Breakdown in the Process of Incipient Speciation in Anopheles gambiae

The Harvard community has made this article openly available. Please share how this access benefits you. Your story matters.

Citation

Published Version
doi:10.1534/genetics.112.148718

Accessed
June 20, 2017 12:19:25 PM EDT

Citable Link
http://nrs.harvard.edu/urn-3:HUL.InstRepos:11370683

Terms of Use
This article was downloaded from Harvard University's DASH repository, and is made available under the terms and conditions applicable to Other Posted Material, as set forth at http://nrs.harvard.edu/urn-3:HUL.InstRepos:dash.current.terms-of-use#LAA

(Article begins on next page)
Breakdown in the Process of Incipient Speciation in Anopheles gambiae

Davis C. Nwakanma,* Daniel E. Neafsey,† Musa Jawara,* Majidah Adiamoh,* Emily Lund,† Amabelia Rodrigues,‡ Kovana M. Loua,** Lassana Konate,†† Ngayo Sy,** Ibrahima Dia,** T. Samson Awolola,*** Marc A. T. Muskavitch,**§§ and David J. Conway*†††

*Medical Research Council Laboratories, Banjul, The Gambia, †Broad Institute, Cambridge, Massachusetts 02142, ‡Harvard School of Public Health, Boston, Massachusetts 02115, §Bandim Health Project, Bissau, Guinea-Bissau, **National Institute of Public Health, Conakry, Republic of Guinea, ††Université Cheikh Anta Diop, Dakar, Senegal, †††Service de Lutte Antiparasitaire, Thies, Senegal, §§Institut Pasteur, Dakar, Senegal, †††Nigerian Institute of Medical Research, Yaba, Lagos, Nigeria, ‡‡Boston College, Chestnut Hill, Massachusetts 02167, and †††London School of Hygiene and Tropical Medicine, London, WC1E 7HT United Kingdom

ABSTRACT Understanding genetic causes and effects of speciation in sympatric populations of sexually reproducing eukaryotes is challenging, controversial, and of practical importance for controlling rapidly evolving pests and pathogens. The major African malaria vector mosquito Anopheles gambiae sensu stricto (s.s.) is considered to contain two incipient species with strong reproductive isolation, hybrids between the M and S molecular forms being very rare. Following recent observations of higher proportions of hybrid forms at a few sites in West Africa, we conducted new surveys of 12 sites in four contiguous countries (The Gambia, Senegal, Guinea-Bissau, and Republic of Guinea). Identification and genotyping of 3499 A. gambiae s.s. revealed high frequencies of M/S hybrid forms at each site, ranging from 5 to 42%, and a large spectrum of inbreeding coefficient values from 0.11 to 0.76, spanning most of the range expected between the alternative extremes of panmixia and assortative mating. Year-round sampling over 2 years at one of the sites in The Gambia showed that M/S hybrid forms had similar relative frequencies throughout periods of marked seasonal variation in mosquito breeding and abundance. Genome-wide scans with an Affymetrix high-density single-nucleotide polymorphism (SNP) microarray enabled replicate comparisons of pools of different molecular forms, in three separate populations. These showed strong differentiation between M and S forms only in the pericentromeric region of the X chromosome that contains the molecular formspecific marker locus, with only a few other loci showing minor differences. In the X chromosome, the M/S hybrid forms were more differentiated from M than from S forms, supporting a hypothesis of asymmetric introgression and backcrossing.

The major malaria vector mosquito Anopheles gambiae sensu stricto (s.s.) exists throughout most of Sub-Saharan Africa, but there are many polymorphisms including chromosomal inversions that appear to be involved in the adaptation of subpopulations to different environments (Coluzzi et al. 2002), and molecular forms (M and S) have been identified that appear to be reproductively isolated (della Torre 2002). The S form is distributed widely throughout the species range, whereas the M form is common but restricted to western parts of Africa, and hybridization between them is rare in most areas of sympathy (Della Torre et al. 2005). Scanning of large numbers of polymorphic markers initially indicated the molecular forms were very highly differentiated at only a small number of discrete regions within the two autosomes and the pericentromeric region of the X chromosome, which contains the form-specific markers in the ribosomal (r)RNA genes (Turner et al. 2005). However, a finding that transposable element insertion sites showed marked differentiation between the forms indicated that reproductive isolation might affect a larger portion of the genome (Esnault et al. 2008). A high-density array to type 400,000 single-nucleotide polymorphisms (SNPs) has recently enabled more thorough genome-wide analyses, confirming that the molecular forms are differentiated at many loci throughout the genome in addition to those previously shown (Lawniczak et al. 2010; Neafsey et al. 2010; Reidenbach et al. 2012).
It is vital to understand such differentiation and genetic subdivision and its importance in vector evolution, as this complexity can affect malaria control, including resistance to insecticides (Dabire et al. 2009; Djogbenou et al. 2010; Lynd et al. 2010) and susceptibility to malaria parasites and other infections (Rottschaefer et al. 2011; White et al. 2011). Differences in the adult mosquito transcriptome between the M and S molecular forms appear to be minimal (Cassone et al. 2008; Aguilar et al. 2010), but evidence is accumulating that the larval stages are differentially adapted to particular features of breeding sites, with the M forms being generally more common in large areas of irrigation for crop cultivation (Diabate et al. 2008; Gimonneau et al. 2011). Studies of mosquito behavior suggest assortative mating may be the means of preventing natural hybridization between the forms, as most mating swarms consisted of single forms in an area of sympatry in Mali (Diabate et al. 2009), although some mixed swarms were seen in Burkina Faso (Diabate et al. 2006), and very close-range barriers to interbreeding may also operate (Pennetier et al. 2010; Sanford et al. 2011).

Surveys of populations in the extreme west of Africa show substantial local variation in relative frequencies of A. gambiae s.s. M and S molecular forms (della Torre et al. 2005). For example, the M form predominates in most of The Gambia, but <100 km farther inland in eastern Senegal almost all members of the species are S form (Caputo et al. 2008). Of particular interest are areas in which both forms exist, as the occurrence of natural hybrids may be possible. Elsewhere in Africa, areas of sympatry consistently exhibit very low frequencies of hybrid forms, but a few years ago exceptionally high proportions of M/S hybrids were reported at a few sites near the west coast, with 3% at Dielmo in Senegal (Ndiiath et al. 2008), 7% at Njabakunda in The Gambia (Caputo et al. 2008), and 24% at Antula in Guinea-Bissau (Oliveira et al. 2008). Analysis of an insertion polymorphism linked to the form-specific marker on the X chromosome, as well as an unlinked SNP on chromosome 3, in a subset of the samples from The Gambia and Guinea-Bissau suggested that there may be introgression between the forms (Caputo et al. 2011), and separate studies using broader scans of genomic polymorphisms in samples from Guinea-Bissau have supported this inference (Marsden et al. 2011; Weetman et al. 2012).

To thoroughly discover and map the area with high frequencies of hybrids and assess its impact on genomic differentiation, we conducted new surveys of diverse sites in the coastal areas of four contiguous countries (The Gambia, Senegal, Guinea-Bissau, and Republic of Guinea). To investigate the stability of molecular form and hybrid frequencies over time throughout different seasons, we conducted a longitudinal survey over a 2-year period in the Njabakunda area of The Gambia. We performed high-density genome-wide scans for differentiation between sympatric M and S forms, as well as M/S hybrids, at the Njabakunda site and at single sites from each of Senegal and Guinea-Bissau. We employed a pooled hybridization approach for expediency, allowing use of a genotyping array with much higher marker density than that of previous surveys for introgression in West Africa (Marsden et al. 2011; Weetman et al. 2012). Results show extensive hybridization throughout the area and that mosquitoes with M and S form-specific markers are largely homogenized throughout the genome, with evidence supporting a hypothesis of asymmetric hybridization and frequent backcrossing particularly between the M/S hybrid forms and the S forms.

Materials and Methods

**Sampling sites for A. gambiae mosquitoes**

Twelve sites were surveyed in four countries (Figure 1). These were chosen to encompass the few areas where unusually high frequencies of M/S hybrids had previously been noted and to extend the sampling to the north and south of these, within 100 km of the west coast of Africa. The northern part of the sampling range has Sudan Savannah-type vegetation, with most annual rainfall of 600–1000 mm normally occurring within 4 months (June to September). The south of the sampling range has Guinea Savannah-type vegetation including more woodland, with annual rainfall of up to 2000 mm extending over a longer season (May to October). In all areas, the majority of A. gambiae s.s. breeding occurs during and at the end of the annual rains, and highest densities of adult mosquitoes are found between August and October. The 12 sites are numbered and described below (sites 1 and 2 represent Sudan Savannah, sites 3–6 represent northern Guinea Savannah, and sites 7–12 represent southern Guinea Savannah).

---

**Figure 1** Map of sampling locations for surveys of Anopheles gambiae s.s. molecular forms between 2007 and 2009 in The Gambia, Senegal, Guinea-Bissau, and Republic of Guinea. Each location is indicated by a yellow circle, and the frequencies of the M form, the S form and M/S hybrid forms sampled at each are indicated by an adjacent pie chart (sample sizes and exact frequencies are given in Table 1).
Table 1 Proportions of M/S hybrid heterozygote forms and M and S homozygote forms of Anopheles gambiae s.s. in each of 12 sites surveyed from four West African countries

<table>
<thead>
<tr>
<th>Country</th>
<th>Site</th>
<th>No. mosquitoes</th>
<th>M</th>
<th>S</th>
<th>M/S</th>
<th>$H_{exp}$</th>
<th>$F_{IS}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gambia</td>
<td>Njabakunda</td>
<td>1474</td>
<td>0.164</td>
<td>0.760</td>
<td>0.076</td>
<td>0.322</td>
<td>0.76</td>
</tr>
<tr>
<td>Senegal</td>
<td>Madina Djikoye</td>
<td>77</td>
<td>0.325</td>
<td>0.350</td>
<td>0.325</td>
<td>0.500</td>
<td>0.35</td>
</tr>
<tr>
<td>Senegal</td>
<td>Bounkiling</td>
<td>145</td>
<td>0.683</td>
<td>0.138</td>
<td>0.179</td>
<td>0.354</td>
<td>0.49</td>
</tr>
<tr>
<td>Senegal</td>
<td>Bignona</td>
<td>30</td>
<td>0.767</td>
<td>0.133</td>
<td>0.100</td>
<td>0.295</td>
<td>0.66</td>
</tr>
<tr>
<td>Senegal</td>
<td>Marsassoum</td>
<td>434</td>
<td>0.270</td>
<td>0.387</td>
<td>0.343</td>
<td>0.493</td>
<td>0.30</td>
</tr>
<tr>
<td>Senegal</td>
<td>Sediou</td>
<td>389</td>
<td>0.653</td>
<td>0.211</td>
<td>0.136</td>
<td>0.402</td>
<td>0.66</td>
</tr>
<tr>
<td>Guinea-Bissau</td>
<td>Caio</td>
<td>12</td>
<td>0.417</td>
<td>0.167</td>
<td>0.417</td>
<td>0.469</td>
<td>0.11</td>
</tr>
<tr>
<td>Guinea-Bissau</td>
<td>Antula</td>
<td>464</td>
<td>0.194</td>
<td>0.470</td>
<td>0.336</td>
<td>0.461</td>
<td>0.27</td>
</tr>
<tr>
<td>Guinea-Bissau</td>
<td>Prabis</td>
<td>91</td>
<td>0.363</td>
<td>0.385</td>
<td>0.253</td>
<td>0.500</td>
<td>0.49</td>
</tr>
<tr>
<td>Guinea-Bissau</td>
<td>Buba</td>
<td>194</td>
<td>0.907</td>
<td>0.041</td>
<td>0.052</td>
<td>0.130</td>
<td>0.60</td>
</tr>
<tr>
<td>Guinea-Bissau</td>
<td>Mansoo</td>
<td>152</td>
<td>0.467</td>
<td>0.322</td>
<td>0.210</td>
<td>0.490</td>
<td>0.57</td>
</tr>
<tr>
<td>Guinea</td>
<td>Boke</td>
<td>37</td>
<td>0.622</td>
<td>0.270</td>
<td>0.108</td>
<td>0.435</td>
<td>0.75</td>
</tr>
</tbody>
</table>

$H_{exp}$, expected proportion of M/S heterozygotes under Hardy-Weinberg equilibrium, assuming random mating. There was a significant heterozygote deficiency ($p < 0.005$) in each of the populations except for Caio. $F_{IS}$, inbreeding coefficient (proportion of heterozygotes missing compared to expectations under random mating).

The Gambia: Site 1, the Njabakunda village area (13°33’S, 15°54’W) in the North Bank region of the country (30 km west of Farafenni town), was sampled, as previous surveys (in 2005 and 2006) had shown this area to contain a higher frequency of M/S form hybrids than elsewhere in The Gambia (Caputo et al. 2008). The site is ~4 km away from the Gambia River on free-draining laterite soil, covered with open woodland savannah and farmland mainly for cultivation of subsistence and cash crops. Four hamlets (Maria Samba Nyado, Sare Illo Buya, Kerr Birom Kardo, and Kerr Sama Kuma) around Njabakunda and within 1 km of each other were selected for longitudinal sampling for a 2-year period between April 2007 and March 2009. Fortnightly (mid-month and end of the month) collections were conducted from June to December covering the rainy season period, and monthly (end of the month) collections were done from January to May covering the dry season.

Senegal: Five sites were sampled in Senegal. One of these (site 2), Madina Djikoye (clustered with nearby villages Kerr Samba Gueye and Kerr Ousainiou Dieng) (13°37’S, 16°18’W) is in the Kaolack region immediately to the north of the Gambian border. The other four sites are south of The Gambia in the lower Casamance region: (site 3) Sediou (12°43’N, 15°4’W) adjacent to the Cassamance River, (site 4) Bounkiling (13°2’N, 15°42’W), (site 5) Bignona (12°47’N, 16°14’W), and (site 6) Marsassoum (12°50’N, 15°58’W). The sites have free-draining laterite sand or aluvial soil and are covered with open woodland savannah or farmland for groundnut and cereal cultivation. These sites were sampled in August 2009, except for Sediou, which was sampled in October 2008.

Guinea-Bissau: Five sites were sampled in Guinea-Bissau: (site 7) Caio village (11°55’N, 16°12’W) is in a coastal area of rice and cashew plantations mixed with woodland with traditional ritual significance, (site 8) Antula (11°53’N, 15°35’W) is a village east of the capital Bissau, (site 9) Prabis (11°48’N, 15°44’W) is a village in a peri-urban area of Bissau with marsh vegetation and rice cultivation, (site 10) Mansoa (12°4’N, 15°19’W) is a small town in the north of the country in a rice cultivation area, and (site 11) Buba (11°35’N, 15°0’W) is in the south of the country on the River Rio Grande de Buba near the National Park Contanhez containing a canopy of tropical rain forest, within which the village of Banta Furu was sampled. These sites were sampled in August 2009, and Prabis was also sampled in October 2008.

Republic of Guinea: One area in Guinea was sampled in August 2009, to the south of the border with Guinea-Bissau: (site 12) near Boke town (10°56’N, 14°18’W) four villages (Korera, Dabaya, Balangdougou, and Bintoumodia) in terrain of flat plains interspersed with hilly slopes divided by fast-flowing streams, fed by a higher rainfall than at any of the other sites studied here.

Collection and identification of mosquitoes

Mosquitoes were sampled from houses or inhabited huts in each site, using indoor pyrethrum spray collections (PSC) in most cases for all the sites, with some sampling by indoor overnight light trap collections (LTC) in addition to PSC in Guinea-Bissau and Republic of Guinea sites. All mosquitoes that were collected were identified morphologically in the field, and A. gambiae sensu lato specimens were stored individually in 1.5-ml polyethylene tubes with desiccant or in Carnoy’s solution if they were semigravid, for subsequent DNA typing of species and molecular forms. DNA was extracted from individual mosquito specimens, using the Corbett Robotics X-Tractor Gene automated DNA extraction platform (QIAGEN, Crawley, UK) according to the manufacturer’s protocol for tissue extraction. Whole mosquito material was extracted, except for a few legs of each specimen retained for confirmatory PCR testing in case the initial result indicated a hybrid molecular form. Each of the three species of the A. gambiae complex that exist in West Africa (A. gambiae s.s., A. arabiensis, and A. melas) were discriminated in the laboratory.
by species-specific PCR of sequences within the rRNA gene locus on the X chromosome (Scott et al. 1993), and A. gambiae s.s. mosquitoes were differentiated into molecular forms M and S (and M/S hybrids) by form-specific restriction enzyme digestion of the amplified fragment (Fanello et al. 2002).

**Genome-wide scans for differentiation between pools of A. gambiae s.s. mosquitoes**

A custom Affymetrix oligonucleotide array for genome-wide typing of 400,071 A. gambiae s.s. SNPs (Neafsey et al. 2010), termed the 400K array, was used for population genotyping. DNA hybridization was performed with separate pooled samples of 20 homozygous M-form and 20 homozygous S-form A. gambiae s.s. mosquitoes from each of three sites sampled (Njabakunda in The Gambia, Sedhiou in Senegal, and Antula in Guinea-Bissau). The Njabakunda site was the primary one selected for this genome-wide SNP analysis, as we studied this site intensively. Therefore, it had the largest sample size and most accurate estimation of frequencies. We added the other two sites to include one from Senegal and one from Guinea-Bissau, each of which had large sample sizes with higher proportions of hybrids. In addition, a pool of DNA from 20 M/S hybrid mosquitoes was tested and compared with the homozygous samples, for each of these three sites. Each of the 180 individual mosquitoes that contributed to the pooled arrays (20 M form, 20 S form, and 20 M/S forms, selected from each of the three sites noted) was also genotyped for the SINE200x6.1 transposon insertion site polymorphism that is linked to the molecular form marker on the X chromosome (Santolamazza et al. 2011). Affymetrix oligonucleotide array hybridization was performed following methods already described (Neafsey et al. 2010), as previous analysis revealed a very high correlation between aggregate individual hybridizations and pooled hybridizations for pools of 20 individuals (Pearson’s $r^2 = 0.96$, Supporting Information, Figure S1), leading to the repetition of that assay design here. Following Robust Multi-array Average (RMA) background correction and quantile normalization using Affymetrix Power Tools, allelic balance at assayed loci within the pools was inferred using the Contrast statistic generated by BRLMM-P, using a $K$ value of 1 (Rabbee and Speed 2007). Such plots result in a modal background mean Contrast difference of $\approx 0.25$ rather than 0, which is the result of noise in the signal rather than a genome-wide divergence signal. Plots of local divergence along the chromosomes were generated using a stepping window approach, by calculating the mean of the absolute value of the arithmetic difference in Contrast for 50 adjacent assays. The mean physical distance spanned by 50 adjacent assays was 28.2 kb (range = 9.1–280 kb, standard deviation = 16.6 kb). Thresholds for statistical significance ($\alpha = 0.05$ after Bonferroni correction) for these windowed analyses were calculated using a bootstrapping approach, in which mean Contrast difference was calculated for each pairwise comparison for 50 SNPs that were sampled randomly from the genome a total of 10 million times.

**Results**

**Quantifying proportions of molecular forms and hybrids at different sites**

Molecular form typing was performed on a total of 3499 A. gambiae s.s. mosquitoes sampled from the 12 sites surveyed in the four countries (Senegal, The Gambia, Guinea-Bissau, and Republic of Guinea) (Figure 1). In each site, M and S molecular forms coexisted sympatrically and substantial proportions of M/S hybrid forms were found (from 5 to 42%) (Table 1). The
estimated inbreeding coefficients for this rRNA gene locus, which has previously been considered a putative speciation marker, showed a wide spectrum of values (from 0.11 to 0.76) (Table 1). Seven of the sites each had samples of >100 mosquitoes analyzed, allowing highly accurate estimations of frequencies, and we note that these also show a wide range of M/S hybrid proportions (from 5 to 34%) and estimated inbreeding coefficients (from 0.27 to 0.76). Thus, the proportions of M/S hybrids were less than expected under Hardy–Weinberg equilibrium with complete panmixia, but in some cases not much less.

**Analysis of proportions of molecular forms and hybrids at one site throughout a 2-year period**

To investigate the stability of frequencies over time, we sampled the Njabakunda site in The Gambia throughout a 2-year period.
(annual periods extending from April to the following March to capture full seasonal dynamics due to rainfall), yielding 1474 typed mosquitoes from this site (1048 in the first annual period and 426 in the second). The relative frequencies of M/S hybrid forms were stable in both years, accounting for 8.3% in the first and 5.6% in the second year (chi-square test, $P = 0.077$) (Figure 2). During each year, S-form mosquito numbers peaked early in the rainy season, and the peak of the less abundant M form occurred later in the season, but M/S hybrid forms were seen throughout. In 2007, M/S forms had seasonally stable frequencies of 8.6% (32/374) in April–July and 8.1% (50/620) in August–October (chi-square test, $P = 0.78$), while proportions of M forms increased from 1.9% (7/374) to 22.6% (140/620) during those respective periods (chi-square test, $P < 10^{-7}$); in 2008, M/S forms had frequencies of 4.9% (9/184) in April–July and 5.9% (12/205) in August–October (chi-square test, $P = 0.67$), while proportions of M forms increased from 8.1% (15/184) to 36.6% (75/205) in those periods (chi-square test, $P = 10^{-7}$).

**Table 2 Number of 50-SNP windows exhibiting significant ($P < 0.05$) mean contrast differences according to pairwise pool comparison and chromosomal location**

<table>
<thead>
<tr>
<th>Total windows</th>
<th>2R: $n = 2256$</th>
<th>2L: $n = 1846$</th>
<th>3R: $n = 1692$</th>
<th>3L: $n = 1374$</th>
<th>X: $n = 829$</th>
<th>Chi-square $P$-value: $2R$: $2L$: $3R$: $3L$: X: Comparative with Senegal and Guinea-Bissau</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gambia M vs. S</td>
<td>3</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>42</td>
<td>$1.70 \times 10^{-04}$</td>
</tr>
<tr>
<td>Senegal M vs. S</td>
<td>9</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>98</td>
<td>$7.17 \times 10^{-11}$</td>
</tr>
<tr>
<td>Mali M vs. S</td>
<td>20</td>
<td>30</td>
<td>21</td>
<td>11</td>
<td>112</td>
<td>Comparator</td>
</tr>
<tr>
<td>Guinea-Bissau M vs. S</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>58</td>
<td>$7.20 \times 10^{-11}$</td>
</tr>
<tr>
<td>Gambia S vs. M/S</td>
<td>5</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>37</td>
<td>$1.83 \times 10^{-03}$</td>
</tr>
<tr>
<td>Gambia S vs. M/S</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>Not applicable</td>
</tr>
</tbody>
</table>

To test whether minor signals of differentiation may have been being obscured by our windowed analysis approach, we examined the region between 28 and 42 Mb on chromosome 2R in closer detail, at the level of individual SNP assays, for the comparison between M- and S-form pools in Guinea-Bissau (Figure S2). This region was focused on as it contains loci that showed differentiation between the M and S forms in a recent study, using a panel of several hundred SNPs with a sample from Guinea-Bissau (Weetman et al. 2012). Although some individual SNP assays in the region showed high Contrast differences between the pools, the Contrast distributions were similar to those observed in a control region of chromosome 3R (19–32 Mb) and much lower than those observed in the highly differentiated X centromeric region (Figure S2). To test whether signals of differentiation might have been obscured by noise due to poorly performing SNP genotyping on the array, we repeated the genome-wide analysis with a subset of 65,974 SNPs that had previously been validated and shown to be in Hardy–Weinberg equilibrium for individual molecular forms in Mali (Neafsey et al. 2010). This confirmed that, outside of the pericentromeric X-chromosomal region, there was no major differentiation between the forms in the populations studied here, in contrast to the interform differentiation previously seen in Mali (Figure S3). We cannot fully reconcile this observation with reports of very narrow regions of differentiation on 2R in another population sample from Guinea-Bissau (Weetman et al. 2012), as differences in findings between the studies may result from fine differences in spatial or temporal sampling or in the sensitivity of the respective assays.
and 20 M/S forms, in each of the three selected sites) gave results that were concordant with the molecular form typing in 159 (88%) of the individuals. While there was 98% (59/60) concordance for the M form and 100% (60/60) for the S form, confirming appropriate sample selection and robust comparison of the forms here, the lower concordance of 67% (40/60) observed for the M/S forms confirms that many of these are not F1 hybrids, but that backcrossing must have occurred over multiple generations. The profile of windows with significant differentiation in M vs. M/S comparisons is highly similar among the three countries sampled (Figure 5). Across the pairs of countries, M vs. M/S comparisons exhibit Spearman’s rank correlations ranging between 0.77 and 0.84, whereas S vs. M/S comparisons have Spearman’s rank correlations of only 0.15–0.42 between the same pairs (Table S1).

**Discussion**

It is widely considered that the major malaria vector *A. gambiae s.s.* is undergoing a process of speciation into at least two reproductive units defined as the M and S molecular forms (della Torre et al. 2001). Although the divergence of these forms is likely proceeding in many parts of west and central Africa (Reidenbach et al. 2012), our results and those of other recent surveys of populations in the extreme west of Africa (Caputo et al. 2011; Marsden et al. 2011; Oliveira et al. 2008; Weetman et al. 2012) indicate that hybridization is common. A contiguous region is now outlined, covering ecologically diverse sites sampled in a contiguous area within 100 km of the West African coast within four countries in a zone of <400 km from north to south, where frequencies of M/S hybrid forms are consistently much higher than elsewhere, and there is minimal interforn genomic differentiation outside of the pericentromeric region of the X chromosome. This contrasts significantly with the results obtained from populations farther east, using the same methods (Reidenbach et al. 2012), and is important for understanding evolution and implementing control of this malaria vector and for investigation of the processes of speciation.

A wide range of proportions of M/S hybrid forms was detected within both Guinea-Bissau and Senegal, with the Gambian site in the north and the Guinean site in the south both showing lower proportions than many of the intervening sites. It appears likely that the area we have surveyed, extending across these four countries, probably covers most of the current geographical range of the *A. gambiae s.s.* populations that exhibit extensive hybridization. Surveys immediately to the south in Guinea have shown mostly S-form mosquitoes near the coast, and both M and S forms, with a very low frequency of hybrids, further inland (della Torre et al. 2005; Vezenegho et al. 2009; Carnevale et al. 2010). In northern Senegal, *A. gambiae s.s.* is less common than the related vector species *A. arabiensis* and exists mostly as the M form (della Torre et al. 2005; Dia et al. 2008), while surveys in the eastern part of Senegal have shown the S

---

**Figure 4** Genome-wide comparison of an M/S pool of 20 hybrid form mosquitoes with M and S homozygous pools from Njabakunda in The Gambia, using data from all SNPs on the 400K genome-wide array: (top) M homozygotes vs. M/S hybrid forms; (bottom) S homozygotes vs. M/S hybrid forms. The more complete lack of differentiation between S and M/S suggests asymmetric gene flow between the forms or selection to maintain the residual differentiation in the M form. (Replicate comparisons between the pooled hybrid forms and each of the major forms are shown for separate populations in Figure S4.)

---

**Asymmetric minimal differentiation between hybrid forms and homozygous molecular forms**

We also performed pooled array hybridizations, using 20 mosquitoes genotyped as M/S heterozygote “hybrid forms” from each site and compared these with the M and S homozygote pools. Results for the Gambian population sample (Figure 4, Table 2) show no divergence in the X pericentromeric region between S and M/S, whereas some divergence remains between M and M/S. The degree of differentiation observed in the X pericentromeric region (megabases 15–24.2) is significantly higher in the M vs. M/S comparison relative to the S vs. M/S comparison (Wilcoxon’s sign-rank test, \( V = 25,996, P = 2.2 \times 10^{-19} \)). Replication of these comparisons for samples from Sedhiou in Senegal and Antula in Guinea-Bissau showed similar results (Figure S4), except that the S and M/S pools showed some detectable X pericentromeric differentiation in Senegal (less than observed for the comparison of M and M/S). This suggests that although the forms are now highly homogenized, the speed of the process has been asymmetric, with partial isolation or a lower recombination rate allowing maintenance of greater X chromosome pericentromeric divergence in the M form. Genotyping of the SINE200 transposon insertion site polymorphism in the 180 mosquitoes contributing to the pooled arrays (20 M form, 20 S form, and 20 M/S forms, in each of the three selected sites) gave
form to be more abundant than the M form, with hybrid forms very rarely detected (della Torre et al. 2005; Caputo et al. 2008), as has been observed in Mali and further eastward (della Torre et al. 2005; Diabate et al. 2009; Aboagye-Antwi et al. 2010).

It is possible that our results reflect consequences of the reversal of a previous process that promotes speciation, with the genomic integrity of one or both of the molecular forms now being substantially compromised by introgression within these western populations. It was previously suggested that areas might exist within which there is extensive gene flow between the molecular forms of *A. gambiae* s.s., while reproductive barriers are maintained at other sites (Black and Lanzaro 2001; Lehmann et al. 2003). A more recent view, also supported by pooled array hybridizations, is that sporadic bouts of hybridization mediated by changing ecological conditions or a very low background rate of gene flow between M and S forms could be responsible for the relative homogeneity of M and S genomes outside of the “speciation islands” (Reidenbach et al. 2012). Such processes would not be expected to disrupt the divergence at well-established pericentromeric islands of speciation, however. Our results enable sites to be specifically selected for population genomic studies to investigate mechanisms of reproductive isolation. Studies of male mating swarm composition and behavior will be important to conduct in these areas, to identify whether there are proximal determinants of hybridization (Diabate et al. 2006, 2009). Further sampling and measurement of multiple ecological parameters at different times of the year are also needed to characterize these and additional sites more fully, which could enable exploration of correlations between environmental variables, population genetic structure, and reproductive isolation.

If the M and S forms were undergoing genome-wide reciprocal introgression, it is expected that the pericentromeric divergence on the X chromosome should be gradually eliminated in both forms by recombination. The observation that the X pericentromeric region remains relatively distinct in M-form populations in this area, as also reported recently by others sampling in Guinea-Bissau (Marsden et al. 2011), supports a hypothesis that partial reproductive isolation or selective pressure preserves a narrow genomic island linked to the M-form-specific marker (Caputo et al. 2011; Marsden et al. 2011; Weetman et al. 2012). A high degree of similarity in the specific pericentromeric divergence profile among sites (Figure 5, Table S2) further indicates the likely role of

Figure 5. Comparison of M vs. M/S divergence among geographic sites in the X pericentromeric region (megabases 15–24.2). Each point represents a 50-SNP window. The profile of differentiation is maintained in a highly similar manner in all pairwise comparisons of geographic sites: (top) Gambia vs. Guinea-Bissau, (middle) Senegal vs. Guinea-Bissau, and (bottom) Gambia vs. Senegal. The locations sampled in each country for these comparisons were Njabakunda (Gambia), Sedhiou (Senegal), and Antula (Guinea-Bissau).
selection in limiting gene flow in this pericentromeric region. This also illustrates that mosquitoes typed as M/S heterozygotes in our study generally do not represent F1 hybrids between the molecular forms, but are members of a thoroughly backcrossed and homogenized population, together with S/S homozygotes. Elsewhere in the range of A. gambiae s.s., major introgression between M- and S-form mosquitoes appears to have been very rare, although it is strongly suggested by the distribution of insecticide resistance genotypes. For example, the kdr mutation conferring resistance to pyrethroids has apparently introgressed from the S form into the M form (Weill et al. 2000; Diabate et al. 2003), and the ace-1(R) mutation has been observed in both M- and S-form populations in several West African countries, although it is unclear in which population this latter mutation originated (Djogbenou et al. 2008).

Reinforcement might occur during the speciation process by strengthening premating isolation mechanisms, in a situation where postmating Isolation is already operating due to reduced fitness of hybrids (Wallace 1889). In areas where M and S forms have long been in contact, it is possible that they have evolved premating isolation mechanisms to reduce the frequency of hybridization, such as selective swarm formation (Diabate et al. 2009) or male–female flight-tone matching (Penninget et al. 2010). As the S form is more widespread, it is possible that S-form populations that have had no contact with M populations would have had no opportunity to evolve such reinforcement. If M-form populations are gradually expanding or shifting their range over time due to ecological changes and carrying reinforcement mechanisms developed through preceding contact with members of S-form populations, then it may expected that the M form would be generally less susceptible to introgression. The demographic and geographic range history of the forms is currently unclear, however. Behavioral mechanisms, such as the relative importance of male or female mate choice in determining prezygotic isolation, could also play an important role. Further investigation of the ecology and range-wide demographic history of these forms may be required to understand the nature of the observed introgression.

Reproductive isolation in this most important African malaria vector species is complex and might not orient primarily around the commonly typed M and S forms within A. gambiae s.s. There is evidence of some genetic substructure within each of the forms (Slotman et al. 2007; Weetman et al. 2010), of ecologically important variation and genomic divergence due to inversion polymorphisms that are not routinely typed (Coluzzi et al. 2002; White et al. 2007, 2009), and of some discrepancies among different methods used for molecular typing of the forms (Santolamazza et al. 2011). Recent findings even suggest that there may be other subpopulations of A. gambiae s.s. that have not yet been adequately sampled (Riehle et al. 2011). Implications of our findings for the evolution and spread of genetic traits relevant to malaria control will warrant further investigation, within the known geographical region of hybridization and throughout the species range. The application of whole-genome resequencing to such studies promises to further increase the power to map loci under selection and track ongoing changes in population genetic structure (Cheng et al. 2012).

Acknowledgments

We thank the staff of our institutes who were involved in entomological field collections, particularly Sainey Kanteh, Lamin Camara, Alhadji Kaba Sylla, Tolho Gnouma Benoit, and Aboubacarr Conteh, and those who assisted in the laboratory, transport, or administration. We appreciate the encouragement and strong support from institute and departmental heads including Tumani Corrah and Moussa Dieng Sarr. We acknowledge the expert efforts of members of the Biological Samples Platform and Genetic Analysis Platform of the Broad Institute. The genome-wide SNP array was supported by joint funding from several sources, including Burroughs Wellcome Fund Request 1008238, the Broad Institute Director’s Fund, Harvard School of Public Health Department of Immunology and Infectious Diseases under direction of D. F. Wirth, Wellcome Trust Programme grant 077229/Z/05/Z to F. C. Kafatos and G. K. Christophides, and the DeLuca Professorship from Boston College to M.A.T.M. This work was enabled by funding from the United Kingdom Medical Research Council (MRC) and Foundation for the National Institutes of Health (FNHI)/Gates Grand Challenges in Global Health to the MRC Unit in The Gambia.

Literature Cited


Cheng, C., B. J. White, C. Kamdem, K. Mockaitis, C. Costantini et al., 2012 Ecological genomics of Anopheles gambiae along


Communicating editor: B. P. Lazzaro
Breakdown in the Process of Incipient Speciation in Anopheles gambiae

Figure S1  Scatterplot showing correlation of the distribution of values of pooled Contrast ratios for a pool of DNA from 20 mosquitoes, compared with the average values across the 20 DNA samples from the individual mosquitoes, with each point corresponding to one feature of the 400K SNP array, for a pilot assay with 20 An gambiae s.s. mosquitoes from Mali (Neafsey et al. 2010).
Figure S2  Focused profile of differentiation between M and S pools from Guinea Bissau on chromosome 2R (A), 3R (B), and X (C). Black dots indicate Contrast differences between the pools for individual SNP assays. Red dots indicate mean Contrast differences for windows of 50 adjacent SNPs.
Figure S3  Test for genomic differentiation between pooled DNA from samples of 20 homozygous M form and 20 homozygous S form Anopheles gambiae s.s. from each of three sites in this study: (A) Njabakunda in The Gambia, (B) Sedhiou in Senegal, (C) Antula in Guinea Bissau, using data from the 66K sub-set of SNPs that had previously shown Hardy-Weinberg equilibrium within molecular forms in Mali (Neafsey et al. 2010). The vertical axis represents divergence measured as the absolute value of mean Contrast difference for stepping windows of 50 assays (this has a modal background of approximately 0.25 which is due to noise rather than a genome-wide divergence signal). The horizontal blue lines indicate the Bonferroni-corrected threshold for statistical significance obtained via bootstrapping. For comparison, panel (D) shows differentiation between similarly pooled DNA from M and S forms in Mali (Neafsey et al. 2010).
Figure S4  Comparison of M and S homozygous genotypes with heterozygous genotypes from two study sites: (A) Sedhiou M homozygotes vs. M/S heterozygotes, (B) Sedhiou S homozygotes vs. M/S heterozygotes, (C) Antula M homozygotes vs. M/S heterozygotes, (D) Antula S homozygotes vs. M/S heterozygotes.
Table S1  Spearman’s rank correlation coefficients between pairwise pool comparisons of mean Contrast difference in the X pericentromeric region (Mb 15 – 24.2).

Table S1 is available for download at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.112.148718/-/DC1.