Genetic Analysis of Erythrocyte Binding Antigen 175 (EBA-175), Apical Membrane Antigen (AMA-1) and Merozoite Surface Protein 3 (MSP-3) Allelic Types in Plasmodium Falciparum Isolates From Rural Area in Senegal

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Abstract

**Background:** Several of the intended *P. falciparum* vaccine candidate antigens are highly polymorphic and could render a vaccine ineffective if their antigenic sites were not represented in the vaccine. This study aimed to characterize genetic diversity of vaccine candidate antigens merozoite surface protein-3 (MSP-3), apical membrane antigen-1 (AMA-1) and erythrocyte binding antigen (EBA-175) in *P. falciparum* isolates from Senegal.

**Methods:** DNA analysis was completed on 170 isolates of *P. falciparum* collected from Keur Soce in Senegal between 2006 and 2008. Genetic diversity was determined in the three *P. falciparum* genes by, PCR followed by restriction fragment length polymorphism (RFLP).

**Results:** From 170 samples collected, successful, PCR products were obtained from 135 (79%), 140 (82%) and 129 (75%) for AMA-1, MSP-3 and EBA-175, respectively. The results showed that the EBA-175 gene presented 4 different alleles (EBA-175F loop (62.3%), EBA-175C loop (46.1%), EBA-175—400bp (17.6%), EBA-175—360bp (8.4%). Regarding the MSP-3 patterns, the analysis revealed the presence of three alleles MSP-3_K1 (49.2%), MSP-3—3D7 (54.2%) and MSP-3—350bp (15%). For AMA-1, the results showed three different alleles AMA-1_K1 (39%), AMA-1—HB3 (33%), AMA-1—3D7 (32%).

**Conclusion:** Characterization of the genetic diversity in *Plasmodium* isolates from Keur Soce in Senegal in the three genes investigated showed a high degree of polymorphism. These findings are helpful in the formulation of a vaccine considering restricted repertoire populations.

Keywords: Malaria; *Plasmodium falciparum*; Genetic diversity; MSP3; EBA-175; AMA-1; Vaccine

Background

Malaria remains a major public health problem in tropical regions. In most African countries such as Senegal, the vast majority of cases and deaths occur in young children [1]. Currently key interventions recommended by WHO for the control of malaria are the use of Insecticidal Treated Nets (ITNs) or Indoor Residual Spraying (IRS) for vector control, and prompt access to diagnosis and treatment of clinical malaria by using Rapid Diagnostic Test (RDT) and Artemisinin Combination Therapy (ACT) respectively [2]. For malaria prevention, an additional strategy such as Intermittent Preventive Treatment (IPT) is recommended specifically in risk group (pregnancy women and infancy) in area of high malaria transmission [2]. In areas of markedly seasonal malaria transmission, such as the Sahel and sub-Sahel regions of Africa, the main burden of malaria is in older children rather than infants, and the risk of clinical malaria is restricted largely to a few months each year [3,4]. In such areas, administration of IPT to children (IPTc) named seasonal malaria chemoprevention (SMC) 3 months to 5 years of age monthly during the seasonal peak in malaria is recently recommended by WHO [5]. All these strategies have met with some success due to the declining of malaria in many African countries such as Senegal, will probably be accomplished by the development of an effective vaccine in addition of vector control strategies [6]. The complexity of the malaria parasite life-cycle stages combined with an exuberant genetic diversity constitute major problem to the development of a successful malaria vaccine [7,8]. The antigen polymorphism greatly enhances the parasites ability to evade immune recognition, making it difficult to bring forth adequate responses against variants of the circulating parasite population [9]. Fluctuations in genetic diversity across transmission seasons can further complicate controlling the disease [10-12]. It is therefore important to understand the genetic diversity in polymorphic antigens in endemic populations before the introduction of any malaria vaccine, including the prevalence of different genetic variants and their natural dynamics. Several *P. falciparum* stage-specific antigens such as the erythrocyte binding antigen 175 (EBA-175), the apical membrane antigen (AMA-1) and the merozoite surface protein 3 (MSP-3) have been suggested as vaccine candidates through molecular epidemiological studies [13]. However, the comparative distribution of the malaria parasite genotypes circulating across a wide geographical endemic area provides important genetic information which could be helpful for malaria vaccines design. The AMA-1 is expressed in the late schizont
stage of the parasite and is required for both merozoite invasion of erythrocytes and sporozoite invasion of hepatocytes. Recombinant AMA-1 induces protective immune responses in mouse and monkey models of malaria [7,8] and both monochon and polyclonal antibodies to AMA-1 inhibit merozoite invasion of erythrocytes [9]. Antibodies raised against AMA-1 have been shown to block parasite invasion of human red blood cells. The main concerns related to AMA-1 as a vaccine candidate is the fact that Pfama-1 is highly polymorphic with most of polymorphisms occurring in domain I [10-13] making a broadly effective vaccine difficult to create. Plasmodium falciparum uses also a 175-kDa sialic acid binding protein ligand, known as erythrocyte binding antigen EBA-175, for erythrocyte invasion [14, 15]. EBA-175 is a potential vaccine candidate as it induces antibodies which inhibit malaria merozoite invasion. The gene encoding EBA-175 is well established to be dimorphic the FCR-3 (referred to as the F loop and CAMP (referred to as the C loop) strains of P. falciparum [16]. The role that dimorphism plays in host-parasite interactions (for example, potential difference in efficiency of red blood cell invasion between genotypes) remains unclear.

Another antigen that is considered as vaccine candidate for P. falciparum is the MSP-3 protein which is encoded by a single locus on parasite chromosome 10. MSP-3 is an important target for protective immunity as antibodies against it could also prevent erythrocyte invasion by merozoites [17]. Previous analysis of the MSP-3 gene from P. falciparum isolates shows that polymorphism in the gene is predominantly due to sequence in the N-terminal extremity within MSP-3 polypeptides [18]. The C-terminal domain (corresponding to amino acids 196–379 in the K1 allele sequence) is highly conserved among various parasites isolates [19]. There are several sequence differences among MSP-3 alleles, but the sequence polymorphism defined 2 major allele types (MSP-3_K1 and MSP-3_3D7), with only very limited recombination [20].

The purpose of this study is to determine in the context of malaria vaccine development, the diversity of three P. falciparum vaccine antigens candidate (AMA-1; EBA-175 and MSP-3) in Senegal. To accomplish this, Plasmodium falciparum field isolates collected from endemic area in Senegal during year 2006 to 2008 were used to assess the frequency of the major alleles of these three candidates vaccines antigens by PCR-RFLPs. Knowledge of the distribution of polymorphic malaria antigens may contribute to rational vaccine development.

Material and Methods

The study took place between 2006 and 2008 in the rural community of Keur Soce located some 200 km south-east of Dakar and 17 km south of Kaolack city in the center of Senegal. Malaria transmission in this locality is seasonal with entomological inoculation rates varying between 9 and 12 infected bites per person per night during the rainy season from September to November (unpublished data from Kanate L et al.). The population is about 20,415 inhabitants and 20% of the population is children under five years old. In this locality, malaria morbidity was 35% at high transmission season from September to November during our study period.

Samples collection

Samples were collected at Keur Soce rural area during a clinical trial study comparing once daily Artesunate plus Amodiaquine (AS/AQ) or twice-daily Artemether plus Lumeftantrine (AL) [21] from patients of any age with symptoms of uncomplicated P. falciparum malaria. A total number of 170 subjects infected with P. falciparum at day zero living in Keur Soce area were included in the study. Thick and thin blood films were done for P. falciparum microscopical identification. Whole blood from P. falciparum positive subjects were blotted on sterile, Whatman 3 MM filter paper and stored at room temperature protected with silica gel in individual plastic bags for P. falciparum DNA extraction.

Microscopic examination

Giemsa stained blood smears were microscopically examined to identify mono-infections with P. falciparum. The slides were independently examined by two experienced microscopists. An individual was considered positive if malaria parasites were detected in the blood smear and negative if parasites were not detected after examining 200 oil-immersion fields of the thick smear. The parasite density was determined by multiplying the number of parasites present per 200 white blood cells in a thick smear by 40 to arrive at an approximate parasite count per microliter of blood. This was based on the assumption that the average WBC count was 8,000/l blood.

P. falciparum DNA extraction

Extraction of P. falciparum DNA from positive filter paper was carried out by means of the QIAmp DNA blood mini kits (manufacture Qiagen, www.qiagen.com/gDNA). Extraction via the Qiagen kit method followed the manufacturers’ protocol [22]. All DNA samples were stored at -20°C for PCR genotyping.

PCR amplification

Nested and semi-nested polymerase chain reaction (PCR) methods were applied to analyze polymorphism of EBA-175 and MSP-3 respectively [23]. The 50 μl of EBA-175 or MSP-3 outer PCR mixture consisted of 4 μl of extracted DNA, in 13 μl of water, 2.5 μl of 1X buffer, 1.0 μl of 2.0 mM MgCl₂, 1.5 μl of 200 μM dNTP mix, 2 μl of primers [[159F/745R for MSP-3] or (EBA1 /EBA1 for EBA-175)] and 1 unit of Platinum Taq polymerase. For the nested and semi-nested mixture, 2.5 μl of outer of each reaction and the primers set EBA3/ EBA4 and 188F/745R was used for EBA-175 and MSP-3 respectively. Genomic DNA preparation K1 and 3D7 were included as references for both genes.

The ama-1 haplotypes were analyzed by PCR-RFLP method [24]. The 50 μl of AMA-1 outer PCR mixture consisted of 4 μl of extracted DNA, 34 μl of water, 5 μl of 1X buffer, 2.0 μl of 2.0 mM MgCl₂, 2 μl of 200 μM dNTP mix, 2 μl of primers VM785/3 /VM990 and 1 μl of primers VM815/3/VM990 was used for both genes.

All the reactions were performed using PCR 96 wells micro-plates (sigma manufacture, www.sigma.com) on a classic Thermocycler 96 wells (PTC-100). Primers sequences of each gene for the outer and nested PCR and cycling conditions were listed in Table 1.

P. falciparum AMA-102, MRA-149, MRA152, MRA153, MRA157, MRA 159, MRA 176 and MRA731 lines provided by MR4 (www.mr4.org) were used as positives controls during the amplification reactions. The nested PCR products were directly separated on a 2.0% ethidium bromide stained agarose gel and visualized on GEL LOGIC 220 UV-translumination cabine. 12 μl of the nested AMA-1 product
was digested with 4 μl of the three different restriction enzymes: MseI, SspI, and BfuCI specific to 3D7, K1 and HB3/7G8 AMA-1 haplotypes groups respectively.

### Table 1: List of Primers sequences and cycling conditions.

<table>
<thead>
<tr>
<th>Primer name</th>
<th>Sequence length 5’-----3’</th>
<th>Conditions cycling</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>EBA-175</strong>&lt;br&gt; 1st round&lt;br&gt; 2 hrs 10 m</td>
<td>EBA1:&lt;br&gt; CAAGAAGGCATTCTGGAGGAA&lt;br&gt; EBA2:&lt;br&gt; TCTCAACTGTCATTAATACAA TTC</td>
<td>94°C x 1:30m 68°C x 2:0 m aides cycles 68°C x 5 m 4°C x Hold</td>
</tr>
<tr>
<td><strong>EBA-175</strong>&lt;br&gt; 2nd round&lt;br&gt; 2 hrs 20 m</td>
<td>EBA3:&lt;br&gt; GAGGAAAACACTGAAATAGCAAC&lt;br&gt; EBA4:&lt;br&gt; CAATCTCTCCAGACTTGGAACTAT</td>
<td>94°C x 1:30 m 94°C x 30 s 54°C x 30 s, 68°C x 2:0 m aides cycles 68°C x 5 m 4°C x Hold</td>
</tr>
<tr>
<td><strong>MSP 3</strong>&lt;br&gt; 1st round&lt;br&gt; 2 hrs 45 m</td>
<td>VM785/3:&lt;br&gt; CCGGATCCCCTCTTGAGTTTACAT ATG&lt;br&gt; VM990:&lt;br&gt; AATTCTTTCTAGGCCAAC</td>
<td>94°C x 1:30 m 94°C x 30 s, 54°C x 30 s, 68°C x 2:0 m aides cycles 68°C x 5 m 4°C x Hold</td>
</tr>
<tr>
<td><strong>MSP 3</strong>&lt;br&gt; 2nd round&lt;br&gt; 3 hrs</td>
<td>VM815/3:&lt;br&gt; GGAACCTAAATAGACTTCC&lt;br&gt; VM990:&lt;br&gt; AATTCTTTCTAGGCCAAC</td>
<td>95°C x 2:30 m 94°C x 30 s, 51°C x 30 s, 68°C x 45 s aides cycles 68°C x 5 m 4°C x Hold</td>
</tr>
</tbody>
</table>

### Statistical analysis

Allelic data were entered in Microsoft Excel format and exported to Epi Info 6.04a (http://www.cdc.gov/epiinfo/Epi6/EI6dnjp.html) for analysis. The data comparisons were made using the Chi square or Fisher’s exact test, or Student’s t-test data with a statistical significance threshold of p<0.05.

### Ethical considerations

Ethical clearance from the Conseil National de Recherche en Santé (National Council for Health Research) in Senegal was obtained (SEN42/06), and a signed informed consent from the parent or the child legal guardian was required prior to blood sample collection.

### Results

**Patient characteristics**

A total of 601 patients were screened. Out of these patients 170 were *P. falciparum* positive and meet the inclusion criteria. Patient characteristic are consign in Table 2.

<table>
<thead>
<tr>
<th>2006 (n=288)</th>
<th>2008 (n=313)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Malaria prevalence, n (%)</strong></td>
<td>101 (35.0)</td>
<td>69 (22.0)</td>
</tr>
<tr>
<td><strong>Sex, male n (%)</strong></td>
<td>55 (44.4)</td>
<td>36 (52.1)</td>
</tr>
<tr>
<td><strong>PD: Geometric mean</strong></td>
<td>31713.7 ± 37253</td>
<td>37253 ± 37253</td>
</tr>
</tbody>
</table>

Table 2: Patient characteristics; PD: Parasite density.

### PCR efficacy

Overall 170 *P. falciparum* mono-infection parasites isolated confirmed by microscopy and collected in Keur Soce area (Senegal) were used for DNA extraction. Out of these, 101 samples were collected in 2006 and 69 in 2008.

Out of the 170 *P. falciparum* isolates, 79% [135/170; n=77 (2006); n=58 (2008)], 82% [140/170; n=83 (2006); n=57 (2008)] and 75% [128/170; n=76 (2006); n=52 (2008)] were successfully analysed for Eba-175, MSP-3 and AMA-1, respectively. PCR negative samples were excluded from further analysis.

### Size polymorphism and alleles frequencies

At each locus different types of alleles found were analysed to assess their frequencies. Based on the molecular weight of amplicons, the isolates were classified according to the two allelic type of EBA-175 (F-loop and C-loop), the two allelic type of MSP-3 (K1 and 3D7) and the three allelic types of AMA-1 (K1, 3D7 and HB3).

The analysis of the EBA-175 dimorphic alleles showed that F-Loop was predominant [EBA-175 F-loop (62.3%), EBA-175 C-loop (37.7%)] (p=0.008) Figure 1. In addition of the two main alleles, we noted frequencies of 15% and 5% for EBA-175 400 bp and EBA-175 360 pb respectively in the study area.

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For MSP-3 alleles results showed frequencies of 49.2% and 54.2% for K1 and 3D7, respectively. In addition, excepted the high frequency observed in MSP3_350 bp allele (15%), no statistically significant difference was observed in the major (K1 and 3D7) MSP-3 alleles frequencies (p=0.40).

For AMA-1 pattern, results showed a comparable frequency between the three main AMA-1 alleles identified in this study. We found 39%, 33% and 32% for AMA-1_K1, AMA-1_Hb3 and AMA-1_3D7 alleles respectively. No significant difference was observed in the AMA-1 allele frequencies (p=0.46).

**Plasmodium falciparum genetic diversity**

The results showed that the EBA-175 gene presented 4 different alleles identified. The two main alleles [F loop (60%) and C_loop (46%)] are more frequent. But the other alleles found (EBA-175_400 bp, EBA-174_360 bp) had frequencies higher than 5% in the parasite population (Figure 1).

![Figure 1: Allele frequencies of EBA-175.](image)

Regarding the MSP-3 patterns, the analysis revealed the presence of 3 different alleles in Keur Soce study population: MSP-3_K1 (50%), MSP-3_3D7 (54%) and MSP-3_350 pb (14%) (Figure 2).

![Figure 2: Allele frequencies of MSP-3.](image)

For AMA-1 pattern, the three main alleles are found. Analysis of AMA-1 alleles showed comparable frequencies between the three main alleles found. More than 30% for all AMA-1 alleles identified in our study [AMA-1_K1 (39%), AMA-1_3D7 (32%) and AMA-1_Hb3 (33%)] was found (Figure 3).

![Figure 3: Allele frequencies of AMA-1.](image)

**Haplotype frequencies over time**

For EBA-175 pattern, the haplotype single allele was more frequent than the haplotype with two or three alleles over year (Table 3). The difference was significant from 2006 to 2008 (p=0.003) while EBA-175 haplotype two alleles, showed no significant difference between 2006 and 2008 (p=0.020). The haplotype with three alleles was missed in 2008.

<table>
<thead>
<tr>
<th></th>
<th>2006</th>
<th>2008</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>EBA-175_1allele</td>
<td>51 (66.23%)</td>
<td>47 (88.68%)</td>
<td>0.003</td>
</tr>
<tr>
<td>EBA-175_2alleles</td>
<td>22 (28.57%)</td>
<td>6 (11.32%)</td>
<td>0.020</td>
</tr>
<tr>
<td>EBA-175_3alleles</td>
<td>4 (5.20%)</td>
<td>0 (0.00%)</td>
<td></td>
</tr>
</tbody>
</table>

Table 3: frequency of different haplotypes of EBA-175.

Regarding MSP3 pattern, the MSP-3_1 allele was also more frequent than the MSP-3_2 alleles with no significant difference between 2006 and 2008 (p=0.028) (Table 4). For haplotype MSP-3_2 alleles, results showed that, these haplotype was more frequent in 2006 than in 2008 with no significant difference (p=0.028). The MSP-3_3 alleles were missed in our study.

<table>
<thead>
<tr>
<th></th>
<th>2006</th>
<th>2008</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>MSP3_1allele</td>
<td>66 (70.5%)</td>
<td>53 (92.9%)</td>
<td>0.028</td>
</tr>
<tr>
<td>MSP3_2alleles</td>
<td>17 (20.5%)</td>
<td>4 (7.0%)</td>
<td>0.028</td>
</tr>
</tbody>
</table>

Table 4: frequency of MSP-3 haplotypes.

**Discussion**

The malaria parasite was shown to exhibit extensive genetic diversity, particularly in the surface antigens that have been under selective pressure and historically considered as the targets of subunit
vaccines. Unfortunately, this extreme genetic diversity poses a big challenge for an effective vaccine development as it could lead to "vaccine-resistant malaria" with non-vaccine type parasites in vaccinated individual [8]. Therefore, to make the vaccine more efficacious against any natural P. falciparum infection, multiple allelic forms of an antigen may need to be incorporated in a vaccine formulation [10,25].

The present study based on the assessment of the genetic diversity of malaria vaccine candidates (EBA-175, MSP-3 and AMA-1) in Keur Soce area (Senegal), provides a pre-vaccine, baseline data of the distribution of major allelic classes.

Here the study reported evidence of the presence of the main allele types of EBA-175 (F-loop and C-loop), MSP-3 (K1 and 3D7) and ama-1 (K1, 3D7 and HB3) at high frequencies. But when looking at the individual loci and the corresponding alleles, it emerges clearly that substantial differences exist in the allelic distributions between other countries. Overall, for eba-175 gene, our results showed that the F-loop was the predominant allele. These results were similar to the previous observations made in comparable area [26]. This trend in EBA-175 allelic form distribution in keur socé confirmed the previous report in Central and Southern Senegal [25].

The analysis of the polymorphic sequence of MSP-3 gene which present many amino acid substitutions leading to the two major allele types (K1 like and 3D7 like) [27]          is of interest to determine how a vaccine candidate antigen that is polymorphic in nature and under immune selection was distributed in such malaria endemic area. These two major allelic types showed comparable frequency in our study area. In addition to the major dimorphic alleles (K1 like and 3D7 like), the presence of MSP-3_350 bp in our study showed that MSP-3 gene is a polymorphic gene [28]. The predominance of the two major allele types (K1 like and 3D7 like) noted in our study confirmed previous studies results showing that the major dimorphic alleles of MSP-3 were maintained in the species, intact within populations with low level of recombination [29].

Regarding AMA-1 gene, P. falciparum isolates from our study belonged to three (3D7, K1 and HB3) of the four groups of alleles previously identified based on the hypervariable region (HVR) of AMA-1(4). The fourth group alleles was not identified because in our study we used only three restriction enzymes, specific to the first three allelic groups which difference may probably pose a problem for a vaccine based on this antigen. Although a remarkable conservation of the AMA-1 molecules were previously reported [11], it is very important to understand the extent to which variation in AMA-1 gene may compromise vaccine development.

Conclusion

The main allelic families found in other African countries were also found in Keur Soce area. These major allelic families circulating (in Keur Soce area should be considered for the successful malaria vaccine in Senegal.

Conflict of interest

No conflict of interest was noted.

Author’s contribution

MN conceived the study, designed the experiments and carried out the molecular genetic analysis. BF supervised the study and corrected the manuscript. RT performed the statistical analysis. AL and AA participated on samples collection. OG coordinated the study and provided conceptual advice. All the authors read and approved the final manuscript.

Acknowledgements

We would like to express our gratitude to all study participants, particularly the Keur Soce population and administrative authorities, the entire staff of the Parasitology and Mycology Department. My sincere thanks also go to MR4 staff (ATCC_, Manassas, VA, USA) for providing us with malaria parasites, primers.

References

2. WHO Policy recommendation on Intermittent Preventive Treatment during infancy with sulphadoxine-pyrimethamine (SP-IPTi) for Plasmodium falciparum malaria control in Africa March 2010.


