Temporal Changes in Prevalence of Molecular Markers Mediating Antimalarial Drug Resistance in a High Malaria Transmission Setting in Uganda

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Abstract. Standard therapy for malaria in Uganda changed from chloroquine to chloroquine + sulfadoxine-pyrimethamine in 2000, and artemether-lumefantrine in 2004, although implementation of each change was slow. *Plasmodium falciparum* genetic polymorphisms are associated with alterations in drug sensitivity. We followed the prevalence of drug resistance-mediating *P. falciparum* polymorphisms in 982 samples from Tororo, a region of high transmission intensity, collected from three successive treatment trials conducted during 2003–2012, excluding samples with known recent prior treatment. Considering transporter mutations, prevalence of the mutant *pfcrt* 76T, *pfmdr1* 86Y, and *pfmdr1* 1246Y alleles decreased over time. Considering antifolate mutations, the prevalence of *pfdhfr* 51I, 59R, and 108N, and *pfdhps* 437G and 540E were consistently high; *pfdhfr* 164L and *pfdhps* 581G were uncommon, but most prevalent during 2008–2010. Our data suggest sequential selective pressures as different treatments were implemented, and they highlight the importance of genetic surveillance as treatment policies change over time.

INTRODUCTION

Despite the recent endorsement of malaria elimination as a worldwide goal, the malaria burden has not decreased notably in Uganda, where *Plasmodium falciparum* is responsible for most episodes of malaria, and millions of cases occur each year.[1] Uganda has undergone two recent changes in policy for the treatment of uncomplicated malaria, driven by the development of resistance to older antimalarials.[2] In 2000, chloroquine (CQ) was replaced by CQ plus sulfadoxine-pyrimethamine (SP), and in 2004 this regimen was replaced by the artemisinin-based combination therapy (ACT) artemether-lumefantrine (AL), although implementation of new treatment practices was slow. Alternate ACTs for uncomplicated malaria in Uganda are artesunate-amodiaquine (AS-AQ) and dihydroartemisinin-piperaquine (DP). Each ACT consists of a potent and rapid-acting artemisinin and a longer-acting partner drug.[3] Leading ACTs have shown outstanding antimalarial efficacy,[4,5] but early signs of resistance to artemisinins, manifested as delayed parasite clearance after therapy, have been seen in parts of Southeast Asia,[6] and resistance has been seen to most ACT partner drugs.[7]

Resistance to a number of antimalarial drugs has been linked to genetic polymorphisms in *P. falciparum*. Single nucleotide polymorphisms (SNPs) in *pfcrt* and *pfmdr1*, which encode putative transport proteins, affect responses to multiple drugs. A single mutation, *pfcrt* 76T, is the key mediator of resistance to CQ and AQ.[8] In addition, polymorphisms in *pfmdr1,* which is homologous to proteins that mediate drug sensitivity in mammalian cells,[9] modulate sensitivity of parasites to multiple drugs.[10,11] Considering *pfmdr1* mutations that are common in Africa, 86Y and 1246Y are associated with decreased sensitivity to CQ and AQ, but wild-type (WT) sequences at the same alleles mediate decreased sensitivity to lumefantrine, mefloquine, and artemisinins.[12–14] Another *pfmdr1* polymorphism, Y184F, is common, but of uncertain significance, and two others, S1034C and N1042D, are seen in Asia, but rare in Africa.[9]

In Uganda and many other African countries the prevalence of the key mediator of CQ resistance, *pfcrt* 76T, increased to saturation levels by the 1990s.[15–17] With cessation of CQ use, reduction in the prevalence of *pfcrt* 76T has been seen. Notably, in Malawi, over 8 years after CQ withdrawal, the prevalence of parasites with *pfcrt* 76T decreased from 85% to 13%,[18] and in 2005 excellent antimalarial efficacy of CQ was shown.[19] Decreases in the prevalence of *pfcrt* 76T have also been seen in eastern Kenya and Zanzibar, although changes have not been as dramatic as in Malawi.[20,21] Changes have also been seen in the prevalence of key *pfmdr1* genotypes in Kenya, Tanzania, and Zanzibar, with WT N86 and D1246 genotypes increasing over time.[11,21–23]

The SNPs in folate enzyme genes are associated with decreased sensitivity to antifolate antimalarials such as SP.[24] Antifolate resistance develops in a stepwise manner. Parasites containing five mutations, *pfdhfr* 51I, 59R, and 108N plus *pfdhps* 437G and 540E, which together mediate clinically relevant resistance, have recently been seen to be common in East Africa and near fixation in Uganda,[16,25] where continued selection is presumably caused by continued use of antifolates for intermittent preventive therapy and other uses. However, mutations that mediate a higher level of resistance and are seen elsewhere, notably *pfdhfr* I164L and *pfdhps* A581G, are generally uncommon in Africa,[26] although some reports have noted increased prevalence in parts of east Africa.[27,28] Notably, *pfdhfr* 164L was reported in 14% of *P. falciparum* isolates collected from symptomatic patients in southwestern Uganda in 2005.[29]

Considering the impacts of parasite polymorphisms in both transporter and folate genes on drug sensitivity and changing malaria treatment practices over time, it was of interest to examine the prevalence of key SNPs in Uganda over time. We therefore examined sequences of interest in *P. falciparum* isolates from patients enrolled in drug efficacy trials from 2003 to 2012 in a high malaria transmission area of Uganda.

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MATERIALS AND METHODS

Clinical trials. We analyzed 982 archived *P. falciparum* isolates obtained from treatment trials in Tororo District. Details of the clinical studies have been published (Table 1).[30–33] For the first study, which enrolled patients ≥ 6 months of age with uncomplicated *P. falciparum* malaria from December 2002 to May 2004 and compared the efficacies of CQ+SP, AQ+SP, and AS+AQ,[31] we analyzed 198 pretreatment DNA samples collected from September to November 2003 for *pfmdr1* and *pfdhps* 581 polymorphisms, and included data on other polymorphisms that were already published.[16] For the second study, which enrolled patients 1–10 years of age that presented with uncomplicated *P. falciparum* malaria from December 2004 to July 2005 and compared the efficacies of AS+AQ, and AL,[32] we analyzed 201 pretreatment DNA samples for *pfdhfr* and *pfdhps* polymorphisms, and included data on *pfcrt* and *pfmdr1* SNPs that were already published.[34] For the third study, a longitudinal trial in which 351 children 4–12 months of age were enrolled and randomized to receive either AL or DP for each episode of uncomplicated malaria,[33] we analyzed 584 samples, including 204 from all first episodes of falciparum malaria and 380 from all recurrent episodes presenting 84 or more days after a prior treatment. For this trial, in a subset of samples that were genotyped, < 1% of recurrent infections within 28 days were caused by recrudescence; we anticipate that no infections occurring ≥ 84 days after a prior infection were the result of recrudescence.[33,35]

Target gene amplification and mutation analysis. Parasite DNA was extracted from dried filter paper blood spots using Chelex, as previously described.[36] The DNA from control strains 3D7, Dd2, 7G8, FCR3, V1/S, K1, and Peru was obtained from the Malaria Research and Reference Reagent Resource Center. Genes of interest were amplified, and polymorphisms in *pfcrt*, *pfmdr1*, *pfdhfr*, and *pfdhps* were analyzed by nested polymerase chain reaction (PCR) followed by restriction fragment length polymorphism (RFLP) analysis, as previously described.[37–39] Target sequences were amplified (see Supplemental Table 1 for primers), and PCR products were treated with polymorphism-specific restriction endonucleases (*Apo*I for *pfcrt* K76T; *Afl*III, *Dra*I, and *Bgl*II for *pfmdr1* N86Y, Y184F, and D1246Y, respectively; *Mlu*CI, *Xmn*I, *Bsr*I and *Dra*I for *pfdhfr* N51I, C59R, S108N and I164L, respectively; and *Ava*II, *Fok*I and *Bst*UI for *pfdhps* A437G, K540E and A581G, respectively). Reaction products were resolved on 2.5% agarose gels, and electrophoretic band patterns were categorized as WT, mixed, or mutant genotypes by visual inspection of gels and comparison with DNA from control strains.

Data analysis. Data were entered into a Microsoft (Microsoft Corp., Redmond, WA) access database and exported into Statistical Package for the Social Sciences (SPSS Inc., Chicago, IL) software 17.0, which was used for analysis. For these analyses, mixed genotypes were grouped with either mutant or WT, as indicated. Graphs were generated with GraphPad Prism 5.0 (GraphPad Prism, La Jolla, CA). Temporal changes in SNP frequencies were analyzed using logistic regression with date of collection as a continuous or categorical variable, as indicated, to evaluate for trends over time or differences between discrete time periods, respectively. A *P* value < 0.05 was considered statistically significant.

RESULTS

We evaluated the prevalence of polymorphisms of interest in *pfcrt*, *pfmdr1*, *pfdhfr*, and *pfdhps* from *P. falciparum* isolates collected in three clinical trials, all conducted in Tororo District over the course of a decade during which standard antimalarial treatment in Uganda underwent major changes. To minimize the influence of prior therapies on parasite genetics, samples were collected before treatment in the two older trials, and in the newer longitudinal trial, samples were from first episodes of malaria and from episodes ≥ 84 days since a prior episode. The SNPs of interest were categorized as WT, mixed, or mutant, based on sequences of the reference *3D7* strain (Table 2).

For *pfcrt* K76T, the prevalence of mutant parasites was nearly 100% throughout the early years of observation, consistent with other reports from Uganda,[15,16,40,41] and likely due in part to widespread use of chloroquine even after the national treatment policy changed in 2004. The prevalence of WT and mixed K76T genotypes increased modestly from 2008 to 2011, and then a marked change was seen in 2012, with 16% mixed and 17% pure WT genotypes seen (Figure 1). Considering the period from 2007 to 2012, the probability of being infected with a WT or mixed (versus mutant) genotype increased significantly over time (*P* < 0.001).

For *pfmdr1*, the N86Y, Y184F, and D1246Y alleles were highly polymorphic throughout the period of observation. Although results varied from year to year, clear patterns were seen at the N86Y and D1246Y alleles, with increasing prevalence of WT genotypes over time (Figure 1). At Y184F, increasing prevalence of the mutant genotype was seen. Considering the entire period of observation, statistically significant increases in the probability of infection with a WT or mixed genotype for the N86Y (*P* < 0.001) and D1246Y (*P* < 0.001) alleles, and with a mutant (versus mixed or WT) genotype for the Y184F allele (*P* < 0.001) were seen. Prevalence of

TABLE 1
Description of trials that provided samples for the molecular study*

	Antimalarial regimens studied		
Baseline study characteristics	CQ+SP vs. AQ+SP vs. AS+AQ†	AL vs. AS+AQ†	AL vs. DP‡
Study period	2002–04	2004–05	2007–12
Age at enrollment	≥ 6 months	1–10 years	4–12 months
Number of participants	347	403	351
Median age (years)	1.27	1.83	0.98
Geometric mean parasite density	18,484/μL	22,071/μL	16,349/μL
Samples successfully genotyped	189/198 (95%)	188/201 (93%)	561/584 (96%)

*CQ = chloroquine; SP = sulfadoxine-pyrimethamine; AQ = amodiaquine; AL = artemether-lumefantrine; DP = dihydroartemisinin-piperaquine.
†Pretreatment samples obtained from clinical studies.[31,32]
‡Samples from all first episodes and recurrent episodes ≥ 84 days after prior treatment.[33]

TABLE 2
Proportions of patients infected with *Plasmodium falciparum* parasites containing polymorphisms in *pfcrt*, *pfmdr1*, *pfdhfr*, and *pfdhps**

				Year				
Genotype	2003–2004†	2005‡	2007	2008	2009	2010	2011	2012
				pfcrt K76T				
WT	0	0	0	0	4 (4%)	0	0	13 (17%)
Mixed	1 (1%)	0	0	3 (2%)	2 (2%)	4 (4%)	9 (8%)	12 (16%)
Mutant	79 (99%)	201 (100%)	38 (100%)	144 (98%)	87 (94%)	104 (96%)	102 (92%)	52 (67%)
				Pfmdr1 N86Y				
WT	20 (10%)	19 (9%)	12 (32%)	34 (23%)	23 (26%)	48 (44%)	52 (47%)	40 (51%)
Mixed	136 (71%)	76 (38%)	7 (19%)	88 (61%)	27 (30%)	41 (37%)	41 (37%)	32 (41%)
Mutant	36 (19%)	106 (53%)	18 (49%)	23 (16%)	39 (44%)	21 (19%)	18 (16%)	6 (8%)
				Pfmdr1 Y184F				
WT	141 (75%)	169 (85%)	25 (68%)	103 (71%)	75 (83%)	41 (37%)	63 (59%)	50 (68%)
Mixed	43 (23%)	28 (14%)	7 (19%)	22 (15%)	6 (7%)	45 (41%)	7 (7%)	4 (6%)
Mutant	3 (2%)	3 (1%)	5 (13%)	20 (14%)	9 (10%)	25 (22%)	36 (34%)	19 (26%)
				Pfmdr1 D1246Y				
WT	3 (2%)	32 (17%)	9 (23%)	35 (24%)	16 (17%)	22 (19%)	22 (20%)	42 (53%)
Mixed	89 (48%)	80 (40%)	12 (31%)	50 (34%)	22 (23%)	55 (50%)	53 (48%)	27 (34%)
Mutant	93 (50%)	86 (43%)	18 (46%)	61 (42%)	58 (60%)	34 (31%)	35 (32%)	10 (13%)
				Pfdhfr N51I				
WT	0	1 (1%)	0	1 (1%)	1 (1%)	0	0	0
Mixed	5 (6%)	5 (2%)	0	0	0	1 (1%)	0	0
Mutant	75 (94%)	185 (97%)	34 (100%)	144 (99%)	92 (99%)	110 (99%)	109 (100%)	79 (100%)
				Pfdhfr C59R				
WT	24 (7%)	13 (7%)	3 (8%)	4 (3%)	6 (7%)	10 (9%)	5 (4%)	6 (8%)
Mixed	122 (37%)	60 (31%)	1 (3%)	9 (6%)	3 (3%)	12 (11%)	14 (13%)	5 (6%)
Mutant	187 (56%)	117 (62%)	33 (89%)	132 (91%)	84 (90%)	87 (80%)	92 (83%)	65 (86%)
				Pfdhfr S108N				
WT	0	1 (1%)	0	0	0	1 (1%)	0	0
Mixed	0	4 (2%)	20 (59%)	29 (23%)	10 (11%)	18 (16%)	10 (9%)	2 (2%)
Mutant	80 (100%)	186 (97%)	14 (41%)	99 (77%)	83 (89%)	92 (83%)	101 (91%)	77 (98%)
				Pfdhfr I164L				
WT	80 (100%)	152 (99%)	34 (100%)	137 (99%)	83 (91%)	98 (88%)	105 (100%)	77 (100%)
Mixed	0	2 (1%)	0	1 (1%)	7 (8%)	12 (11%)	0	0
Mutant	0	0	0	0	1 (1%)	1 (1%)	0	0
				Pfdhps A437G				
WT	5 (2%)	3 (2%)	0	1 (1%)	1 (1%)	1 (1%)	1 (1%)	0
Mixed	48 (14%)	24 (12%)	0	1 (1%)	1 (1%)	2 (2%)	1 (1%)	4 (5%)
Mutant	280 (84%)	170 (86%)	33 (100%)	142 (98%)	91 (98%)	108 (97%)	108 (98%)	75 (95%)
				Pfdhps K540E				
WT	8 (2%)	2 (1%)	0	0	0	1 (1%)	1 (1%)	0
Mixed	86 (26%)	25 (13%)	0	6 (4%)	4 (4%)	4 (4%)	14 (13%)	3 (4%)
Mutant	239 (72%)	165 (86%)	33 (100%)	138 (96%)	89 (96%)	106 (95%)	95 (86%)	76 (96%)
				Pfdhps A581G				
WT	193 (100%)	195 (98%)	37 (100%)	129 (88%)	83 (89%)	97 (87%)	95 (88%)	76 (98%)
Mixed	0	1 (1%)	0	17 (11%)	9 (10%)	4 (4%)	9 (8%)	1 (2%)
Mutant	0	2 (1%)	0	1 (1%)	1 (1%)	10 (9%)	4 (4%)	0

WT = wild-type.
*Data shown are numbers (proportions in parentheses) of samples with each genotype.
†Data from 2003–2004 (samples obtained from November 2003 to May, 2004) are combined.
‡Data obtained from December 2004 to July 2005 are included for 2005; 98% of samples from this trial were collected in 2005.

the 86Y/Y184/1246Y haplotype decreased markedly over time, with increases in haplotypes including WT sequences at positions 86 and 1246 (Table 3). Based on known selective effects of antimalarial drugs that have been commonly used in Uganda, these results suggest decreasing selective pressure of CQ and/or increasing selective pressure of AL over time in Uganda.

For mutations associated with resistance to antifolate antimalarials, five well-described mutations in *pfdhfr* (N51I, C59R, S108N) and *pfdhps* (A437G, K540E) were all very common throughout the period of observation (Table 2). Considering uncommon genotypes associated with high-level resistance, both *pfdhfr* 164L and *pfdhps* 581G were nearly absent early and late in our study, but more common from 2008 to 2010, with peak prevalence of mixed or mutant sequences at *pfdhfr* 164 at 9–12% in 2009 and 2010, and at *pfdhps* position 581 at 11–13% in 2008–2011 (Figure 2). The prevalence of the *pfdhfr* 164 WT genotype was significantly lower in 2009–10 than in other years ($P < 0.001$) and the prevalence of the *pfdhps* 581 WT genotype was significantly lower in 2009–12 than in earlier years ($P = 0.01$).

DISCUSSION

We examined changes in the prevalence of *P. falciparum* polymorphisms associated with drug resistance over a decade during which standard antimalarial treatment in Uganda underwent major changes. All evaluated samples were from the same region of Uganda, and from patients without known recent antimalarial treatment before analysis, limiting selective pressure from prior therapy, and thus providing a reasonable assessment of the prevalence of polymorphisms in parasites circulating in Tororo each year. Important changes were seen in the prevalence of a number of SNPs of interest.
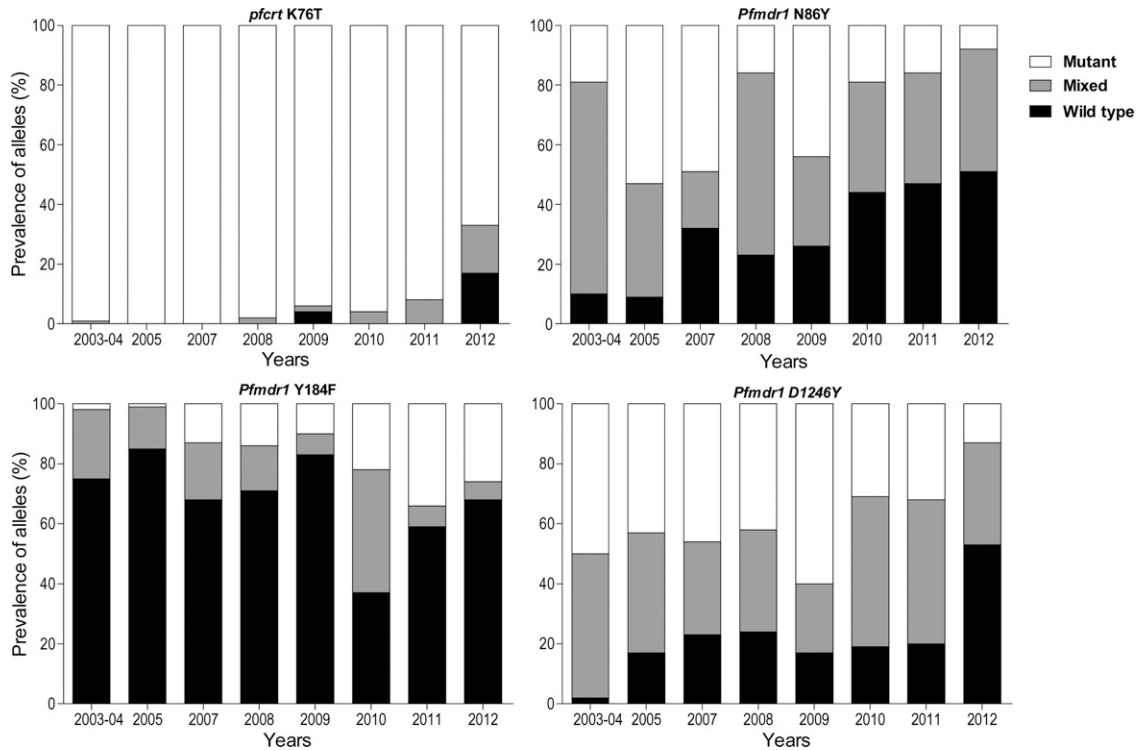
FIGURE 1.   Prevalence of polymorphisms over time at codon 76 of *pfcrt*, and codons 86, 184, and 1246 of *pfmdr1*.

For *pfcrt* K76T, which is known to mediate CQ and AQ resistance, WT parasites were nearly absent in the early years of observation, but these became much more common by 2012. For *pfmdr1* N86Y and D1246Y, which impact upon sensitivity to multiple drugs, the prevalence of WT alleles increased steadily over time. For polymorphisms in *pfdhfr* and *pfdhps*, which mediate resistance to antifolates, five well-described mutations remained common over time, and mutations at two additional alleles associated with high level resistance showed modest prevalence only from 2008–11. Overall, the identified changes in prevalence seem to be consistent with differing selective drug pressures caused by changes in treatment practices in Uganda over time.

How can we explain the observed changes in the prevalence of *P. falciparum* drug resistance-mediating SNPs in Uganda over time? The mutant *pfcrt* 76T genotype persisted in Uganda at high (> 90%) prevalence levels through 2011, long after it had decreased elsewhere in East Africa. For example, the prevalence of the 76T genotype was 63% in eastern Kenya in 2008,[22] 63% in Zanzibar in 2010,[21] and 32% in western

Kenya in 2011.[11] The persistence of the mutant *pfcrt* 76T genotype in Uganda suggests that continued selective pressure from CQ persisted long after the national treatment policy changed in 2004, when the standard therapy for malaria was changed from CQ + SP to AL. The CQ remains available in Uganda, and in fact it continues to be recommended for regular chemoprophylaxis in children with sickle cell disease.[42] Very recently, the prevalence of parasites with the CQ-sensitive *pfcrt* K76 genotype increased markedly in Tororo, suggesting a decrease in community use of CQ.

For *pfmdr1*, the prevalence of mutant 86Y and 1246Y genotypes gradually decreased in Uganda from 2003 to 2012. These changes were likely due both to decreased use of CQ and gradual establishment of AL as the standard antimalarial drug in Tororo, because both decreasing CQ exposure and increased lumefantrine exposure will select for WT sequences at these alleles.[3,43,44] In other parts of East Africa, the prevalence of *pfmdr1* N86 and D1246 have been observed to increase following widespread use of ACTs.[11,23,45] Of note, *pfmdr1* WT genotypes have been associated with decreased sensitivity to lumefantrine.[46,47] Taken together, available data suggest that, although the efficacies of leading ACTs appear to remain excellent, parasites in East Africa are undergoing changes rendering them less sensitive to lumefantrine. Continued selection may lead to highly resistant parasites, jeopardizing the antimalarial efficacy of AL, the first-line therapy for malaria in Uganda and surrounding countries.

Considering changes in the prevalence of SNPs that mediate antifolate resistance, five well-characterized mutations in *pfdhfr* (N51I, C59R, and S108N) and *pfdhps* (A437G, K540E) were very common in Tororo throughout the last 10 years. These data suggest continued strong selective pressure despite the withdrawal of SP from treatment guidelines in 2004. Of interest was whether selection of additional polymorphisms in

TABLE 3
Pfmdr1 haplotype distribution over time

Year	86Y/1246Y	N86/D1246	N86/184F/D1246	86Y/Y184/1246Y
2003	15/180 (8%)	0/180 (0%)	0/197 (0%)	70/197 (36%)
2005	70/198 (35%)	15/198 (8%)	2/197 (1%)	67/197 (34%)
2007	13/37 (35%)	7/37 (19%)	1/37 (3%)	12/37 (32%)
2008	13/144 (9%)	19/144 (13%)	8/150 (5%)	11/150 (7%)
2009	24/89 (30%)	9/89 (10%)	3/87 (4%)	23/87 (26%)
2010	9/110 (8%)	14/110 (13%)	0/110 (0%)	3/110 (3%)
2011	9/110 (8%)	10/110 (9%)	4/105 (4%)	5/105 (5%)
2012	2/78 (3%)	22/78 (28%)	7/73 (10%)	0/73 (0%)

Data from 2003–2004 and late 2004–2005 were combined as explained in Table 2. The results shown represent the proportion and percentage of each haplotype found among all those with successful analysis for each allele, considering only results with pure wild-type (WT) or mutant genotypes.
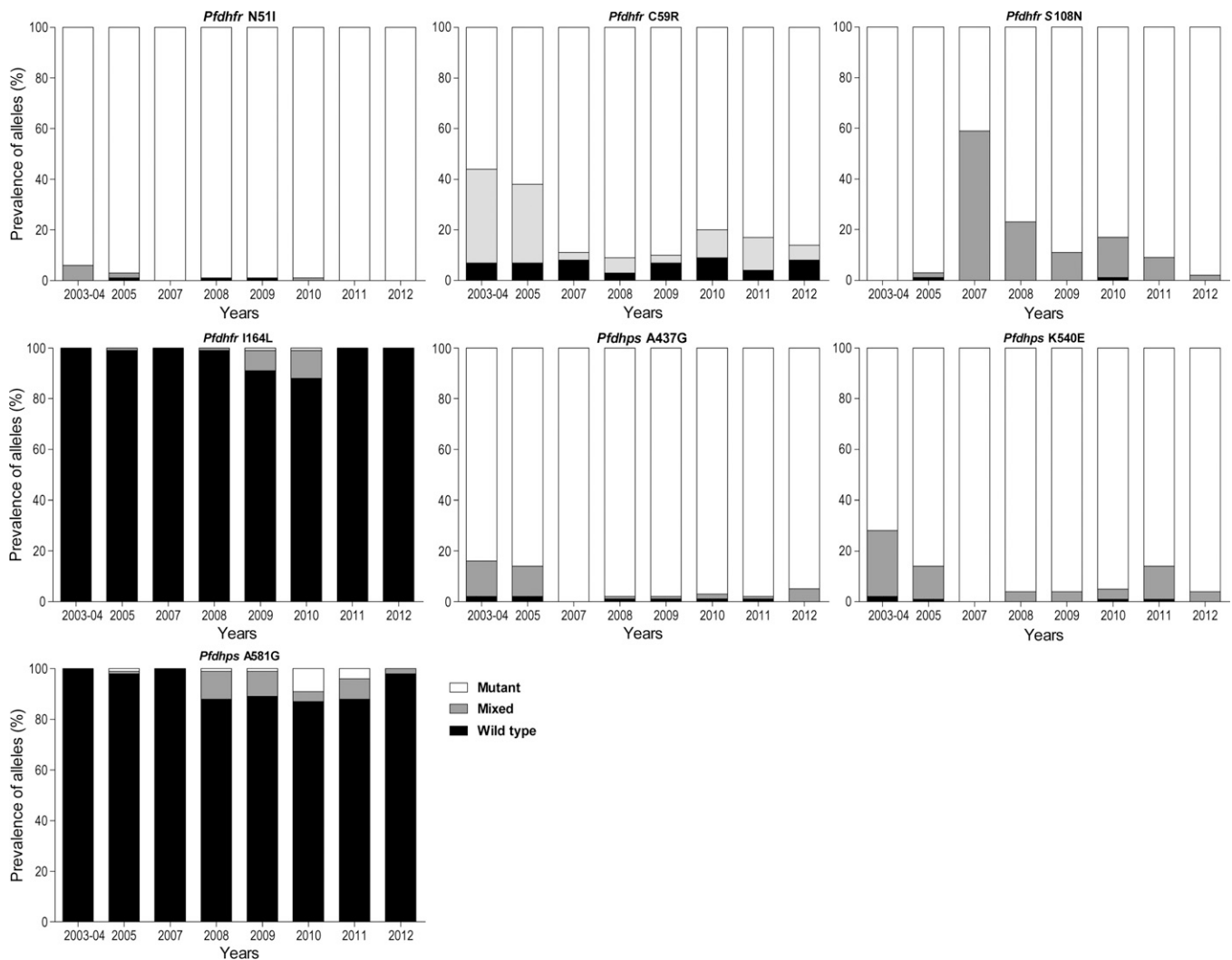
FIGURE 2.   Prevalence of polymorphisms over time in the indicated alleles of *pfdhfr* and *pfdhfr*.

pfdhfr or *pfdhps* was seen, in particular the *pfdhfr* 164L and *pfdhps* 581G mutations that are associated with high-level antifolate resistance.[24] In Kenya, an increase in prevalence of the five common mutations, and also emergence of *dhps* 581G, was reported over a 13-year period of observation,[48] despite withdrawal of SP for the treatment of malaria in 2006. Other reports have noted a fairly high prevalence of SNPs that mediate high-level antifolate resistance in some settings, including a *pfdhfr* 164L prevalence of 14% in *P. falciparum* from an area of Uganda with low malaria transmission intensity[29] and modest prevalence of both the *pfdhfr* 164L and *pfdhps* 581G mutations in human immunodeficiency virus (HIV)-infected Ugandan children receiving regular trimethoprim-sulfamethoxazole prophylaxis.[49,50] In other recent studies from East Africa, the prevalence of *pfdhps* 581G was > 50% in samples from eastern Kenya and Tanzania.[27,28] In our results from Tororo, the *pfdhfr* 164L and *pfdhps* 581G mutations were very uncommon, except for increased prevalence from 2008 to 2011. Reasons for continued antifolate selective pressure likely include continued use of SP to treat malaria, treatment of bacterial infections with antifolates, use of SP in intermittent preventive treatment in pregnant women, which remains the World Health Organization (WHO) policy, and widespread use of another antifolate, trimethoprim-sulfamethoxazole, as prophylaxis against opportunistic infections in HIV-infected individuals. The decreased prevalence of both the *pfdhfr* 164L and *pfdhps* 581G mutations in Tororo in the most recent years suggests decreasing use of SP to treat malaria quite recently and fitness disadvantages of genotypes that mediate the highest levels of antifolate resistance; these fitness disadvantages may most effectively prevent selection in areas with very high malaria transmission intensity, such as Tororo.[7]

Our study had some limitations. First, samples were collected from studies with different designs. In the two older treatment efficacy trials subjects were enrolled and samples obtained immediately before treatment of malaria, but information on prior treatment before enrollment was necessarily limited. The more recent trial was a longitudinal trial in which children were treated with the same regimen, either AL or DP, for every episode of malaria over 5 years. In this trial, to limit impacts of prior treatments on infecting parasites, we studied only parasites causing first infections in the study and those without prior therapy within 84 days. Another limitation was that data were derived from a combination of older and recent assays, and for the oldest trial different numbers of samples were assessed for different alleles. Although we used

the same RFLP methods for all assessments, assays done at different points in time after sample collection may have led to somewhat different results, in particular in the case of minority strains within populations.

Despite some limitations, our data offer the best available description of changes in the prevalence of key resistance-mediating *P. falciparum* polymorphisms over time in Uganda. Indeed, parasites changed notably from 2003 to 2012. Our results suggest continued use of CQ and SP well beyond the establishment of AL as the national treatment regimen in 2004. However, our most recent results suggest decreasing selective pressure from both CQ and SP, with increasing prevalence of the *pfcrt* K76 WT genotype and loss of folate gene polymorphisms associated with high level resistance. In addition, increasing prevalence of the WT *pfmdr1* N86 and D1246 alleles has been seen over time. These results are reassuring, in suggesting that recommended use of AL to treat uncomplicated malaria has increased. However, the results also raise the concern that continued heavy use of AL may select for parasites with decreased lumefantrine sensitivity, potentially leading to AL treatment failures. Continued surveillance of *P. falciparum* polymorphisms will be important, both to provide insight into the evolution of drug resistance and to offer feedback regarding national treatment practices. In future surveillance higher throughput assays,[51] and deep sequencing methods to identify minority strains,[52] may improve our ability to assess changes in allele prevalence over time.

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