RESEARCH NOTE

Mitochondrial genomes of *Anopheles arabiensis*, *An. gambiae* and *An. coluzzii* show no clear species division [version 1; peer review: 1 approved, 1 approved with reservations]

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v1 First published: 21 Mar 2018, 7:347
<https://doi.org/10.12688/f1000research.13807.1>
 Latest published: 15 Mar 2019, 7:347
<https://doi.org/10.12688/f1000research.13807.2>

Abstract

Here we report the complete mitochondrial sequences of 70 individual field collected mosquito specimens from throughout Sub-Saharan Africa. We generated this dataset to identify species specific markers for the following *Anopheles* species and chromosomal forms: *An. arabiensis*, *An. coluzzii* (The *Forest* and *Mopti* chromosomal forms) and *An. gambiae* (The *Bamako* and *Savannah* chromosomal forms). The raw Illumina sequencing reads were mapped to the NC_002084 reference mitogenome sequence. A total of 783 single nucleotide polymorphisms (SNPs) were detected on the mitochondrial genome, of which 460 are singletons (58.7%). None of these SNPs are suitable as molecular markers to distinguish among *An. arabiensis*, *An. coluzzii* and *An. gambiae* or any of the chromosomal forms. The lack of species or chromosomal form specific markers is also reflected in the constructed phylogenetic tree, which shows no clear division among the operational taxonomic units considered here.

Keywords

Mitogenome, species identification, Africa, malaria vector, mosquitoes, *Anopheles*, single nucleotide polymorphisms, phylogenomics

Open Peer Review

Approval Status

	1	2
version 2 (revision) 15 Mar 2019		 view
version 1 21 Mar 2018	 view	 view

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Competing interests: No competing interests were disclosed.

Grant information: We thank University of California - Irvine, Malaria Initiatives (UCIMI) for their support.

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

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How to cite this article: Hanemaaijer MJ, Houston PD, Collier TC *et al.* **Mitochondrial genomes of *Anopheles arabiensis*, *An. gambiae* and *An. coluzzii* show no clear species division [version 1; peer review: 1 approved, 1 approved with reservations]** F1000Research 2018, 7:347 <https://doi.org/10.12688/f1000research.13807.1>

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Introduction

Historically, mtDNA sequence has been used in taxonomy as a source of species diagnostic markers (Cronin *et al.* (1991); De Barba *et al.* (2014); Pegg *et al.* (2006)) or in population genetics and evolutionary studies (Fu *et al.* (2013); Harrison (1989); Llamas *et al.* (2016)). One advantage of using mitochondrial over nuclear DNA for such studies is that the mutation rate of mtDNA is about 10 times faster than nuclear DNA (Brown *et al.* (1979); Haag-Liautard *et al.* (2008)), hence amplifying the evolutionary trajectory of populations and species. In addition, mtDNA is easy to amplify, because there are more copies of mitochondrial DNA relative to nuclear DNA. Also, universal primers can be applied to a wide range of species. Widely used universal primers target the cytochrome b and cytochrome oxidase 1 genes (Tahir *et al.* (2016)), because both have conserved and highly variable regions. In addition to these, other genes as described in De Mandal *et al.* (2014), can also be used as markers. However, phylogenetic trees based on mtDNA can deviate from the ones that are derived from nuclear DNA (Phillips *et al.* (2013); Shaw (2002); Sota & Vogler, 2001).

The *Anopheles gambiae* species complex consists of eight morphologically identical species that can only be distinguished with molecular markers (Scott *et al.* (1993)) or, for some of the species, by cytological examination of polytene chromosomes (Green, 1972; Pombi *et al.*, 2008). The currently used molecular markers are located within genomic islands of divergence located proximal to the centromeres (Lee *et al.* (2014); Turner *et al.* (2005)). Monitoring additional species-specific markers on mitochondrial DNA (mtDNA) could increase the ease of application and accuracy of species detection assays. In addition, mtDNA markers could enhance our understanding of divergence times among taxa within the complex.

In this study we wished to identify species-specific markers within the mtDNA for *Anopheles arabiensis*, *An. coluzzii* and *An. gambiae*, including among the chromosomal forms currently subsumed under the designations *An. gambiae* and *An. coluzzii*, with the goal of adding these to our existing *Anopheles* species detection assay (Lee *et al.* (2014)). We sequenced the whole mitogenomes of 70 individual mosquito specimens collected throughout Sub-Saharan Africa. The raw Illumina sequencing reads were mapped to the AgamP4 reference sequence, which included both nuclear and mitochondrial sequences. We explore the relationship among *An. arabiensis*, *An. coluzzii*, *An. gambiae* and four of the sub-specific chromosomal form mitogenome sequences.

Methods

Sample collection

Anopheles arabiensis raw Illumina sequencing reads were obtained from our previous study (Marsden *et al.* (2014)). These included 20 samples from three villages in Tanzania collected in 2012 (Lupiro ((-8.38000°N, 36.66912°W), Sagamaganga

((-8.06781°N, 36.80207°W), and Minepa ((-8.25700°N, 36.68163°W) in the Kilombero Valley) and 4 samples from Cameroon collected in 2005 (9.09957°N, 13.72292°W). The *An. gambiae* and *An. coluzzii* samples were collected as resting adults using mouth aspirators in Kela, Mali (11.88683°N, -8.44744°W) in 2012 and Mutengene, Cameroon (4.0994°N, 9.3081°W) in 2011. We subdivided the *An. coluzzii* specimen into the *Forest* and *Mopti* chromosomal forms. Similarly, we did this for the *An. gambiae* *Savannah* and *Bamako* chromosomal forms. We used the same definitions and methods to characterize the chromosomal forms as in Lanzaro & Lee, 2013.

Genome sequencing

Sequencing methods for *An. arabiensis* samples are as described in Marsden *et al.* (2014). In short, individually barcoded Illumina paired-end sequencing libraries, with insert sizes of 320-400 basepairs (bp) using NEXTflex Sequencing kits (NOVA-5144) and barcodes (NOVA-514102) (Bio Scientific, Austin, TX, USA), were sequenced on an Illumina HiSeq2000 (Illumina, San Diego, CA, USA) with 100-bp paired-end reads using twelve samples per lane. For the *An. coluzzii* and *An. gambiae* samples we used the same methods as described in Norris *et al.* (2015) and Main *et al.* (2015). For the latter species, libraries were created using the Nextera DNA Sample Preparation Kit (FC-121-1031) and TruSeq dual indexing barcodes (FC-121-103) (Illumina) and the samples were sequenced on an Illumina HiSeq2500 with 100-bp paired end reads.

Data analysis

De-multiplexed raw reads were trimmed using Trimmomatic (Bolger *et al.* (2014)) version 0.36 and mapped to the mitogenome reference sequence of *An. gambiae* (Genbank accession number = NC_002084 (Beard *et al.* (1993))). Freebayes (v1.0.1) (Garrison & Marth, 2013) was used for mitochondrial variant calling assuming single ploidy and without population prior. Mapping statistics were calculated using qualimap version 2.2 (Okonechnikov *et al.* (2016)) and the data is represented in Table 1. Following the recommendation of Crawford and Lazarro (Crawford & Lazzaro, 2012), we used a minimum depth of 8 to call variants for each individual. Between positions 1-13,470bp of the mitogenome, we obtained consistently high quality reads for all samples, which were used for further analysis. An AT-rich region located between 13,471 and 15,388 suffers from low or zero coverage for sequences generated with the Nextera library preparation kit. Therefore, we excluded these regions from further analysis. The Vcf2fasta program (Danecek *et al.* (2011)) was used to extract mitogenome sequences from vcf file to fasta format. Geneious version 10.1.3 was used for mitogenome alignments. The phylogenetic tree was generated using the Jukes-Cantor genetic distance model and Neighbor-Joining tree methods available in Geneious version 10.1.3. We used scikit-allel (v1.1.9), a software package for Python (Miles & Harding (2017)), to identify species specific markers.

Table 1. List of samples that are used for the study. Mapped reads indicates the reads that are mapped to the reference genome. Mean coverage indicates the average depth of reads on the mitochondrial DNA and standard deviation indicates the coverage deviation across the mitochondrial DNA.

Species	Banked_id	Year	Country	Village	Mapped bases	Mean coverage	Standard deviation
<i>An. coluzzii-Forest</i>	11MUTE470	2011	Cameroon	Mutengene	4265836	277.7	144.5
<i>An. coluzzii-Forest</i>	11MUTE472	2011	Cameroon	Mutengene	1862892	121.3	23
<i>An. coluzzii-Forest</i>	11MUTE476	2011	Cameroon	Mutengene	2130531	138.7	50.5
<i>An. coluzzii-Forest</i>	11MUTE477	2011	Cameroon	Mutengene	806611	52.5	16.7
<i>An. coluzzii-Forest</i>	11MUTE480	2011	Cameroon	Mutengene	804015	52.3	21
<i>An. coluzzii-Forest</i>	11MUTE483	2011	Cameroon	Mutengene	1702247	110.8	42.9
<i>An. coluzzii-Forest</i>	11MUTE487	2011	Cameroon	Mutengene	812839	52.9	21.2
<i>An. coluzzii-Forest</i>	11MUTE490	2011	Cameroon	Mutengene	1882088	122.5	52.4
<i>An. coluzzii-Forest</i>	11MUTE491	2011	Cameroon	Mutengene	1422997	92.6	46.6
<i>An. coluzzii-Forest</i>	11MUTE493	2011	Cameroon	Mutengene	627590	40.9	17.3
<i>An. coluzzii-Mopti</i>	12KELA022	2012	Mali	Kela	3695920	240.6	64.4
<i>An. coluzzii-Mopti</i>	12KELA024	2012	Mali	Kela	574282	37.4	30.8
<i>An. coluzzii-Mopti</i>	12KELA046	2012	Mali	Kela	4152520	270.3	87.2
<i>An. coluzzii-Mopti</i>	12KELA085	2012	Mali	Kela	10883282	708.4	345
<i>An. coluzzii-Mopti</i>	12KELA087	2012	Mali	Kela	3351158	218.1	79.8
<i>An. coluzzii-Mopti</i>	12KELA088	2012	Mali	Kela	1704283	110.9	91.3
<i>An. coluzzii-Mopti</i>	12KELA099	2012	Mali	Kela	349531	22.8	11
<i>An. coluzzii-Mopti</i>	12KELA112	2012	Mali	Kela	8550102	556.5	198.2
<i>An. coluzzii-Mopti</i>	12KELA161	2012	Mali	Kela	33794208	2199.7	629.3
<i>An. gambiae-Savannah</i>	12KELA210	2012	Mali	Kela	3007375	195.8	53.3
<i>An. gambiae-Bamako</i>	12KELA214	2012	Mali	Kela	26441050	1721.1	566.4
<i>An. gambiae-Bamako</i>	12KELA219	2012	Mali	Kela	3617355	235.5	130.2
<i>An. gambiae-Savannah</i>	12KELA228	2012	Mali	Kela	7783776	506.7	262.8
<i>An. gambiae-Savannah</i>	12KELA233	2012	Mali	Kela	7827363	509.5	138.6
<i>An. gambiae-Savannah</i>	12KELA234	2012	Mali	Kela	6721204	437.5	205.9
<i>An. gambiae-Bamako</i>	12KELA239	2012	Mali	Kela	6683521	435	126.4
<i>An. gambiae-Bamako</i>	12KELA240	2012	Mali	Kela	15131480	984.9	270.8
<i>An. gambiae-Bamako</i>	12KELA244	2012	Mali	Kela	12851754	836.5	306.5
<i>An. gambiae-Savannah</i>	12KELA285	2012	Mali	Kela	407888	26.6	119.8
<i>An. gambiae-Savannah</i>	12KELA321	2012	Mali	Kela	1034014	67.3	43.8
<i>An. gambiae-Savannah</i>	12KELA334	2012	Mali	Kela	20949015	1363.6	400.4
<i>An. gambiae-Savannah</i>	12KELA348	2012	Mali	Kela	12053890	784.6	280.9
<i>An. gambiae-Bamako</i>	12KELA367	2012	Mali	Kela	12109235	788.2	240.1
<i>An. coluzzii-Mopti</i>	12KELA400	2012	Mali	Kela	13707820	892.3	398.2
<i>An. gambiae-Bamako</i>	12KELA406	2012	Mali	Kela	17605437	1146	463.2
<i>An. gambiae-Savannah</i>	12KELA409	2012	Mali	Kela	10526480	685.2	259.1
<i>An. coluzzii-Mopti</i>	12KELA420	2012	Mali	Kela	31785953	2069	845.5
<i>An. gambiae-Bamako</i>	12KELA443	2012	Mali	Kela	25740781	1675.5	669.1
<i>An. gambiae-Bamako</i>	12KELA457	2012	Mali	Kela	1360654	88.6	36.6
<i>An. coluzzii-Mopti</i>	12KELA458	2012	Mali	Kela	153686	10	10.4

Species	Banked_id	Year	Country	Village	Mapped bases	Mean coverage	Standard deviation
<i>An. gambiae</i> -Bamako	12KELA467	2012	Mali	Kela	10499093	683.4	249.1
<i>An. gambiae</i> -Savannah	12KELA468	2012	Mali	Kela	10315033	671.4	197.1
<i>An. gambiae</i> -Bamako	12KELA481	2012	Mali	Kela	20308589	1321.9	307.6
<i>An. coluzzii</i> -Mopti	12KELA496	2012	Mali	Kela	2975297	193.7	162.9
<i>An. gambiae</i> -Bamako	12KELA651	2012	Mali	Kela	376689	24.5	11.3
<i>An. gambiae</i> -Savannah	12KELA812	2012	Mali	Kela	799071	52	29.3
<i>An. arabiensis</i>	12LUPI001	2012	Tanzania	Lupiro	2843317	185.1	34.9
<i>An. arabiensis</i>	12LUPI007	2012	Tanzania	Lupiro	6288802	409.3	40
<i>An. arabiensis</i>	12LUPI024	2012	Tanzania	Lupiro	6328898	412	78.5
<i>An. arabiensis</i>	12LUPI056	2012	Tanzania	Lupiro	5440256	354.1	39.2
<i>An. arabiensis</i>	12LUPI059	2012	Tanzania	Lupiro	39721262	2585.5	801.8
<i>An. arabiensis</i>	12LUPI071	2012	Tanzania	Lupiro	3433158	223.5	59.2
<i>An. arabiensis</i>	12LUPI074	2012	Tanzania	Lupiro	10096062	657.2	100.5
<i>An. arabiensis</i>	12LUPI082	2012	Tanzania	Lupiro	5732773	373.2	69.6
<i>An. arabiensis</i>	12MINE001	2012	Tanzania	Minepa	7768923	505.7	66.9
<i>An. arabiensis</i>	12MINE040	2012	Tanzania	Minepa	2784428	181.2	54.9
<i>An. arabiensis</i>	12MINE100	2012	Tanzania	Minepa	10753877	700	93.9
<i>An. arabiensis</i>	12MINE101	2012	Tanzania	Minepa	5684230	370	41.9
<i>An. arabiensis</i>	12MINE105	2012	Tanzania	Minepa	1526829	99.4	32.8
<i>An. arabiensis</i>	12MINE111	2012	Tanzania	Minepa	5578562	363.1	76.3
<i>An. arabiensis</i>	12SAGA066	2012	Tanzania	Sagamaganga	12745079	829.6	142.3
<i>An. arabiensis</i>	12SAGA107	2012	Tanzania	Sagamaganga	14460217	941.2	259.2
<i>An. arabiensis</i>	12SAGA131	2012	Tanzania	Sagamaganga	15333239	998.1	282.9
<i>An. arabiensis</i>	12SAGA133	2012	Tanzania	Sagamaganga	3792945	246.9	62.5
<i>An. arabiensis</i>	12SAGA134	2012	Tanzania	Sagamaganga	2439101	158.8	34.5
<i>An. arabiensis</i>	12SAGA141	2012	Tanzania	Sagamaganga	3130504	203.8	33.3
<i>An. arabiensis</i>	05OKJ017	2005	Cameroon	Ourodougoudje	9041052	588.5	78.8
<i>An. arabiensis</i>	05OKJ042	2005	Cameroon	Ourodougoudje	148752684	9682.5	785.7
<i>An. arabiensis</i>	05OKJ045	2005	Cameroon	Ourodougoudje	35514980	2311.7	262.8
<i>An. arabiensis</i>	05OKJ070	2005	Cameroon	Ourodougoudje	22847478	1487.2	400.5

Dataset 1. Aligned FASTA file of mitogenome samples

<http://dx.doi.org/10.5256/f1000research.13807.d192892>

Results and discussion

We identified a total of 783 single nucleotide polymorphisms (SNPs) over the entire mitogenome. The majority of these (58.7%) were singletons (found on one of the 70 mitogenomes). We did not identify any SNPs unique to the species or chromosomal

forms (Table 2) and therefore conclude that mtDNA is not suitable for *Anopheles gambiae* complex species identification.

The lack of species-specific markers is also reflected in the phylogenetic tree (Figure 1). *An. arabiensis*, *An. coluzzii* and *An. gambiae* did not cluster separately, which is consistent with previous reports that compared mitochondrial genome sequence data from specimens originating from Kenya, Senegal and South Africa (Besansky *et al.* (1997)) and Burkina Faso, Cameroon,

Table 2. List of SNP variants in the different *Anopheles* species and chromosomal forms.

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			<i>An. arabiensis</i>	<i>An. coluzzii-Forest</i>	<i>An. coluzzii-Mopti</i>	<i>An. gambiae-Bamako</i>	<i>An. gambiae-Savannah</i>
55	C	T/-/-	21/3/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
71	C	T/-/-	0/24/0/0	0/11/0/0	0/13/0/0	1/11/0/0	0/11/0/0
117	A	G/-/-	23/1/0/0	9/2/0/0	13/0/0/0	12/0/0/0	11/0/0/0
126	T	C/-/-	11/13/0/0	1/10/0/0	0/13/0/0	0/12/0/0	1/10/0/0
205	C	T/-/-	23/1/0/0	11/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
223	T	C/-/-	23/1/0/0	11/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
248	G	A/-/-	24/0/0/0	11/0/0/0	12/0/0/0	12/0/0/0	10/1/0/0
250	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
298	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
340	T	C/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
373	A	G/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
391	T	C/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
396	C	T/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
409	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
441	T	C/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
469	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
488	T	C/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
502	A	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
503	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
514	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
520	T	A/C/-	22/0/2/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
526	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	10/1/0/0
562	A	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
572	G	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	10/2/0/0	11/0/0/0
583	A	G/-/-	24/0/0/0	11/0/0/0	10/3/0/0	12/0/0/0	11/0/0/0
611	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
665	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
685	A	G/-/-	24/0/0/0	11/0/0/0	12/0/0/0	12/0/0/0	10/1/0/0
688	T	A/-/-	24/0/0/0	10/1/0/0	12/0/0/0	11/1/0/0	11/0/0/0
700	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
706	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
712	A	C/-/-	24/0/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
757	A	G/-/-	24/0/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
763	A	G/-/-	11/13/0/0	3/8/0/0	0/13/0/0	2/10/0/0	1/10/0/0
787	A	G/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
788	T	C/-/-	24/0/0/0	9/1/0/0	12/1/0/0	12/0/0/0	10/1/0/0
796	A	G/-/-	22/2/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
811	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
821	T	C/-/-	11/13/0/0	1/9/0/0	1/12/0/0	0/12/0/0	1/10/0/0
832	A	G/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
887	T	C/-/-	16/8/0/0	10/0/0/0	12/0/0/0	12/0/0/0	10/1/0/0
908	A	G/-/-	18/6/0/0	10/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
934	G	A/-/-	22/2/0/0	9/1/0/0	12/0/0/0	12/0/0/0	10/1/0/0
949	A	G/-/-	24/0/0/0	10/0/0/0	11/2/0/0	11/1/0/0	11/0/0/0
955	T	C/-/-	12/12/0/0	5/5/0/0	9/4/0/0	4/8/0/0	2/9/0/0
1012	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1029	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1042	T	C/-/-	24/0/0/0	11/0/0/0	11/1/0/0	12/0/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			<i>An. arabiensis</i>	<i>An. coluzzii-Forest</i>	<i>An. coluzzii-Mopti</i>	<i>An. gambiae-Bamako</i>	<i>An. gambiae-Savannah</i>
1045	A	G/-/-	24/0/0/0	11/0/0/0	11/1/0/0	12/0/0/0	11/0/0/0
1114	C	T/-/-	24/0/0/0	11/0/0/0	12/0/0/0	11/1/0/0	11/0/0/0
1150	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1153	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1155	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1163	T	C/-/-	0/24/0/0	0/11/0/0	0/13/0/0	0/12/0/0	0/11/0/0
1189	G	A/-/-	24/0/0/0	9/2/0/0	11/2/0/0	11/1/0/0	11/0/0/0
1198	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1308	T	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
1465	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1474	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
1486	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1504	A	G/-/-	23/1/0/0	9/2/0/0	13/0/0/0	11/1/0/0	10/1/0/0
1507	G	A/-/-	23/1/0/0	9/2/0/0	11/2/0/0	11/1/0/0	11/0/0/0
1523	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1538	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
1540	A	T/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
1543	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1546	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1549	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
1558	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1561	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
1567	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
1618	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
1624	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1636	T	C/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
1639	A	G/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
1642	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1645	A	G/T/	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	10/0/1/0
1648	G	A/-/-	23/1/0/0	10/0/0/0	9/4/0/0	12/0/0/0	10/1/0/0
1681	A	C/-/-	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1693	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1729	G	A/-/-	23/1/0/0	7/4/0/0	13/0/0/0	10/2/0/0	11/0/0/0
1735	T	C/-/-	23/1/0/0	9/2/0/0	13/0/0/0	10/2/0/0	11/0/0/0
1738	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1751	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1765	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1780	G	A/-/-	23/1/0/0	10/1/0/0	11/2/0/0	12/0/0/0	11/0/0/0
1792	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
1807	T	C/-/-	23/1/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1837	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	11/1/0/0	10/1/0/0
1876	A	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1879	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1903	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1906	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
1918	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1930	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
1933	G	A/-/-	23/1/0/0	10/0/0/0	11/2/0/0	7/5/0/0	7/4/0/0
1964	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
1972	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			<i>An. arabiensis</i>	<i>An. coluzzii-Forest</i>	<i>An. coluzzii-Mopti</i>	<i>An. gambiae-Bamako</i>	<i>An. gambiae-Savannah</i>
1978	G	A/-/-	22/2/0/0	11/0/0/0	9/4/0/0	8/4/0/0	11/0/0/0
2026	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2068	A	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
2071	T	C/G/-	23/1/0/0	11/0/0/0	12/0/1/0	12/0/0/0	10/0/1/0
2080	T	C/-/-	22/2/0/0	11/0/0/0	13/0/0/0	10/2/0/0	11/0/0/0
2098	T	C/-/-	23/1/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2101	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2110	T	C/-/-	23/1/0/0	10/1/0/0	11/2/0/0	11/1/0/0	10/1/0/0
2116	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2149	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2164	T	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2179	T	C/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
2182	G	A/-/-	22/2/0/0	6/5/0/0	11/2/0/0	4/8/0/0	8/3/0/0
2206	A	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2209	G	A/-/-	19/5/0/0	10/1/0/0	12/1/0/0	11/1/0/0	9/2/0/0
2227	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2233	A	G/T/-	24/0/0/0	11/0/0/0	13/0/0/0	11/0/1/0	11/0/0/0
2239	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
2260	C	T/-/-	2/22/0/0	0/11/0/0	0/13/0/0	0/12/0/0	0/11/0/0
2269	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2284	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2329	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2359	G	A/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
2374	G	A/-/-	23/1/0/0	11/0/0/0	10/3/0/0	11/1/0/0	10/1/0/0
2401	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2410	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2411	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2413	G	A/-/-	0/24/0/0	0/11/0/0	0/13/0/0	0/12/0/0	0/11/0/0
2426	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2432	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2434	G	A/-/-	22/2/0/0	9/2/0/0	11/2/0/0	11/1/0/0	10/1/0/0
2449	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2473	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2474	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
2482	A	G/-/-	20/4/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2521	C	T/-/-	24/0/0/0	10/1/0/0	12/1/0/0	11/1/0/0	10/1/0/0
2530	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2558	T	C/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2569	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2599	A	G/T/-	23/1/0/0	10/1/0/0	13/0/0/0	11/0/1/0	11/0/0/0
2608	T	C/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2612	T	C/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2615	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2635	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2692	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2719	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2722	A	G/-/-	23/1/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2728	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2731	A	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2737	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			An. arabiensis	An. coluzzii-Forest	An. coluzzii-Mopti	An. gambiae-Bamako	An. gambiae-Savannah
2752	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2755	C	A/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
2758	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
2774	G	A/-/-	23/1/0/0	11/0/0/0	11/2/0/0	11/1/0/0	11/0/0/0
2782	T	A/C/-	23/0/1/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
2791	T	A/C/-	23/0/1/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2797	C	T/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
2806	C	T/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
2818	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2848	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2851	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2859	C	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2872	T	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2902	C	T/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
2908	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
2938	G	A/-/-	23/1/0/0	10/1/0/0	13/0/0/0	11/1/0/0	10/1/0/0
2945	C	T/-/-	15/9/0/0	9/2/0/0	13/0/0/0	11/1/0/0	11/0/0/0
2975	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
3055	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	10/2/0/0	11/0/0/0
3124	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3136	T	C/-/-	24/0/0/0	9/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
3199	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3202	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3205	A	G/-/-	24/0/0/0	9/2/0/0	12/1/0/0	12/0/0/0	11/0/0/0
3238	T	A/C/	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3277	A	T/-/-	24/0/0/0	11/0/0/0	11/1/0/0	11/1/0/0	8/3/0/0
3286	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3304	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3307	A	C/G/T	24/0/0/0	11/0/0/0	9/0/1/3	12/0/0/0	11/0/0/0
3310	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
3325	G	A/-/-	24/0/0/0	11/0/0/0	11/2/0/0	10/2/0/0	11/0/0/0
3331	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
3334	T	C/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3337	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3352	T	C/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
3400	A	G/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3401	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3403	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
3412	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3413	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
3424	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3451	C	T/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
3457	G	A/T/	12/12/0/0	6/4/1/0	12/1/0/0	3/9/0/0	5/6/0/0
3458	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3466	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3508	A	G/-/-	24/0/0/0	11/0/0/0	11/2/0/0	11/1/0/0	10/1/0/0
3511	C	A/T/-	22/1/1/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3514	C	T/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
3523	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3544	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			An. arabiensis	An. coluzzii-Forest	An. coluzzii-Mopti	An. gambiae-Bamako	An. gambiae-Savannah
3595	A	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3613	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
3619	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3652	G	A/-/-	22/2/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
3773	A	G/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3838	G	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/1/0/0	10/1/0/0
3870	C	T/-/-	12/12/0/0	3/8/0/0	6/7/0/0	1/11/0/0	3/8/0/0
3882	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3924	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
3960	T	C/-/-	24/0/0/0	10/0/0/0	10/3/0/0	11/1/0/0	11/0/0/0
3976	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4002	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
4011	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
4034	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4037	G	A/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
4052	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/1/0/0	11/0/0/0
4100	C	T/-/-	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4104	G	T/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
4112	C	T/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4115	A	G/-/-	11/13/0/0	1/9/0/0	0/13/0/0	0/12/0/0	2/9/0/0
4121	A	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4145	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4157	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4181	T	A/-/-	3/21/0/0	0/11/0/0	0/13/0/0	0/12/0/0	0/11/0/0
4190	A	G/-/-	0/24/0/0	1/10/0/0	0/13/0/0	0/12/0/0	0/11/0/0
4196	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4206	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4208	A	G/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
4214	T	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4220	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4256	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
4259	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4292	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4310	T	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
4332	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
4352	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4367	A	G/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4368	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4373	T	C/-/-	22/2/0/0	11/0/0/0	13/0/0/0	10/2/0/0	11/0/0/0
4430	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4442	G	A/-/-	14/10/0/0	10/1/0/0	11/2/0/0	12/0/0/0	9/2/0/0
4451	G	A/-/-	24/0/0/0	10/1/0/0	12/1/0/0	11/1/0/0	11/0/0/0
4484	A	T/-/-	20/4/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4487	T	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
4490	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	10/2/0/0	11/0/0/0
4494	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4526	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4529	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
4538	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			<i>An. arabiensis</i>	<i>An. coluzzii-Forest</i>	<i>An. coluzzii-Mopti</i>	<i>An. gambiae-Bamako</i>	<i>An. gambiae-Savannah</i>
4559	A	G/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
4562	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	10/2/0/0	11/0/0/0
4565	T	A/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
4566	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
4579	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4603	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4620	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4637	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4649	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
4652	A	G/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
4715	G	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
4747	C	A/T/-	24/0/0/0	10/0/1/0	13/0/0/0	10/1/1/0	11/0/0/0
4750	A	G/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
4756	C	T/-/-	21/3/0/0	9/2/0/0	13/0/0/0	9/3/0/0	10/1/0/0
4774	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4777	A	C/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
4795	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4846	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
4847	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4867	G	A/-/-	24/0/0/0	9/1/0/0	12/1/0/0	11/1/0/0	11/0/0/0
4885	T	C/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
4969	A	C/-/-	16/8/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5011	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5020	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
5029	T	C/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
5044	A	G/-/-	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5056	T	C/-/-	23/1/0/0	10/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
5059	A	T/-/-	11/13/0/0	1/9/0/0	0/13/0/0	0/12/0/0	1/10/0/0
5062	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
5065	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5072	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5074	A	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
5077	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/1/0/0	11/0/0/0
5080	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5128	A	G/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5131	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5137	C	T/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5165	G	A/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5167	T	A/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5173	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5182	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
5215	A	G/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
5216	G	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5221	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	11/1/0/0	10/1/0/0
5254	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5257	T	C/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
5272	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
5278	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
5279	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			<i>An. arabiensis</i>	<i>An. coluzzii-Forest</i>	<i>An. coluzzii-Mopti</i>	<i>An. gambiae-Bamako</i>	<i>An. gambiae-Savannah</i>
5287	A	G/-/-	19/5/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5308	A	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5314	C	T/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
5320	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5323	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5359	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	11/1/0/0	11/0/0/0
5398	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5428	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
5431	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5513	A	G/-/-	24/0/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
5540	C	T/-/-	23/1/0/0	7/4/0/0	7/5/0/0	7/5/0/0	9/2/0/0
5564	T	C/-/-	23/1/0/0	11/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
5572	A	G/-/-	21/3/0/0	10/1/0/0	11/1/0/0	11/1/0/0	11/0/0/0
5622	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5652	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5661	A	G/-/-	20/4/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5664	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
5670	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5679	T	C/-/-	24/0/0/0	11/0/0/0	10/3/0/0	12/0/0/0	11/0/0/0
5682	G	A/-/-	23/1/0/0	7/4/0/0	5/8/0/0	6/6/0/0	11/0/0/0
5688	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
5691	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5700	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5712	T	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
5850	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
5865	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5871	C	T/-/-	16/8/0/0	10/1/0/0	13/0/0/0	11/1/0/0	10/1/0/0
5883	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
5898	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
5941	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6021	A,T	A/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
6054	G	A/-/-	21/3/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
6222	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6252	A	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6277	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
6289	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	10/1/0/0
6315	A	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6388	A	G/-/-	24/0/0/0	10/1/0/0	11/2/0/0	12/0/0/0	11/0/0/0
6421	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6425	A	G/-/-	9/15/0/0	1/10/0/0	0/13/0/0	0/12/0/0	0/11/0/0
6430	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
6439	C	T/-/-	24/0/0/0	10/0/0/0	12/1/0/0	11/1/0/0	11/0/0/0
6442	T	C/G/-	14/9/1/0	10/0/0/0	12/1/0/0	12/0/0/0	8/3/0/0
6450	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
6466	A	G/-/-	16/8/0/0	7/4/0/0	13/0/0/0	7/5/0/0	6/5/0/0
6469	G	A/-/-	21/3/0/0	9/2/0/0	11/2/0/0	12/0/0/0	10/1/0/0
6482	G	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6488	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
6501	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			An. arabiensis	An. coluzzii-Forest	An. coluzzii-Mopti	An. gambiae-Bamako	An. gambiae-Savannah
6517	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6529	G	A/-/-	12/12/0/0	1/10/0/0	0/13/0/0	0/12/0/0	1/10/0/0
6551	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
6556	G	A/-/-	9/15/0/0	1/10/0/0	0/13/0/0	0/12/0/0	0/11/0/0
6563	T	C/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
6571	G	A/-/-	23/1/0/0	9/2/0/0	13/0/0/0	11/1/0/0	10/1/0/0
6578	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
6580	G	A/-/-	21/3/0/0	7/4/0/0	11/2/0/0	10/2/0/0	6/5/0/0
6616	T	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
6619	G	A/-/-	21/3/0/0	9/2/0/0	13/0/0/0	11/1/0/0	7/4/0/0
6628	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	11/1/0/0	10/1/0/0
6631	T	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6637	G	A/-/-	23/1/0/0	9/2/0/0	11/2/0/0	10/2/0/0	11/0/0/0
6649	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
6661	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6662	G	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6670	C	T/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
6684	G	A/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
6687	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
6699	C	T/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
6718	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
6726	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
6730	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
6731	C	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6733	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6753	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6764	C	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
6791	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6793	A	G/-/-	24/0/0/0	11/0/0/0	10/3/0/0	11/1/0/0	11/0/0/0
6805	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	10/1/0/0
6808	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6829	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
6841	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
6847	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6928	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
6933	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
6982	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
6985	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
7027	C	T/-/-	24/0/0/0	9/2/0/0	13/0/0/0	10/2/0/0	10/1/0/0
7045	G	A/-/-	15/9/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
7075	T	C/-/-	24/0/0/0	8/2/0/0	12/1/0/0	12/0/0/0	11/0/0/0
7090	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
7099	T	C/G/-	24/0/0/0	11/0/0/0	13/0/0/0	9/2/1/0	11/0/0/0
7105	T	C/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
7108	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	10/2/0/0	10/1/0/0
7116	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
7135	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
7168	T	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
7195	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
7207	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	10/2/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			An. arabiensis	An. coluzzii-Forest	An. coluzzii-Mopti	An. gambiae-Bamako	An. gambiae-Savannah
7231	C	T/-/-	24/0/0/0	9/2/0/0	13/0/0/0	11/1/0/0	11/0/0/0
7240	G	A/-/-	9/15/0/0	1/10/0/0	0/13/0/0	0/12/0/0	0/11/0/0
7255	G	A/-/-	3/21/0/0	1/10/0/0	0/13/0/0	1/11/0/0	1/10/0/0
7261	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7282	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7290	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
7351	A	G/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
7360	T	C/-/-	11/13/0/0	2/9/0/0	4/9/0/0	1/11/0/0	1/10/0/0
7381	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
7396	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7402	A	G/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
7423	T	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
7432	A	C/-/-	24/0/0/0	11/0/0/0	12/0/0/0	12/0/0/0	10/1/0/0
7450	G	A/-/-	23/1/0/0	10/1/0/0	12/1/0/0	12/0/0/0	9/2/0/0
7478	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7479	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
7483	C	G/T/	24/0/0/0	10/1/0/0	11/0/2/0	11/1/0/0	11/0/0/0
7486	C	T/-/-	11/13/0/0	5/6/0/0	4/9/0/0	0/12/0/0	2/9/0/0
7525	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7555	A	G/-/-	24/0/0/0	9/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
7578	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
7588	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7603	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7606	G	A/-/-	24/0/0/0	10/1/0/0	11/2/0/0	12/0/0/0	11/0/0/0
7627	A	G/-/-	13/11/0/0	7/4/0/0	12/1/0/0	5/7/0/0	5/6/0/0
7672	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7687	G	A/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
7693	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
7735	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	11/1/0/0	11/0/0/0
7777	C	T/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
7797	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
7798	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
7822	A	G/-/-	24/0/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
7861	T	C/-/-	23/1/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
7923	T	C/-/-	24/0/0/0	11/0/0/0	10/3/0/0	11/1/0/0	11/0/0/0
7952	A	G/-/-	0/24/0/0	0/11/0/0	0/13/0/0	0/12/0/0	0/11/0/0
8001	T	C/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8034	C	T/-/-	13/11/0/0	6/4/0/0	11/1/0/0	3/9/0/0	5/6/0/0
8091	A	AT/-/-	22/2/0/0	9/1/0/0	12/1/0/0	12/0/0/0	9/2/0/0
8122	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
8123	C	T/-/-	22/2/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8149	G	A/-/-	2/22/0/0	0/10/0/0	0/13/0/0	0/12/0/0	0/11/0/0
8196	G	A/-/-	23/1/0/0	10/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
8201	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8261	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
8297	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8302	G	A/-/-	23/1/0/0	10/0/0/0	10/3/0/0	12/0/0/0	11/0/0/0
8303	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8309	C	T/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8339	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			<i>An. arabiensis</i>	<i>An. coluzzii-Forest</i>	<i>An. coluzzii-Mopti</i>	<i>An. gambiae-Bamako</i>	<i>An. gambiae-Savannah</i>
8342	C	T/-/-	24/0/0/0	11/0/0/0	10/3/0/0	12/0/0/0	11/0/0/0
8372	C	T/-/-	24/0/0/0	9/2/0/0	11/2/0/0	11/1/0/0	11/0/0/0
8375	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8382	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
8384	A	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
8393	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
8399	G	A/-/-	2/22/0/0	0/11/0/0	0/13/0/0	0/12/0/0	0/11/0/0
8404	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
8414	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8425	A	G/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8450	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8465	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8471	G	A/T/-	24/0/0/0	6/5/0/0	7/6/0/0	10/2/0/0	10/1/0/0
8513	A	G/-/-	22/2/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8528	A	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8546	A	T/-/-	24/0/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
8564	C	A/T/-	23/0/1/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
8582	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
8588	T	C/-/-	24/0/0/0	11/0/0/0	9/4/0/0	11/1/0/0	10/1/0/0
8612	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8645	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
8657	T	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
8663	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
8678	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
8684	T	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	10/2/0/0	11/0/0/0
8714	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
8720	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	10/2/0/0	11/0/0/0
8722	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
8725	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
8726	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
8740	G	A/-/-	24/0/0/0	10/1/0/0	9/4/0/0	9/3/0/0	10/1/0/0
8744	G	A/-/-	23/1/0/0	8/3/0/0	11/2/0/0	10/2/0/0	10/1/0/0
8765	G	A/-/-	22/2/0/0	10/1/0/0	12/1/0/0	11/1/0/0	8/3/0/0
8807	T	C/-/-	22/2/0/0	9/2/0/0	12/1/0/0	11/1/0/0	11/0/0/0
8819	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	11/1/0/0	8/3/0/0
8840	C	T/-/-	11/13/0/0	1/10/0/0	0/13/0/0	0/12/0/0	1/10/0/0
8842	A	G/-/-	24/0/0/0	10/1/0/0	10/3/0/0	12/0/0/0	9/2/0/0
8855	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
8882	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	9/2/0/0
8893	G	A/-/-	24/0/0/0	7/4/0/0	8/6/0/0	9/3/0/0	11/0/0/0
8903	C	T/-/-	23/1/0/0	11/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0
8913	A	C/-/-	24/0/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
8915	G	A/-/-	23/1/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
8927	A	G/-/-	11/13/0/0	2/9/0/0	0/14/0/0	1/11/0/0	2/9/0/0
8942	A	G/-/-	24/0/0/0	11/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0
8995	A	G/-/-	21/3/0/0	11/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0
8996	A	T/-/-	24/0/0/0	11/0/0/0	13/1/0/0	12/0/0/0	11/0/0/0
9014	A	T/-/-	24/0/0/0	11/0/0/0	14/0/0/0	12/0/0/0	10/1/0/0
9035	C	T/-/-	23/1/0/0	11/0/0/0	14/0/0/0	12/0/0/0	10/1/0/0
9041	C	T/-/-	3/21/0/0	0/11/0/0	0/14/0/0	0/12/0/0	0/11/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			An. arabiensis	An. coluzzii- Forest	An. coluzzii- Mopti	An. gambiae- Bamako	An. gambiae- Savannah
9062	C	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9122	T	C/-/-	24/0/0/0	9/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
9152	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
9158	C	T/-/-	23/1/0/0	7/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
9210	G	A/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9236	C	T/-/-	24/0/0/0	9/2/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9244	G	A/-/-	22/2/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9245	C	A/T/-	23/0/1/0	10/0/1/0	13/0/0/0	12/0/0/0	9/1/1/0
9278	G	A/-/-	24/0/0/0	10/1/0/0	12/1/0/0	11/1/0/0	11/0/0/0
9287	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9311	G	A/-/-	9/15/0/0	1/10/0/0	0/13/0/0	0/12/0/0	0/11/0/0
9353	C	T/-/-	24/0/0/0	11/0/0/0	11/1/0/0	12/0/0/0	11/0/0/0
9359	G	A/-/-	9/15/0/0	1/10/0/0	0/13/0/0	0/12/0/0	0/11/0/0
9365	T	C/-/-	24/0/0/0	9/2/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9421	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
9422	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
9459	A	G/-/-	24/0/0/0	10/0/0/0	10/3/0/0	11/1/0/0	11/0/0/0
9493	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
9529	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9532	C	A/-/-	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9535	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9550	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9575	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9583	A	G/-/-	20/4/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9611	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9631	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
9660	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9688	T	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
9690	T	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9711	T	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9724	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
9795	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
9808	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9911	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
9930	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
9976	C	T/-/-	24/0/0/0	10/1/0/0	14/0/0/0	12/0/0/0	11/0/0/0
10011	A	G/-/-	24/0/0/0	11/0/0/0	13/1/0/0	12/0/0/0	10/1/0/0
10047	A	G/-/-	24/0/0/0	11/0/0/0	13/1/0/0	12/0/0/0	11/0/0/0
10063	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10068	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10104	A	G/-/-	24/0/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
10156	G	A/C/-	24/0/0/0	8/1/2/0	13/1/0/0	10/1/1/0	8/3/0/0
10168	C	A/T/-	24/0/0/0	7/4/0/0	9/5/0/0	9/2/1/0	10/0/1/0
10176	A	G/-/-	11/13/0/0	2/9/0/0	3/11/0/0	0/12/0/0	2/9/0/0
10177	G	A/-/-	24/0/0/0	11/0/0/0	13/1/0/0	12/0/0/0	10/1/0/0
10185	C	A/T/-	16/0/8/0	11/0/0/0	13/1/0/0	12/0/0/0	10/0/1/0
10187	T	C/-/-	24/0/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
10252	A	G/-/-	24/0/0/0	10/0/0/0	14/0/0/0	12/0/0/0	10/1/0/0
10253	C	T/-/-	23/1/0/0	10/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			An. arabiensis	An. coluzzii-Forest	An. coluzzii-Mopti	An. gambiae-Bamako	An. gambiae-Savannah
10269	C	T/-/-	24/0/0/0	7/3/0/0	9/5/0/0	10/2/0/0	11/0/0/0
10284	A	G/-/-	24/0/0/0	10/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0
10311	A	G/-/-	24/0/0/0	10/0/0/0	14/0/0/0	12/0/0/0	10/1/0/0
10324	T	C/-/-	24/0/0/0	10/0/0/0	14/0/0/0	12/0/0/0	10/1/0/0
10332	A	G/-/-	24/0/0/0	10/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
10341	T	C/-/-	24/0/0/0	10/0/0/0	10/3/0/0	12/0/0/0	11/0/0/0
10371	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10383	A	G/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10396	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10401	G	A/-/-	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10424	T	A/-/-	16/8/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
10427	T	C/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10454	C	T/-/-	24/0/0/0	10/0/0/0	12/1/0/0	10/2/0/0	10/1/0/0
10463	T	C/-/-	24/0/0/0	7/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
10466	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
10481	T	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10482	G	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10499	C	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10502	C	T/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10535	C	T/-/-	23/1/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10536	T	C/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10542	C	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	9/2/0/0
10559	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10566	C	T/-/-	23/1/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10568	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10583	C	T/-/-	23/1/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10598	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10607	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10628	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10640	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10664	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10670	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	10/1/0/0
10691	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10700	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10715	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10718	A	G/-/-	24/0/0/0	9/2/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10719	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10724	T	C/-/-	22/2/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10727	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10737	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10742	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10763	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10784	A	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
10796	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	10/1/0/0
10805	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
10808	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10820	A	G/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
10841	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10863	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			<i>An. arabiensis</i>	<i>An. coluzzii-Forest</i>	<i>An. coluzzii-Mopti</i>	<i>An. gambiae-Bamako</i>	<i>An. gambiae-Savannah</i>
10872	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10877	T	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10880	C	T/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
10881	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10886	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
10889	G	A/-/-	22/2/0/0	9/2/0/0	11/2/0/0	9/3/0/0	11/0/0/0
10892	T	C/-/-	23/1/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10898	T	A/C/-	11/0/13/0	2/0/9/0	0/0/13/0	1/0/11/0	1/0/10/0
10910	A	G/-/-	20/4/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10913	G	A/-/-	22/2/0/0	9/2/0/0	10/3/0/0	10/2/0/0	8/3/0/0
10916	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	10/2/0/0	11/0/0/0
10931	C	T/-/-	24/0/0/0	8/3/0/0	8/5/0/0	10/2/0/0	11/0/0/0
10934	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
10955	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
10988	T	C/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
10997	G	A/-/-	23/1/0/0	9/1/0/0	11/2/0/0	10/2/0/0	10/1/0/0
10998	A	G/-/-	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11042	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11060	A	G/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
11093	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11117	A	G/-/-	24/0/0/0	10/0/0/0	11/2/0/0	12/0/0/0	11/0/0/0
11150	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11159	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11160	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11171	T	C/-/-	23/1/0/0	9/2/0/0	11/2/0/0	11/1/0/0	8/3/0/0
11174	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11204	T	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11213	A	G/T/-	24/0/0/0	10/1/0/0	12/1/1/0	12/0/0/0	10/0/1/0
11216	T	C/-/-	24/0/0/0	11/0/0/0	13/1/0/0	10/2/0/0	10/1/0/0
11222	A	G/-/-	24/0/0/0	8/3/0/0	9/5/0/0	10/2/0/0	11/0/0/0
11234	C	T/-/-	24/0/0/0	11/0/0/0	12/2/0/0	11/1/0/0	11/0/0/0
11249	C	T/-/-	24/0/0/0	10/1/0/0	13/1/0/0	12/0/0/0	9/2/0/0
11276	G	A/-/-	23/1/0/0	11/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0
11282	A	G/-/-	24/0/0/0	11/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0
11301	C	T/-/-	9/15/0/0	2/9/0/0	0/14/0/0	0/12/0/0	0/11/0/0
11318	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11339	C	T/-/-	24/0/0/0	8/3/0/0	7/6/0/0	10/2/0/0	11/0/0/0
11348	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11351	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	10/2/0/0	10/1/0/0
11354	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11363	A	G/-/-	24/0/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11390	C	T/-/-	24/0/0/0	10/1/0/0	14/0/0/0	12/0/0/0	9/2/0/0
11414	G	A/-/-	23/1/0/0	10/1/0/0	10/4/0/0	10/2/0/0	11/0/0/0
11415	T	C/-/-	24/0/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
11432	A	G/-/-	23/1/0/0	11/0/0/0	14/0/0/0	10/2/0/0	10/1/0/0
11450	C	T/-/-	13/11/0/0	1/10/0/0	1/13/0/0	0/12/0/0	2/9/0/0
11475	T	C/-/-	24/0/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
11492	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11537	G	A/-/-	24/0/0/0	9/2/0/0	8/5/0/0	10/2/0/0	8/3/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			<i>An. arabiensis</i>	<i>An. coluzzii-Forest</i>	<i>An. coluzzii-Mopti</i>	<i>An. gambiae-Bamako</i>	<i>An. gambiae-Savannah</i>
11538	C	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11592	G	A/-/-	0/24/0/0	0/11/0/0	0/13/0/0	0/12/0/0	0/11/0/0
11599	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11610	A	AT/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
11655	G	A/-/-	8/16/0/0	1/9/0/0	0/13/0/0	0/12/0/0	0/11/0/0
11673	G	A/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
11729	G	A/-/-	24/0/0/0	9/2/0/0	11/2/0/0	12/0/0/0	8/3/0/0
11739	A	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11745	T	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11748	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11757	C	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11760	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11763	A	G/-/-	18/6/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
11787	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11793	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11829	A	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11862	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11868	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
11899	G	A/-/-	24/0/0/0	9/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
11907	C	T/-/-	20/4/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
11910	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11916	G	A/-/-	20/4/0/0	5/5/0/0	2/11/0/0	5/7/0/0	8/3/0/0
11925	A	G/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11931	T	C/-/-	23/1/0/0	9/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
11982	A	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
11988	A	C/-/-	12/12/0/0	6/4/0/0	11/2/0/0	3/9/0/0	3/8/0/0
12005	G	A/-/-	23/1/0/0	9/1/0/0	12/1/0/0	9/3/0/0	8/3/0/0
12006	C	T/-/-	23/1/0/0	10/0/0/0	13/0/0/0	11/1/0/0	10/1/0/0
12009	G	A/T/-	24/0/0/0	6/4/0/0	8/2/3/0	8/4/0/0	11/0/0/0
12015	A	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
12020	A	G/-/-	24/0/0/0	9/1/0/0	13/0/0/0	11/1/0/0	11/0/0/0
12036	A	G/-/-	13/11/0/0	2/8/0/0	1/12/0/0	2/10/0/0	4/7/0/0
12039	A	G/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12061	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12078	A	G/-/-	24/0/0/0	9/2/0/0	13/0/0/0	11/1/0/0	11/0/0/0
12084	A	G/-/-	24/0/0/0	11/0/0/0	10/3/0/0	11/1/0/0	11/0/0/0
12092	C	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12159	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
12165	C	A/T/-	19/4/1/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12168	C	T/-/-	22/2/0/0	10/1/0/0	12/1/0/0	12/0/0/0	9/2/0/0
12171	C	T/-/-	24/0/0/0	9/2/0/0	13/0/0/0	11/1/0/0	10/1/0/0
12204	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
12210	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/1/0/0	11/0/0/0
12225	T	C/-/-	24/0/0/0	11/0/0/0	11/2/0/0	12/0/0/0	10/1/0/0
12228	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
12258	A	G/-/-	24/0/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
12273	A	G/-/-	23/1/0/0	11/0/0/0	14/0/0/0	12/0/0/0	11/0/0/0
12278	A	G/-/-	24/0/0/0	11/0/0/0	14/0/0/0	11/1/0/0	11/0/0/0
12333	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	9/2/0/0
12336	A	T/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			<i>An. arabiensis</i>	<i>An. coluzzii-Forest</i>	<i>An. coluzzii-Mopti</i>	<i>An. gambiae-Bamako</i>	<i>An. gambiae-Savannah</i>
12339	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12348	A	G/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
12420	T	C/-/-	24/0/0/0	11/0/0/0	13/1/0/0	12/0/0/0	11/0/0/0
12471	G	A/-/-	23/1/0/0	11/0/0/0	14/0/0/0	10/2/0/0	10/1/0/0
12480	A	G/-/-	24/0/0/0	10/1/0/0	14/0/0/0	12/0/0/0	11/0/0/0
12499	G	A/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12501	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12536	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
12558	T	C/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12601	T	TTA/-/-	24/0/0/0	10/0/0/0	14/0/0/0	12/0/0/0	10/1/0/0
12607	A	T/-/-	24/0/0/0	10/0/0/0	11/3/0/0	12/0/0/0	11/0/0/0
12633	G	A/-/-	23/1/0/0	9/1/0/0	12/2/0/0	11/1/0/0	10/1/0/0
12784	C	T/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
12890	T	C/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
12964	T	G/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
12967	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
13109	A	G/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
13123	G	A/-/-	22/2/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
13310	T	A/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
13311	T	C/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
13489	G	A/-/-	23/1/0/0	10/0/0/0	12/0/0/0	12/0/0/0	10/1/0/0
13579	T	C/-/-	24/0/0/0	11/0/0/0	11/0/0/0	12/0/0/0	10/1/0/0
13641	A	G/-/-	23/1/0/0	11/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
13683	C	T/-/-	24/0/0/0	11/0/0/0	12/0/0/0	11/1/0/0	11/0/0/0
13696	G	A/-/-	22/2/0/0	11/0/0/0	12/0/0/0	11/1/0/0	10/1/0/0
13741	G	A/-/-	23/1/0/0	11/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
13776	A	G/-/-	23/1/0/0	11/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
13876	A	G/-/-	24/0/0/0	10/1/0/0	12/1/0/0	12/0/0/0	11/0/0/0
13882	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
13941	A	AT/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/0/0/0
13943	T	A/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	10/0/0/0
13955	A	G/-/-	24/0/0/0	10/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
13989	T	C/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
14105	G	A/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
14115	G	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14194	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/1/0/0
14233	T	C/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14291	C	T/-/-	21/3/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14359	G	A/-/-	23/1/0/0	10/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14373	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14384	C	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
14439	A	G/-/-	21/3/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14454	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14536	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/1/0/0	11/0/0/0
14540	C	T/-/-	24/0/0/0	11/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
14543	T	C/-/-	24/0/0/0	11/0/0/0	13/0/0/0	12/0/0/0	10/1/0/0
14549	A	T/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14582	T	TTA/-/-	24/0/0/0	11/0/0/0	12/0/0/0	12/0/0/0	11/0/0/0
14602	T	C/-/-	24/0/0/0	9/2/0/0	12/1/0/0	11/1/0/0	11/0/0/0

Position	Reference nucleotide	Alternative nucleotides	SNP variant counts per group (first value is count of reference allele)				
			<i>An. arabiensis</i>	<i>An. coluzzii-Forest</i>	<i>An. coluzzii-Mopti</i>	<i>An. gambiae-Bamako</i>	<i>An. gambiae-Savannah</i>
14642	C	T/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14686	T	C/-/-	24/0/0/0	10/1/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14691	T	A/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14741	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0
14847	T	C/-/-	11/13/0/0	1/9/0/0	2/10/0/0	1/11/0/0	1/9/0/0
14875	A	G/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	10/0/0/0
14881	T	TA/-/-	24/0/0/0	11/0/0/0	11/1/0/0	12/0/0/0	9/0/0/0
14912	T	C/-/-	24/0/0/0	11/0/0/0	10/1/0/0	10/0/0/0	9/0/0/0
14916	C	T/-/-	23/1/0/0	11/0/0/0	11/0/0/0	10/0/0/0	8/1/0/0
14930	A	G/-/-	23/1/0/0	11/0/0/0	9/0/0/0	11/0/0/0	10/0/0/0
14936	A	G/-/-	24/0/0/0	11/0/0/0	9/1/0/0	11/0/0/0	11/0/0/0
14976	T,A	T/-/-	23/1/0/0	10/1/0/0	8/2/0/0	9/1/0/0	7/3/0/0
14978	A	C/T/	20/4/0/0	3/8/0/0	4/6/0/0	3/7/0/0	5/4/1/0
14984	A,T,T	TTT/AT/A	14/2/7/1	2/2/0/3	3/2/0/0	5/2/0/1	4/0/0/2
15002	A	T/-/-	22/2/0/0	5/2/0/0	4/1/0/0	3/5/0/0	4/2/0/0
15012	T	C/-/-	24/0/0/0	9/0/0/0	11/0/0/0	11/1/0/0	10/0/0/0
15035	T	TA/-/-	23/1/0/0	10/0/0/0	12/0/0/0	9/0/0/0	11/0/0/0
15036	A	G/-/-	24/0/0/0	10/0/0/0	12/0/0/0	9/0/0/0	9/2/0/0
15038	A	AATT/-/-	22/2/0/0	7/3/0/0	10/0/0/0	11/0/0/0	7/2/0/0
15039	A	G/-/-	24/0/0/0	10/0/0/0	10/0/0/0	7/4/0/0	8/1/0/0
15049	T	C/-/-	24/0/0/0	10/0/0/0	10/0/0/0	11/0/0/0	7/2/0/0
15050	T	TTA/-/-	23/1/0/0	10/0/0/0	10/0/0/0	11/0/0/0	9/0/0/0
15052	A	G/-/-	23/1/0/0	10/0/0/0	7/1/0/0	11/0/0/0	9/0/0/0
15057	C	T/-/-	23/1/0/0	10/0/0/0	8/0/0/0	8/0/0/0	9/0/0/0
15058	A	G/-/-	22/2/0/0	5/5/0/0	3/5/0/0	4/4/0/0	7/2/0/0
15066	T	C/-/-	23/1/0/0	10/0/0/0	10/0/0/0	11/0/0/0	8/0/0/0
15069	T	C/-/-	23/1/0/0	10/0/0/0	10/0/0/0	11/0/0/0	8/1/0/0
15082	A	G/-/-	22/2/0/0	10/0/0/0	10/0/0/0	11/0/0/0	8/2/0/0
15098	A	G/-/-	23/1/0/0	9/1/0/0	10/0/0/0	8/1/0/0	8/0/0/0
15115	T	C/-/-	21/3/0/0	8/1/0/0	8/2/0/0	8/1/0/0	8/0/0/0
15116	G	A/-/-	14/10/0/0	9/1/0/0	10/0/0/0	8/1/0/0	3/5/0/0
15128	A	G/-/-	23/1/0/0	8/1/0/0	6/1/0/0	8/0/0/0	7/0/0/0
15129	G	A/-/-	1/23/0/0	0/9/0/0	0/7/0/0	1/7/0/0	0/7/0/0
15144	T	A/-/-	24/0/0/0	10/0/0/0	13/0/0/0	11/1/0/0	11/0/0/0
15189	A	G/-/-	18/6/0/0	10/1/0/0	11/0/0/0	10/0/0/0	7/0/0/0
15243	T	C/-/-	15/9/0/0	10/1/0/0	7/1/0/0	7/0/0/0	6/0/0/0
15282	T	C/-/-	24/0/0/0	11/0/0/0	12/1/0/0	12/0/0/0	11/0/0/0
15301	C	A/-/-	24/0/0/0	11/0/0/0	12/1/0/0	11/0/0/0	11/0/0/0
15304	A	G/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/0/0/0	11/0/0/0
15305	T	TA/-/-	24/0/0/0	10/1/0/0	13/0/0/0	11/0/0/0	11/0/0/0
15321	C	T/-/-	23/1/0/0	11/0/0/0	11/2/0/0	11/0/0/0	11/0/0/0
15327	A	G/-/-	23/1/0/0	11/0/0/0	13/0/0/0	12/0/0/0	11/0/0/0

Figure 1. Phylogenetic tree inferred from mtDNA genome sequence data. With the exception of the outgroup, *An. quadriannulatus*, this analysis fails to reveal a clear division of the operational taxonomic units included in this analysis. Colors indicate the species or chromosomal form and numbers at the branches indicate the accuracy of the inferred branches on a scale of 0–100, where 100 represents the highest confidence.

Kenya, Mali, South Africa, Tanzania and Zimbabwe (Fontaine *et al.* (2015), supplemental material).

Of note, 36 of the samples that we used in our study originated from Kela (Mali). Kela is located near the village of Selinkenyi, where previous studies have shown a history of hybridization and introgression between *An. gambiae* and *An. coluzzii*

(Lee *et al.* (2013); Main *et al.* (2015); Norris *et al.* (2015)), which may have resulted in shared polymorphisms in their mitochondrial genomes. Shared polymorphisms in their mitochondrial genomes, where history has not been reported, also appeared to have occurred in Mutengene (Cameroon), where both *An. gambiae* and *An. coluzzii* occur sympatrically. Hybridization between either *An. coluzzii* or *An. gambiae* with *An. arabiensis*

yields sterile males (Slotman *et al.* (2004)), but phylogenomic analysis of these species show patterns of introgression between all of them (Fontaine *et al.* (2015)). Our mitochondrial genome study does not provide conclusive evidence for hybridization and introgression among the taxa under study. However, our data suggest that this is a possibility.

Data availability

Aligned sequences were submitted to the National Center for Biotechnology Information (NCBI) Accession number:

MG930826 - MG930896

Dataset 1. Aligned FASTA file of mitogenome samples [10.5256/f1000research.13807.d192892](https://doi.org/10.5256/f1000research.13807.d192892) (Hanemaaijer *et al.*, 2018)

Competing interests

No competing interests were disclosed.

Grant information

We thank University of California - Irvine, Malaria Initiatives (UCIMI) for their support.

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Acknowledgments

We thank Michelle Sanford for her assistance in the field collection in Cameroon in 2011. We thank Clare Marsden for providing the raw data of *An. arabiensis* samples.

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Current Peer Review Status:

Version 1

Reviewer Report 14 May 2018

<https://doi.org/10.5256/f1000research.15009.r33371>

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General comment

Phylogenetic analysis need to be improved, and the choice for NJ methods and JC model, justified in the article. There are several programs that have been largely employed for phylogenetic analysis, including for mitogenome data. The paper authored by Foster et al.¹ contains useful information about analyses that have been carried out for inferring phylogenetic relationships within Anophelinae mosquitoes. I strongly suggest authors to verify how analyses were done.

Sample collection

Authors - "The *An. gambiae* and *An. coluzzii* samples were collected as resting adults using mouth aspirators in Kela, Mali (11.88683°N, -8.44744°W) in 2012 and Mutengene, Cameroon (4.0994°N, 9.3081°W) in 2011."

Comment - Can you please give more details the micro environment where your specimens of *An. gambiae* and *An. coluzzii* were resting?

Authors - "Similarly, we did this for the *An. gambiae* Savannah and Bamako chromosomal forms. We used the same definitions and methods to characterize the chromosomal forms as in Lanzaro & Lee, 2013."

Comment - It is not clear to me if you examined the polytene chromosome of each specimen you identified as the Savannah, Bamako, Forest and Mopti forms. Please clarify.

Genome sequencing

Authors - "For the *An. coluzzii* and *An. gambiae* samples we used the same methods as described in Norris et al. (2015) and Main et al. (2015). For the latter species, libraries were created using the Nextera DNA Sample Preparation Kit (FC-121-1031) and TruSeq dual indexing barcodes (FC-121-103) (Illumina) and the samples were sequenced on an Illumina HiSeq2500 with 100-bp paired end reads."

Comment - Please add a short sentence to clarify if you sequenced the whole genome and from the full sequence data you obtained the positions 1-13,470 of the mitogenome.

Data analysis

Authors - "The phylogenetic tree was generated using the Jukes-Cantor genetic distance model and Neighbor-Joining tree methods available in Geneious version 10.1.3."

Comment - Authors should clarify their choice for sequence analysis. The Geneious software has been developed for editing and aligning DNA / amino acid sequences. There are several softwares, which have been largely used to infer phylogenetic relationships. I suggest authors to refining and improving the phylogenetic analysis using appropriate programs and models that have been chosen for the mitogenome data you have at hand.

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1. Foster PG, de Oliveira TMP, Bergo ES, Conn JE, et al.: Phylogeny of Anophelinae using mitochondrial protein coding genes. *R Soc Open Sci.* 2017; **4** (11): 170758 [PubMed Abstract](#) | [Publisher Full Text](#)

Is the work clearly and accurately presented and does it cite the current literature?

Yes

Is the study design appropriate and is the work technically sound?

Yes

Are sufficient details of methods and analysis provided to allow replication by others?

No

If applicable, is the statistical analysis and its interpretation appropriate?

Partly

Are all the source data underlying the results available to ensure full reproducibility?

Yes

Are the conclusions drawn adequately supported by the results?

Partly

Competing Interests: No competing interests were disclosed.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Reviewer Report 30 April 2018

<https://doi.org/10.5256/f1000research.15009.r32266>

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General comments

The present research note entitled: "Mitochondrial genomes of *Anopheles arabiensis*, *An. gambiae* and *An. coluzzii* show no clear species division" is well analysed, reported and written. As already reported in previous study the submitted manuscript suggested the absence of any species-specific differences in the mitogenome of the three species examined. Although the manuscript is not innovative and the research is not based on any previous evidence, the present note confirms previous suggestions by examining the whole mitogenome of 70 specimens from field specimens and find the lack of species or chromosomal form specific markers.

Title and abstract

Title and abstract are appropriate and summarize well the content of the article.

Introduction

The introduction gives a good description of the aims of the present study, although I would have added some references to previous studies performed on mtDNA of the examined species (for example Besansky 1997) and why you expected to obtain different results compared to previous studies.

Please revise also:

"morphologically identical species that can only be distinguished with molecular markers" (Scott *et al.*, 1993; Coetzee *et al.*, 2013)

The currently used molecular markers are located within genomic islands of divergence located proximal to the centromeres (Lee *et al.* (2014); Turner *et al.* (2005)) please rephrase the citation and refer it only to detect genomic differences between *An.gambiae* and *An.coluzzii*.

Please insert a sentence about chromosomal forms of *An.gambiae*.

Methods

Please specify the method for collecting *An. arabiensis* as you already described for *An.gambiae* (e.g. indoor specimens, mouth aspirators, PSC collections).

Please insert a table with inversion polymorphism of chromosomal forms analyzed.

Please add the source of the *An. quadriannulatus* specimens you included in the phylogenetic analysis.

Results

Study design is well explained and results are given concisely.

Please add in Table 2 also the number of specimens you included for each species in the analysis.

Please add in Figure two an explanation of what "lineage" means for *An. arabiensis* specimens.

Please give results (also without table or figure) for each country separately.

Discussion

Discussion is very concise but deals with most major points of interest. We would just suggest to explain better the conclusion on possible introgression (the more plausible hypothesis) between taxa and to evaluate other possible explanations for the absence of fixed differences between species (e.g. absence for divergent selection, or evolutionary characteristic of mitogenomes).

Is the work clearly and accurately presented and does it cite the current literature?

Yes

Is the study design appropriate and is the work technically sound?

Yes

Are sufficient details of methods and analysis provided to allow replication by others?

Yes

If applicable, is the statistical analysis and its interpretation appropriate?

Yes

Are all the source data underlying the results available to ensure full reproducibility?

Yes

Are the conclusions drawn adequately supported by the results?

Yes

Competing Interests: No competing interests were disclosed.

We confirm that we have read this submission and believe that we have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

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