

# Resistance to Antimalarial Drugs: Molecular, Pharmacologic, and Clinical Considerations

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**ABSTRACT:** One of the greatest obstacles to the control of malaria has been the spread of resistance to drugs used on a large scale. This review provides an update of the current understanding of the molecular basis for antimalarial drug resistance. Parasite intrinsic resistance is just one component that determines the *in vivo* efficacy of a drug. Human immune responses and pharmacologic properties play important roles in determining the clinical outcome of treatment. The emergence and spread of resistance also results from an interplay of these factors. Current efforts to characterize and deter resistance to new combination therapy are also discussed. (*Pediatr Res* 65: 64R–70R, 2009)

One of the greatest obstacles to the control of malaria has been the spread of resistance to drugs used on a large scale. Malaria continues to cause hundreds of millions of infections per year, and the annual toll of one million deaths is exacted predominantly on African children (1). Until several years ago, the armamentarium to battle malaria was essentially limited to two drugs for the treatment of uncomplicated malaria and one drug to treat severe disease. Resistance to chloroquine and sulfadoxine-pyrimethamine (SP) has fueled the on-going burden of *Plasmodium falciparum* malaria. In response, the World Health Organization (WHO) has recommended the use of combination treatments that include artemisinin derivatives as first-line therapy. Seventy-seven of the 81 countries worldwide with endemic *P. falciparum* have now adopted the WHO recommendation (1). New drugs, even when used in combination, are not impervious to resistance. In this review, we will discuss our current understanding of the mechanisms of resistance to antimalarial drugs, factors that affect the clinical response to therapy aside from intrinsic resistance and also features that contribute to the spread of resistance.

## Overview of Important Drugs for the Treatment of Malaria in Endemic Countries

Until recently, chloroquine was the most widely used drug to treat and prevent malaria infection. The spread of chloroquine resistance in Africa led to a rise in the disease burden in the 1980s (2,3), a setback that has plagued the region to this day. Chloroquine acts by interfering with the detoxification of

hemin, a toxic byproduct of Hb degradation, in the *Plasmodium* parasite's food vacuole. Although it is no longer recommended for the treatment of *P. falciparum*, it is the drug of choice to treat *P. vivax* and *P. ovale*, less severe forms of malaria that can cause recurrent infections.

With the spread of chloroquine resistance, many countries adopted SP as the first-line antimalarial treatment. SP is composed of two drugs that act on sequential enzymes in the folate synthesis pathway. When both drugs are used together, they act synergistically. Although SP is a coformulation of two drugs, it is not considered combination therapy because the mechanisms of action are closely linked. Resistance to SP spread more quickly than to chloroquine. In Southeast Asia, its use was abandoned after only 5 years (4). SP resistance is more common in East Africa than West Africa (5). SP use is likely to continue even as first-line therapy for uncomplicated malaria changes. SP is increasingly used for the intermittent preventive treatment of malaria in vulnerable groups including pregnant women, a widely adopted practice, and infants and children, tools that have not been implemented on a large scale.

In response to resistance to the widely available antimalarials used as monotherapy, artemisinin-based combination therapy (ACTs) have been introduced first in Asia and now throughout Africa and South America. The artemisinins are derived from the Chinese sweet wormwood plant, *Artemisia annua*. Their mechanism of action has not been fully elucidated, but they may inhibit the sarco/endoplasmic reticulum calcium ATPase found in *Plasmodium* parasites (6). Artemisinins are potent antimalarials, acting rapidly and killing *Plasmodium* parasites throughout the asexual blood stages (7,8). Artemisinins may also decrease malaria transmission because they act on the gametocytes, the parasite stage that is infectious to the mosquito vector (9). Artesunate cannot be administered alone because if the duration of therapy is less than 5–7 d, there is a high risk of recrudescence. The recurrent parasites are not resistant to artemisinins but evade their very short duration of action (10). When combined with a longer-acting partner drug, the artemisinins can be administered as an ACT over 3 days. The commonly used ACTs are artemether-

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**Abbreviations:** ACT, artemisinin-based combination therapy; DHFR, dihydrofolate reductase; DHPS, dihydropteroate synthetase; PfCRT, *Plasmodium falciparum* chloroquine-resistance transporter; PfMDR, *Plasmodium falciparum* multidrug resistance gene; SP, sulfadoxine-pyrimethamine; WHO, World Health Organization

lumefantrine, amodiaquine-artesunate, and mefloquine-artesunate.

### The Molecular Basis of Drug Resistance

***P. falciparum* chloroquine-resistance transporter.** Among chloroquine-resistant parasites, there is a decrease in the accumulation of drug within the food vacuole. Genetic crosses have identified the role of the *P. falciparum* chloroquine-resistance transporter (PfCRT) (11,12). When present in a mutated form, it is associated with decreased chloroquine accumulation. Multiple polymorphisms in the gene are associated with chloroquine resistance both *in vitro* and *in vivo*, but the essential mutation seems to be the replacement of lysine with threonine at residue 76 (13–15). However, PfCRT is not the sole molecular determinant of chloroquine resistance. Mutations in the homolog of the major multidrug-transporter *P. falciparum* multidrug resistance gene (PfMDR) seems to modulate the extent of chloroquine resistance conferred by mutations in PfCRT. *In vitro* studies suggest that the genetic background of the strain also influences the degree of resistance conferred by these mutations in PfCRT and PfMDR (16,17).

***Dihydrofolate reductase and dihydropteroate synthetase.*** *De novo* folate synthesis is essential to parasite survival. The antifolate medications interrupt this process by targeting two enzymes: pyrimethamine and proguanil target dihydrofolate reductase (DHFR), and sulfa drugs such as sulfadoxine target dihydropteroate synthase (DHPS). Resistance to antifolate drugs is the result of the accumulation of mutations in *DHFR* and *DHPS*. Nonsynonymous nucleotide changes occur in a stepwise fashion leading to increasing parasite resistance to antifolate drugs (18). The order in which mutations occur is likely due to changes in enzymatic activity with each additional mutation, although the data are not clear (19). The highest levels of antifolate resistance are found in Southeast Asia and South America. In these two regions, a polymorphism at *DHFR* residue 164 is almost always found. In contrast, *DHFR* I164L has not spread through sub-Saharan Africa, despite extensive use of the drug (4). Although SP is ineffective in treating symptomatic disease in malaria-naïve children in many parts of Africa, it has retained some efficacy in preventing malaria in pregnant women (20). This may be due to the moderate level of resistance conferred by the polymorphisms in *DHFR* and *DHPS* typically found in Africa and the absence of the I164L polymorphism associated with very high-level SP resistance (up to 20,000-fold decrease in susceptibility in comparison with the wild type). It is unclear as to why this final mutation has not taken hold in Africa, despite extensive drug pressure. It has been hypothesized that this amino acid change carries a high fitness cost to the parasite, such that it is unable to survive the immune response of malaria-experienced hosts in Africa (21).

***The worldwide spread of drug resistance.*** Tracing the spread of the chloroquine-resistant genotype of PfCRT has led to the current understanding that chloroquine resistance developed in several independent locations in Asia, Papua New Guinea, and South America (22). The chloroquine-resistant

gene that originated in Southeast Asia spread across the Asian continent and reached Africa in the late 1970s (17,23). Over the course of a decade, chloroquine resistance became widespread in sub-Saharan Africa. Resistance did not emerge within infected individuals on a regular basis, as might be expected based on the inherent mutation rate of the parasite and the high rate of replication within the human host. Rather, resistant strains emerged a limited number of times and those ancestral strains spread in the permissive environment of drug pressure.

Faced with widespread chloroquine resistance, many countries in sub-Saharan Africa adopted SP as first-line therapy in the 1990s. Resistant parasites appeared shortly thereafter. Low-level antifolate resistance arises within a population independently. This was suspected based on early studies of pyrimethamine prophylaxis (24) and has since been supported by microsatellite analysis demonstrating diverse origins of *DHFR* genes carrying one or two mutations. However, moderate antifolate resistance, the highest level of resistance found in Africa is associated with three mutations in *DHFR* and has limited ancestral origins. In parasites carrying these “triple mutations” the gene seems to have originated in southeast Asia and migrated to Africa, much like chloroquine resistance, with no or limited evidence of recent local evolution (25,26).

There has been one example of the effect of the removal of drug pressure on the prevalence of drug-resistant parasites. In 1993, Malawi was the first country to replace chloroquine with SP for the oral treatment of malaria, due to high rates of chloroquine resistance. Immediately after chloroquine use was stopped, there was a decrease in the prevalence of the PfCRT 76T polymorphism that is associated with chloroquine resistance (27). From 2001 until today, no chloroquine-resistant parasites have been identified in the major cities where surveillance has occurred [(28) and F. Dzinjalama, unpublished data]. A clinical trial demonstrated that chloroquine is now highly effective in the treatment of malaria, after high rates of failure documented just 12 y prior (29). Chloroquine should not be used in sub-Saharan Africa at this time because chloroquine-resistant parasites predominate in most countries. As chloroquine is withdrawn from use throughout the region, it is possible that chloroquine-susceptible parasites will return and chloroquine may once again play a role in the treatment or prevention of malaria in the future.

***P. falciparum* multidrug resistance gene.** The gene encoding PfMDR is an ortholog of P-glycoproteins found in mammals that mediate multidrug resistance in cancer cells. The protein is found on the digestive vacuole membrane and seems to play a role in regulating traffic across the membrane, including a variety of antimalarial drugs (16,30). The substitution N86Y in PfMDR modulates but is not essential to chloroquine resistance. In clinical studies, this polymorphism is not associated with changes in treatment outcome (13,31). Mutations in this gene have also been linked to *in vitro* susceptibility of other drugs, but the effects depend on the genetic background of the malaria strain and are not uniform. The allele associated with chloroquine resistance (86Y) has also been associated with hypersensitivity to mefloquine,

when assessed *in vitro*. The clinical implications of the decrease in 50% inhibitory concentration ( $IC_{50}$ ) are not known (32). Of recent interest, *PfMDR* N86, the chloroquine susceptible-allele has been proposed as a molecular marker for lumefantrine resistance. Artemether-lumefantrine treatment selects for N86 in recurrent infections (33).

Differences in *pfmdr* copy number are linked to changes in clinical efficacy of several drugs. Increases in copy number are associated with increased risk of treatment failure after treatment with mefloquine, artesunate-mefloquine, or artemether-lumefantrine (34–36). Relating copy number to *in vitro* susceptibility testing has been difficult because copy number can change during the process of culture adaptation of field isolates, a process that is necessary for reliable assessment of drug sensitivity. Sidhu *et al.* (37) have succeeded in altering *pfmdr* copy number and have demonstrated increases in susceptibility to mefloquine, quinine, halofantrine, and artemisinin with lower copy number.

There may be other genes in the *Plasmodium* genome with increased copy numbers in response to drug pressure. GTP-cyclohydrolase I (*gch1*), the first gene in the folate biosynthesis pathway, is increased in copy number in regions with extensive antifolate drug usage. The increased *gch1* copy number (ranging from 1 to 11) is exclusively found in parasites with polymorphisms in DHFR and DHPS associated with antifolate resistance. It has been suggested that this increase in copy number plays a role in compensating for the changes in enzyme activity associated with antifolate resistance, rather than mediating the decrease in susceptibility (38).

**PfATP6.** Another transporter, PfATP6, is an ortholog of the mammalian sarcoendoplasmic reticulum  $Ca^{2+}$  ATPase (SERCA). There is evidence that this pump is inhibited by artemisinins, suggesting that mutations may alter artemisinin susceptibility (6). One molecular marker for artemisinin resistance has been proposed, PfATP6 S769N, based on an ecological study in Senegal, French Guiana, and Cambodia and supported by differences in  $IC_{50}$  values (39). The most susceptible parasites were found in Cambodia, where the nucleotide substitution was not identified, and the most resistant parasites were found in French Guiana in association with the polymorphism at residue 769. The role of this polymorphism in conferring or serving as a marker for artemisinin resistance has not been confirmed. This single nucleotide polymorphism (SNP) is not found in China, where the artemisinins have been used the longest (40) nor has it been identified in Africa (41,42).

### Pharmacologic Contributions to Drug Resistance and Impaired Efficacy

When used as monotherapy, artemisinins are associated with recurrent parasitemia unless the medication is administered for 5–7 d. The need for prolonged therapy has been considered a significant obstacle to adherence. As a result, the artemisinins are administered with longer acting partner drugs in a fixed-dose combination treatment regimen that is used to protect against recrudescence infections. The artemisinin deriv-

ative rapidly reduces parasitemia, with the remaining parasites are eliminated by the longer-acting partner drug. For example, artemether-lumefantrine was the first fixed-dose combination commercially produced for use in Africa. Artemether acts rapidly, with a half-life of 1–3 h, whereas lumefantrine, with a half-life of 3–6 d, is responsible for preventing the recurrent parasitemia associated with short course artemisinin therapy.

For long-acting drugs, blood levels persist for days, a period during which a patient essentially has antimalarial monotherapy. This time interval has been referred to as the “selective window,” a period of time when the drug level is adequate to suppress the growth of susceptible parasites but too low to prevent the replication of drug-resistant parasites (43,44). Watkins and Mosobo (45) were the first to characterize the selective window of pyrimethamine. They sampled children who were treated with SP and collected parasites from cases of recurrent parasitemia. They found that parasites that occurred before 52 d after initial therapy were almost all pyrimethamine-resistant, whereas after 52 d, the  $IC_{50}$  values were similar to the baseline distribution. This study was performed before the validation of molecular markers for resistance. Using PfMDR 86 as the marker of lumefantrine resistance, the selective window of lumefantrine has been estimated to last approximately 12 d, based on a model derived from one clinical trial (46). This value is a rough estimate, since the basis of lumefantrine resistance has not been completely elucidated and is not fully represented by the single polymorphism.

ACTs combine the short-acting artemisinins with longer-acting partner drugs, and were initially introduced in Southeast Asia, where transmission intensity is low and exposure to a new infection after therapy is rare. In contrast, in sub-Saharan Africa, where transmission is intense, individuals who have recently been treated for malaria infection are frequently exposed to new infections during the period of time when the partner drug level is waning. If new infections occur during the selection window of the partner drug, drug-resistant parasites will have a survival advantage. There is concern that frequent exposures of parasites to subtherapeutic drug levels may allow for the rapid emergence of drug resistance. Data from studies in Africa indicate that the use of ACTs leads to the selection of parasites resistant to the long-acting partner drugs (47–49). The long-term effect of this selection is not yet known.

The role of pharmacokinetics in determining antimalarial efficacy and in promoting the emergence and spread of drug resistance has recently gained increased attention (50). In the past, drug levels were rarely measured, so that all episodes of clinical treatment failure were thought to be due to inherent parasite resistance. In fact, if therapeutic drug levels are not achieved, clinical outcomes are an inaccurate reflection of drug efficacy and parasite susceptibility. This has become especially clear with the use of lumefantrine, a compound that has highly variable absorption, determined by fat consumption, among other factors. Low lumefantrine level 7 d after therapy is an independent risk factor for recurrent parasitemia (35). Because pharmacokinetic analysis of drugs is beyond the scope of standard drug efficacy trials, some investigators have



proposed including the assessment of the drug level at d 7 as a key data point to determine whether therapeutic concentrations were achieved in the blood (51). This will offer important information about the contribution of pharmacokinetic factors to the observed clinical efficacy of a drug.

Incomplete understanding of pharmacokinetic factors may shorten the useful life of antimalarial drugs and may hasten the spread of resistance. When dose-finding studies are conducted, they take place before resistance to the study drug has emerged. The dose selected is usually the lowest dose that achieves a good response so as to minimize adverse effects. As resistance spreads, low levels of drug allow the spread of resistant parasites because the therapeutic levels required to clear mildly resistant parasites is higher than the level required to eliminate fully susceptible ones (52). A PK mathematical model has suggested that had mefloquine been deployed at a dose of 24 mg/kg rather than 15 mg/kg, mefloquine resistance would have emerged much more slowly (53). One such natural experiment has occurred in Guinea Bissau, where chloroquine has been used at two to three times the dose administered in other countries (50–75 mg/kg vs. 25 mg/kg administered over 3 d) (54). Chloroquine resistance is rare there in contrast to most of its neighbors (55). These observations should be taken with caution: the causal relationship between high dose and low prevalence of resistance has not been established, and the safety of the dosing regimen has not been rigorously evaluated.

**Counterfeit medication.** During the past decade, the malaria community has become aware that antimalarial drug quality is a cause for concern. Counterfeit and low quality antimalarial medications are found worldwide. The most thoroughly investigated drugs are the artemisinins. Recently, an international, multidisciplinary team was established to identify and trace fake artemisinins and hold their producers accountable. The group obtained specimens from most countries in Southeast Asia and discovered that half of the samples were counterfeit. Counterfeit drugs contained much less than the labeled amount of active drug or none at all. In tablets labeled as artesunate and other artemisinin derivatives, the contents included antimicrobials, nonartemisinin antimalarials, antipyretics, and even illicit drugs and carcinogenic compounds (56). Although fake artemisinins brought attention to the issue of antimalarial quality, the integrity of all antimalarials has undergone investigation on a small scale. Testing of a variety of different antimalarials across sub-Saharan Africa found substandard medication in seven countries (57,58). Aside from the obvious threat of counterfeit antimalarials administered to sick patients who require full doses of the medication, drugs that contain less than the labeled amount of drug may contribute to the spread of drug resistance.

### The Human Host

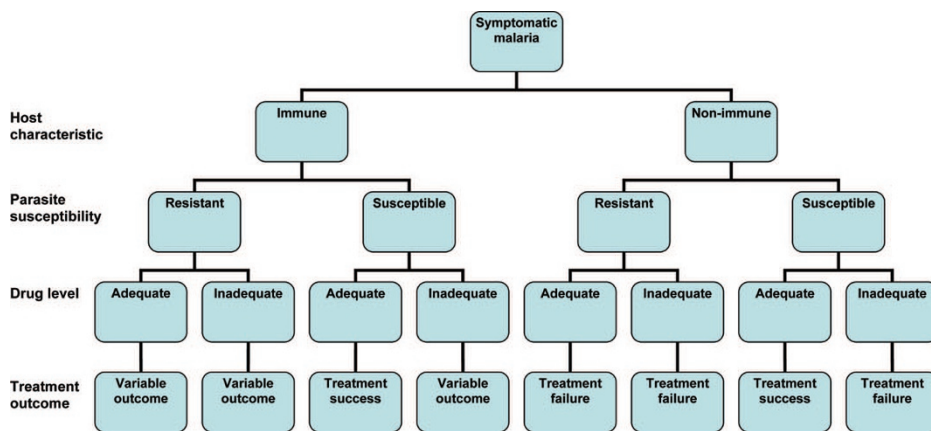
The host immune response to malaria infection likely influences the speed of spread of drug resistance and also the extent to which drug resistance translates into clinical drug

failure (59). Immunity to malaria is acquired through repeated exposure to infection and is maintained through boosting by infectious bites throughout an individual's lifetime. In high transmission settings, children are susceptible to symptomatic and severe malaria infection, whereas adults are considered semi-immune because they can acquire infection, but are not at risk for severe disease and often experience asymptomatic infection. Malaria parasites in these semi-immune adults are not under drug pressure because infection is not usually recognized or treated. In contrast, individuals in low and sporadic transmission settings, such as Southeast Asia, are not exposed to malaria with enough frequency to develop immunity. As a result, all infected individuals develop symptomatic infection, and the infections always prompt treatment with an antimalarial drug. It is possible that the difference in the extent of drug pressure on the parasite population drives the spread of drug resistance. As described above, resistant parasites have emerged in low transmission settings, where most parasites in human hosts are under selective drug pressure, and later spread to high transmission settings, where many parasites survive without drug pressure.

Another factor that has limited the spread of drug resistance in high transmission settings is the ability of the host immune response to clear resistant infections. Individuals with acquired immunity are cured even if the parasites are resistant to the administered drug. Because no laboratory correlate for immunity has been established for malaria, age is used as a surrogate measure of acquired immunity in endemic areas. Several studies have demonstrated that with increasing age, there is improved ability to clear resistant parasites. Some of this impaired clearance in children may be due to subtherapeutic dosing (52), but lack of acquired immunity is likely also a major factor. Intrinsic parasite drug resistance may be less apparent in endemic areas as drugs retain clinical efficacy even against resistant parasites due to host factors (60–62). Figure 1 demonstrates the lack of consistency between the results of clinical drug efficacy studies and intrinsic parasite resistance when host and pharmacokinetic factors are taken into account.

**Red blood cell abnormalities.** There are a number of human genetic polymorphisms that offer protection against malaria, including enzyme deficiencies such as glucose-6-phosphate dehydrogenase deficiency and pyruvate kinase deficiency and Hb variants such as thalassemia and Hb S (63). Little is known about how effectively patients with these polymorphisms respond to antimalarial drugs. There is evidence that antimalarials in patients with hemoglobinopathies have different pharmacokinetic properties (64,65), and that standard doses of antimalarials may be less efficacious (66). In human populations with high prevalence of these hemoglobinopathies, drug efficacy may seem impaired, even in the absence of intrinsic resistance or may be threatened by even minimal increases in  $IC_{50}$ s.

**HIV.** The interaction between HIV and malaria has been difficult to measure. Although malaria does not act like an opportunistic infection for people living with HIV infection who have previously acquired malaria immunity, it is significantly more severe in malaria-naïve hosts with HIV coinfection than without HIV infection (67). In most settings, HIV infection is associated with higher parasite densities than in the absence of



**Figure 1.** Schematic depiction of the clinical outcomes of drug efficacy studies when taking into account parasite, pharmacokinetic, and host factors.

HIV infection. This trend has led to the suggestion that HIV infection leads to an increase in the parasite biomass by 18% (68). Increased biomass raises the possibility that mutations associated with drug resistance may emerge more frequently than in the absence of coinfection.

### Identifying and Deterring Resistance to New Drugs

Like resistance to chloroquine and SP, resistance to the artemisinins may be emerging in Southeast Asia. Thailand and Cambodia adopted the ACT mefloquine-artesunate in 1995 and 2000, respectively. Several studies reported decreases in the efficacy of the combination (69,70), but it has been difficult to ascertain whether the decline was due to the artesunate or mefloquine. In 2006, Noedl *et al.* conducted a randomized trial comparing artesunate monotherapy for 7 d to treatment with quinine and tetracycline (a regimen that is expected to be very effective) in western Cambodia. Four of the 60 participants treated with artesunate had recurrent parasitemia 3 to 4 wks after therapy. Two of these individuals were found to have subtherapeutic drug levels, so the clinical failure was not attributed to parasite drug resistance. The parasites from the other two individuals were found to have artemisinin  $IC_{50}$ s that were four times higher than those of the parasites collected from study subjects with a good response to therapy. The proposed molecular markers for artemisinin resistance, *pfmdr* copy number and SERCA polymorphisms, were not associated with artemisinin resistance in this pilot study (71).

An international initiative is underway to further investigate the possibility of artemisinin resistance in the region of the Thai-Cambodian border. Led by the WHO and funded by the Bill and Melinda Gates Foundation, the Artemisinin Resistance Confirmation, Characterization and Containment project (ARC3), is conducting trials of artesunate monotherapy to assess its efficacy without the complication of a partner drug. Parasites collected from these studies will undergo *in vitro* susceptibility testing and extensive genomic analysis to understand the molecular basis of artemisinin resistance. If resistance is confirmed, genomic tools will be applied to identify markers of artemisinin resistance and to begin to understand its molecular basis. Investigators, policy makers, and donors will work together to contain artemisinin-resistant malaria so that ACTs can remain as effective therapy in the regions hardest-hit by malaria.

The proactive effort to identify and contain the very earliest sign of artemisinin resistance is an example of a new, aggressive international effort to not just control, but to eradicate malaria from the world (<http://rbm.who.int/gmap/gmap.pdf>, last accessed January 17, 2009). A cornerstone of the current malaria eradication plan is deterring the emergence and spread of drug resistance. The Worldwide Antimalarial Resistance Network (WWARN) has been established to monitor antimalarial drug efficacy so as to maximize the useful therapeutic lives of current drugs and to detect emergence as rapidly as possible [(72) and website [www.wwarn.org](http://www.wwarn.org)]. Drugs alone will not be able to eradicate this disease: other key elements to the strategy include vector control and vaccine development. Nevertheless, malaria will not be controlled without effective medication for treatment and prevention. The loss of antimalarial drug efficacy has led to the tragic persistence of malaria transmission in many regions of the world and is a cycle that cannot be repeated.

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