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Plasmodium falciparum sulfadoxine resistance is geographically and genetically clustered within the DR Congo

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Understanding the spatial clustering of *Plasmodium falciparum* populations can assist efforts to contain drug-resistant parasites and maintain the efficacy of future drugs. We sequenced single nucleotide polymorphisms (SNPs) in the dihydropteroate synthase gene (*dhps*) associated with sulfadoxine resistance and 5 microsatellite loci flanking *dhps* in order to investigate the genetic backgrounds, genetic relatedness, and geographic clustering of falciparum parasites in the Democratic Republic of the Congo (DRC). Resistant haplotypes were clustered into subpopulations: one in the northeast DRC, and the other in the balance of the DRC. Network and clonal lineage analyses of the flanking microsatellites indicate that geographically-distinct mutant *dhps* haplotypes derive from separate lineages. The DRC is therefore a watershed for haplotypes associated with sulfadoxine resistance. Given the importance of central Africa as a corridor for the spread of antimalarial resistance, the identification of the mechanisms of this transit can inform future policies to contain drug-resistant parasite strains.

A ntimalarial drug resistance continually threatens to undermine global efforts to contain and control malaria. Molecular analyses have demonstrated that parasite mutations conferring resistance to chloroquine[1] and to pyrimethamine[2] originated in Southeast Asia and spread first to East Africa and thence across the African continent. Consequently, these mutations are highly prevalent across sub-Saharan Africa and the clinical drug resistance they confer bedevils malaria control efforts. A better understanding of the geographic spread of drug-resistant malaria may enhance efforts to contain nascent resistance to newer antimalarials[3].

In contrast to mutations which confer resistance to chloroquine and pyrimethamine, those which confer resistance to sulfadoxine are not yet fixed in Africa[4]. This resistance is mediated by the stepwise accumulation of single nucleotide polymorphisms (SNPs) in the dihyropteroate synthase (*dhps*) gene which encodes the drug's target[5]; the most common SNPs encode single amino acid changes at codons 436, 437, 540, and 581 of *dhps*. The ancestral wildtype haplotype is denoted SAKA to indicate wildtype amino acids at these 4 codons; the S436**A** mutation is not clearly associated with reduced drug susceptibility and is considered an alternate wildtype (haplotype **A**AKA). Prior analyses of these *dhps* mutations in sub-Saharan Africa have demonstrated that resistant *dhps* haplotypes have multiple origins and are geographically restricted to finite regions[4,6]. Specifically, resistant parasites in East Africa typically harbor haplotypes with the A437**G** and K540**E** mutations (S**GE**A), sometimes with the addition of the A581**G** mutation (S**GEG**); those in West Africa more typically display haplotypes with the single A437**G** mutation (S**G**KA) or coupled with the alternate wildtype codon 436 (**AG**KA)[4,7,8].

Sulfadoxine, when co-formulated with pyrimethamine (SP), is no longer a recommended antimalarial therapy in sub-Saharan Africa, but it remains an important tool for malaria prevention owing to its use as intermittent preventive therapies during pregnancy (IPTp), in infancy (IPTi), and in childhood (IPTc)[9–11]. Additionally, it is employed in some countries as a partner drug for artemisinin-based therapies. Because resistance to

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pyrimethamine is more prevalent than against sulfadoxine, these interventions may be undermined by the ongoing accumulation of parasites bearing SNPs in *dhps*. These SNPs confer reduced susceptibility to sufladoxine *in vitro* that is broadly proportional to the number of amino acid changes in *dhps*[12]; clinical studies of therapeutic efficacy in children from across Africa suggest differential patterns of sulfadoxine susceptibility *in vivo*, with treatment failure closely linked to parasites bearing the A437**G** mutation in Congo-Brazzaville[13], the K540**E** mutation in Burkina Faso[14] and Uganda[15], both the A437**G** and K540**E** mutations in the Democratic Republic of the Congo (DRC)[16], and to the triple-mutant parasites bearing the A437**G**, K540**E**, and A581**G** mutations in Tanzania[17]. These clinical data underscore the importance of molecular surveillance as a surrogate tool to monitor evolving trends in clinical efficacy.

The DRC suffers one of the greatest burdens of falciparum malaria, but the epidemiology of parasite populations across this vast nation is poorly described. We recently described the epidemiology and estimated the consequences of *P. falciparum* for children[18] and pregnant women[19] in the DRC using specimens collected from a 2007 nationally-representative cross-sectional survey of DRC adults. Herein, we use a random sample of these *P. falciparum* parasites to describe the prevalence of *dhps* mutations across the DRC, explore the origins of resistance-mediating haplotypes, and investigate the geographic clustering of *dhps* haplotypes. We hypothesized that parasites harboring resistant haplotypes would be spatially restricted, with single-mutant (S**G**KA, **A**GKA) haplotypes predominating in the West and double (S**GE**A) and triple-mutant (S**GEG**) haplotypes in the East, and that these resistant haplotypes would manifest distinct genetic lineages.

Results

Prevalence and distribution of dhps haplotypes. From 179 randomly-selected *P. falciparum* parasitemias, we obtained pure (i.e. non-mixed) *dhps* haplotypes from 151 parasites: 53 (35.1%) were SAKA, 30 (19.9%) were **A**AKA, 2 (1.3%) were **C**AKA, 41 (27.2%) were S**G**KA, 3 (2%) were **AG**KA, 17 (11.3%) were S**GE**A, and 5 (3.3%) were S**GEG**. There were no mutations at codon 613 of *dhps*. Of these 151 parasites, the geographic coordinates were missing for 15 (6 SAKA, 4 **A**AKA, 3 S**G**KA, 1 S**GE**A, and 1 S**GEG**), allowing us to geo-locate 136 pure *dhps* haplotypes across the DRC (**Figure 1**). Inspection of the geographic distribution of haplotypes revealed that the single-mutant S**G**KA and **A**GKA haplotypes were largely clustered in the west and the double- and triple-mutant haplotypes S**GE**A and S**GEG** were more prevalent in the east. This pattern is

consistent with prior analyses in regions bordering the east and west of the DRC[4].

Geographic clustering of parasite populations. We investigated this visually-apparent geographic clustering of parasites using an ecological clustering algorithm that measures phylogenetic diversity between microbial communities and assigns confidence to the resolved clusters using jackknifing[20]. This algorithm clustered the overall parasite population into two communities with >99.9% confidence: an eastern (comprised of North and South Kivu, Orientale, and Maniema provinces) and a western subpopulation (comprised of Bandundu, Equateur, Katanga, Bas-Congo, Kinshasa, Kasai-Occidental, and Kasai-Oriental provinces) (**Figure 2**). Predicted splits between provinces within these eastern and western subpopulations were not significant. We repeated the clustering algorithm using only microsatellite profiles harbored by parasites with wildtype *dhps* haplotypes. In this repeat analysis only Maniema was partitioned from the other provinces with >99.9% confidence. This finding may reflect a reduction in statistical power owing to the presence of fewer wildtype *dhps* parasites in North and South Kivu and Orientale, or that geographic clustering is largely driven by the distributions of mutant *dhps* haplotypes.

This east-west division of parasites was supported by calculation of nearest-neighbor statistics (S_{nn}), which quantify the likelihood that a closely-related parasite microsatellite profile will be found within the same DRC province[21]; S_{nn} values close to 1 indicate substantial genetic differentiation between populations while values near 0.5 indicate that the two populations likely belong to a single, panmictic population. Between provinces that were grouped by the Unifrac analysis above into eastern and western subpopulations, several pairwise comparisons returned S_{nn} values close to 1 that were significant despite correction for multiple comparisons by the Bonferroni method (Maniema vs. Bas-Congo/Kinshasa, N/S Kivu vs. Bas-Congo-Kinshasa, Maniema vs. Katanga, and Orientale vs. Katanga) (**Table 1**). This is consistent with segmentation into different parasite populations. Other pairwise comparisons were non-significant to this stringent level, but mean S_{nn} values were significantly different for pairwise comparisons between eastern and western provinces (0.728) than for those between eastern provinces (0.696) or those between western provinces (0.577; p-value < 0.001 for comparisons of means by ANOVA).

Divergence of dhps haplotypes. Consistent with previous studies in African *P. falciparum*[22], we observed high degrees of expected heterozygosity (H_e) at microsatellite loci: the overall mean H_e was
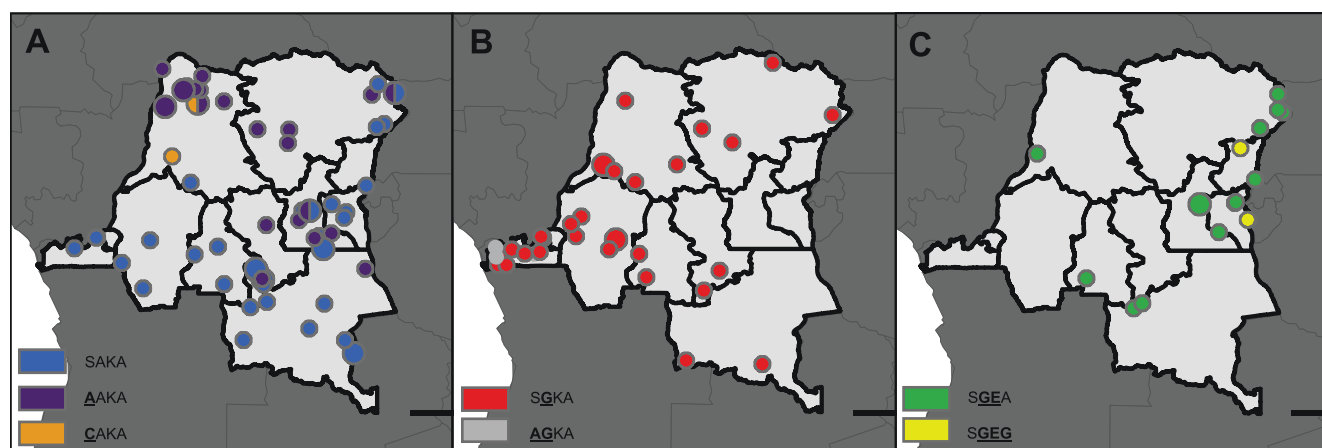
Figure 1 | Distributions of wildtype (A), single-mutant (B), and double- and triple-mutant (C) *dhps* haplotypes across the DRC. Size of circles is proportional to the number of samples in that location. Haplotypes are indicated by the amino acids at codons 436, 437, 540, and 581 of DHPS; mutant amino acids are underlined and bolded.
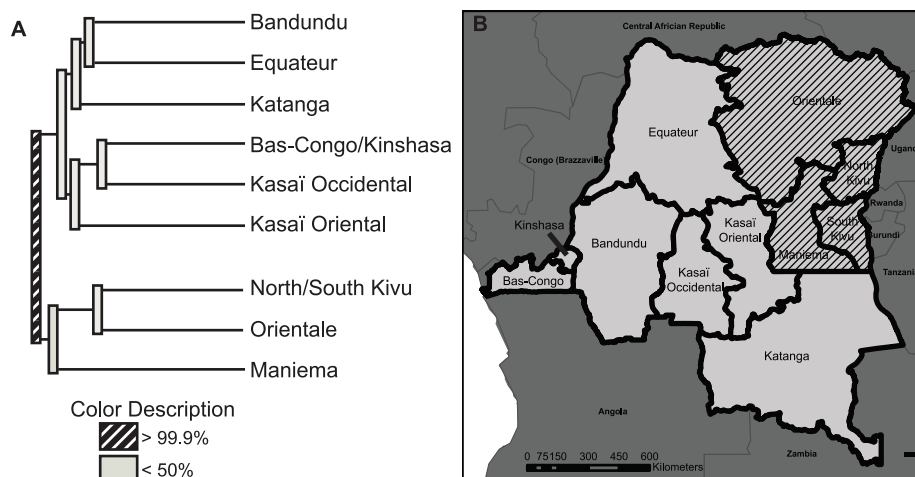
Figure 2 | Clustering of provincial falciparum parasite populations. (A) Predicted clustering of microsatellite profiles between DRC provinces into two distinct parasite subpopulations from western DRC (Bandundu, Equateur, Katanga, Bas-Congo/Kinshasa, Kasaï Occidental, Kasaï Oriental) and eastern DRC (North/South Kivu, Orientale, Maniema). Computed by UniFrac with jackknifing and 1000 replicates[20]. (B) Predicted provincial subpopulations in the DRC. The parasites in the hatched provinces were partitioned by the analysis in (A) to be distinct from those of the un-hatched provinces.

0.564 (standard error [SE] 0.06), and individual loci ranged from 0.404 (for locus −0.13; SE 0.135) to 0.723 (for locus 0.03; SE 0.132) when calculated for the major allele at each locus. These H_e estimates were not substantially different from those calculated by inputting all alleles that were obtained at mixed loci (data not shown). After partitioning into the 7 unique *dhps* haplotypes described above, there was evidence of mild selective pressure upon mutant haplotypes: mean H_e (SE) for SAKA was 0.801 (0.062), for AAKA was 0.765 (0.071), for SGKA was 0.480 (0.081), for AGKA was 0 (0), SGEA was 0.508 (0.110), and for SGEG was 0.393 (0.167) (**Figure 3**).

We first investigated the divergence of mutant and wildtype haplotypes by comparing genetic and geographic distances of the 136 parasites for which we had both *dhps* haplotypes and geographic coordinates. Overall, there was minimal correlation between geographic and genetic distance by Mantel testing (Rxy = 0.098, p = 0.010) (**Figure 4A**). However, this relationship was modified by *dhps* haplotypes: after stratification into wildtype (SAKA, AAKA, and CAKA) and mutant (SGKA, AGKA, SGEA, SGEG) parasites, there was no significant correlation between wildtype parasites (Rxy = 0.046, p = 0.213) but significant correlation for the mutant parasites (Rxy = 0.277, p < 0.001). These results suggest that while wildtype *dhps* haplotypes are genetically and geographically intermixed, mutant *dhps* haplotypes are isolated by distance across the DRC.

We further explored pairwise divergence between *dhps* haplotypes using both Nei's unbiased distance and Φ_{PT}, the latter estimated using AMOVA (**Table 2**). Nei's distance measures divergence between populations accounting for both mutation and drift[23], while AMOVA estimates the degree of differentiation into subpopulations and is an analog of Wright's F-statistics[24]. As expected, the ancestral wild-type SAKA and alternate wild-type AAKA were closely related by both measures, with distance of 0.174 and Φ_{PT} of 0.032 (p = 0.29). Additionally, the double- and triple-mutants SGEA and SGEG were closely related to each other with distance of 0.081 and Φ_{PT} of 0 (p = 0.310). Surprisingly, the single-mutant SGKA (prevalent in Western DRC) was divergent from all other major haplotypes, with distance values over 0.540 and pairwise Φ_{PT} values of 0.133 (p = 0.010) with SAKA, 0.362 (p = 0.010) with SGEA, and 0.380 (p = 0.020) with SGEG (prevalent in Eastern DRC). These data suggested that the SGKA mutant did not arise from the sampled SAKA wildtype parasites and, furthermore, did not give rise to the more resistant SGEA and SGEG haplotypes that we sampled in the DRC.

Origins of dhps *haplotypes.* In order to further investigate the origins of the *dhps* haplotypes in the DRC, we partitioned the 129 specimens with full microsatellite profiles into 111 unique haplotypes. Inspection of a median-joining network built from these 111 haplotypes demonstrated clear segmentation of the

Table 1	Pairwise Hudson's nearest neighbor (S$_{nn}$) analyses of parasite populations by DRC province								
	Bas-Congo/ Kinshasa	Bandundu	Equateur	Kasai-Occidental	Katanga	Kasai-Oriental	Orientale	Maniema	N./S. Kivu
Bas-Congo/ Kinshasa		0.59417	0.59201	0.61019	0.63696	0.69097	0.61067	***0.9315***	***0.87987***
Bandundu	0.1800		0.46556	0.30556	0.5098	0.56739	0.69767	0.63167	0.65521
Equateur	0.1260	0.9180		0.59928	0.61228	0.59928	0.56332	0.70914	0.68651
Kasai-Occidental	0.3820	0.8350	0.7460		0.47778	0.67908	0.77366	0.76597	0.64428
Katanga	0.0710	0.4110	0.1680	0.6490		0.70833	***0.78204***	***0.87154***	0.71491
Kasai-Oriental	0.0070	0.4360	0.1140	0.2180	0.0250		0.7022	0.76597	0.64428
Orientale	0.1460	0.1890	0.1910	0.1360	0.0010	0.0040		0.65208	0.67641
Maniema	<0.0001	0.1150	0.0090	0.0240	0.0010	0.0030	0.0580		0.73507
N./S. Kivu	<0.0001	0.0640	0.0460	0.1080	0.0230	0.0890	0.1210	0.0090	

Global S$_{nn}$ 0.233046 (p = < 0.0001).
S$_{nn}$ values are above the diagonal, and p-values are below. S$_{nn}$ values that are significant at a level of p < 0.0014 (adjusted for multiple comparisons by the Bonferroni method) are bold and italicized. Genetic distances were calculated by the Cavalli-Sforza method, and S$_{nn}$ calculated with 1000 permutations[21].
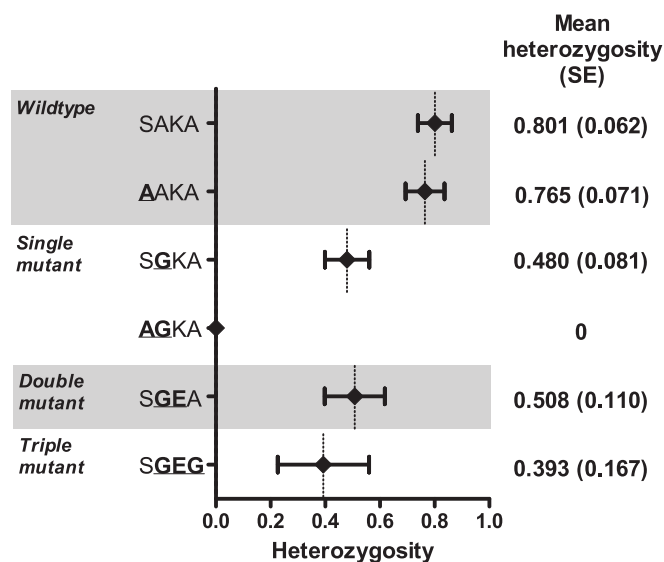
Figure 3 | **Reductions in mean heterozygosity by** *dhps* **haplotype.**
Haplotypes are indicated by the amino acids at codons 436, 437, 540, and 581 of DHPS; mutant amino acids are underlined and bolded. Diamonds are point estimates of the mean, and bars represent standard error. Calculated with GenAlEx v6.5 [39].

resistance lineages in the DRC (**Figure 5**). Specifically, on a background of unclustered SAKA and AAKA haplotypes (blue and purple circles in **Figure 5**, respectively), we note clustering of the majority of SGKA and AGKA haplotypes (red and grey circles in **Figure 5**, respectively) clearly distinct from the major cluster of SGEA and SGEG haplotypes (green and yellow circles in **Figure 5**, respectively). This segmentation of the single-mutants (SGKA and AGKA) from the double- and triple-mutants (SGEA and SGEG) haplotypes suggested that the *dhps* haplotypes arose on different genetic backgrounds.

We analyzed this observation further with eBURST, which utilizes multi-locus sequence tags to predict founding genotypes and clusters of descendants[25]. This algorithm, which is agnostic to *dhps* haplotype, identified two major clonal clusters against a background of unrelated haplotypes: one cluster contained 15 of 18 SGEA and SGEG haplotypes, and the second cluster contained 33 of 38 of the SGKA and AGKA haplotypes (**Figure 6**). Thus the genetic origins of the single-mutants SGKA and AGKA were distinct from those of the double- and triple-mutants SGEA and SGEG. Taken together, our spatial and genetic analyses indicated that, among the parasites sampled in our study, haplotypes associated with sulfadoxine resistance are genetically and geographically clustered across the DRC.

Discussion

In this cross-sectional study of *P. falciparum* haplotypes in the DRC, parasite populations were geographically clustered into two subpopulations along provincial boundaries running from north-central to southeast DRC. Furthermore, these subpopulations manifested *dhps* mutant haplotypes with independent lineages, with single-mutant SGKA and AGKA haplotypes in the west largely unrelated to the double- and triple-mutant SGEA and SGEG haplotypes in the east. These twin findings suggest a significant barrier to parasite population flow between eastern and western DRC. Because this corridor across central Africa has been critical to past spread of drug-resistant haplotypes, the identification of these barriers to gene flow may assist in future efforts to control and contain parasite drug resistance.

Central Africa is a known watershed for sulfadoxine-resistant falciparum parasites: in a prior analysis of the origins of *dhps* haplotypes in sub-Saharan Africa, mutant haplotype prevalences were sharply
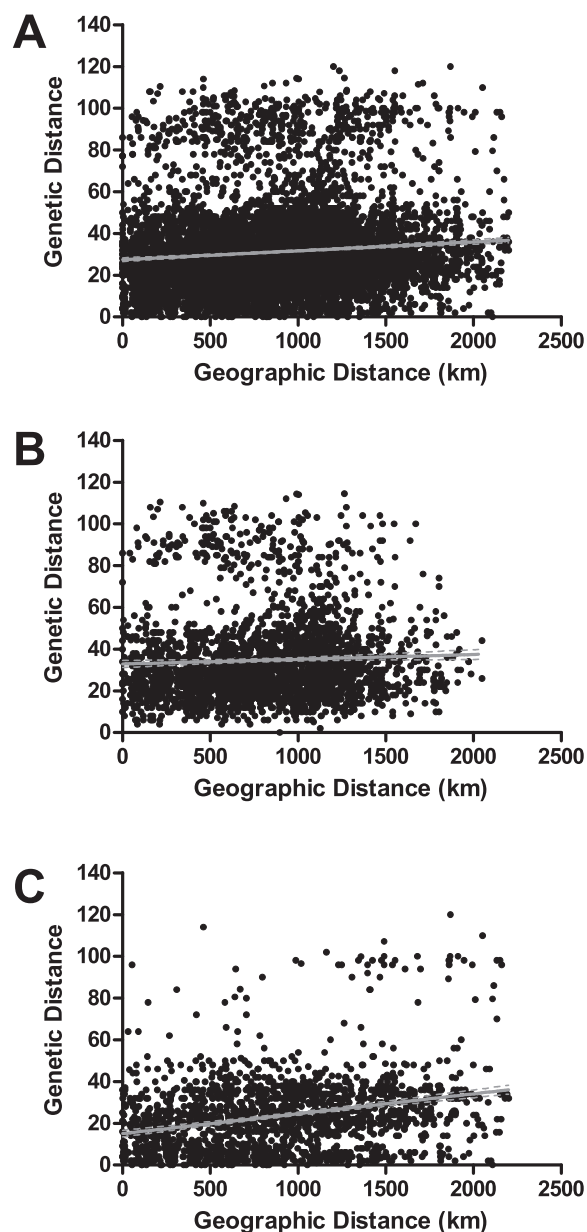
Figure 4 | **Correlations of genetic and geographic distance for all parasites (A), wildtype parasites (SAKA, AAKA, CAKA) only (B), and mutant parasites (SGKA, AGKA, SGEA, SGEG) only (C) in the DRC.**
Black dots represent pairwise comparisons, gray line is the best-fit regression line, and dotted gray line is the 95% confidence interval of best-fit line. Mantel values were 0.098 (p = 0.010) for all parasites, 0.046 (p = 0.213) for wildtype parasites only, and 0.277 (p < 0.001) for mutant parasites only. Pearson product-moment correlation coefficient (PMCC) values were 0.09828 (p < 0.0001) for all parasites, 0.04580 (p = 0.0158) for wildtype parasites only, and 0.2771 (p < 0.0001) for mutant parasites only. Genetic and geographic distances and Mantel tests computed using 999 permutations with GenAlEx v6.5, and PMCC computed with GraphPad Prizm.

divided between eastern and western Africa, but few parasites from the DRC were included[4]. We report a relatively high prevalence of wildtype haplotypes, with 55% (83/151) of parasitemias harboring either the SAKA or AAKA haplotype. These data indicate that resistance to sulfadoxine is still evolving in the DRC and there is minimal selective pressure applied by the relatively infrequent use of sulfadoxine-pyrimethamine for childhood fever[18] or IPTp[26].

Table 2 | Pairwise Nei's genetic distance (above diagonal) and Φ_{PT} values (below diagonal) between the major *dhps* haplotypes in the DRC*

	SAKA	SGKA	SGEA	SGEG	AAKA	AGKA
SAKA		0.540	0.765	0.735	0.174	0.879
SGKA	*0.133*		0.746	0.978	0.371	0.133
SGEA	0.037	*0.362*		0.081	0.351	1.249
SGEG	0	*0.380*	0		0.509	1.220
AAKA	0	*0.124*	0.009	*0*		0.666
AGKA	0.032	0	0.217	0.588	0.008	

Calculated using GenAlEx v6.5 using 149 specimens with pure (i.e. non-mixed) *dhps* haplotypes, using 999 permutations over full population and 99 permutations for pairwise comparisons[39]. *Φ_{PT} values with a p < 0.05 are indicated in italics and bold. Haplotypes are indicated by the amino acids at codons 436, 437, 540, and 581 of DHPS; mutant amino acids are underlined and bolded.

Nevertheless, as expected based upon prior studies, there were marked differences in the distributions of mutant *dhps* haplotypes: single-mutant SGKA and AGKA predominated in the west while double- and triple-mutant SGEA and SGEG haplotypes clustered in the east. These distributions mirror the prevailing mutant haplotypes in neighboring countries: Congo-Brazzaville[13] and the Central African Republic[27] in the west and Uganda[28] and Rwanda[29] in the east. We do note, however, a cluster of double-mutant SGEA haplotypes near Mbuji-Mayi in south-central DRC, which may represent the incursion of more highly-resistant parasites into western DRC. The region around Mbuji-Mayi was a major destination for refugees from eastern DRC during the protracted civil war in the DRC[30], possibly providing a corridor for parasite transit across geographic and political boundaries.

Microsatellite genotyping of our parasites revealed a high degree of heterozygosity both within and between parasitemias. These findings are consistent with prior studies of African *P. falciparum*[22]. Reductions in mean heterozygosities across microsatellites linked to *dhps* were consistent with selective pressure on haplotypes bearing the A437G, K540E, and A581G mutations, and greatest upon those with all three mutations. These haplotype H_e values are similar to those from other African studies[4,31,32], though our study allows a fuller characterization owing to the DRC's greater scope of haplotypes and our number of microsatellites analyzed. Interestingly, the degrees of selection upon the mutant SGKA (mean H_e 0.480), SGEA (mean H_e 0.508), and SGEG (mean H_e 0.393) haplotypes were similar to those reported from other regions in which these mutant haplotypes are nearly fixed in the parasite populations[6,32,33], despite the DRC continuing to harbor a relatively high prevalence of wildtype haplotypes (55%).

Based upon genetic distance (**Figure 4**, **Table 2**), network (**Figure 5**), and clonal lineage analyses (**Figure 6**), the lineages of these sulfadoxine-resistant haplotypes appear to be distinct: These analyses largely grouped the SGKA haplotype microsatellite profiles into a cluster distinct from those of the SGEA and SGEG haplotypes. This is supported by prior studies[4], though we employed alternate analytic tools to characterize lineages of fine-scale microsatellite profiles in order to more specifically describe these relationships. Because the mutations in *dhps* are believed to accumulate in a stepwise manner[5], we would expect single-, double-, and triple-mutant *dhps* haplotypes to cluster together in these analyses, but we sampled few SGEA and SGEG haplotypes that were related to the single-mutant SGKA parasites, and few single-mutant SGKA parasites that were closely related to the SGEA and SGEG haplotypes. In western DRC where the SGKA mutant haplotypes predominate, SP use may not be frequent enough to produce sufficient selective pressure to favor the emergence of a related double-mutant: In Congo-Brazzaville to the West, the *dhps* SGKA haplotype, when combined with the triple-mutant *dhfr* which is common in the DRC[34,35], confers significant clinical resistance to SP as evidenced by clinical treatment failure[13]. More puzzling is the absence of an abundant ancestral single-mutant SGKA related to the double- and triple-mutant SGEA and SGEG haplotypes. Though several phenomena may account for this, one explanation is that these parasites were imported from neighboring East African countries such as Uganda and Rwanda, where these haplotypes are prevalent[28,29]. This hypothesis is supported by their increased preponderance in eastern DRC; though one might expect that we would have also detected imported parasites bearing an ancestral SGKA haplotype, the K540E mutation was near fixation in these neighboring countries by the early 2000s[28], thus eliminating this ancestral haplotype from their parasite populations. We note the presence of the double-mutant SGEA haplotype in parasitemias from Kasaï-Occidental, Kasaï-Oriental, and Equateur provinces that are far from the eastern borders of the DRC; their clustering with eastern mutant haplotypes indicates that this lineage has migrated across the DRC. Identifying the route and mechanisms of this migration will be critical to controlling and containing drug-resistant parasite populations.

Similar to this genetic divergence of drug-resistant haplotypes, the parasite populations overall in the DRC were geographically divided into one cluster in the West and one in the Northeast (**Figure 2B**), and pairwise comparisons of parasite genotypes between provinces supported this split (**Table 1**). These findings suggest that parasite populations are circumscribed within the DRC, despite the absence of obvious barriers to gene flow owing to geography or ecology. Differentiation into divergent populations is dependent upon complex relationships between malaria endemicity, human population density and migration, vector prevalence and efficiency, and malaria treatment and control practices. Future studies to better characterize the mediators of this phenomenon will be critical to understanding the impact of parasite subpopulations on malaria control and elimination.

Our study is subject to several limitations. Multiplicities of infection in our asymptomatic adults were high as evidenced by the return of multiple alleles for many microsatellite loci, from which we selected the dominant allele. Though we may have underestimated minor variants in these mixed parasitemias, this approach has been applied in other studies[22] and our analyses were limited to those parasitemias which were pure *dhps* haplotypes. Additionally, we had no clinical data on the survey recipients who harbored the parasitemias we studied, and thus we cannot gauge the potential impact of personal or aggregate antimalarial use upon the distribution of *dhps* haplotypes. Nevertheless, this may not have a major impact given the uniformly low use of SP across the DRC: the proportion of febrile children under 5 who received SP ranged from 1.1% (in Kinshasa) to 8.2% (in Bandundu). Finally, we did not have contemporary parasites from neighboring countries with which to compare our *dhps* lineages. Therefore, future studies will be needed to assess the relationships between our DRC haplotypes and those of East and West Africa.

In our sampling of falciparum parasites across the DRC, we report a full range of *dhps* haplotypes as well as geographically- and genetically-distinct sulfadoxine-resistant parasites. Our data suggest that more resistant parasite lineages were imported into the DRC from east Africa, and that, despite the overall divergence of parasites into eastern and western subpopulations, these parasites are spreading into western DRC. Given 1) the importance of sulfadoxine to preventive measures in children and pregnant women, 2) the appearance of more highly-resistant *dhps* haplotypes in East Africa, and 3) the importance of the DRC as a corridor for parasite flow across sub-Saharan Africa, continued molecular surveillance in central Africa is necessary both to characterize the evolving pattern of sulfadoxine-resistant haplotypes and to identify factors governing the spread of drug-resistant parasites.
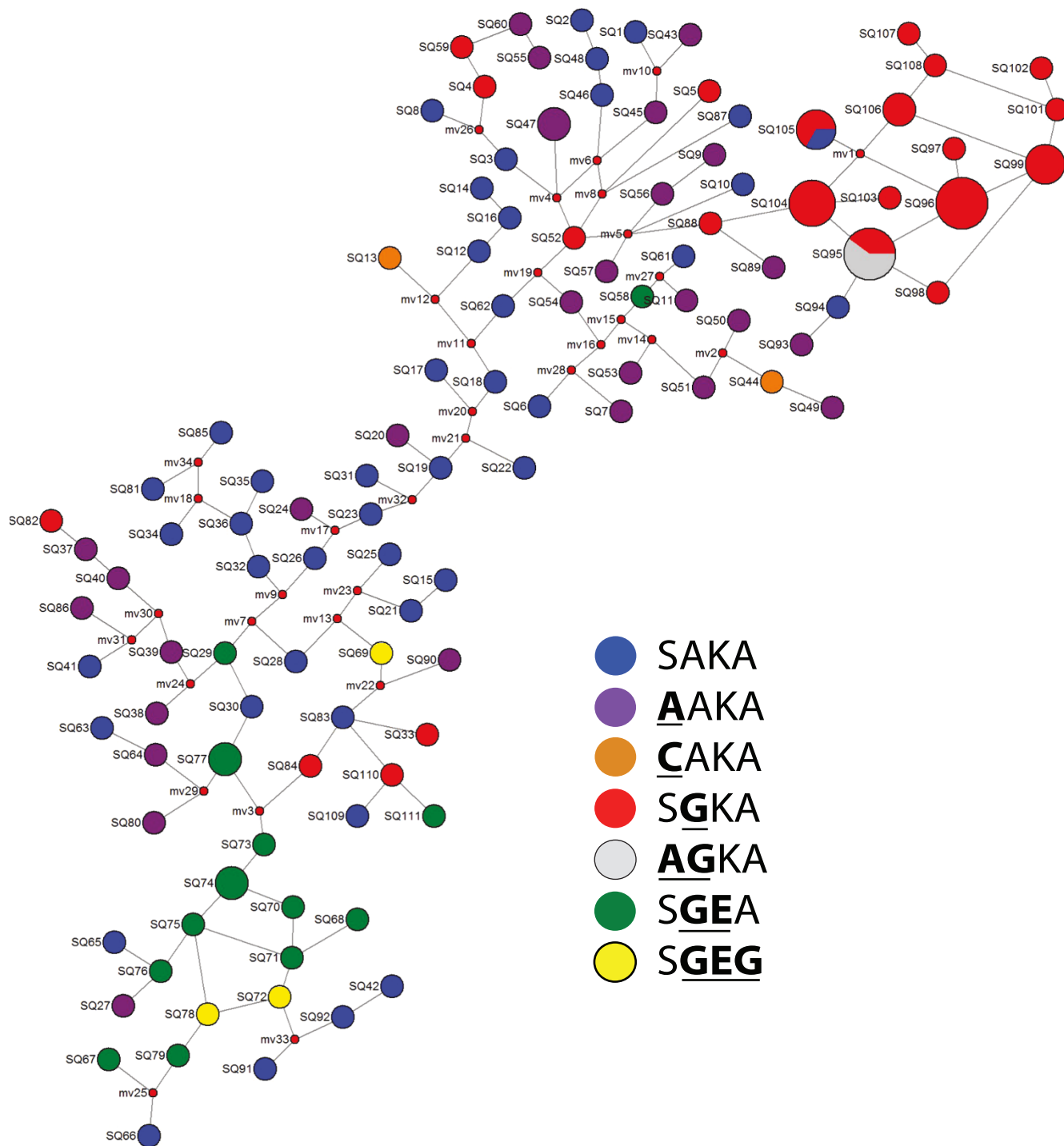
Figure 5 | Median-joining network of _dhps_ haplotypes in the DRC. ''SQ'' numbers designate microsatellite profile, circles are proportional to the number of parasites bearing that microsatellite profile, and _dhps_ haplotypes are indicated by the color key and are indicated by the amino acids at codons 437, 540, and 581 of DHPS; mutant amino acids are underlined and bolded. Small red nodes are hypothetical median vectors created by the program to connect sampled haplotypes into a parsimonious network. Distances between nodes are arbitrary. Constructed in NETWORK v4.6.10 [40,41].

Methods

Ethics statement. All survey respondents provided verbal informed consent for the collection of blood spots in one of the five main languages spoken in the DRC. Consent was verbally acquired owing to the need for immediate de-identification of all data. Consent procedures, survey administration, and blood sample collection were approved by the Ethics Committees of Macro International and the School of Public Health of the University of Kinshasa, and testing of malaria parasites was approved by the Institutional Review Board of the University of North Carolina.

Specimen collection. The methods of the 2007 Demographic and Health Survey (DHS) in the DRC have been described elsewhere[18]. Briefly, adults aged over 15 years

were selected from 9000 randomly selected households within 300 randomly-selected clusters identified across the DRC based upon the 2006 DRC national census. Survey respondents contributed a finger-prick blood sample which was stored on filter paper as a dried blood spot (DBS), from which three 0.3-inch discs were punched into plastic 96-well plates, with genomic DNA (gDNA) extracted using the invitrogen PureLink 96 kit (invitrogen, Carlsbad, CA, USA). Real-time PCR detection of _P. falciparum_ was performed as previously described[18]. The DHS was conducted in February and March for clusters in and near Kinshasa, and between May and August for the balance of the DRC.

The original molecular survey of malaria in the DRC identified 2,435 _P. falciparum_ mono-parasitemias in 8,838 adult respondents[18]. A random subset of 867 specimens

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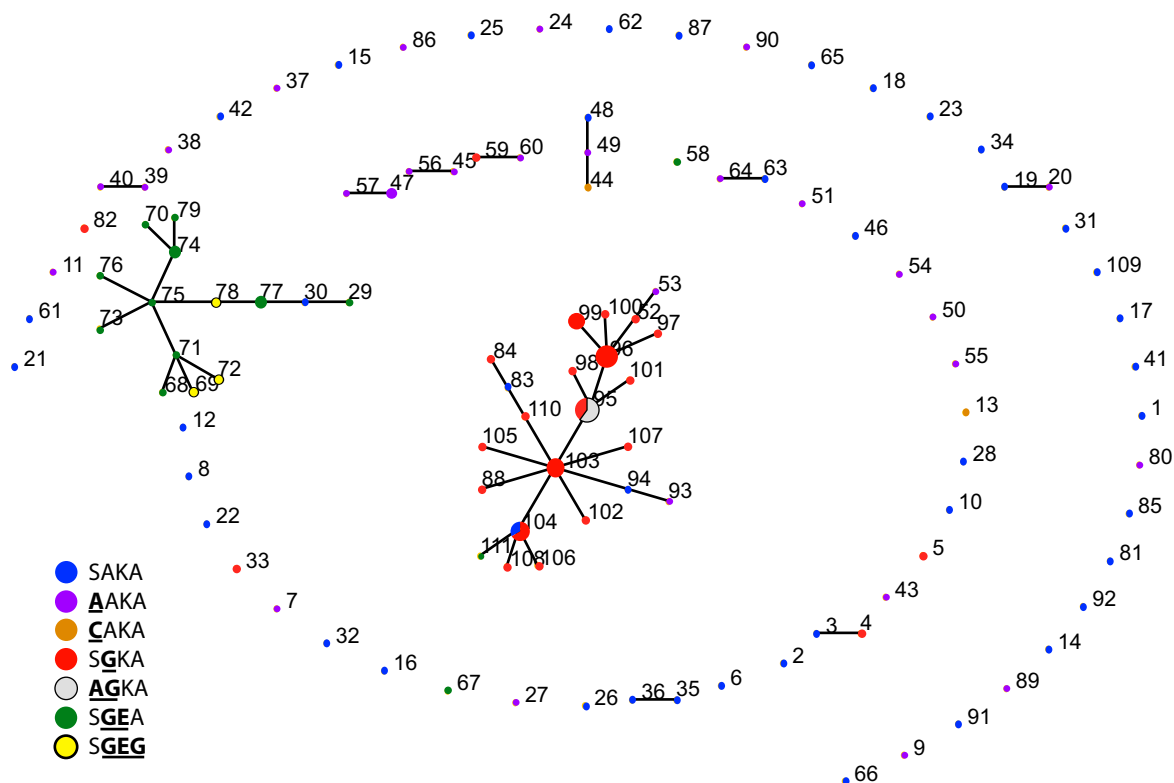
Figure 6 | Hypothesized lineages of *dhps* haplotypes in the DRC. Numbers designate microsatellite profile, nodes are proportional to the number of parasites bearing that profile, and *dhps* haplotypes are indicated by the color key and are indicated by the amino acids at codons 437, 540, and 581 of DHPS. Nodes with more than one color indicate that the microsatellite profile was borne by more than one type of *dhps* haplotype. Connected haplotypes are clonal complexes that are hypothesized by the algorithm to have descended from the same founder haplotype. Haplotypes that are connected vary in their microsatellite profile at one locus; unconnected haplotypes are those that do not share 4 loci with any other haplotype. Calculated with eBURST v3 [25].

that were chosen irrespective of demographic or geographic characteristics yielded 229 *P. falciparum* parasitemias, of which 50 failed to return *dhps* genotype data. The resulting 179 parasitemias constitute the unit of analysis for this study. These patients harboring parasitemias did not differ significantly from non-selected parasitemic patients with regard to province or demographics (data not shown).

Genotyping procedures. Specimens were genotyped for SNPs at codons 436, 437, 540, 581, and 613 of *dhps* by amplification and sequencing as previously described[6]. Parasites with multiple peaks at any locus in the manually-inspected eletropherogram were scored as mixed at that locus. All parasites were assayed for allele length at five microsatellite loci flanking the *dhps* gene: −2.9 and −0.13 kB upstream, and 0.03, 0.5, and 9 kB downstream of *dhps*. Microsatellite loci were amplified as previously described[6], PCR products were sized on a 310 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA), and allele lengths were scored using GeneMapper (v4.1, Applied Biosystems). In specimens with multiple peaks, additional allele lengths were recorded if peak heights were > 20% of the major peak. All specimens were amplified and sized in parallel with gDNA from *P. falciparum* isolate 3d7; the known length of the 5 microsatellites in the 3d7 genome was used to correct allele lengths in the experimental specimens in order to account for inter-run variability in fragment sizing.

Data analyses. For specimens for which geographical coordinates were available, we first mapped *dhps* haplotypes across the DRC using ArcGIS (v10, ESRI, Redlands, CA, USA). We classified SAKA, **A**AKA, **C**AKA haplotypes as wildtype and other haplotypes as mutant consistent with prior studies[4], because of the unclear association of mutations at codon 436 with sulfadoxine susceptibility. Prior to mapping, all DHS cluster coordinates are randomly offset by 0 – 2 km (in urban areas) or 0 – 5 km (in rural areas) in order to maintain privacy.

Based upon the microsatellite profiles, we investigated the geographic structure of haplotypes by DRC political province. Pairwise genetic distances between parasites were calculated using the Cavalli-Sforza and Edwards model as implemented in Populations v1.2.23[36]. The genetic distance matrix created in Populations was used as input for FastME to construct neighbor-joining trees with balanced branch-length estimation[37,38]. The FastME output in Newick format was used in Fast UniFrac to assess for geographic clustering. Fast UniFrac compares communities of microbes and clusters them with confidence estimates derived from permutation[20]. 1000 permutations were used to determine significance. For these analyses, we first input

microsatellite profiles of all *dhps* haplotypes, and then repeated them using only parasites bearing wildtype haplotypes as defined above.

To corroborate the conclusions of these geographic phylogenies, we also tested the overall parasite populations for genetic differentiation into subpopulations by calculating pairwise Hudson's nearest-neighbor statistics (S_{nn}) between DRC provinces[21]. S_{nn} measures how frequently the nearest neighbors of closely linked genetic marker data are located within the same geographic locality and employs permutation in order to estimate p-values of these measures. Typically, genetically distant populations have values near 1; panmictic populations have values close to 0.5. Populations were defined by DRC province, though we combined Bas-Congo with Kinshasa and North with South Kivu; the resulting 9 geographic categories produced 36 pairwise comparisons, and for this analysis a p-value < 0.0014 (0.05 / 36) was considered significant after correction using the Bonferroni method for multiple comparisons. Means of pairwise provincial S_{nn} values between subpopulations that were identified by UniFrac were compared by analysis of variance (ANOVA) using Stata/IC v10 (Stata Corp, College Station, TX, USA).

We calculated the number of alleles and expected heterozygosity (H_e) per microsatellite locus in the overall dataset using GenAlEx 6.5[39]. In order to assess the degree of selection on different *dhps* haplotypes, we calculated H_e across all five loci for each *dhps* haplotype. Based upon the microsatellite fragment lengths, we calculated pairwise Nei's genetic distances between *dhps* haplotypes in order to estimate genetic relatedness[23]. We assessed isolation-by-distance using pairwise comparisons of genetic and geographic distance and computing Mantel tests using 999 permutations in GenAlex. We first included all parasites for which dhps haplotype and geographic coordinates were available, then repeated testing among only wildtype parasites and among only mutant parasites. In order to further assess the divergence of wildtype and mutant *dhps* haplotypes, we calculated Φ_{PT} via an Analysis of Molecular Variance (AMOVA) in GenAlEx using 999 permutations over the full population and 99 pairwise permutations[24,39].

In order to further explore the origins of the prevailing *dhps* haplotypes in the DRC, we first partitioned into unique haplotypes the microsatellite profiles from each specimen that was successfully genotyped at all five loci. Next, we calculated a median-joining network of these unique microsatellite haplotypes using NETWORK v4.6.10[40,41]; for network construction, we assigned weights to each locus in inverse proportion to the locus's H_e, as calculated above. The unique microsatellite haplotypes were then analyzed using eBURST v3, which groups multi-locus sequence types into clonal clusters that are hypothesized to have derived from a common

ancestor[25]. Analyses with NETWORK and eBURST were performed in an unsupervised fashion with regard to *dhps* haplotype; these haplotypes were added post-hoc to the median-joining network and hypothesized clonal clusters.

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Author contributions

Conceived and designed experiments: SMT, ALA, ME, MTA, VU, AKT, SRM. Performed the experiments: SMT, ALA, MJ, MTA. Analyzed the data: SMT, ALA, CMP, MTA, JJJ, SRM. Contributed reagents/materials/analysis tools: KM, CMP, JJJ, MJ, ME, MTA, VU, AKT. Wrote the paper: SMT, ALA, JJJ, SRM.

Additional information

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