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The Pharmacogenetics of the Antimalarial Amodiaquine

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1. Introduction

Malaria is globally the most lethal parasitic disease. With an annual number of new cases reaching hundreds of millions and a mortality of circa 800,000 (WHO, 2010), this disease represents a worldwide major public health concern.

Malaria generally occurs in tropical and subtropical areas, with most of the lethality focused in the African continent, particularly among children under five. The disease further commands a major economic impact in the Developing World estimated as a Gross Internal Product reduction of more than US$ 6 billion for the year 2010 alone (Sachs and Malaney, 2002)(WHO, 2010). Such burden has significantly slowed down the social development of these regions in the last decades.

Malaria is caused by an intracellular Protozoan belonging to the genus Plasmodium. P. falciparum, P. vivax, P. ovale, P. malariae and P. knowlesi are the five different species able to infect humans (Levine, 1988)(Cox-Singh et al., 2008). P. falciparum is responsible for the most severe forms of the disease, and hence the near totality of the mortality.

The parasites are transmitted through an arthropod vector, the dynamics of the disease being the result of a complex interplay between the human host, the parasite and its mosquito vector.

2. Plasmodium falciparum – A brief reference to its life-cycle

As a referential example, the 48-hour life cycle of P. falciparum, the major malaria pathogen – and the principal target of complex chemotherapeutic measures – is herein presented.
We assume as an arbitrary starting point the moment when a female *Anopheles* mosquito infected with *P. falciparum* penetrates the human skin to obtain a blood meal. If the mosquito saliva is infected with parasite sporozoites, these will be injected into the bloodstream of the host. These forms travel in the bloodstream to the liver where they invade hepatocytes. In this intracellular environment it rapidly divides asexually, generating the next life cycle stage form, the merozoites. These, following the rupture of the hepatocyte, are released in the bloodstream. Here, they invade erythrocytes. Once inside the erythrocyte, the merozoite develops towards the mature trophozoite stage. After these, the parasite undergoes a series of asexual divisions to produce a large segmented schizont filled with mono-nucleated merozoites. The erythrocyte then ruptures releasing the merozoites, a clinically important event associated to the characteristic malaria peaks of fever and chills. These merozoites swiftly reinvade new red blood cells, reinitiating the intra-erythocytic cycle. In parallel, a small proportion of merozoites take a new development route towards becoming sexual forms: the male and female gametocytes. These can reinvade the mosquito vector during its blood meal. Inside the mosquito, zygotes will form after meiotic events. Further development will lead to the formation of oocysts. These, after repeated mitotic divisions, produce a large number of sporozoites, which actively migrate to the salivary glands of the mosquito, ready to be injected into the bloodstream of a human. The cycle is hence restarted.

3. Malaria chemotherapy

Chemotherapy has been the mainstay for the clinical control of malaria for hundreds of years. Starting with the introduction of artemisinin rich teas in China 1500 years ago (Hsu, 2009) and the use of barks containing quinine in South America in the XVII Century (Peters, 1970), the XX Century saw the development of several synthetic and semi-synthetic compounds. Quinine prevailed as the major antimalarial drug used worldwide for near 300 years, until the advent of the Second World War. The extension of this conflict drove the search for alternative synthetic variants. Derived from these efforts, chloroquine (CQ), a highly effective 4-aminoquinoline, emerged in the immediate post-War as the global mainstay for the treatment and control of malaria (Coatney et al., 1963). By the end of the 1950s the next major malaria challenge emerged: *P. falciparum* have been able to develop resistance to this drug (Young and Moore, 1961). From two main foci in South East Asia and South America, resistance parasites invaded most of the other malaria-affected regions. In the late 1970s reached Africa. By the end of the Century the burden of malaria topped in a calculated multi-million death toll and an uncontrolled situation in large regions, particularly in the African Continent (Marsh, 1998).

The severity of the situation demanded a change in concept. This came from South East Asia. In the late 1980s, Thailand - a region known to be a major cradle for the development of drug resistance - was fighting with a steep decrease of efficacy of their main national control programme drug, mefloquine (Nosten et al., 1991). A strategy of combining this long half-life drug with the fast acting/short half-life antimalarials of the artemisinin class (re-discovered in China during the 1970s) saved the former during the next decade (Nosten et al., 2000).

The success of artemisinin combination therapy (ACT) in the Thai national malaria programme drove the rapid adoption, and progressive worldwide implementation of this strategy for the treatment of uncomplicated malaria.
This relatively new antimalaria strategy is based on the powerful pharmacodynamic action of the artemisinin derivatives (ARTs). These, typically artesunate or artemether, are known to have a Parasite Reduction Ratio of 1:10,000 (i.e., a reduction towards 0.01% of the initial parasitaemia in 48 hours of treatment), orders of magnitude above the typically found with long lasting quinoline drugs (White, 1997). This effect is short-lived, due to the characteristic very short half live of the ARTs, typically 20 minutes to 2-3 hours (Gautam et al., 2009).

Upon this first impact, the long-standing partner is expected to handle more efficiently the remaining parasite population. The association of drugs with different expected mechanisms of action and associated modes of parasite resistance has been deemed as a strong deterrent for the development of the latter (Eastman and Fido, 2009).

The two global main ACTs in use are artemether-lumefantrine and artesunate-amodiaquine. (WHO, 2010). The latter represents the main drive for this review.

4. Amodiaquine

Amodiaquine (AQ) emerged in the shadow of CQ success, in the late 1940s (Burckhalter et al., 1948). Similar to CQ, AQ has a core 4-aminoquinoline structure. Contrarily to CQ it also represents a Mannich base.

AQ was never used to the same extent as CQ due to the large prevalence of the latter in the global malaria control programmes until the end of the XX Century. Also, its use was severely curtailed in the beginning of the 1990s, upon its removal from the WHO list of recommended antimalarials for the treatment of uncomplicated malaria (WHO, 1990). This decision followed the emergence of a number of clinical reports on rare (ca. 1:2000) but life-threatening secondary events associated to its use in prophylaxis regimens among Caucasian travellers (Larrey et al., 1986)(Rouveix et al., 1989)(Neftel et al., 1986)(Hatton et al., 1986). These included in most cases acute agranulocytosis, but also severe liver damage. During the 1990s, research - mainly based on in vitro approaches and the use of animal models - have pointed for the causing agent to be a toxic short lived quinone-imine (QI) metabolite of AQ (Jewell et al., 1995)(Tingle et al., 1995)(Naisbitt et al., 1997). The mode of action of this putative metabolite is still under discussion, but it is generally accepted that it operates by binding covalently to cell structures or/and as an hapten associated to a specific anti-AQ IgG antibody driven immunological response (Clarke et al., 1990).

The described prophylaxis effects were never formally confirmed in circumstances of the regular treatment of uncomplicated malaria. This lack of confirmatory data has raised some criticisms concerning a possible over-cautious decision at WHO (Olliaro et al., 1996). In fact, the actual usefulness of this decision in a time when the efficacy of CQ was collapsing worldwide is still open to discussion. Nevertheless, AQ as a monotherapy kept being used in many African and South American regions for decades, both in the public and in the private sector.

Interestingly, the fact that AQ has not been as intensively used as CQ possibly slowed down the development of parasite resistance against this drug. AQ was recovered for global use in the XXI Century as combination therapy partner, due its low price and capacity to handle CQ resistance parasites. Two combinations are available, artesunate-AQ (an ACT), and AQ-sulfadoxine-pyrimethamine, although the latter has been recently considered to be withdrawn from the WHO list of recommended drugs for the treatment of uncomplicated malaria (WHO,
Artesunate-AQ (AS-AQ) is particularly prevalent in the African continent, the epicentre of malaria mortality and morbidity. The combination represents the first or second line antimalarial treatment for uncomplicated malaria in more than twenty sub-Saharan countries (www.who.int/entity/malaria/am_drug_policies_by_region_afro/en/).

AS-AQ is administrated orally in one daily dose, for three days. The present guideline is: 4mg/Kg/day artesunate + 10mg/Kg/day AQ (WHO, 2010). Contrarily to other antimalarials (e.g. lumefantrine, CQ, piperazine), the age of the patient does not seem to affect the plasma concentrations of AQ. The present dosing has shown to be effective in areas where resistance to AQ monotherapy was not widespread (<20% of the infections). In the event of rising resistance, changes in the formulation might be necessary, namely increasing the dosing in AQ. Such changes in the dosing have been applied in the past, e.g. with CQ (Peters, 1970) and mefloquine (Carrara et al., 2009).

Presently, AS-AQ is available as a fixed formulation in three tablet options: 25 mg AS/67.5 mg AQ, 50 mg AS/135 mg AQ or 100 mg AS/270 mg AQ (Coarsucam®/Winthrop®, Sanofi-Aventis, Paris; DNDi, Geneva).

Both AQ and desethylamodiaquine (DEAQ, AQ main active metabolite) show significant inter-individual variation on their pharmacokinetic parameters. AQ has a relatively short half-life of 4-12 hours (Giao and de Vries., 2000), being readily biotransformed in the liver towards DEAQ. DEAQ is a fully active antimalarial that, albeit less potent than AQ (Gerstner et al., 2003)(Echeverry et al., 2007) is the main responsible for the long pharmacodynamic effect of AQ therapy (Winstanley et al., 1990). DEAQ has a longer half-life of 3-20 days (Hombhanje et al., 2005)(Hietala et al., 2007). Although AQ has been even considered as a pro-drug due to its short half-life, circumstances of extreme AQ exposure have been documented where this drug was detected in the urine of patients, months after its administration (Winstanley et al., 1987).

AQ has been associated with both mild and severe adverse events. Mild events include mainly gastro-intestinal effects, particularly vomiting (Brasseur et al., 1999)(Adjuik et al., 2002)(Cairns et al., 2010)(Nankabirwa et al., 2010) and self-reported abdominal pain (Parikh et al., 2007)(Bojang et al., 2010), both frequently observed in amodiaquine efficacy clinical trials. Most importantly, several studies have noted situations of (clinically asymptomatic) neutropenia upon AQ therapies in subsets of the treated population (Staedke et al., 2001)(Adjuik et al., 2002). Although this relatively common drop in neutrophil count is not an exclusive effect of this drug (Nankabirwa et al., 2010), it is possibly linked with the rare severe adverse events observed in AQ prophylaxis. Accordingly, in this (now abandoned) higher dose regimens of typically 400 mg/week, the most documented serious adverse event was agranulocytosis (~1:2000 prevalence), followed by hepatic toxicity (~1:16000)(Phillips-Howard and West, 1990)(Hatton et al., 1986).

The few data available suggest that the AQ adverse events are drug dose dependent (Hatton et al., 1986)(Cairns et al., 2010). Although drug associated severe and lethal reactions have not been generally observed in AQ regimens for the treatment of uncomplicated malaria (Olliaro et al., 1996)(Olliaro and Mussano, 2003), mild events are relatively frequent, being a threat for full regimen compliance (e.g. Gerstl et al., 2010), leading to incomplete cure and potential selection of resistant parasites. This effect can be decreased through genetic evidence-based adjustment of the dose, at a personalized level.
In addition, the knowledge of the frequencies of rare genetic variants associated with documented AQ-driven adverse events in certain ethnic groups and regions under AQ exposure can be useful as a pharmacovigilance tool. As an example, and taking into account the surpassing of a specific (evidence-based) threshold of allele frequency, the use of alternative first line ACTs (e.g. aminoalcohol quinoline based, as artemether-lumefantrine) for those regions could be decided. Such type of measures - although not totally preventing - have the potential of decreasing the occurrence of serious events.

It should be noted that such a population pharmacogenetics approach can be of great importance: the effect of fatal adverse events in the public opinion can be very significant, especially after the 1990s temporary withdrawal of AQ from the WHO list of recommended antimalarials. Such dramatic events - in particular involving the typical children under five - could lead to a further mistrust of the public about a drug that is pivotal in a large number of national malaria control programmes.

5. The main players of AQ disposition

As previously mentioned, upon oral absorption AQ is readily metabolized towards the pharmacologically active DEAQ. This biotransformation occurs mostly in the liver and is almost exclusively performed by the cytochrome P450 (CYP) 2C8 (Li et al., 2002). The high specificity of CYP2C8 for this reaction has even led to the proposal of AQ as a specific probe drug for this P450 isoform (Walsky et al., 2004). Besides this main step, other putative AQ metabolites have been proposed and at least partially confirmed (figure 1). These include 2-hydroxy-DEAQ (Churchill et al., 1985), N-Bis-DEAQ (Mount et al., 1986) and M2, the latter initially detected in the microsome-based seminal studies of Li et al (2002), and recently confirmed through in vitro electrochemical approaches (Johansson et al., 2009). A fraction of DEAQ itself is believed to also be transformed in 2-hydroxy-DEAQ through P450 action. Several of these post-CYP2C8 action steps are catalyzed by members of the CYP1 sub-family (Li et al., 2002)(Gil and Gil-Berglund, 2007)(Johansson et al., 2009).

Most importantly, both AQ and DEAQ are able to generate the highly reactive quinone-imine (QI) metabolite responsible for the described serious side affects of AQ therapies. DEAQ is considered less prone to create QIs (Tingle et al., 1995), reinforcing the action of CYP2C8 over AQ as a protective event. The generation of these compounds has been previously proposed to occur spontaneously, but recent investigations have pointed to a fundamental role of CYP1A1 and CYP1B1 as well as the family of myeloperoxidases in the process. In this processes, the M2 metabolite initially identified by Li et al. has been proposed to be a central player in the generation of the toxic QIs (Johansson et al., 2009).

Taking in account the fact that these species are most likely short-lived, it is expected that the enzymes involved in its generation will be present in the location of its toxic action. Suggestively, CYP1A1 and CYP1B1 are essentially extra-hepatic P450 isoforms, with confirmed expression in several blood cell types (e.g. leukocytes)(Furukawa et al., 2004), the most frequent location for these fatal toxicities (neutropenia).

Scarce information is available concerning other ADME phases in AQ metabolism. The analysis of QI adducts in animal models have pointed for the presence of glutathione conjugates, although no specific isoform has ever been determined (Masubuchi et al., 2007). The potential production of phase II metabolites further points to the likely involvement of
phase III (transport) systems. The most common phase III glutathione conjugate transporters are the members of the ATP binding cassette (ABC) superfamily of proteins, and more specifically of the ABCC (also referred as MRP) type of transporters.

A summarized proposal of the complex metabolism of AQ is presented in figure 1.

Fig. 1. The metabolism of AQ. Although the main biotransformation in this process is the synthesis of DEAQ, a constellation of minor – but most likely non-negligible – metabolites have been proposed to result in parallel (Churchill et al., 1985)(Mount et al., 1986)(Li et al., 2002). Most importantly, events leading to the formation of the toxic QIs, involving both AQ and DEAQ are included among them. The presented scheme represents a summary of the available data from in vitro studies with microsomes, animal models, the few available human in vivo data, as well as the most recent information utilizing electrochemical approaches to simulate drug oxidation in vitro (Harrison et al., 1992)(Jewell et al., 1995)(Tingle et al., 1995)(Naisbitt et al., 1997)(Li et al., 2002)(Johansson et al., 2009).
The previously identified M2 metabolite (Li et al., 2002) seems to be a central component in the generation of the QIs from both AQ and DEAQ, with CYP1A1 and CYP1B1 being the main enzymes involved in the process (Johansson et al., 2009). The QIs have been proposed to result from the action of myeloperoxidases, an event that is herein tentatively proposed to involve the M2 metabolite, although a direct action of these enzymes in both AQ and DEAQ cannot be disregarded.

*In vitro* electrochemical approaches have generated a number of putative compounds, the most relevant being indicated here (C8, C9 and C10). This complex of compounds, due to its expected hydroxylated structures has been proposed to most likely represent the previously reported 2-hydroxy-DEAQ (Churchill et al., 1985).

### 6. The pharmacogenetics of AQ metabolism

As described, based on current knowledge, three main drug metabolizing enzymes are involved in the biotransformation of AQ: CYP2C8 (the main one), CYP1A1 and CYP1B1. All of them harbour significant genetic polymorphisms, some with marked effects in the catalytic activities of the respectively coded proteins.

#### 6.1 CYP2C8

The CYP2C8 comprises nine exons. 14 alleles have been annotated in the gene coding for this 490 amino acid enzyme (http://www.cypalleles.ki.se/cyp2c8.htm), most of them rare. Apart from the most prevalent alleles, 2C8*1 (wild type), 2C8*2, 2C8*3, and 2C8*4, the majority of the remaining ones (2C8*5 - 2C8*12, see figure 2) have been identified only in the Japanese population (Soyama et al., 2001)(Nakajima et al., 2003). Few works have evaluated the presence of these minor alleles in other regions (Cavaco et al., 2006)(Suarez-Kurtz et al., 2010), although the output of large consortium projects (e.g. HapMap, www.sanger.ac.uk/resources/downloads/human/hapmap3.html) supports the view of these alleles being specific among the Japanese. On the other hand, 2C8*2, 2C8*3 and 2C8*4 are rare in this population. (Nakajima et al., 2003)(table 1).

African settings represent the major context where AQ therapy is practiced, both in combination with artesunate or sulfadoxine-pyrimethamine. The first CYP2C8 pharmacogenetic study in endemic African populations was performed in East African populations, in the islands of Zanzibar (Cavaco et al., 2005)(table 1). In this population all the most studied mutant alleles, namely 2C8*2, 2C8*3 and 2C8*4, were detected. Further studies in other regions of the continent have confirmed 2C8*2 as the main allele among the native populations (see table 1). Interestingly, outside Zanzibar, 2C8*3 (when found) has been documented at lower frequencies, while 2C8*4 has not been detected at all. These results point to the populations of Zanzibar as somewhat particular, perhaps due to the historical/migration influences from the Arabian Peninsula (Low and Smith, 1976).

The data from native African populations was consistent with previous reports in African-American, where the 2C8*2 allele represents the main mutant allele in Black populations (table 1), with the non-active 2C8*3 mostly present among Caucasians (Cavaco et al., 2006).

A number of *in vitro* studies have been performed to characterize the phenotypic effect of the CYP2C8 polymorphisms.
<table>
<thead>
<tr>
<th>Region (n*)</th>
<th>2C8*2</th>
<th>2C8*3</th>
<th>2C8*4</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Zanzibar (Unguja and Pemba)(n= 165)</td>
<td>13.9%</td>
<td>2.1%</td>
<td>0.6%</td>
<td>Cavaco et al., 2005</td>
</tr>
<tr>
<td>Ghana (Accra)(n= 204)</td>
<td>17.9%</td>
<td>0%</td>
<td>0%</td>
<td>Kudzi et al., 2009</td>
</tr>
<tr>
<td>Ghana (n= 92)</td>
<td>17.9%</td>
<td>n/t</td>
<td>n/t</td>
<td>Adjei et al., 2008</td>
</tr>
<tr>
<td>Ghana (Tamale) (n= 200)</td>
<td>16.8%</td>
<td>0.0%</td>
<td>0.0%</td>
<td>Rower et al., 2005</td>
</tr>
<tr>
<td>Burkina Faso (Bobo-Dioulasso) (n=275)</td>
<td>11.5%</td>
<td>0.4%</td>
<td>n/t</td>
<td>Parikh et al., 2007</td>
</tr>
<tr>
<td>Southern India (n=245)</td>
<td>0.8%</td>
<td>2.9%</td>
<td>n/t</td>
<td>Arun Kumar et al., 2011</td>
</tr>
<tr>
<td>Malaysia(^b)(n= 57)</td>
<td>0.8%</td>
<td>1.2%</td>
<td>0%</td>
<td>Muthiah et al., 2005</td>
</tr>
<tr>
<td>South East Asia (n= 20)(^c)</td>
<td>0.0%</td>
<td>5.0%</td>
<td>0%</td>
<td>Solus et al, 2004</td>
</tr>
<tr>
<td>Papua-New Guinea (Madang) (n = 305)</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
<td>Hombhanje et al, 2005</td>
</tr>
<tr>
<td>Brazil (scattered regions)(n= 1034)(^d)</td>
<td>6.4%</td>
<td>8.6%</td>
<td>3.4%</td>
<td>Suarez-Kurtz et al., 2010</td>
</tr>
</tbody>
</table>

\(^a\)number of subjects analysed; n/t (non tested)
\(^b\)Any 2C8*3 or 2C8*4 alleles present confounded in the 2C8*1 group.
\(^c\)Indian ethnic group
\(^d\)Ethnically mixed populations, originated from several scattered regions of the country. The sample is claimed by the authors to be representative of the present day Brazilian population; when considering self-reporting ethnic origin, the 2C8*3 frequency increased among “White” subjects, while the *2 among “Black” individuals.

*(note: this compilation is intended to be a representative sample of the published information and not an exhaustive collection of the available data)*

Table 1. CYP2C8 main allele frequencies in populations from malaria endemic regions (Africa, Asia, Oceania and South America).

The CYP2C8*2 allele is characterized by the presence of an I269F SNP. Quantitative HPLC/UV analysis of the DEAQ resulting from *in vitro* incubations of recombinant CYP2C8*2 enzyme with AQ pointed to a significant decrease of approximately 30% in the \(V_{\text{max}}\) (maximum substrate transformation rate) as compared with the wild-type (2C8*1) reference (0.16 ± 0.06 µmol/min/µmol P450 *vs* 0.25 ± 0.09 µmol/min/µmol P450). In parallel, the mutant allele was associated with a three-fold increase in its Km (substrate concentration at which the reaction reaches half of the \(V_{\text{max}}\) value) (2.55 ± 1.06 µM *vs* 0.81 ± 0.23 µM) (Parikh et al., 2007). This decreased performance was reflected in a significantly lower intrinsic clearance (\(V_{\text{max}}/K_{\text{m}}\)) of AQ (2C8*2: 0.05 1/min/µmol P450 *vs* 2C8*: 0.30 l/min/µmol P450). As for the CYP2C8*3, the presence of the two linked mutations characterizing this protein (R139K and R399K) had a marked effect on its catalytic capacities, with no AQ metabolism detected at any of the tested substrate concentrations (Parikh et al., 2007). It was concluded that the 2C8*3 protein has very low AQ metabolism activity. These results obtained with AQ are supported by data from previous studies using the CYP2C8 probe drug paclitaxel (Dai et al., 2001).
As for 2C8*4, *in vitro* experiments by Singh *et al.* have reported this protein as having a 10-fold decrease in paclitaxel 6-alpha hydroxylase activity. The associated SNP (I264M, see figure 2) was proposed to affect heme insertion and the correct folding of the protein (Singh *et al.*, 2008). It is expectable that this also represents a low activity allele as for the biotransformation of amodiaquine.

More recently, Gao and collaborators performed tests based on the heterologous expression of 2C8*2, 2C8*3 and 2C8*4 in *Saccharomyces cerevisiae*. Microsomes prepared from the transfected yeast cells were incubated with different concentrations of AQ. The experiments showed a decrease in the overall activity of the mutant alleles towards ~45-75% of the wild type values (Gao *et al.*, 2010). The reasons behind the observed large differences in the capacities of these alleles between the microsome based systems and the *in vitro* based ones (i.e. reconstituted protein) are not fully clear.

Some of the remaining minor alleles have been studied in some detail in Japan. The 2C8*5 allele carries a 475delA mutation causing a frameshift effect leading to a premature translation termination at residue 177, and hence no functional protein (Soyama *et al.*, 2002). Using microsomes obtained from CYP2C8 transfected COS-1 cells, the 2C8*6, 2C8*9 and 2C8*10 proteins were shown not to significantly differ from the wild type (2C8*1) on paclitaxel 6-alpha hydroxylase activity. As for 2C8*8, this allele showed more than ten fold decrease in catalytic activity, associated with a less stable protein. As expected, 2C8*7 – involving the introduction of a translational stop codon - had no detectable enzyme activity (Hichiya *et al.*, 2005). Finally, Hanioka and collaborators have recently used the same yeast system for testing the 2C8*13 and 2C8*14 alleles. While 2C8*13 did not show significant differences in V<sub>max</sub> and K<sub>m</sub> for paclitaxel 6-alpha hydroxylation as compared with 2C8*1, 2C8*14 showed a 3 fold higher K<sub>m</sub> albeit with no changes in the V<sub>max</sub>.

A summary of relevant CYP2C8 SNPs and the associated phenotype characteristics is presented in figure 2.

*In vivo*, there is limited information on the impact of CYP2C8 polymorphisms in AQ therapy, both in terms of efficacy and risk of adverse events.

Parikh and collaborators have performed a retrospective analysis of an AQ monotherapy efficacy trial searching for *in vivo* phenotype/2C8 genotype associations (Parikh *et al.*, 2007). The study involved 275 uncomplicated malaria patients from the region of Bobo-Dioulasso, southwest Burkina Faso. No associations were found between the clinical success of AQ therapy and the presence of minor CYP2C8 alleles (2C8*2 and 2C8*3). This is probably due to the fact that DEAQ, the main AQ metabolite, also represents a fully active antimalarial entity, i.e. enhanced AQ metabolism does not lead to an inactive metabolite that would decrease the clinical (pharmacodynamic) success of the therapy. More importantly, Parikh *et al.* found a positive correlation between harbouring a 2C8*2 allele and events of mild side effects, mainly abdominal pain (self reported): 52% of occurrences among the 2C8*2 carriers versus 30% for the 2C8*1/*1 subjects. This is until now the only reported association between the patient CYP2C8 status and effects of AQ therapy. Another trial, performed in Ghana did not report such an association (Adjei *et al.*, 2008). It also did not find clear associations between the pharmacokinetic parameters of AQ and the presence of less active alleles, although a trend for decreased DEAQ plasma concentrations among the 2C8*2 carriers was noted. It must be noted however, that the smaller size of this study (n=92) might have prevented the detection of such associations.
These are the only two published studies exploring the impact of the CYP2C8 polymorphism in AQ based therapies, while near 100 million treatments performed in the last five years (WHO, 2010). It is evident that there is an urgent need of further research in this area, in order to guarantee the longest “useful life” for this drug, presently a cornerstone in the global control of malaria.

6.2 CYP1A1

CYP1A1 represents a 512 amino acid cytochrome P450 enzyme mainly expressed in extra-hepatic tissues, including the lungs (Willey et al., 1997), intestine (Paine et al., 1999)(Paine et al., 2006), placenta (Hakkola et al., 1996) and, importantly, lymphocytes (Dey et al., 2001, van Duursen et al., 2005). It is usually present at low constitutive baseline levels. The gene is readily inducible through the AHR (Aryl Hydrocarbon Receptor) regulatory pathway, typically by exposure to PAHs (polycyclic aromatic hydrocarbons, e.g. components of tobacco smoke). Upon induction, CYP1A1 can also be found in the liver, where it usually is at very low (pre-induction) baseline levels. CYP1A1 is able to metabolize a number of clinically relevant drugs, including the calcium blocker flunarizine, the anticancer drug toremifene and the cardiovascular disease drug fluvastatin. Significant inter-individual variability in the elimination of these drugs has been described. This variability is probably of minor clinical concern, due to the non-hepatic patterns of expression of the gene. In the context of this review, the importance of CYP1A1 is mainly focused in its probable involvement in the generation of short lived but toxic AQ metabolites (Johansson et al., 2009).

The CYP1A1 gene (15q24.1) is organized in 7 exons. It harbours significant polymorphisms, comprising eleven established alleles (figure 2), as well as a number of SNPs with haplotype associations still to be assigned (http://www.cypalleles.ki.se/cyp1a1.htm). A significant portion of the non-synonymous polymorphisms is concentrated at exon 7 (figure 2)(table 2).

The CYP1A1*2 allele has been documented in vitro to represent a more drug responsive gene upon exposure to the prototype inducer 2,3,7,8-tetrachlorodibenzo-para-dioxin (TCDD)(studies with the 1A1*2A and 1A1*2B haplotypes)(Spurr et al., 1987)(Landi et al., 1994). Also, at least in the case of 1A1*2B and 1A1*2C, this allele was shown to code for more active enzymes (Cosma et al., 1993). The increased transcriptional response is related to the presence of a T3801C transition in the gene’s 3’ UTR, while the referred enhanced enzymatic activity (reflected specifically in an increased $V_{max}$) is linked with a non-synonymous I462V SNP at exon 7 (Cosma et al., 1993). This enhanced activity of the proteins harbouring 462V (1A1*2B and 1A1*2C) was also confirmed in terms of estrone and 17 ß-estradiol 2-hydroxylation, as a 5-10 fold increase in comparison to the wild type (Kisselev et al., 2005).

The T461N SNP (defining 1A1*4) was shown not to alter significantly the behaviour of its coded enzyme (Kisselev et al., 2005). As for the 3’ UTR T3204C transition defining the 1A1*3 allele (proposed to be specific of African populations) it does not seem to influence the levels of CYP1A1 expression (Smart and Daly, 2000). 1A1*7 represents a frameshift mutation leading to the generation of a stop codon and hence precluding the production of an active enzyme. Finally, alleles 1A1*8 (T448N), 1A1*9 (R464C) and 1A1*10 (R477W) carry non-synonymous SNPs located close to the protein heme binding protein, and are hence expected to affect the activity of the enzyme (Saito et al., 2003).
<table>
<thead>
<tr>
<th>Region (n*)</th>
<th>1A1*2</th>
<th>1A1*7</th>
<th>1A1*3</th>
<th>1A1*4</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Namibia* (n= 134)</td>
<td>14.9%b</td>
<td>n/t</td>
<td>n/t</td>
<td>n/t</td>
<td>Fujihara et al., 2009</td>
</tr>
<tr>
<td>Southwest Libya (El Awaynat and Tahala) (n=129)</td>
<td>6.5%d</td>
<td>n/t</td>
<td>0%</td>
<td>18.1%</td>
<td>Martinez-Labarga et al., 2007</td>
</tr>
<tr>
<td>Midwest and Southeast Nigeria (n= 250)</td>
<td>24.2%e</td>
<td>n/t</td>
<td>13%</td>
<td>0%</td>
<td>Okobia et al., 2005</td>
</tr>
<tr>
<td>South Africa (n= 96)</td>
<td>0%s</td>
<td>n/t</td>
<td>n/t</td>
<td>n/t</td>
<td>Dandara et al., 2002</td>
</tr>
<tr>
<td>Zimbabwe (n= 148)</td>
<td>0%e</td>
<td>n/t</td>
<td>n/t</td>
<td>n/t</td>
<td>Dandara et al., 2002</td>
</tr>
<tr>
<td>Tanzania (n= 114)</td>
<td>1.3%s</td>
<td>n/t</td>
<td>n/t</td>
<td>n/t</td>
<td>Dandara et al., 2002</td>
</tr>
<tr>
<td>Mali (n=116)</td>
<td>24.0%s</td>
<td>n/t</td>
<td>n/t</td>
<td>n/t</td>
<td>Garte et al., 1998</td>
</tr>
<tr>
<td>East India (Chennai) (n=150)</td>
<td>33%e</td>
<td>n/t</td>
<td>n/t</td>
<td>n/t</td>
<td>Suneetha et al., 2011</td>
</tr>
<tr>
<td>Southwest India (Kerala) (n = 146)</td>
<td>20.9%</td>
<td>n/t</td>
<td>n/t</td>
<td>n/t</td>
<td>Sreeja et al., 2005</td>
</tr>
<tr>
<td>Northern India (Delhi) (n= 309)</td>
<td>71.4%b</td>
<td>n/t</td>
<td>n/t</td>
<td>0%</td>
<td>Kumar et al., 2010</td>
</tr>
<tr>
<td>Northern Thailand (Lampang)(n= 287)</td>
<td>84.9%hi</td>
<td>n/t</td>
<td>n/t</td>
<td>n/t</td>
<td>Pisani et al., 2006</td>
</tr>
<tr>
<td>China (Peking)(n= 284)</td>
<td>28.2%h</td>
<td>n/t</td>
<td>n/t</td>
<td>0%</td>
<td>Zhang et al., 2010</td>
</tr>
</tbody>
</table>

* number of subjects analyzed; n/t: not tested

** Bantu (Ocambo) ethnicity

† T3798C tested, defining the presence of 1A1*2A or 1A1*2B. As the I462V was not determined (1A1*2C contribution not included) it is not possible to distinguish between these two forms.

‡ Although these are regions not directly affected by malaria, the nomadic characteristics of the Tuareg populations under study puts them in risk when travelling to sub-Saharan areas (e.g. Northern Mali, Mauritania)

§ 1A1*2A= 4.5%, 1A1*2B= 0.2%, 1A1*2C=1.8%

∥ 1A1*2A= 24%, 1A1*2C= 0.2%. Data on 1A1*2B not available.

Venda ethnicity

Only T3798C tested, so the data should be considered as the result of the 1A1*2A + 1A1*2B composite.

T3798C and I462V tested but no information on the composite of the two giving rise to *2B

286 subjects analysed for 1A1*2A

Only the I462V analysed so 1A1*2A not included and 1A1*2B contribution not available (note: this compilation is intended to be a representative sample of the published information and not an exhaustive collection of the available data).

Abbreviation - CYP1A1: 1A1

Table 2. CYP1A1 allele frequencies of population from malaria affected regions of Africa and Asia.

### 6.3 CYP1B1

Similarly to CYP1A1, the expression of the CYP1B1 isoform is also predominantly extra-hepatic, including peripheral blood cells (Hanaoka et al., 2002)(Furukawa et al., 2004), and it is inducible by exposure to several xenobiotics, namely PAHs (Nebert et al., 2004).
Null alleles are rare in the general population. Most were identified among patients with glaucoma, for which these alleles are an established risk factor (Stoilov et al., 1998), and are not a major concern in the context of this review. The main polymorphic positions in this gene are summarized in figure 2.

The functional consequence of the major CYP1B1 alleles has been studied in vitro upon heterologous expression in E. coli and the quantification of the enzyme’s capacity of catalyzing the 4- and 2- hydroxylation of estradiol. The introduction of the R48G, A119S and N453S SNPs did not significantly change the \(V_{\text{max}}\) and \(K_m\) of the resulting proteins, as compared with the wild type (1B1*1) (Li et al., 2000). The L432V SNP was on the other hand associated increased of \(K_m\) values \(<V_{\text{max}}\) values). Interestingly, in these works this effect was only observed in the context of a SNP haplotype including other polymorphic positions (R48G + A119S + L432V)(Aklillu et al., 2002). Finally, several minor allele of this SNP (present in the 1B1*3, 1B1*5, 1B1*6 and 1B1*7 alleles) have been proposed as associated with a transcriptional less active gene (Helmig et al., 2009, 2010).

Presently there is still scarce information available concerning the CYP1B1 allele frequencies in populations living in malaria regions (table 3).

<table>
<thead>
<tr>
<th>Region (n*)</th>
<th>1B1*2</th>
<th>1B1*3</th>
<th>1B1*4</th>
<th>1B1*5</th>
<th>1B1*6</th>
<th>1B1*7</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ethiopia (Adis Ababa)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Aklillu et al., 2002</td>
</tr>
<tr>
<td>(n=150)</td>
<td>36.7%</td>
<td>39.0%</td>
<td>2.0%</td>
<td>0.7%</td>
<td>6.3%</td>
<td>7.0%</td>
<td></td>
</tr>
<tr>
<td>North India (Lucknow)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Shah et al., 2008</td>
</tr>
<tr>
<td>(n=200)</td>
<td>33.0%</td>
<td>21.3%</td>
<td>18.3%</td>
<td>n/t</td>
<td>n/t</td>
<td>n/t</td>
<td></td>
</tr>
<tr>
<td>South Central China (Chengdu) (N= 400)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Wang et al., 2011</td>
</tr>
<tr>
<td>n/t</td>
<td>57.5%</td>
<td>n/t</td>
<td>n/t</td>
<td>n/t</td>
<td>n/t</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Northeast China (Nanjing)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Liang et al., 2005</td>
</tr>
<tr>
<td>(N= 227)</td>
<td>n/t</td>
<td>15.1%</td>
<td>n/t</td>
<td>n/t</td>
<td>n/t</td>
<td>n/t</td>
<td></td>
</tr>
</tbody>
</table>

* number of subjects analyzed; n/t: not tested.

Only women included in the study.

Only the L432V SNP was analysed, meaning that the declared frequency for 1B1*3, also is likely to include also the 1B1*5, 1B1*6 and 1B1*7 alleles.

Only women included in the study. The sole analysis of the A119S does not distinguish between the 1B1*2, 1B1*6 and 1B1*7.

(note: this compilation is intended to be a representative sample of the published information and not an exhaustive collection of the available data).

Abbreviation – CYP1B1: 1B1

Table 3. CYP1B1 allele frequencies of population from malaria affected regions in Africa and Asia.

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a Haplotype not determined yet (reference SNP: rs11572102, NCBI (http://www.ncbi.nlm.nih.gov/SNP/snp_ref.cgi?rs=11572102);
b Discovered by Soyama et al., 2001 and phenotypically characterized by reduced catalytic activity (Soyama et al., 2002)(Jiang et al., 2011).
c The colour code was herein applied according to the data of Aklillu et al. (2002). It is to note that initial studies by Li et al (2000) noticed a significant decrease in the activity of the protein.

Fig. 2. Genetic diversity of CYP2C8, CYP1A1 and CYP1B1, the main polymorphic genes involved in AQ phase I metabolism. Although the gene structures are represented, the locations of established polymorphisms are presented using the amino acid nomenclature as this is more relevant for the present review. For the sake of clarity, only the most studied alleles, with established haplotype structures are presented. Alleles shown in red color indicate protein products reported to be less active than the reference wild type (*1). Alleles in green do not have a significant differences as compared with *1, whereas alleles flagged in blue have higher activity than the wild type. For alleles in black there is currently no experimental information available. In the case of the CYP1B1 the use of the colors is restricted to alleles (and not SNPs) due to the availability of haplotype data (Aklilliu et al., 2002).

7. The CYP2C8, CYP1A1, CYP1B1 trio - Potential implications

In terms of therapeutic efficacy, since DEAQ is a powerful and clinically valuable antimalarial, variations in the CYP2C8 enzymatic capacity are not expected to have significant pharmacodynamic consequences. As mentioned, this expectation is in line with observations by Parikh et al in Burkina-Faso, where the presence of CYP2C8*2 did not influence the treatment outcome of AQ monotherapy. On the other hand, pharmacogenetics might be of particular importance in the identification of individuals in higher risk of
developing AQ-related adverse events. This is supported by the observation in the same study that the presence of CYP2C8*2 (still an allele associated with significant catalytic capacity, as compared with the much less functional 2C8*3 and 2C8*4) can influence the individual risk for mild adverse events, even in heterozygous form could.

Recently in vitro evidence was published supporting the involvement of CYP1A1 and CYP1B1 in the generation of toxic QIs from AQ (and DEAQ) (Johansson et al., 2009). This confirmation of preliminarily reports (Li et al., 2002, I. Cavaco, Universidade do Algarve, unpublished) has opened a new perspective towards individualization of AQ therapy to minimize adverse events. In fact, contrarily to the previous view of a spontaneous formation of QIs (Tingle et al., 1995), the involvement of these polymorphic P450s reinforces a broader genetic basis for the phenomenon, which was until now almost exclusively focused on CYP2C8 (Cavaco et al., 2005). The now recognized more extensive genetic background of AQ adverse drug events underlines the importance of individualized medicine and the possibility to identify appropriate molecular markers for predicting response to treatment/risk of adverse reactions.

With this new data, the hypothetical characterization of the sub-group of subjects in higher risk is starting to emerge. The first assumption is that such individuals carry a deficient CYP2C8 gene (2C8*2, ideally the very low active 2C8*3 or 2C8*4), allowing an extended half-life for AQ (Parikh et al., 2007). This will probably represent the group with T1/2 values >12 hours (Giao and de Vries, 2001), as well as the observed outliers showing very long exposure to the drug (Winstanley et al., 1987). With this increased pool of circulating AQ (as previously referred, a compound more prone than DEAQ for the formation of the QI reactive species (Tingle et al., 1995)), the drug will have higher chances to be extra-hepatically catalysed by CYP1A1 and CYP1B1 - both present in leucocytes, where AQ tends to accumulate (Naisbitt et al., 1997). The rate of QI formation is expected to be further enhanced if particularly efficient versions of CYP1A1 and CYP1B1 are present, namely the CYP1A1*2, and CYP1B1*1 (wild type) enzymes. The resulting enhanced generation of QIs in the blood, coupled with the referred low CYP2C8 activity could be the basis of the previously documented AQ induced severe agranulocytosis.

Interestingly, the involvement of CYP1A1 and CYP1B1 has another implication: In adult patients whom are smokers, both genes are likely to be induced by the polycyclic aromatic hydrocarbons (PAHs), which is present in tobacco smoke, through the activation of the aryl hydrocarbon receptor (AhR) based pathway (Nebert et al., 2004). This will also lead to the expression of these genes in the liver, another location for fatal AQ induced toxicity. Adult patients are characteristic of areas of low transmission, where the low exposure during the earlier periods of life does not allow the development of natural immunity to the diseases as an adult (premunition, frequent in the African continent (Struik and Riley, 2004)). Such malaria settings are the norm in South America regions, where populations carry a significant Caucasian genetic background and hence, an expected high frequency of the CYP2C8*3 allele. This has been confirmed in a pilot screening study conducted in populations of Northern Colombia where the frequency of this allele was ca. 7% (I. Cavaco, Universidade do Algarve, unpublished). In such areas it would be worthwhile to conduct trials in order to understand the influence that tobacco habits might have in the incidence of mild and serious adverse events associated to AQ treatments. Its connection with the CYP2C8/CYP1A1/CYP1B1 polymorphic set would be of interest, e.g. identifying patients that should be advised to decrease their smoking rate in time periods relevant for treatment.
Currently the epicentre of AQ use is in the Africa where the 2C8*3 and 2C8*4 alleles seem to be rare in the native populations. However, this observation is based on a very limited number of small studies, surely not representative of the overall population of the continent, the genetically most diverse on the planet (Lambert and Tishkoff, 2009). In addition, even though these alleles are considered “rare”, one has to take into account the dimensions of the malaria control challenge. A frequency of 1% for the 2C8*3 allele in a universe of at least 20 million AS-AQ treatments performed per year (WHO, 2010 - just the public sector, and not counting with the SP-AQ combination), would translate to ~2,000 homozygotes for 2C8*3 patients per year. Secondly, AQ resistance, although still not globally prevalent, is slowly increasing (Holmgren et al., 2006). Its potential expansion might lead to the need for increased drug dosage, as previously decided in the cases of CQ (Peters, 1970)(Ursing et al., 2009, 2011) and mefloquine (Carrara et al., 2009). By approaching the top of the AQ therapeutic window, the risks of toxicity will increase to a point when serious side effects might be “under the reach” of the less compromised 2C8*2 allele.

8. The CYP2C8, CYP1A1, CYP1B1 trio - Potential applications
Pharmacogenetic markers in AQ therapies are expected to serve mostly as surveillance tools of adverse events of the drug. The identification of individuals with a genetic predisposition to AQ side effects (e.g. a 2C8*2/*2 carrier) would prompt the direct diversion of this patient towards different doses or the available second line treatment (e.g. artemether-lumefantrine or artesunate-mefloquine).

An alternative therapeutic strategy could be the use of a more personalized (i.e. more optimized) AQ dosing, with values below the conventional 10 mg/Kg, or through a different regimen schedule. As the incidence of side effects is dose dependent (Cairns et al., 2010), individualized treatment would be expected to reduce those events. The success of such strategies could boost the patient’s (and specially their guardians) trust on the treatment, leading to increased compliance to the full dosing regimen. This effect has been witnessed with the anti-HIV drug abacavir, where the application of pharmacogenetic testing has increased the use of this drug (Ingelman-Sundberg, 2008)(Chaponda and Pirmohamed, 2011). Unfortunately, clinical studies to support future guidelines concerning the ideal dose for certain pharmacogenetic configurations are clearly missing. Initiatives to address this issue, such as the WANECAM Consortium in East Africa, are presently under way (see: www.edctp.org/annualreport2010/EDCTP_Annual_Report_2010_English.pdf).

The application of pharmacogenetics can contribute to an extended useful life of AQ, through its better use. Chemotherapy represents a central strategy for the long desired global elimination of the disease (malERA Consultative Group on Drugs, 2011), an event fundamental for the social-economical development of the Developing World. AQ is one of its central tools in these efforts (Bhattarai et al., 2007) – its safer and consequently longer use can be pivotal in this process.

But, although promising, are these pharmacogenetic applications possible in the present context of the Developing World health systems? In short, no. The prices of pharmacogenetic testing are still very high, totally eclipsing the costs of the therapy itself. A complete AS-AQ treatment in Africa will cost below US$5, already taking in
consideration a price of US$ 0.5-1 for the Coarsucam®/Winthrop® fixed combination supplied by Sanofi-Aventis (Shillcutt et al., 2008). As previously calculated (Ferreira et al., 2008), the analysis of the CYP2C8*3 allele alone will demand a minimum of US$50, taking in account the local costs of human resources and reagents. An upgrade towards the determination of the CYP2C8*2 allele, plus CYP1B1*2 and CYP1A1*2, would increase the financial burden per patients to values well above US$ 100 per patient, the equivalent of more than one hundred treatments. Besides, the maintenance of a system with the required quality standards for molecular diagnostic analysis would be in the order of many tens of thousands of US$/year. All this has to be put further in the context of populations with an available national health expenditure of less then US$25/year/citizen. The pharmacogenetic testing for AQ therapy alone would consume the funds of four years of health care.

So, what is the translational value of pharmacogenetics in such scenario? In fact there are at least two venues of development.

The first is what will be called here as “population pharmacogenetics”. As explained, the application of individual dose adjusted AQ therapies based on pharmacogenetics is essentially not viable. Alternatively, the study of the allele frequencies of pivotal markers in representative samples of specific populations/regions can be of considerable interest for national and regional health programmes, particularly in countries with a rich ethnic diversity, as it is frequent in the African continent. This would define the populations where therapeutics based in AQ would be safe, and the ones where an alternative antimalarial (like artemether-lumefantrine) would be the better choice. In a way, it would be the equivalent of rationally deciding not to introduce AQ in Europe, due to the high prevalence of the CYP2C8*3 allele (Cavaco et al., 2006). Several malaria endemic countries have more than one first line recommended treatment (e.g. Burkina Faso, Mali, Colombia, Peru (http://www.who.int/malaria/publications/treatment-policies/en/index.html), having as such a start up capacity for implementing region-specific policies. Such a programme could be centralized taking advantage of pre-existing molecular technology facilities used e.g. for molecular parasitology. In this context it is worth mentioning that new techniques are surfacing for the extraction of DNA from Rapid Diagnostic Tests (P. Ferreira, Karolinska Institutet, pers. commun)(Alam et al., 2011). These can be further coupled with novel inexpensive amplification-free genotyping approaches (Aw et al., 2011), allowing the ready molecular characterization of the patient in field settings.

Such an application of pharmacogenetics would aid evidence-based decisions for optimized antimalarial use, at a population level. This would allow the use of safer ACT alternatives for the benefit of specific populations.

The second venue has to do with the target country. Malaria is a significant public health concern in three of the “BRIC” emerging economies: Brazil, India and China. These large countries are rapidly developing economic capacity compatible with a first large scale application of personalised anti-infection therapies. In this context, it should be noted that the populations of Brazil and India (incidentally, the ones with larger malaria burden) have been shown to harbour non-negligible CYP2C8*3 frequencies (Arun Kumar et al., 2011)(Suarez-Kurtz et al., 2010)(table 1). In these countries the resources for personalized medicine as previously described are potentially available.
9. Conclusions

Although tens of millions of AQ doses are prescribed per year, the knowledge of the pharmacogenetics of this drug is still limited. In particular, stronger in vivo phenotype/genotype associations are needed for the definition of genetic markers of AQ overexposure risk.

This must be obtained through several venues. A basic need is the performance of clinical trials designed for the detection of adverse events, mild or eventually serious. These are needed to be relatively large (>500 subjects), due to the non-precise nature of the former (e.g. self reported abdominal pain in children under five), and the rarity of the latter. Such studies must include a long follow up for the detection of possible late onset events, as well as the reaction of the subject upon repetitive treatments. Also, the inclusion of full sequencing approaches in such reference studies would be fundamental, especially in cases of particularly relevant phenotypes. As previously mentioned, studies of this type are presently undergoing. Such trials will allow the establishment of better phenotype/genotype associations that can be further explored in the context of health structures integrated in national malaria programmes. In this second step, technologies like the DNA extraction from Rapid Diagnostic Test devices, coupled with novel simple genotyping methods with applications in the field can be used in order to further establish polymorphisms in CYP2C8, CYP1A1, CYP1B1 or other relevant genes (e.g. myeloperoxidases) as risk markers of AQ over-exposure.

With true personalized medicine being presently out of reach in most malaria affected countries, population pharmacogenetics of such markers will supply information for the use of the best available chemotherapy option, at a public health level. An example of such application would be the use of an alternative second line treatment (e.g. artemether-lumefantrine) as first liner for certain regions and/or populations of a country. Such a strategy would optimize the use of the available antimalarial arsenal in the national control programmes. A more personalized analysis could be potentially applied in the much less frequent (< 10%) situations of AS-AQ use as second liner.

A population-based approach, as described, can offer true benefits for the optimization of national malaria treatment, in particular when integrated in malaria elimination efforts, where the maintenance of the useful life of well established and effective therapies is key. Once the incidence of malaria decreases, as for example witnessed in the Zanzibari islands (Bhattarai et al., 2007), countries will be able to start supporting more personalized application of pharmacogenetics. In conclusion, upon the solid establishment of pharmacogenetics markers, the success of their application at a population level can lay the basis for a future more personalized pharmacogenetics, once the countries would be able to finance it. By the same token, the Developing World would not be left behind in this area of translational medicine.

10. Acknowledgments

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The rapidly evolving field of Pharmacogenetics aims at identifying the genetic factors implicated in the inter-individual variation of drug response. These factors could enable patient sub-classification based on their treatment needs thus expediting drug development and promoting personalized, safer and more effective treatments. This book presents Pharmacogenetic examples from a broad spectrum of different drugs, for different diseases, which are representative of different stages of evaluation or application. It has been designed so as to serve both the unfamiliar reader through explanations of basic Pharmacogenetic concepts, the clinician with presentation of the latest developments and international guidelines, and the research scientist with examples of Pharmacogenetic applications, discussions on the limitations and an outlook on the new scientific trends in this field.

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