Liver Injury in Uncomplicated Malaria is an Overlooked Phenomenon: An Observational Study

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Abstract

Background: Liver injury is a known feature of severe malaria, but is only incidentally investigated in uncomplicated disease. In such cases, drug-induced hepatotoxicity is often thought to be the primary cause of the observed liver injury, and this can be a major concern in antimalaria drug development. We investigated liver function test (LFT) abnormalities in patients with imported uncomplicated malaria, and in Controlled Human Malaria Infection (CHMI) studies.

Methods: Clinical and laboratory data from 484 imported malaria cases and 254 CHMI participants were obtained from the Rotterdam Malaria Cohort database, and the Radboud University Medical Center database (between 2001 and 2017), respectively. Routine clinical LFTs, clinical profiles, parasite densities, hematological, and inflammation parameters were assessed in 217 patients with imported falciparum malaria upon admission, and from longitudinal data of 187 CHMI participants.

Findings: Upon admission, the proportion of patients with imported uncomplicated malaria and elevated liver enzymes was 128/186 (69%). In CHMI, 97/187 (52%) participants showed LFT abnormalities, including mild (64%, N1.0 ≤ 2.5× upper limit of normal (ULN)), moderate (20%, 2.5 ≤ N 5.0xULN) or severe (16%, N 5.0xULN). LFT abnormalities were primarily ALT/AST elevations and to a lesser extent γGT and ALP. LFT abnormalities peaked shortly after initiation of treatment, regardless of drug regimen, and returned to normal within three to six weeks. Positive associations were found with parasite burden and inflammatory parameters, including cumulative inflammatory cytokine responses and oxidative stress markers (r = 0.65, p = 0.008, and r = −0.63, p = 0.001, respectively).

Interpretation: This study shows that reversible liver injury is a common feature of uncomplicated falciparum malaria, most likely caused by an enduring pro-inflammatory response post treatment. The recognition of this phenomenon is of clinical relevance for individual patient care as well as clinical development of (new) antimalarial drugs.

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1. Introduction

Malaria continues to play a critical role in the global infectious disease burden with significant morbidity and mortality, especially in sub-Saharan Africa. International travelers are also at risk in >90 countries worldwide, mainly in Africa, Asia, and the Americas [1]. Clinical malaria is characterized by a systemic inflammatory response induced by asexual Plasmodium parasites. Plasmodium falciparum is responsible for most malaria-related deaths globally [1]. Severity of disease is determined by multiple factors, including parasite species and timing of antimalarial treatment [2]. The majority of severe falciparum malaria manifestations are most likely related to cytoadherence of parasitized red blood cells (RBCs) to the vascular endothelium, to each other (platelet-mediated agglutination) [3], or to uninfected

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The underlying pathogenesis of liver damage is largely unknown. Furthermore, liver involvement has only been incidentally investigated in uncomplicated malaria [14–16].

Previously, we regularly observed pronounced elevations in liver function tests (LFTs) often shortly upon initiation of curative treatment in patients with imported uncomplicated malaria. We hypothesized that liver injury might arise through a mechanism other than drug-induced hepatotoxicity, or the substantial sequestration observed in severe disease [4,17]. Understanding this clinical feature of uncomplicated malaria could support clinicians in drug-related decision making, and in particular drug development, where frequency of adverse hepatic reactions is a leading concern. Here, we performed a retrospective analysis to determine the frequency of LFT abnormalities in patients with imported uncomplicated malaria, and used longitudinal prospective data of controlled human malaria infection (CHMI) studies to further investigate the significance, dynamics and pathophysiological basis of liver injury.

2. Methods

2.1. Study design and population

Clinical and laboratory data from 484 imported malaria cases and 254 individuals participating in 17 CHMI studies were obtained from the Rotterdam Malaria Cohort database, and the Radboud University Medical Center database, respectively. The Rotterdam Malaria Cohort consists of patients diagnosed with imported malaria who presented at the Rotterdam Harbour Hospital or the Erasmus University Medical Center between 2002 and 2017. For this study, clinical and laboratory data from patients with imported P. falciparum malaria were selected (S1 figure). Patients with a known history of liver disease, or concomitant infections at admission were excluded (e.g. hepatitis B, HIV, schistosomiasis, urinary tract infections, and respiratory tract infections). Furthermore, patients that received antimarial treatment prior admission were also excluded. Data on concomitant medication use other than antimalarial treatment, antipyretic therapy (e.g. acetaminophen) or information on (chronic) alcohol intake were not available. Because of the retrospective nature of the analysis and use of anonymized data, ethical approval or informed consent was not necessary, as stated in the Medical Research involving Human Subject Act (WMO).

Healthy malaria-naïve male and female participants aged 18–35 years were recruited for the CHMI studies between 2001 and 2016. Extended screening included hematological and biochemistry parameters, serology for asexual stages of P. falciparum, and hepatitis B, C and HIV, as previously described [16,18]. All study participants provided written informed consent at screening visit. All clinical trials were approved by the Radboudumc Committee on Research Involving Human Subjects (CMO), the Central Committee on Research Involving Human Subjects (CCMO) of the Netherlands, or the Western Institutional Review Board (WIRB). The studies were conducted according to the principles outlined in the Declaration of Helsinki and Good Clinical Practice standards, and registered at ClinicalTrials.gov. Study EHMI-3, conducted in 2001, was not registered in an online database such as ClinicalTrials.gov.

2.2. Controlled human malaria infection

CHMI participants were all challenged by bites of malaria-infected mosquitoes or direct venous inoculation of sporozoites/blood stage parasites. The challenges were conducted with different parasite clones: NF54 (airport malaria) [19], 3D7 (clone of NF54) [20], NF135 (Cambodia) [21], and NF166 (Guinea, West Africa) [22]. Daily blood sampling included parasitological assessment (thick blood smears and qPCR) and/or safety laboratory parameters.
2.3. Laboratory investigations

All clinical laboratory data were assessed by standard hematological and biochemical tests on peripheral blood specimens. Biochemical liver tests included: aspartate aminotransferase (AST), alanine aminotransferase (ALT), gamma-glutamyl transferase (γGT), alkaline phosphatase (ALP), lactate dehydrogenase (LD), and total bilirubin. Reference laboratory values for AST were < 30 or < 35 U/L (female or male); ALT < 35 or < 45 U/L (female or male); γGT < 40 or < 55 U/L (female or male); ALP < 100 or < 115 U/L (female or male); total bilirubin < 17 μmol/L; LD < 250 U/L (S2 table).

2.4. Inflammatory cytokines and oxidative stress analysis

Inflammatory cytokines (IL-1β, IFN-α, IFN-γ, TNF-α, MCP-1, IL-6, IL-8, IL-10, IL-12/70, IL-17A, IL-18, IL-23, and IL-33) were determined in study CHMI-trans1 using flow-based multiplex (Legendplex). For the oxidative stress analysis, TaqMan gene expression Assays (Applied Biosystem) were used to measure antioxidant gene expression levels for Superoxide dismutases (SOD1 and SOD2), Nitric oxide synthase (NOS3), Catalase (CAT), Peroxiredoxin (PRDX1) and Glutathione S-transferase Kappa (GSTK1) from whole blood by using qPCR (S1 Material). The cumulative anti-oxidant and cytokine responses were determined through transformation of data into a Z-score (each value subtracted by the mean of the group and divided by the SD of the group).

2.5. Definitions

Liver function test (LFT) abnormalities were graded using an adaptation of the World Health Organization (WHO) Adverse Event Grading System 2003: mild LFT elevations (>1·0 - 2·5× upper limit of normal (ULN)), moderate (>2·5 - 5·0×ULN), and severe (>5·0×ULN) elevations. Imported malaria patients were classified as having uncomplicated malaria by absence of WHO criteria 2014 [23] for severe P. falciparum malaria on admission or during hospitalization. Abnormal bilirubin levels were not included in the incidence or grading of LFT abnormalities, since the bilirubin increases found in the imported malaria cases most likely reflect haemolysis and could possibly bias the elevated liver enzyme prevalence in imported malaria. Similarly, lactate dehydrogenase (LD) was not included in the incidence or grading of LFT abnormalities, due to its strong relation to haemolysis and low liver specificity. Patients with imported malaria were considered partially-, semi-, or non-immune. In short, patients born in a malaria-endemic country living in the Netherlands were considered partially immune. Patients that were born and still residing in a malaria-endemic area were presumed semi-immune. All other patients were considered non-immune [24]. Data on previous episodes of malaria were not available.

The parasite load was estimated by measuring the area under the curve of parasitaemia over time, and computed by GraphPad Prism 5 (2009, San Diego California USA).

2.6. Statistical analysis

All data were analyzed with GraphPad Prism 5 or SPSS software version 24 (IBM Inc., Chicago, IL, USA). Descriptive analyses are presented as percentages, mean with standard deviation, or median with interquartile range. Mann Whitney U test was used for comparison of non-normal continuous data or independent groups/samples. Chi square test or Fisher’s exact test was used for comparison of qualitative variables and for determining association between various variables. Correlation between different parameters was assessed by Spearman’s rho. A P-value of <0·05 was considered as statistically significant.

3. Results

The general characteristics on admission of the 217 included patients with imported P. falciparum malaria are shown in Table 1 and S1 table. On admission day, LFTs were increased in 128/186 (69%) of patients with uncomplicated falciparum malaria (Table 1) and 27/31 (87%) in severe disease (S1 table). In uncomplicated disease, abnormalities appeared to be mild in 93/186 (50%), moderate in 26/186 (14%), and severe in 9/186 (4·8%) of the cases. The median ALT of all uncomplicated malaria patients with LFT abnormalities was 48 U/L (range 9–236 U/L, IQR 31–63 U/L), and the median AST was 41 U/L (range 9–236 U/L, IQR 31–63 U/L). The median γGT was 71 U/L (range 20–447 U/L, IQR 49–113 U/L), the median ALP was 83 U/L (range 36–265 U/L, IQR 64–101 U/L), the median total bilirubin was 22 μmol/L (range 3–115 μmol/L, IQR 17–43 μmol/L), and the LD was 286 μmol/L (range 52–656 μmol/L, IQR 113–346 μmol/L). No statistically significant differences were found between ages, gender, or immune status in patients with or without LFT abnormalities. Furthermore, LFT abnormalities appeared in all treatment groups (Table 1). In a sub-group analysis of the malaria cohort, increases in LFT abnormalities were also found in 23/50 (46%) of the patients with a Plasmodium vivax infection (S1 table). No significant differences in other parameters than in LFTs between cases with and without LFT abnormalities were observed (S1 table).

<table>
<thead>
<tr>
<th>Table 1 General characteristics of patients with imported uncomplicated falciparum malaria on admission day.</th>
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<tr>
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<tr>
<td>Age</td>
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<tr>
<td>Gender</td>
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<tr>
<td>Female</td>
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<td>Male</td>
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<tr>
<td>Immunity</td>
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<tr>
<td>Unknown</td>
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<tr>
<td>Non-immune</td>
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<tr>
<td>Partially</td>
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<tr>
<td>Semi</td>
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<tr>
<td>Parasitaemia/μL</td>
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<tr>
<td>AST (U/L)</td>
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<tr>
<td>ALT (U/L)</td>
</tr>
<tr>
<td>γGT (U/L)</td>
</tr>
<tr>
<td>Alkaline phosphatase (U/L)</td>
</tr>
<tr>
<td>Bilirubin (total) (μmol/L)</td>
</tr>
<tr>
<td>LD (U/L)</td>
</tr>
<tr>
<td>Haemoglobin (mmol/L)</td>
</tr>
<tr>
<td>Leukocytes (x10⁹/L)</td>
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<tr>
<td>Lymphocytes (x10⁹/L)</td>
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<tr>
<td>Thrombocytes (x10⁹/L)</td>
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<tr>
<td>CRP (mg/L)</td>
</tr>
<tr>
<td>Creatinine (μmol/L)</td>
</tr>
<tr>
<td>Urea (mmol/L)</td>
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<tr>
<td>Sodium (mmol/L)</td>
</tr>
<tr>
<td>Potassium (mmol/L)</td>
</tr>
<tr>
<td>Lactate (mmol/L)</td>
</tr>
<tr>
<td>Temperature (°C)</td>
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<tr>
<td>Treatment</td>
</tr>
</tbody>
</table>

All data are presented as median (IQR) or N (%). LFT# = liver function test abnormalities. Statistical differences are tested using Mann-Whitney or Chi square. Clinical laboratory reference ranges can be found in S2 table.
## Table 2
Overview of CHMI studies.

<table>
<thead>
<tr>
<th>Study</th>
<th>Year</th>
<th>Challenge</th>
<th>Treatment drug</th>
<th>Subjects with parasitaemia (n)</th>
<th>Mean peak parasitaemia (Pf/μL)</th>
<th>Subjects with LFT* (n (%)</th>
<th>Severity</th>
<th>Treatment criterion</th>
<th>LFT timepoints</th>
<th>Registered</th>
</tr>
</thead>
<tbody>
<tr>
<td>EHMI-3</td>
<td>2001</td>
<td>3D7- mosquito bite</td>
<td>chloroquine</td>
<td>5</td>
<td>21.6</td>
<td>4 (80)</td>
<td>mild</td>
<td>48 h after positive TS</td>
<td>multiple timepoints*</td>
<td>–</td>
</tr>
<tr>
<td>EHMI-8A</td>
<td>2007</td>
<td>NF54- mosquito bite</td>
<td>artemether-lumefantrine</td>
<td>5</td>
<td>15.1</td>
<td>18 (100)</td>
<td>moderate</td>
<td>positive TS</td>
<td>–</td>
<td>NCT00442377</td>
</tr>
<tr>
<td>LSA-3</td>
<td>2008</td>
<td>NF54- mosquito bite</td>
<td>artemether-lumefantrine</td>
<td>18</td>
<td>26.7</td>
<td>10 (4)</td>
<td>severe</td>
<td>positive TS</td>
<td>–</td>
<td>NCT00509158</td>
</tr>
<tr>
<td>EHMI-8B</td>
<td>2009</td>
<td>NF54- mosquito bite</td>
<td>atovaquone-proguanil</td>
<td>7</td>
<td>3.7</td>
<td>4 (57)</td>
<td>mild</td>
<td>positive TS</td>
<td>Standardd</td>
<td>–</td>
</tr>
<tr>
<td>TIP1</td>
<td>2010</td>
<td>NF54-NF135 mosquito bite</td>
<td>atovaquone-proguanil</td>
<td>10</td>
<td>17.6</td>
<td>–</td>
<td>severe</td>
<td>positive TS</td>
<td>–</td>
<td>NCT01002813</td>
</tr>
<tr>
<td>TIP2</td>
<td>2010/2011</td>
<td>NF54- PBF2 L.M.*</td>
<td>atovaquone-proguanil</td>
<td>15</td>
<td>43.6</td>
<td>5 (33)</td>
<td>mild</td>
<td>positive TS</td>
<td>–</td>
<td>NCT01086917</td>
</tr>
<tr>
<td>ZonMw1</td>
<td>2011</td>
<td>NF54- mosquito bite</td>
<td>atovaquone-proguanil</td>
<td>12</td>
<td>28.5</td>
<td>4 (33)</td>
<td>moderate</td>
<td>positive TS</td>
<td>–</td>
<td>NCT01218853</td>
</tr>
<tr>
<td>EHMI-9</td>
<td>2011</td>
<td>3D7- mosquito bite or BS challenge</td>
<td>atovaquone-proguanil</td>
<td>19</td>
<td>9.5</td>
<td>11 (58)</td>
<td>severe</td>
<td>positive TS</td>
<td>Standardc</td>
<td>–</td>
</tr>
<tr>
<td>ZonMw2</td>
<td>2012</td>
<td>NF54- mosquito bite</td>
<td>atovaquone-proguanil</td>
<td>9</td>
<td>27.8</td>
<td>6 (67)</td>
<td>mild</td>
<td>positive TS</td>
<td>Standardc</td>
<td>–</td>
</tr>
<tr>
<td>TIP4</td>
<td>2012</td>
<td>NF135- mosquito bite</td>
<td>atovaquone-proguanil</td>
<td>19</td>
<td>81.1</td>
<td>8 (42)</td>
<td>moderate</td>
<td>positive TS</td>
<td>Standardc</td>
<td>–</td>
</tr>
<tr>
<td>TIP3</td>
<td>2012</td>
<td>NF54-NF135-NF166 mosquito bite</td>
<td>atovaquone-proguanil</td>
<td>15</td>
<td>37.4</td>
<td>6 (32)</td>
<td>severe</td>
<td>positive TS</td>
<td>Standardc</td>
<td>–</td>
</tr>
<tr>
<td>TIP5</td>
<td>2012/2013</td>
<td>NF54- mosquito bite</td>
<td>atovaquone-proguanil</td>
<td>21</td>
<td>15.5</td>
<td>11 (52)</td>
<td>mild</td>
<td>positive TS</td>
<td>standardd</td>
<td>–</td>
</tr>
<tr>
<td>BMGF2a</td>
<td>2014</td>
<td>NF54-NF135-NF166 mosquito bite</td>
<td>atovaquone-proguanil</td>
<td>20</td>
<td>20.1</td>
<td>8 (42)</td>
<td>moderate</td>
<td>2 pos. qPCR (&gt;500 Pf/mL)</td>
<td>–</td>
<td>NCT012149550</td>
</tr>
<tr>
<td>BMGF1</td>
<td>2014</td>
<td>NF54- mosquito bite</td>
<td>atovaquone-proguanil</td>
<td>8</td>
<td>0.1</td>
<td>0 (0)</td>
<td>mild</td>
<td>pos. qPCR (&gt;100 Pf/mL)</td>
<td>standardd</td>
<td>–</td>
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<tr>
<td>BMGF2b</td>
<td>2015</td>
<td>NF54-NF135-NF166 mosquito bite</td>
<td>atovaquone-proguanil</td>
<td>31</td>
<td>1.5</td>
<td>7 (23)</td>
<td>severe</td>
<td>pos. qPCR (&gt;100 Pf/mL)</td>
<td>standardd</td>
<td>–</td>
</tr>
<tr>
<td>BCG-EHMI</td>
<td>2016</td>
<td>NF54- mosquito bite</td>
<td>atovaquone-proguanil</td>
<td>19</td>
<td>1.0</td>
<td>7 (37)</td>
<td>mild</td>
<td>pos. qPCR (&gt;100 Pf/mL)</td>
<td>standardd</td>
<td>–</td>
</tr>
<tr>
<td>CHMI-trans1</td>
<td>2016</td>
<td>3D7- mosquito bite</td>
<td>sulfadoxine-pyrimethamine/</td>
<td>16</td>
<td>20.0</td>
<td>16 (100)</td>
<td>severe</td>
<td>positive TS</td>
<td>multiple timepoints*</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>piperaquine</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td>NCT02836002</td>
</tr>
</tbody>
</table>

* Total subjects with LFTs measured: 187
  97 (52) 62 (33) 19 (10) 16 (9)

* Total subjects with LFTs measured (thick smear studies): 129
  83 (64) 50 (39) 18 (14) 15 (12)

* Total subjects with LFTs measured (qPCR studies): 58
  14 (24) 12 (21) 1 (2) 1 (2)

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* liver function test abnormalities.

* TS = thick smear.

* standard LFT measurements at 3 time-points: baseline, 2 days after treatment, and at the end of study.

* LFTs are only measured on baseline and at the end of study.

* >3 LFT measurement time-points (range of 4–13).

* intra-muscular injection.

** blood stage challenge.
To better define the dynamics and basis of liver injury, we used data of CHMI studies, which entails extensive screening to minimise confounding effects. Longitudinal data of 17 CHMI studies with a total of 254 participants with patent parasitaemia, showed that LFTs were elevated in 97/187 (52%) of the participants with LFTs measured during infection (Table 2). In most cases standard LFT measurement time-points were obtained at baseline, 2 days post-treatment, and at the end of study. Elevations were primarily limited to ALT/AST elevations, and to a lesser extent, to γGT and ALP. Increased transaminases were found in 83/129 (64%) of the CHMI participants when treated at positive qPCR (treatment threshold of 5·0xULN) and severe (15/83 (18%), ≤1·0xULN) and moderate (18/83 (22%), >1·0 ≤ 2·5xULN), and severe (15/83 (18%), >5·0xULN) elevations (Table 2). The incidence of LFT elevations was 14/58 (24%) in volunteers treated at positive qPCR (treatment threshold of ~50/83 (60%), N = 5·0xULN) and severe (15/83 (18%), ≤1·0xULN) and moderate (18/83 (22%), >1·0 ≤ 2·5xULN) and severe (15/83 (18%), >5·0xULN) elevations (Table 2).

When more frequently assessed over the course of the study (2 CHMI studies, n = 34), mild LFT elevations became apparent just prior to initiation of treatment (Fig. 1). The majority of LFT abnormalities exceeded the upper limit of normal on the day of treatment, and peaked around 2–6 days after initiation of antimalarials. This corroborates with data from EHM-I-3 (n = 5) where treatment is initiated 48 h after a positive thick smear. The observed abnormalities were transient, normalizing at study end (around day 35–42 after challenge infection). Furthermore, a distinct pattern of timing of peak of transaminase elevations is found between individuals. Some participants show peak elevations early after treatment and others more delayed. These specific patterns, as well as the severity of the observed abnormalities, seem regardless of different drug regimens used.

The association between parasite load & liver function tests

CHMI participants with LFT abnormalities presented with a higher parasite load than those without LFT abnormalities (p < 0.001), although the range was relatively large (Fig. 2A). There was a positive association between LFT values and parasite load in the CHMI studies (r = 0.33, p < 0.001) (Fig. 2B). No significant differences were found between the different groups of LFT severity grades. In addition, in clinical cases with imported uncomplicated P. falciparum infections, a positive association was found between parasite density on admission day, and LFT abnormalities (r = 0.25, p = 0.005).

4. Clinical laboratory parameters and liver function tests

Analysis of clinical laboratory parameters in CHMI participants showed that lowest platelet, leukocyte, and lymphocyte counts, as well as maximum LD levels, independently associated with LFT abnormalities (p < 0.0001, p = 0.01, p < 0.0001, p < 0.0001, respectively) (Fig. 3). However, prior to treatment these parameters poorly predicted LFT abnormalities.

We hypothesized that inflammation, well known to be involved in malaria pathogenesis, might play a role in these abnormalities. In the imported uncomplicated malaria cases, C-reactive protein (CRP) was increased on the day of admission in patients with LFT abnormalities.
lesser extent, to the nature of the induced inflammatory response in relation to LFT abnormalities. A significant reduction in the average of anti-oxidant gene expression SOD1 (p = 0.03), SOD2 (p = 0.001), NOS3 (p < 0.0001), CAT (p < 0.0001), and GTSK1 (p < 0.0001) and an increase in expression of PRDX1 (p = 0.007) was observed during the malaria infection (one day after treatment) (S4 figure). The cumulative anti-oxidant response of these markers through transformation into a Z-score, showed a negative association between the anti-oxidant response and the LFT abnormalities (r = -0.63, p = 0.001) (Fig. 4). All markers normalized by the end of the study.

5. Discussion

This study shows that abnormalities in liver function test (LFT) are a relatively frequent finding in uncomplicated falciparum malaria, and occur regardless of the choice of drug regimen. These abnormalities are transient in nature, resolving within 3–6 weeks. The typical pattern of LFT elevations is primarily limited to ALT/AST elevations, and to a lesser extent, to γGT and ALP, and peaks in particular two to six days after initiation of treatment. Furthermore, the study shows a significant association between LFT elevations and parasite load, inflammatory markers and reduced expression of oxidative stress markers. Early treatment based on qPCR thresholds can decrease the occurrence and severity of LFT abnormalities in CHMI.

Hepatic dysfunction is a well-known feature of severe malaria, contributing to clinically significant complications such as hypoglycaemia, metabolic acidosis, impaired drug metabolism, and finally organ failure [8,12]. Malaria-associated liver damage in uncomplicated malaria, however, has rarely been investigated so far [25]. Observational studies are often restricted in number and limited to admission samples only [15], therefore, underestimating incidence and severity. Other studies do not differentiate non-severe from severe disease in their analysis [9,14,26]. This study specifically advocates the relevance in relation to potential clinical implications in uncomplicated disease, which constitutes the vast majority of clinical malaria cases. This study highlights that LFT abnormalities can be severe (up to >20 xULN), but are apparently fully reversible upon parasitological cure, corroborating previous reports [25–27].

The observed liver injury seems to have a hepatocellular basis, as indicated by the disproportionate elevation in serum transaminases relative to alkaline phosphatase. Peak bilirubin levels precede amimalarial treatment in imported malaria cases but not CHMI. This suggests that these elevations are likely due to haemolysis leading from higher parasitaemia in these patients compared to CHMI volunteers. Similarly, Woodford et al. show that bilirubin elevations in clinical cases peak on admission day, resolving early after treatment in contrast to the later occurring peak of transaminases [14]. The absence of clearly elevated bilirubin levels in CHMI adduces that these events may not result in a functional liver impairment, since conjugation of bilirubin occurred normally. Serum albumin or clotting factors were not tested in the current study, and therefore, it cannot be formally excluded that biosynthetic capacity of the liver may be compromised. The absolute increase in serum transaminases is of little prognostic value since the liver can
recover from most forms of acute injury, due to its large regenerative capacity. In absence of symptoms such as haemorrhage or altered consciousness, significant hepatic dysfunction seems highly unlikely in patients without history of liver disease.

The potential contribution of infection transformation, from the liver stage to blood stage infection, to LFT abnormalities remains uncertain. However, similar LFT abnormalities are found CHMI studies with a blood stage challenge, where the liver stage of the parasite is circumvented [14]. This, together with the observation that no substantial LFT abnormalities are found on day 6–7 (day of liver schizont rupture), makes it less likely that the liver stage can cause significant LFT abnormalities on its own. It is unknown if the liver stage could influence the severity of the observed abnormalities.

This study provides evidence that the underlying pathogenesis of liver injury in uncomplicated malaria conceivably differs from severe malaria. In severe falciparum malaria, tissue damage is thought to be at least partly related to decreased oxygen supply and disturbed metabolisms due to parasite sequestration in the microvascular capillary system [7,17]. However, in CHMI only very low parasite densities are present and sequestration likely limited. Systemic inflammation with leukocytopenia, thrombocytopenia, increased d-dimer, CRP, and IFN-γ concentrations is a typical hallmark of malaria even at the very low density of parasitaemia as observed after CHMI [28,29]. This study shows a clear relationship between these parameters and LFT abnormalities in falciparum malaria. Together with the timing of LFT abnormalities post treatment, and the presence of low-density parasitaemia, this suggests an inflammation-based mechanism of liver injury. Similarly, lung injury with impaired alveolar-capillary function is described to deteriorate after antimalarial treatment, reflecting a prolonged inflammatory response to parasite killing [30]. Histopathology of lung tissue in vivax malaria supports this hypothesis with an increase in alveolar-capillary monocytes and pulmonary phagocytic cell activity after initiation of treatment [31]. An adjacent hypothesis describes platelet sequestration as a downstream promoter of liver injury by exacerbating local inflammation and leukocyte accumulation [32], which correlates with the observed thrombocytopenia and leukocytopenia. Interestingly, although inflammation-induced liver injury is common in other infectious diseases (e.g. extrahepatic bacterial infection and sepsis), it seems to predominantly have a cholestatic nature in contrast to uncomplicated malaria [33].

Fig. 3. Clinical laboratory parameters and liver function test (LFT) abnormalities in CHMI. Maximum lactate dehydrogenase (LD), and minimum platelets, leukocytes, and lymphocytes measured in CHMI participants without- and with LFT abnormalities (LFT#). Error bars represent the mean with SD. **P = 0.004; ***p < 0.001.

Fig. 4. Association between liver function test abnormalities, and cumulative cytokine levels and cumulative anti-oxidant gene expression. The cumulative cytokine score comprises IFNγ, MCP-1, IL-6, IL-8, IL-10, IL12p70, IL-17a, IL-18 and the cumulative anti-oxidant gene expression comprises SOD1, SOD2, NOS3, CAT, GTSK1, and PRDX1 measured on 1 day after treatment (DT + 1) in CHMI-trans1. Values are standardized as a Z-score. xULN of LFTs = x upper limit of normal range of liver function tests (LFTs). The xULN of LFTs values are the peak LFT abnormalities measured from day 2 after treatment and the samples available onwards.
Systemic inflammation is the net result of an interplay between pro- and anti-inflammatory responses, and a shift towards a pro-inflammatory status can cause malfunctioning of the host’s mitochondria in malaria, leading to organ damage [34]. The resulting oxidative stress as observed in uncomplicated malaria is known to play a role in pathogenesis [35]. For instance, lipid peroxidation and antioxidant enzyme activity associate with cholestatic jaundice in Plasmodium vivax patients [36], and oxidative stress causes hepatocyte apoptosis in murine malaria models [37,38]. In this study, we show that anti-oxidant gene expression is down-regulated for SOD1, SOD2, NOS3, CAT, and GSTK1 during infection, and up-regulated for PRDX1. This corroborates with data from rodent studies [39,40] and a non-human primate study with Plasmodium knowlesi [41], where hepatic superoxide scavenging systems, glutathione S-transferase, superoxide dismutase and catalase, decrease during the course of a malaria infection. This net result may be reduced clearance of radicals and subsequent failure to protect cellular constituents from oxidative damage.

Our findings reflect a need to understand and reassess LFT abnormalities in malaria. This will have significant impact on clinical decision-making and in drug development, where they are often interpreted as drug-induced liver injury, particularly in malaria drug studies [27,42]. For example, drug-related serious adverse events in a recent multicentre trial comparing pyronaridine–artesunate or dihydroartemisinin–piperinequine versus current first-line therapies for uncomplicated malaria were associated mainly with increased liver enzymes [43]. Incorrect attribution of liver injury to an antimalarial drug can lead to unnecessary discontinuation or shifts in drug regimens, or impede drug development. Given the diversity of drug regimens used, it is unlikely that the observed LFT abnormalities in this study are caused by antimalarials. Moreover, no marked deterioration of LFTs was observed after a second, higher drug dose [16]. Our data does not support distinct differences between drugs and severity or occurrence of LFT abnormalities. In line with findings from Woodford et al., our data does not show a clear relation between the severity of abnormalities found, the pattern of early- or delayed transaminase elevations, and the different drug regimens used in CHMI. Furthermore, the timing, varied and often limited use of supportive medication (such as paracetamol, known for dose-dependent hepatotoxicity) in CHMI does not support a clear relationship with LFT abnormalities. It seems similarly improbable that the observed injury is parasite strain-specific. Geographically distinct Plasmodium falciparum strains were used in CHMI, and the imported falciparum malaria cases were presumably caused by a wide diversity of strains. In addition, non-falciparum malaria (e.g. Plasmodium vivax) was also shown to increase LFT abnormalities.

The limitations of this study are related to the retrospective observational nature of some of the data. However, the longitudinal CHMI data from healthy participants excludes the majority of confounding factors, and provides a much more thorough description of LFT dynamics. Although, we observed differences between CHMI and naturally-acquired malaria cases, patients with sequential sampling data from the latter seem to have similar LFT dynamics, and affirm previous observations [14].

This study shows that liver function test abnormalities are an underrecognized but common feature of uncomplicated falciparum malaria. The pathophysiological basis is most likely a pro-inflammatory response associated with oxidative stress resulting in transient liver tissue injury. Given the rapid and spontaneous resolution, and the absence of clear functional liver impairment in uncomplicated malaria, these events are unlikely to result in permanent subclinical liver damage. Treatment should remain focused on fast parasite clearance, and a more expectative approach might be warranted to avert unnecessary discontinuation or shifts in antimalarials due to supposed drug-induced liver injury. Nevertheless, supportive drugs with hepatotoxic potential should be limited or given only with appropriate monitoring, and adjunctive therapy that mediates systemic inflammation and oxidative stress may have a potential role in helping to constrain malaria progress into severe disease. Clinical trials testing the safety and efficacy of novel antimalarials should consider the temporal relationship between LFT abnormalities and infection. Importantly, unnecessary early abrogation of further clinical development of promising drugs related to potential or supposed hepatotoxic effects should be carefully considered.

Contributors

IJR, PJJC, and RWS designed the study, which was performed by IJR, LAS, QM, AJV, TB, RWS, IJR, GMJ, JW, LAS, and RK collected the data, and IJR, GMJ, JJH, PJJC, and RWS analyzed and interpreted the clinical data. IJR, XZY, and MA performed, analyzed, and interpreted the cytokine and oxidative stress markers assays, and supervised by AF and RWS. IJR wrote the first manuscript, which was critically reviewed and approved by all authors.

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Declaration of interests

All authors declare no competing interests.

Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

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Appendix A. Supplementary data

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References