 in maternal and fetal tissues during pregnancy. If these findings translate to malaria infection in human pregnancy, altered maternofetal disposition and clearance of endogenous and exogenous substrates may have important clinical consequences.

\textbf{Authorship Contributions}

\textit{Participated in research design}: Cressman, McDonald, Silver, Kain, Piquette-Miller.

\textit{Conducted experiments}: Cressman, McDonald, Silver.

\textit{Performed data analysis}: Cressman, Piquette-Miller.

\textit{Wrote or contributed to the writing of the manuscript}: Cressman, McDonald, Silver, Kain, Piquette-Miller.

\textbf{References}


De-Oliveira AC, Da-Matta AC, and Paumgartten FJ (2006) Plasmodium berghei (ANKA): inflammation-mediated changes in gene expression. Although expression of \textit{Abcb1a} and \textit{Abcb1b} is much lower in fetal liver than that of adult levels (Sharma et al., 2013), levels are thought to increase rapidly postgestation (Lee et al., 2011); therefore inflammation-mediated alterations in gene expression could impact ontogenic changes and potential function in fetal and neonatal livers.


