rRNA encoding gene showed a high genetic similarity between *P. vivax* and *P. simium*, and between *P. malariae and Plasmodium brasilianum*, as demonstrated by other authors. This high identity is also observed in the phylogenetic reconstruction of isolates studied here. Three *loci* of microsatellite and two polymorphic blocks of PvMSP-1 showed that there is a great genetic diversity among the circulating parasites. The data from microsatellites will be also very useful for comparing recurrent infections in the same animal, to verify if they are the same chronic infection or a different one. The present results provide evidence that non-human primates may act as reservoirs for parasites of the genus *Plasmodium*, highlighting the potential of zoonotic transmission of the parasite in areas of the Atlantic forest, hamperin the elimination of malaria in the country.

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DRAMATIC CHANGES IN MALARIA POPULATION GENETIC COMPLEXITY IN DIELMO AND NDIOP, SENEGAL REVEALED USING GENOMIC SURVEILLANCE

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The challenges of calculating traditional estimates of malaria transmission in low transmission areas emphasize the need for exploring innovative strategies, including harnessing genomics. A simple genotyping tool comprised of 24 independent single nucleotide polymorphisms (SNPs) revealed changes in *Plasmodium falciparum* transmission dynamics across multiple years of intervention application in Thiès, Senegal, including declines and rebounds in transmission through epidemiological modeling of *R*0. We applied this tool to an extensive longitudinal collection in Dielmo and Ndiop Senegal, where determinants of malaria infection have been conducted for decades. Using blinded samples from two distant time-points in this longitudinal cohort, we applied the molecular barcode tool to detect changes in parasite genotypes related to changes in transmission intensity. The goal of this genetic surveillance study was to validate the molecular barcode as a tool to assess parasite population diversity changes related to transmission dynamics and to track parasite genotypes across space and time. We observed a striking difference in the genetic diversity between the two parasite populations. In one population, we detected a high percentage (50%) of polygenomic infections, no shared genotypes, and no previously detected genotypes. In the alternate population we detected only monogenomic infections, three shared parasite genotype clusters representing two-thirds (67%) of the population. Upon unblinding it was revealed that the first population was from 2001-2002 where EIR was high (~350 in Dielmo and 79 in Ndiop) and that the second population was from 2014 where EIR was low (26 in Dielmo and 0 in Ndiop). Using neighbor-joining tree analysis we found no strict clustering of barcodes suggesting that parasite genotypes were shared between Dielmo and Ndiop. However, when we compared these genotypes with over 1000 other Senegal parasite genotypes from distinct locales, we detected that one of the 2014 genotypes from Dielmo had been previously detected in Thiès, Senegal in 2007 and again in 2010, suggesting possible importation of malaria.

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SURVEILLANCE OF PFMDR1, PFATPASE SINGLE NUCLEOTIDE POLYMORPHISM (SNP) PREVALENT AMONG *PLASMODIUM FALCIPARUM* UNCOMPLICATED MALARIA CASES OF NORTHEAST INDIA (YEAR 2015) AS ANTIMALARIAL DRUG RESISTANT MARKER

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North east India is corridor to south east asian countries that historically remained first to report antimalarial drug resistance. Though Artemisinin combined therapy (ACT) is still effective in region but there is serious concern about progressive decline in parasite clearance rate to therapy. Study districts Mizoram, Meghalaya, Tripura are endemic with high proportion of *Plasmodium falciparum* malaria cases. Membrane transporter Pfmdr1 and Pfatp6 polymorphism is reported to be associated with lumefantrine and artemisinin tolerance respectively worldwide. Pfmdr1 86,184, 1246 codons and Pfatp6 codons 402, 431 polymorphism were studied by nested PCR, restriction fragment length polymorphism (RFLP) and Sanger sequencing techniques. There observed significant trend towards predominance of Pfmdr1 N86 allele among population since introduction of Artemether-Lumefantrine in year 2013. Pfatp6 codon L402V, E431K polymorphism was observed among 3/73 and 7/73 samples respectively. Predominance of Pfmdr1 N86 allele in malaria parasite isolates of north East India establishes its increased tolerance to lumefantrine. Insufficient pfatp6 polymorphism based reports from region limits to determine its efficacy as Artemisinin resistant marker. Continued molecular surveillance should take place to develop robust markers to track disease and to take timely action measures.

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PREVALENCE OF *PFMDR1* AND *PFK13* POLYMORPHISMS IN THREE PROVINCES IN ANGOLA, 2015

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Artemisinin-based combination therapy is the first-line anti-malarial treatment for uncomplicated *Plasmodium falciparum* infection in Angola. With the recent emergence of artemisinin resistance in the Greater Mekong sub-region and suspected lumefantrine resistance in Angola, it is important to characterize the background prevalence of polymorphisms in *pfk13*, associated with artemisinin resistance, and *pfmdr1*, associated with lumefantrine resistance. DNA was isolated from 506 dried blood spots collected at enrollment during the 2015 round of therapeutic efficacy studies in Benguela, Zaire and Lunda Sul Provinces in Angola. The *pfk13* propeller domain and *pfmdr1* segments were sequenced using the Sanger method and analyzed for polymorphisms. Additionally, *pfmdr1* copy number was assessed using a real-time PCR method. The majority of samples, 99% (413/416), were wildtype for *pfk13*, and all three non-wildtype samples (1%) carried the A578S mutation commonly observed in Africa and not associated with artemisinin resistance. The *pfmdr1* wildtype NYD haplotype (N86Y, Y184F, D1246Y) was predominant in all three provinces, with a frequency of 63% (133/209) of isolates in Benguela, 46% (105/227) in Zaire and 62% (69/109) in Lunda Sul, counting mixed infections as single infections. The NFD (N86Y, Y184**F**, D1246Y) haplotype, was found in 23% (49/209) of isolates in Benguela, 31% (72/227) in Zaire and 31% (35/109) in Lunda Sul. A total of 98% (497/506) samples were