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Drug-Resistance and Population Structure of *Plasmodium falciparum* Across the Democratic Republic of Congo Using High-Throughput Molecular Inversion Probes

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A better understanding of the drivers of the spread of malaria parasites and drug resistance across space and time is needed. These drivers can be elucidated using genetic tools. Here, a novel molecular inversion probe (MIP) panel targeting all major drug-resistance mutations and a set of microsatellites was used to genotype *Plasmodium falciparum* infections of 552 children from the 2013–2014 Demographic and Health Survey conducted in the Democratic Republic of the Congo (DRC). Microsatellite-based analysis of population structure suggests that parasites within the DRC form a homogeneous population. In contrast, sulfadoxine-resistance markers in dihydropteroate synthase show marked spatial structure with ongoing spread of double and triple mutants compared with 2007. These findings suggest that parasites in the DRC remain panmictic despite rapidly spreading antimalarial-resistance mutations. Moreover, highly multiplexed targeted sequencing using MIPs emerges as a cost-effective method for elucidating pathogen genetics in complex infections in large cohorts.

**Keywords.** Democratic Republic of the Congo; malaria; drug resistance; molecular inversion probe; targeted sequencing.

Malaria, particularly drug-resistant malaria, remains a global public health problem [1]. However, little is known about the drivers that modulate its spread over space and time [2]. Over short distances, parasite distribution depends on both human and mosquito movement among local populations, but over larger distances, human population movement is the main determinant [3]. Understanding such movement is important in the context of malaria control, especially with regard to the spread of drug-resistant parasites [4–7].

The Democratic Republic of the Congo (DRC) is the second largest country by area in Africa, and it has the second highest malaria burden [1]. It is centrally located, bordering 9 other countries. Because of this, the flow of parasites between the DRC and its neighbors and within the DRC needs to be better understood. Previously, using 5 neutral microsatellites (MSs), we were able to show that *Plasmodium falciparum* parasites in the DRC were different from those in other countries, but we could not find any differentiation within the country [8, 9]. However, we found notable geographic structure in more recently introduced genotypes, such as those resistant to sulfadoxine [10]. Parasites that harbor recently described deletions in the *pfhrp2* gene also showed spatial structure, clustering in a few sites in eastern DRC and in Kinshasa [11]. Based on these initial insights, information from more genetic markers and samples can likely further elucidate the population structure and flow of drug resistance.

Analyses of *P. falciparum* population genetics have been hampered by several factors. First, the AT richness of the genome makes sequencing difficult [12]. Second, individuals are often infected with multiple genotypes, making haplotype reconstruction challenging [13]. Third, balancing selection may independently lead to identical parasite populations in geographic regions that are not spatially connected, thereby giving the false impression of high connectivity [14]. Finally, a substantial portion of infections contain very low levels of circulating parasites, making it difficult to obtain enough parasite DNA relative to the human host for genotyping.
Here we introduce a panel of molecular inversion probes (MIPs) that can alleviate some of these problems through cost-effective targeted sequencing at multiple loci. Molecular inversion probe sequencing is a novel tool that has been used extensively for targeted capture and resequencing of human candidate genes, allowing tens of thousands of individual samples to be rapidly assessed at hundreds of loci (Figure 1A) [15–18]. Key strengths compared with other capture methods are scalability and minimal costs in terms of reagents and labor. Here, for the first time, we optimize MIPs for efficient capture from dried blood spots and use them to genotype and characterize malaria parasites across the DRC.

**METHODS**

**Study Population**

Dried blood spot samples were collected from children as part of cluster-based household surveys in the 2013–2014 DRC Demographic and Health Survey (DHS) from November 2013 to February 2014, as described previously [19]. DNA samples were extracted from 1622 dried blood spots and analyzed for *P. falciparum* by real-time quantitative polymerase chain reaction (qPCR). Each sample included global positioning system (GPS) coordinates that provide a location of the cluster of households from which they were collected [20]. The resulting 601 malaria-positive samples were selected and underwent MIP capture and sequencing at the University of Massachusetts.

**Figure 1.** Molecular inversion probe (MIP) assay and performance on laboratory control mixtures. A, The MIP capture is illustrated showing the key steps of MIP arm hybridization, polymerase extension, and gap ligation to form a single-stranded circle. Exonuclease digestion removes linear template DNA, thereby relatively enriching for the circular captures, which are then amplified using universal primers along with a sample barcode. Important components are color coded: extension arm (blue), ligation arm (red) molecular identifiers (green), and backbone (pink+purple). B, An example of microsatellite (MS) stutter seen in standard capillary electrophoresis versus MIPs where stutter is detected and removed based on inconsistency within unique molecular identifiers. C, The coverage of the 21 assessed MSs, demonstrating that apart from a few failed reactions the vast majority of MSs are detected in every sample until dilutions of 29 parasites/μL. D, Frequency estimates of the 4-strain mixture compared with expected frequency (last bar on right, drawn wider for emphasis) based on relative amounts of DNA from each strain. Abbreviations: CE, capillary electrophoresis; MIP, molecular inversion probe; MS, microsatellite.
These positive samples came from 299 geographically distinct household cluster sites across all provinces within the country.

Control Samples
The sensitivity and accuracy of the MIP panel was assessed using serial dilutions of a control mixture of DNA isolated from the laboratory strains 3D7, HB3, 7G8, and DD2 mixed at relative frequencies of 67%, 14%, 13%, and 6%, respectively (Supplementary Tables 1 and 2). Quantification was based on Quant-iT PicoGreen dsDNA Assay (Invitrogen, catalog no. P11496). These DNA mixtures were supplemented with 1 ng/μL of human DNA to better mimic DNA isolated from dried blood spots and whole blood and were included not only in initial testing but also as a positive control for every capture and sequencing run.

*Plasmodium falciparum* Molecular Inversion Probe Design
Molecular inversion probes are approximately 100 nucleotide long, single-stranded oligos that have a shared backbone and specific sequence complementary to the target region in the arms (Figure 1A, Supplementary Figure 1A). *Plasmodium falciparum* MIPs were designed to capture known and candidate drug-resistance mutations (Table 1), as well as 11 previously described [21, 22] and 18 newly designed flanking MSs (Yaobao et al., unpublished data) (Table 2, Supplementary Table 3, Supplementary Methods). Nine of these MSs were removed from analysis for failing quality controls (Supplementary Methods).

Molecular Inversion Probe Capture, Amplification, and Sequencing
Our molecular inversion probe library sequencing is a multistep protocol modified from published protocols [23] to improve *Plasmodium falciparum* molecular inversion probe library sequencing (Supplementary Methods, Supplementary Figures 1–4) with the following key steps. First a panel is created by pooling all desired MIPs (43 for MS MIP panel and 42 for drug-resistance MIP panel; Supplementary Table 3, probe sets MS1 and DR1, respectively), followed by 5′ end phosphorylation. Each panel can be used separately or combined to create a larger panel if desired. Each capture reaction is carried out as a single reaction per MIP panel per sample, combining sample DNA, MIP panel, polymerase, and ligase. With isothermal incubation, MIPs bind to their targets, followed by polymerase extension and single-stranded circle formation by ligase. After capture, all remaining linear DNA (unbound probes, original template DNA) is removed by exonuclease treatment. All captured products are then amplified by 1 forward and 1 reverse primer binding to the universal priming site on each circle. Polymerase chain reaction (PCR) primers also include Illumina sequencing adapters and 8-nucleotide-long sample barcodes. Once barcoded, samples are pooled into a single tube to create a sequence-ready library that is further cleaned prior to sequencing using solid phase reversible immobilization (SPIR) beads and agarose gel purification (Supplementary Figure 1A).

Molecular Inversion Probe Data Processing
Sequencing data was processed using MIPWrangler software (Hathaway, unpublished data) in combination with other software. Briefly, sequences were demultiplexed by their dual sample barcode using bcl2fastq software (Illumina). Paired-end reads were then stitched together using FLASH [24] and filtered on expected length and on per base quality scores by discarding a sequence if the fraction of quality scores >30 was <70% (Q30 < 70%). Quality filtered stitched sequences were then further demultiplexed by target using the extension and ligation arm sequences to produce a file for each target for each sample (Supplementary Figure 1B). Target sequences for each sample were then corrected using their unique molecular identifiers (UMIs). This was done by clustering sequences on their UMIs and then creating a consensus sequence for each specific UMI. This UMI redundancy removes a substantial proportion of PCR errors that occur in late cycles, including polymerase stutter and subsequent sequencing errors (Supplementary Figure 1B). The UMI corrected sequences were then further clustered by using the cluster algorithm from SeekDeep, allowing accurate detection of single base differences and indels at levels ≤1% [25]. Given the variable depth, we set minimum threshold defaults at ≥2 UMIs and ≥0.5% relative abundance for a cluster to be included in final analysis.

Differences between the observed sequence and the reference sequence for each probe were obtained by pairwise alignment using LastZ software [26]. Single nucleotide variants and indels from the LastZ output were annotated using Annovar software [27].

Population Genetic Analyses of Microsatellites
Quality checks were carried out on the distribution of MS lengths, and all 20 loci were tested for independence through pairwise correlation tests using a Bonferroni-adjusted
significance threshold of \( \alpha = 0.05 \) to account for multiple testing. Principal component analysis (PCA) was conducted to look for any signal of population structure, using the dominant allele only in each individual and imputing missing values using the mean. Population structure was also assessed using the program \textit{Maverick} [28], which builds on the Bayesian mixture model approach developed by Pritchard and colleagues [29] but provides more accurate estimates of the number of clusters. \textit{Maverick} was run under the nonadmixture model with 500 burn-in iterations, 10,000 sampling iterations, and 20 thermodynamic rungs. Finally, we looked for a signal of isolation by distance by regressing the absolute difference in MS lengths against geographic distance between sample GPS locations; under isolation by distance we would expect a positive relationship between these quantities.

**Spatial Analysis of Drug-Resistant Mutations**

All drug-resistance loci were analysed separately using the R package \textit{PrevMap} [30], which implements model fitting and spatial prediction under a range of geostatistical models. First, allele frequencies within each cluster were transformed to the real line using the transformation \( y_i = \log((p_i + \varepsilon)/(1 - p_i + \varepsilon)) \), where \( p_i \) is the mutant allele frequency of cluster \( i \), \( y_i \) is the transformed value, and \( \varepsilon \) is a small value that ensures that \( y_i \) values are always finite even when allele frequencies are 0 or 1 (we used \( \varepsilon = 0.001 \), although results were not highly sensitive to this parameter). A geostatistical model of the form \( y_i = S(x_i) + Z_i \) was then fit to the transformed data, where \( S(x) \) is a stationary isotropic Gaussian process (GP) with variance \( \sigma^2 \) and Matérn correlation function with scale \( \phi \) and shape parameter \( \kappa = 2 \), and \( Z_i \) is an independent Gaussian noise term with variance \( \tau^2 \). Hence, the 3 free parameters of the model were \( \{\sigma^2, \phi, \tau^2\} \). These parameters were jointly estimated in \textit{PrevMap} using maximum likelihood, and fitted values were used to produce spatially continuous estimates of the underlying allele frequency distribution through 10,000 simulations. These simulations capture the predictive error that occurs due to the stochastic nature of the underlying model. Standard errors of prediction were calculated and used to measure confidence at each point in space.

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**Table 2. Summary of Microsatellite Molecular Inversion Probes**

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**Abbreviations:** MIC, molecular inversion probe; QC, quality control.
RESULTS

Molecular Inversion Probe Performance Controls
The accuracy and sensitivity of the designed MIP assay were tested using 15 serial dilutions of a DNA mixture of 4 laboratory strains (Supplementary Table 1) containing from 7469 down to 0.5 of Plasmodium haploid genome copies and 1 ng of human DNA (~1650 haploid genome copies) per microliter. Unique molecular identifiers associated with each arm allowed correction of errors introduced during PCR amplification (Supplementary Figure 1B), including MS stutter (Figure 1B). Based on these control mixtures, MIPs captured the vast majority of targets down to inputs of approximately 29 parasites per microliter (Figure 1C). The frequency estimates were consistent down to approximately 29 parasites per microliter, closely following the expected frequencies based on picogreen quantification of input DNA (Figure 1D).

Sequencing the Parasitic Demographic and Health Survey Blood Spots
Among these 601 samples submitted for analyses, after a single MIP capture and sequencing run each for the drug-resistance and MS panels, 552 samples yielded a usable sequence. The sequenced individuals were well distributed across the country (Figure 2). Overall, 293 and 154 samples showed good coverage of 50% and 80%, respectively, across all of the targeted loci. In terms of density of infection, we found that MIP coverage began to drop off at qPCR cycle threshold (Ct) values of 31, which equates to a parasite level of approximately 100 parasites/μL (Supplementary Figure 5). This represents low parasitemia but may also be a consequence of the quality of the dried blood spots, as well as the large number of samples multiplexed. The median Ct value of the samples that yielded no MIP coverage was 34. The raw sequence data used in this study has been deposited to Sequence Read Archive of National Center for Biotechnology Information with the accession number SRP144456.

Microsatellite Population Genetics
We first explored population structure using the 20 well-validated MSs from the MIP panel. Consistent with their known sequence, 19 MSs showed clear trinucleotide repeat distributions, with only MS B7M19 having a more complex repeat distribution (Supplementary Figure 6). Among the 19 trinucleotide MSs, just 2 of 7515 MS length calls fell outside the trinucleotide pattern, and these were removed from subsequent analyses. There was correlation in MS lengths in only 2 of the 190 pairwise comparisons—between Ara2 and AS1 and between AS12 and AS13. These MSs occur in close physical proximity, so this correlation indicates likely linkage disequilibrium. Principal component analysis indicated no clear signal of population structure, and the first 2 components accounted for a minimal amount of the total variation in the data (17% for PCA1, 14% for PCA2) (Figure 3, Supplementary Figure 7). Analysis in Maverick also failed to detect any population structure, with K = 1 clusters having the highest model evidence, indicating a single freely mixing population (Supplementary Figure 8). This was further supported by regression of genetic and geographic distance, which revealed no strong signal of isolation by distance (Supplementary Figure 9).

Drug-Resistance Profiling
Using the MIPs we designed to target known and putative drug-resistance mutations based on the literature. We first, quantified the prevalence of known drug-resistance mutations. The pfαfr-ts gene mutations N51I, C59R, and S108N showed the highest prevalence (>80%) among all tested drug-resistance loci. Similar to the previous studies, the levels of evolutionarily older pfαps mutations A437G and K540E showed higher prevalence compared with A581G [10, 31]. The mutations A613S/T and I431V seen in Western Africa [32] were not observed in the DRC. Mutations at the highest prevalences include those in pfαt and pfmdr. Importantly, known artemisinin-resistance mutations in pfk13 (M476I, Y493H, R539T, I543T, C580Y) were not observed in any sample (Figure 4; Supplementary Table 6) consistent with previous studies [33, 34]. With deep sequencing, in addition to prevalence, we can also examine overall population frequencies of mutations. As expected, mutant allele frequencies were nearly identical to prevalences (Supplementary Figure 10) [35, 36].

Spatial Assessment of Drug Resistance
Given the country-wide sampling scheme, we modeled the spatially referenced prevalence data using PrevMap to look for
differences based on geographic location. For each mutation, we generated estimated prevalences and standard errors of prediction (Supplementary Figures 11 and 12). These predictions are generated using the maximum likelihood model parameters, so, although we present the most likely prevalence surfaces, it is important to emphasize there are alternative predictive surfaces that are plausible. Various spatial patterns were observed. Generally, older initial mutations or mutations that confer resistance to previous generations of drugs were relatively uniform in distribution. For instance, key mutations for chloroquine resistance and pyrimethamine resistance had relatively uniform prevalences across the DRC. Interestingly, what are thought to be relatively more recent adaptive mutations associated with sulfadoxine resistance showed strong spatial structure (Figure 5). The pf dhps K540E mutation was predominantly localized in the northeast, and, interestingly, the pf dhps A581G mutation was always found against a background of K540E. Conversely, the A437G mutation is seen in association with K540E and A581G
mutations, as well as a single mutant *pfdhps* in the western side of the country. The S436A variant, not associated with drug resistance, occurs at high prevalence in the north of the country toward central Africa where it is most prevalent [37]. For *pfdhps*, the frequency of parasite mutations has significantly changed in comparison with our previous assessment of the 2007 DHS (*p* = 2.6 × 10⁻⁵, χ² test, 3 df) [10]. Filtering our data to nonmixed *pfdhps* haplotypes equivalent to the 2007 analysis, the overall frequency of mutant parasites has increased markedly (43.5% in 2007 vs 72.1% in 2013; *p* = 1.5 × 10⁻⁶, Fisher exact test). The number of strains with sequential mutations, double *pfdhps* mutations (436S/437G/540E/581A—SGEA), and triple *pfdhps* mutations (SGEG) has increased significantly from 14.6% to 27.2% (*p* = .009). Overall, the single (SGKA and AGKA), double (SGEA), and triple (SGEG) mutants have increased 1.5-, 1.8-, and 2.2-fold, respectively, consistent with a greater selective advantage for triple mutant, fitting with its rapid spread where it was only observed approximating the northeast border in the 2007 DHS.

**DISCUSSION**

Making statistically robust inferences from population genetics has been challenging for malaria. Many *P. falciparum* population genetic studies have used convenience samples, which may not be representative of the true parasite population and have the potential for substantial selection bias. Accordingly, we have used samples taken from the 2013–2014 DHS, which was a cluster-based household survey designed to be representative of the national population as a whole. To our knowledge, this is the first study to attempt to use a population-based sample of the malaria parasite to understand its subpopulation and drug-resistance structure and possible mechanisms of gene flow in the DRC.

Our results indicate that the parasite population is best characterized as a single population that exhibits weak isolation-by-distance. This is perhaps surprising given the country’s poor infrastructure and transportation network, which should lead to differentiation over relatively short spatial scales. Hence, it may be the case that transmission in the DRC is too high.

![Figure 5](https://academic.oup.com/jid/article-abstract/218/6/946/4989954) **Figure 5.** Spatial distribution of pfdhps mutations. Estimated prevalence of *pfdhps* K540E, A581G, A437G, and S436A mutations in the Democratic Republic of the Congo. White circles indicate clusters where only wild-type alleles were found; black stars indicate clusters where at least 1 mutation was found. Contours are at 10% prevalence levels.
Finally, all previous studies aggregate case reports or individual to existing panels. Molecular inversion probes also minimize the design and synthesis of new oligos that can be added much richer genetic data. Addition of new targets requires sim-
"...
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Potential conflicts of interest. All authors: No reported conflicts of interest. All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

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