Plasmodium falciparum Genetic Diversity in Western Kenya Highlands

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Abstract. The present study examined the genetic diversity and population structure of Plasmodium falciparum in western Kenya by analyzing the polymorphism of 12 microsatellite loci and two antigen loci. Malaria in highland areas is unstable and epidemic whereas malaria in lowland areas is endemic. Transmission intensity and malaria prevalence are substantially lower in the highlands than in the lowlands. Despite that the highland parasite populations exhibited reduced number of alleles, lower expected heterozygosity, and infection complexity in comparison to the surrounding lowland population, genetic diversity of the highland populations remained high in comparison to parasites from other meso-endemic regions. More than 70% of infections from western Kenya highland study sites were mixed genotype infections. Small but statistically significant genetic differentiation between highland and lowland populations was detected. These findings are discussed in the context of human travel and local transmission in the study area.

INTRODUCTION

Epidemic malaria is a major public health problem in the African highlands (highlands are generally referred to areas with elevation more than 1,500 meters above sea level). For instance, since the 1980s a series of Plasmodium falciparum epidemic malaria has occurred in the western Kenyan highlands, a region that was previously free of malaria or exhibited low incidences of the disease.1–4 The epidemic malaria in the western Kenyan highlands is characterized by expanded geographic areas,5 increased frequencies,6 and increased case-fatality rates.7 Previous studies have examined the risk factors associated with clinical malaria in the highlands.8–10 Population dynamics of mosquito vectors,11 effects of topography and land use on the spatial distribution of vectors and malaria infections,12–14 and the potential role of climate factors8,15,16 and drug resistance on malaria epidemics.10,17

Genetic diversity and population structure of malaria parasites have profound impacts on clonal diversity,18 competitive or positive interactions among the clones,19,20 dynamics of drug resistance,21 persistence of asexual infection and gametocyte production,22 infectivity in mosquito vectors,23,24 and malaria vaccine development.25,26 Global-scale studies on P. falciparum genetic diversity using specimens with varying transmission intensities from sites in Africa, South America, and Asia found a general pattern of low genetic diversity, strong linkage disequilibrium, and high genetic differentiation in low transmission areas, whereas in areas of high transmission intensity, parasite populations exhibited a panmictic pattern with high genetic diversity and weak linkage disequilibrium.18 Previous studies established that infection complexity within a host was dependent on exposure (transmission intensity) and age of the host (reflective of level of immunity), and negatively associated with the severity of the disease.27–32 A recent study found that allelic diversity of the merozoite surface protein 1 gene (msp-1) is affected not only by transmission intensity, but also by other factors such as the number of alleles prevalent and infection complexity.33 Moreover, studies of daily parasite population dynamics showed that such complex patterns of multiple infections would undergo rapid changes.34 To date, few studies have examined the genetic diversity and population structure of malaria parasites in highland areas where malaria transmission is unstable and occurrences of epidemic is common.

The objective of this study was to determine genetic diversity of P. falciparum in two highland sites (Kakamega and Kisii districts) in western Kenya. We then compared our results with those found in a surrounding, malaria-endemic lowland site (Kisumu district), also in western Kenya. The transmission intensity and malaria prevalence in the highlands was substantially lower than in the lowlands.11 If transmission intensity is an important determinant of the genetic diversity of malaria parasites, one would expect that epidemic malaria in the highlands would lead to few major genotypes in the population, thus low genetic diversity and low infection complexity. To the contrary, high genetic diversity and infection complexity is expected in the malaria-endemic lowlands because of frequent meiotic recombination events in mosquito vectors resulting from high infection rates. Conversely, travel to malaria-endemic areas was found to be significantly associated with increased malaria risk in highland residents.19 Introduction of new alleles by travelers from malaria-endemic areas to the highlands would increase population genetic diversity. We examined genetic diversity of block 2 of msp-1 and block 3 of msp-2 genes that code for major blood-stage surface antigens. In malaria-endemic areas in Africa, allelic types of block 2 of msp-1 were strongly associated with protection from P. falciparum malaria,35 demonstrating that these genes are under strong selection by human immune systems.36,37 Thus, interpretation of population structure and diversity results based on a small number of strongly selected markers such as msp-1 and msp-2 is problematic because the results are confounded by population history and natural selection.18 Therefore, we also included 12 microsatellite markers that are presumably selective neutral.38,39

MATERIALS AND METHODS

Parasite sampling. Blood samples were collected from malaria outpatients attending three clinics, Iguhu (1,500–1,580

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In this method, the forward primer for each marker and two allelic families (FC27 and IC1) for gene on chromosome 2. A nested PCR were performed individually using previously published primer sequences and conditions that distinguish three major allelic families (K1, MAD20, and RO33) for msp-1 and two allelic families (FC27 and IC1) for msp-2. The PCR products were subjected to electrophoresis on a 2.0% agarose gel. Fragment length was determined using the Kodak Digital Science 1D Image Analysis Software (Eastman Kodak Company, New Haven, CT). Each P. falciparum infection was characterized on the basis of the allele size for each locus. Sizes of alleles were allocated into bins of 40-basepair size ranges.

**Microsatellite marker must be fluorescently labeled (infrared dye, IRD800). To reduce the cost associated with synthesis of fluorescently labeled primers, we used the tailed primer method.** In this method, the forward primer for each marker was synthesized with an additional 19-basepair M13 sequence (5'-CACGACGTTGTAAAACGAC-3') added to the 5' end of the oligonucleotide. A primer with the same 19-basepair sequence was directly labeled with the fluorescent dye (IRD800) and was used as the sole type of labeled primer for the detection of microsatellite alleles for all 12 markers. The tailed primer method dramatically reduced the synthesis cost of fluorescently labeled primers.

The PCR was carried out in a total volume of 25 μL for each sample and locus and contained 20 μL of 1× PCR Master Mix (Abgene, Rochester, NY), 0.25 μL of 10 μM each primer, 0.5 μL of M13 primer, an additional 1 μL of 25 mM MgCl₂, and 10 ng of template DNA. An initial denaturation period of for 5 minutes at 95°C preceded the 45 amplification cycles (annealing for 30 seconds at 45°C, extension for 45 seconds at 65°C, and denaturation for 30 seconds at 94°C), followed by a final extension of 7 minutes. A Gene ImagIR 4.33 software (Li-Cor) program was used to quantify allele size on the basis of the height pattern of signal peaks. Multiple alleles were scored at a given locus if minor peaks were more than one-third the height of the predominant peak. An infection was considered to contain multiple clones if one or more loci showed more than one allele. Infection complexity provides a surrogate indicator of the level of transmission within populations, as well the opportunity for genetic recombination between different malaria clones.
linkage disequilibrium, and genetic differentiation. Genetic diversity was measured by the number of alleles per locus and expected heterozygosity on the basis of allele frequency data in each population. In the case of the presence of multiple alleles at a locus within an infection, only the predominant allele defined by the allele with the highest peak in pherograms was used for calculation of allele frequency. This procedure is appropriate for estimation of population allele frequency if the composition of PCR products is representative of the composition of templates. The unbiased expected heterozygosity, \( H_e \), was calculated as \( H_e = \frac{n(n-1)}{\Sigma r} \), where \( n \) is the number of infections sampled and \( r_i \) is the frequency of the \( i \)th allele. \(^{18}\) Observed infection complexity is defined as the largest number of alleles at any \( msp \) locus detected in the sample; it is often referred to as minimum number of clones.\(^{46,50}\) For example, an infection with two \( msp-1 \) alleles and one \( msp-2 \) allele is scored as two clones. This measure is conservative and it likely underestimates the number of clones likely to be present.\(^{50}\) Therefore, we used the maximum likelihood methods described by Hill and Babiker\(^{46,50}\) to estimate the mean number of clones, the support limit and \( msp \) allele frequencies, assuming a Poisson distribution of number of clones per individual. Because detection of multiple alleles per locus depends critically on the polymorphism of the markers and sensitivity of the methods used, the data provides relative assessment rather than absolute measures of infection complexity. The non-parametric Wilcoxon test was used to determine the statistical differences in genetic diversity among populations.

Linkage disequilibrium (LD), which characterizes statistical independence of alleles at pairs of loci, was determined for all pairs of microsatellite loci, using the LIAN 3.0 software developed for multilocus haplotype data.\(^{51}\) This software tests the null hypothesis of no linkage by a Monte Carlo simulation (10,000 permutations) on the variance of genetic distances between isolates (\( V_{pe} \)). The sample variance is then compared with the variance expected under linkage equilibrium \( V_{le} \). A distribution of \( V_e \) is generated by Monte Carlo simulations, and its percentiles provide 95% confidence intervals. The output file gives \( V_{pe} \) and \( V_{le} \) values, as well as a standardized index of association (\( I_{AS} = (V_{pe}/V_{le}) - 1)/1-r \), where \( r \) is the number of loci, a measure of haplotype-wide linkage and the 95% confidence limits determined by Monte Carlo simulations (I\(_{MC} \)).\(^{51}\) Because \( msp \) markers are not selectively neutral,\(^{35-37}\) population genetic structure was determined using microsatellite markers alone. The analysis of molecular variance (AMOVA) was conducted using the Arlequin genetic analysis software.\(^{52}\) The AMOVA partitions the molecular variance (microsatellite allele size) into three categories: among groups (highland and lowland), among populations within groups, and among individuals within populations. A Permutation test (\( n = 1,000 \)) was used to test the null hypothesis that the variance component is zero. Wright’s F-statistics between pairs of populations is also computed using the FSTAT computer software.\(^{53}\)

Structure 2.0 computer program was used to assign individuals from all populations to a predetermined number of clusters (K) based on multilocus microsatellite data.\(^{54}\) For each run, a burn-in period of 50,000 steps was followed by 1,000,000 iterations under the admixture model and the assumption of correlated allele frequencies. Various values of K (2 to 4) were tested. Individuals were assigned to the cluster only if the proportion ancestry was \( \geq 0.8 \).\(^{55}\) The individual was unassigned when the proportion ancestry from any single cluster was < 0.8.

**RESULTS**

**Microsatellite polymorphism.** High levels of polymorphism were shown among parasites because all 12 microsatellite markers used were polymorphic for the three populations studied. The number of microsatellite alleles per locus ranged from 7 (TA42) to 16 (Polya). The lowland population showed the highest level of diversity, and the highland samples showed a significantly lower level of diversity (Table 1). For example, an average of 8.6 alleles was detected in the lowland Kombewa population (range = 3–14), whereas the two highland populations, Kakamega and Kisii, showed an average of 6.7 alleles (range = 4–9) and 5.8 alleles (range = 2–9), respectively (\( \chi^2 = 7.44, df = 2, P = 0.02 \)). The levels of unbiased expected heterozygosity of the lowland Kombewa population were marginally higher than those observed in the highland population (\( \chi^2 = 4.86, \) degrees of freedom [df] = 2, \( P = 0.09 \)). The estimated expected heterozygosity (\( He \)) was 0.75 (range = 0.55–0.89) in Kombewa, 0.69 (range = 0.53–0.78) in Kakamega, and 0.66 (range = 0.38–0.81) in Kisii (Table 1).

The overall infection complexity (minimum number of clones in an infection detected by all 12 microsatellite markers) was marginally higher in the lowland Kombewa population than in the two highland populations (\( \chi^2 = 5.54, df = 2, P = 0.06 \); Table 2). The proportion of infections with more than one clone was 87.0%, 82.4%, and 80.9% in Kombewa, Kakamega and Kisii, respectively (\( \chi^2 = 1.44, df = 2, P = 0.49 \)).

**Genetic diversity of \( msp-1 \) and \( msp-2 \) genes.** The \( P. falciparum \) parasite populations exhibited a high degree of diversity on the basis of length polymorphism of the two antigen loci. Using a conservative bin size range of 40 basepairs for \( msp-1 \) and \( msp-2 \), a total of 13 alleles were identified for \( msp-1 \) and 15 alleles for \( msp-2 \) for the three locations (Table 3). At the \( msp-1 \) locus, a total of six alleles of the K1 family (size range = 140–370 basepairs), five MAD20 alleles (range = 120–320 basepairs) and two alleles of the RO33 family (range = 180–260 basepairs) were detected in the three

<table>
<thead>
<tr>
<th>Locus</th>
<th>Chromosome</th>
<th>Kombewa</th>
<th>Kakamega</th>
<th>Kisii</th>
</tr>
</thead>
<tbody>
<tr>
<td>Polya</td>
<td>4</td>
<td>14</td>
<td>0.89</td>
<td>0.79</td>
</tr>
<tr>
<td>TA42</td>
<td>5</td>
<td>1</td>
<td>0.66</td>
<td>0.53</td>
</tr>
<tr>
<td>TA81</td>
<td>5</td>
<td>10</td>
<td>0.80</td>
<td>0.72</td>
</tr>
<tr>
<td>TA1</td>
<td>6</td>
<td>10</td>
<td>0.58</td>
<td>0.55</td>
</tr>
<tr>
<td>TA7</td>
<td>6</td>
<td>10</td>
<td>0.86</td>
<td>0.73</td>
</tr>
<tr>
<td>TA109</td>
<td>6</td>
<td>10</td>
<td>0.82</td>
<td>0.73</td>
</tr>
<tr>
<td>ARA2</td>
<td>11</td>
<td>8</td>
<td>0.81</td>
<td>0.72</td>
</tr>
<tr>
<td>2409</td>
<td>10</td>
<td>5</td>
<td>0.64</td>
<td>0.71</td>
</tr>
<tr>
<td>TA40</td>
<td>10</td>
<td>10</td>
<td>0.75</td>
<td>0.69</td>
</tr>
<tr>
<td>PIPK2</td>
<td>12</td>
<td>9</td>
<td>0.85</td>
<td>0.76</td>
</tr>
<tr>
<td>PIG377</td>
<td>12</td>
<td>3</td>
<td>0.55</td>
<td>0.59</td>
</tr>
<tr>
<td>TA60</td>
<td>13</td>
<td>9</td>
<td>0.84</td>
<td>0.78</td>
</tr>
<tr>
<td>Mean</td>
<td>8.6</td>
<td>0.75</td>
<td>6.7</td>
<td>0.69</td>
</tr>
</tbody>
</table>

* \( Na \) = number of alleles for microsatellite loci; \( He \) = expected heterozygosity.
populations. Alleles of the RO33 family in the msp-1 gene were not found in the Kisii population. At the msp-2 locus, seven IC1 alleles (range = 440–760 basepairs) and eight FC27 alleles (range = 300–720 basepairs) were observed. Overall, the Kombewa population showed the highest number of alleles, and the Kisii population showed the lowest number of alleles (Table 3). The K1 and IC1 allele families were dominant alleles in western Kenya study sites. The minimum number of clones was 1.98, 1.92, and 1.58 in Kombewa, Kakamega, and Kisii, respectively (P > 0.05). The number of clones estimated by the maximum likelihood method was substantially higher than the observed number of clones (Table 3), but the trend on the difference between highland and lowland sites was similar to those detected by the minimum number of clones. The proportion of mixed infections based on msp-1 and msp-2 genes was 81.7%, 76.7%, and 73.3% in Kombewa, Kakamega, and Kisii, respectively (x^2 = 1.21, df = 2, P = 0.55). This result indicated that multiple infections in western Kenya highlands were as frequent as in the lowland populations.

### Linkage disequilibrium.
For microsatellite analysis, 9 and 17 of the 66 possible tests for LD showed significant results at P ≤ 0.05 in the lowland and highland populations, respectively. None of the significant pairwise associations involved loci located on the same chromosome. The LD estimated by the LIAN program was significant in the lowland population (observed mismatch variance V_D = 3.66, expected mismatch variance V_E = 1.93, standardized index of association I_A = 0.082, simulated 5% critical value L_M = 2.09, P = 10^-4) and in the highland populations (V_D = 3.92, V_E = 1.94, I_A = 0.093, L_M = 2.16, P = 10^-4).

### Population structure.
The AMOVA found that most (92.2%) of the variance in allele frequencies was among individuals within populations; only 6.9% of the variation was explained by differences between highland and lowland populations (P < 0.001) (Table 4). Wright's F-statistics indicated that 9 of 12 microsatellite markers detected significant population structure (Table 5). The overall genetic differentiation index among the three populations (F_S) was 0.027 (P <...
0.0001), whereas differences between highland and lowland populations were pronounced ($F_{ST} = 0.036$, $P < 0.0001$). Seven of 12 microsatellite markers detected significant structure between Kombewa and Kisii, which had the lowest transmission intensity ($F_{ST} = 0.032$, $P < 0.0001$). Between the two highland populations, four of 12 markers detected significant structure, giving an average differentiation index of 0.017 ($P < 0.05$).

**Assignment test.** Two clusters, each representing parasites with similar microsatellite genotypes, were identified by the structure analysis. Assignment test found that 91.1–94.0% individuals could be assigned to particular locations (Table 6). From the location perspective, most (76%) of the malaria parasites from the lowland site (Kombewa) were assigned to one cluster, whereas parasites from the two highland sites represented a mixture of both clusters in similar frequencies (Table 6). These results indicate a high rate of parasite infiltration from lowland to highland areas.

**DISCUSSION**

In this study, microsatellite markers detected a significantly lower number of alleles, marginally lower expected heterozygosity, and reduced infection complexity in the highland populations in comparison to the lowland population. Similar trends in genetic diversity measures were found in *msp-1* and *msp-2*; however, the difference between highland and lowland populations was not statistically significant. Malaria in the lowland site used in this study is hyperendemic according to its transmissions intensity (annual EIR = 31.1) and prevalence in asymptomatic children (< 50%). The lack of statistical significance in population genetic diversity by *ms* is likely due to the fact that *ms* genes are under strong selection pressure, the limited sample size analyzed in this study, and limited difference in malaria transmission intensities among the study sites.

The expected heterozygosity of microsatellite markers in our highland samples ($He$ range = 0.66–0.69) was substantially higher than that observed in South America (Colombia, Bolivia, and Brazil; $He$ range = 0.30–0.40) and in Thailand ($He$ = 0.51), but was comparable to the samples from cosmopolitan Africa (Benin, Cameroon, The Gambia, Ghana and Uganda; $He$ range = 0.69). In comparison to other malaria-endemic African regions, genetic diversity of malaria parasites in western Kenya highlands was slightly lower. Studies with microsatellite markers showed expected heterozygosity of 0.76–0.80 for *P. falciparum* from malaria-endemic sites in Uganda, Congo, and Zimbabwe, and 0.79 for those from the Republic of the Congo. These estimates were comparable with our lowland Kombewa sample.

Interestingly, although highland parasite populations exhibited reduced infection complexity in comparison with the lowland population, the proportion of mixed infections was similar between the highland and lowland populations. Both microsatellite markers and *msp* gene detected a high proportion of mixed infections in the highland populations. The high proportion of mixed infections paralleled high genetic diversity in the highland. This observation raises a question of how high genetic diversity and high prevalence of mixed infections are generated and maintained in the highlands where malaria transmission intensity is generally low (e.g., EIR was estimated as merely 0.4 infectious bites per person in Kisii). One possible mechanism is the introduction of parasite clones from malaria-endemic lowland areas through human travel. Human travel is an important risk factor for malaria in the highlands. During the epidemic season, malaria transmission intensity is increased substantially over that in the non-epidemic season. Diversity in microsatellite alleles or *msp* haplotypes may be generated through meiotic recombination during the epidemic, a period with enhanced parasite infection rates in vector populations. If low-transmission during non-epidemic seasons did not lead to a substantial genetic diversity increase, the population may experience substantial bottlenecks during the non-epidemic season.

### Table 4
Results of analysis of molecular variance for genetic variation of microsatellite markers in *Plasmodium falciparum* populations from highland and lowland areas in western Kenya

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>Degrees of freedom</th>
<th>Sum of squares</th>
<th>Expected mean squares</th>
<th>Variance component</th>
<th>Percentage of variation</th>
<th>$P$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Among groups</td>
<td>1</td>
<td>32.4</td>
<td>32.4</td>
<td>0.65</td>
<td>6.9</td>
<td>&lt; 0.001</td>
</tr>
<tr>
<td>Among populations within groups</td>
<td>1</td>
<td>11.6</td>
<td>11.6</td>
<td>0.08</td>
<td>0.9</td>
<td>0.113</td>
</tr>
<tr>
<td>Among individuals within populations</td>
<td>147</td>
<td>1,231.6</td>
<td>8.4</td>
<td>8.63</td>
<td>92.2</td>
<td>&lt; 0.001</td>
</tr>
<tr>
<td>Total</td>
<td>149</td>
<td>1,275.6</td>
<td>52.4</td>
<td>9.36</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### Table 5
$F_{ST}$ indices of the 12 microsatellite loci for *Plasmodium falciparum* populations from highland and lowland areas in western Kenya

### Table 6
Results of Bayesian cluster analysis and assignment test for *Plasmodium falciparum* populations from highland and lowland areas in western Kenya

<table>
<thead>
<tr>
<th>Population</th>
<th>Sample size</th>
<th>Cluster 1*</th>
<th>Cluster 2*</th>
<th>Not assigned</th>
<th>Percent assigned</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kombewa</td>
<td>50</td>
<td>38</td>
<td>8</td>
<td>4</td>
<td>92.0</td>
</tr>
<tr>
<td>Kakamega</td>
<td>50</td>
<td>26</td>
<td>21</td>
<td>3</td>
<td>94.0</td>
</tr>
<tr>
<td>Kisii</td>
<td>45</td>
<td>21</td>
<td>20</td>
<td>4</td>
<td>91.1</td>
</tr>
<tr>
<td>Total</td>
<td>145</td>
<td>85</td>
<td>49</td>
<td>11</td>
<td></td>
</tr>
</tbody>
</table>

* Numbered clusters represent distinct groups identified by Bayesian cluster analysis using Structure computer software.
† Not assigned refers to the number of individuals that could not be assigned to any cluster statistically.
bottleneck effect, population diversity and mixed infection could be maintained in the population. The question of whether low transmission intensity in the long non-epidemic season leads to parasite selfing and thus dramatic reduction in genetic diversity has not been determined. Evidence from the lack of significant seasonal fluctuations in the allele frequencies of msp-1, msp-2, and the gene coding for glutamate-rich protein in Sudan, after a six-month dry season during which malaria transmission was not even detectable, suggests that genetic bottleneck in P. falciparum during low transmission season should not be severe.46 It would be interesting to determine the changes in genetic diversity and infection complexity throughout an epidemic season in the highland areas.

We observed small, but statistically significant population structure between the highland and lowland malaria populations \( (F_{ST} = 0.036, P < 0.0001) \). The lack of strong genetic differentiation between highland and lowland parasite populations is consistent with the notion of parasite introduction by human travel from the malaria-endemic lowland to the epidemic highland region. Shanks and others10 found that travel to malaria-endemic areas was significantly associated with increased malaria risk in highland residents. In addition to human travel, genetic structure of malaria parasite populations may be affected by parasite life history, site-specific epidemiology, and malaria control measures such as insecticide-treated bed nets and indoor residual spray. Selection by antimalarial drugs would also result in unique genetic imprints on parasite populations.

We found significant linkage disequilibrium in both highland and lowland populations in the present study. None of the significant linkage disequilibrium involved loci located on the same chromosome, which suggested that these loci are only statistically linked and not physically linked. Linkage disequilibrium in our highland populations was consistent with the expectation of low transmission. However, linkage disequilibrium in our lowland population present with a substantially stronger index of association \( (I_{AS} = 0.082) \) than those reported in other African sites \( (I_{AS} < 0.02) \) with comparable malaria prevalence.18 Sakihama and others33 also reported strong linkage disequilibrium in the msp-1 gene in P. falciparum populations from the Solomon Islands where the EIR exceeds several hundred infectious bites per person per year. These investigators suggested that transmission intensity is not the sole determinant of the strength of linkage disequilibrium. Other variables such as the number of prevalent alleles, the prevalence of mixed infections, and infection complexity may also be involved. In our study, more than 70% of infection cases were mixed genotype infections in the highlands and lowlands on the basis of microsatellite or msp markers. Multiple repeated multilocus genotypes may have contributed to the observed linkage disequilibrium. No significant linkage disequilibrium was found in P. falciparum populations from hypo-endemic areas in Africa when only genotypes of the mono-infected isolates were used.44

In summary, the present study examined the genetic diversity of P. falciparum from symptomatic infections in western Kenya highland and lowland areas with contrasting transmission intensities. Despite reduced genetic diversity in the highland populations in comparison to populations in the surrounding endemic lowland, population genetic diversity in the highland area remained high. More than 70% of the infections were mixed genotype infections, even in areas of with an EIR < 1 infectious bite per person per year. Small geographic differentiation was detected between highland and lowland populations. Together with the results of risk factor analysis19 and malaria infection dynamics1,11,12 in the highlands, these results suggest that both human travel and local transmission may be important in shaping the genetic structure of malaria parasites in the highlands.

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