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Human Candidate Polymorphisms in Sympatric Ethnic Groups Differing in Malaria Susceptibility in Mali

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Abstract

Malaria still remains a major public health problem in Mali, although disease susceptibility varies between ethnic groups, particularly between the Fulani and Dogon. These two sympatric groups share similar socio-cultural factors and malaria transmission rates, but Fulani individuals tend to show significantly higher spleen enlargement scores, lower parasite prevalence, and seem less affected by the disease than their Dogon neighbours. We have used genetic polymorphisms from malaria-associated genes to investigate associations with various malaria metrics between the Fulani and Dogon groups. Two cross sectional surveys (transmission season 2006, dry season 2007) were performed. Healthy volunteers from the both ethnic groups (n=939) were recruited in a rural setting. In each survey, clinical (spleen enlargement, axillary temperature, weight) and parasitological data (malaria parasite densities and species) were collected, as well as blood samples. One hundred and sixty six SNPs were genotyped and 5 immunoassays (AMA1, CSP, MSP1, MSP2, total IgE) were performed on the DNA and serum samples respectively. The data confirm the reduced malaria susceptibility in the Fulani, with a higher level of the protective O-blood group, and increased circulating antibody levels to several malaria antigens (p<10-15). We identified SNP allele frequency differences between the 2 ethnic groups in CD36, IL4, RTN3 and ADCY9. Moreover, polymorphisms in FCER1A, RAD50, TNF, SLC22A4, and IL13 genes were correlated with antibody production (p-value<0.003). Further work is required to understand the mechanisms underpinning these genetic factors.

Introduction

Malaria remains the major public health problem in more than 90 countries inhabited by more than 40% of the world’s population, with at least one million deaths every year. More than 90% of all malaria cases occur in sub-Saharan Africa [1]. In Mali, there are over 800,000 recorded cases of malaria among the 14 million people affected worldwide every year, and it accounts for 17 percent of child deaths overall [2]. It is therefore a major burden for the public health system, where prevention, treatment and control measures are administered by the Ministry of Health.

Malaria is a complex disease with many genetic and environmental determinants influencing the natural variation in
response to infection, progression and severity. Several factors are important for the different phenotypes observed, such as parasite genetic make-up, and host age, state of immunity and host genetic background [3]. There are differences in malaria infection and susceptibility between ethnic groups. In the Gambia and Nigeria, studies have indicated that the Fulani ethnic group has a higher frequency of splenomegaly than other sympatric groups despite similar exposure [4,5]. In Burkina Faso, a similar study showed that the Fulani have lower parasite incidence, higher levels of humoral immune responses to a variety of malaria parasite antigens than Rimaibe and Mossi living in the same area [6,7]. There are also inter-ethnic differences in susceptibility to malaria between the two sympatric groups from Manterou in Mali, namely the Fulani (also known as Peulh) and Dogon [8]. In particular, the Fulani, tend to develop larger spleens, have lower parasite densities and malaria prevalence than Dogon. The classical genetic markers involved in malaria resistance, such as haemoglobin C (Hbc) and S (Hbs) (in the HBB gene), glucose-6-phosphate dehydrogenase (G6PD) and blood group polymorphisms [9], are not sufficient to explain the differences between Fulani and Dogon.

The main advantage of studying sympatric populations is that geographical, environmental and epidemiological factors are either the same or very similar between the groups, and therefore it is believed that differences is the adaptation to the environment may arise genetically [10]. Given the observations from Burkina Faso and Mali of lower infection rates and higher anti-malarial antibody levels in the Fulani compared to other sympatric populations living in neighbouring villages [6,7,11], one can hypothesize that there are genetic factors affecting the underlying the humoral immune response to malaria. In Mali, the Fulani ethnic group also shows a higher level of anti-malarial humoral immune responses to a variety of Plasmodium falciparum malaria antigens (CSP, AMA1, MSP1, MSP2) in a context of similar malaria exposure [8]. Some of the genes underlying these immune responses, particular those mediated by inflammatory cytokines, have been associated with susceptibility/resistance to severe malaria. These include genes underlying cytokine production (e.g. TNF, LTA, interleukins IL3, IL4, IL5, IL13, IL10, and interferon-γ) (reviewed in 12). Other genes relevant to innate immunity have also been reported, and include Toll-like receptors (TLR-2, 4, and 9) [13]. The chromosomal region 5q31–33 contains many of the genes above, as well as others related to cytokines, growth factors and their receptors. By comparing the polymorphisms in these genes, it will allow an assessment of differences in allele frequency between the Fulani and other sympatric populations.

In this study, we investigated a set of polymorphisms from candidate genes linked to antibody production, malaria susceptibility and resistance, in the Fulani and Dogon ethnic groups in Mali, West Africa. This study consists of 939 subjects genotyped at 166 single nucleotide polymorphisms (SNPs) from genes involved in known malaria resistance (e.g. HBB, G6PD), cytokine production (e.g. TNF, LTA, IL1, 3, 4, 5, 7, 10, and 13), innate immunity (e.g. TLR 4,9) and the 5q31-33 region (117 SNPs). The polymorphisms were correlated with antibody levels to four P. falciparum antigens (CSP, AMA1, MSP1, MSP2), which have been used as candidates in vaccines trials. Ethnic differences in SNP allele frequencies and antibody levels on clinical phenotypes, such as spleen enlargement, parasitaemia and malaria outcome, are also assessed.

Materials and Methods

Study participants

The study was performed in a rural village of Manteourou, 875 km from Bamako, where people from the Dogon and Fulani ethnic group live together in sympathy. This village lies within the region known as the African Sahel. This region is characterized by a dry season from October to May and a rainy season from June to October [8]. The two groups live within 0.5 km of each other where the Dogon (n=505, 53.8%) are farmers who migrated from Bandiagara (110 km) to their present location 50 years ago, while the nomadic Fulani (Fulani, n=434, 46.2%) are cattle breeders who migrated 200 years ago from the area of Douentza situated 150 km from the study area. Cultural and ethnic differences mean that there are no inter-marriages between these two ethnic groups. According to the general census before the study began, the population size was estimated to be ~5000 inhabitants with 50% Dogon, 45% Fulani and 5% other ethnicities (Rimaibe, Mossi). The way subjects are recruited is described in Diallo DA et al. 2005 [14]. Two cross sectional surveys were performed, the first at the end of the transmission or rainy season (October/November 2006) and the second during the dry season (March/April 2007). The study included unrelated healthy volunteers, children and adults, males and females, belonging to both ethnic groups. At each survey, we have collected clinical (spleen enlargement, auxillary temperature, body weight) and parasitological data (malaria parasite densities and species) as well as blood samples.

Clinical information

Auxiliary temperature and spleen size were measured in all participants. The spleen size was scored by Hackett’s method and dichotomized as enlarged or not enlarged [15]. Thick blood smears were collected and stained with 3% Giemsa and examined for malaria parasites. Parasites and leukocytes were counted. Parasite densities were estimated using an assumed leukocyte count of 7500 leukocytes per microlitre of blood [8]. A film was determined to be negative if no parasites were identified in the course of examining sufficient fields for a total of 300 leukocytes to be counted. Quality control through double reading was also conducted on 10% of the slides randomly selected by a separate physician. Parasitaemia was defined as being present or absent. Clinical (mild) malaria was defined as the presence of fever (auxillary temperature of at least 37° 5C) accompanied by detection of P. falciparum parasites on a thick blood smear, in the absence of any other known illnesses. Asymptomatic malaria was defined as the presence of P. falciparum parasites, but no clinical symptoms. As this is a cross-sectional survey there are no severe malaria cases of malaria. Volunteers were followed-up for malaria incidence by active and passive methods by the research team, which
included a physician and biologist based in the health center of the village of Manteourou.

Genotyping and immunoassays

All Genomic DNA samples (n=939) underwent whole genome amplification through either Primer Extension Pre-amplification (PEP) [16] before genotyping using the Sequenom iPLEX MassArray platform [17,18]. One hundred and sixty-six single nucleotide polymorphisms (SNPs), predominantly located in genomic regions of malaria candidate genes (e.g. sickle cell polymorphism HbS) were designed into 5 multiplexes. A full list of SNPs typed can be found in Tables S1 and S2.

Serum was separated from the clotted blood samples by centrifugation (12,000 rpm for eight minutes) and analysed by ELISA for antibodies against four malarial antigens (AMA1, MSP1<sub>10</sub>, MSP2, CSP) and total IgE. Fifty microlitres of each antigen at a dilution of 0.5 µg/mL (for AMA1 [3D7], MSP2 [3D7] and IgE) or 1 µg/mL (for MSP1 [Wellcome genotype] and NAP [NANP]) were coated on ELISA plates (Immulon4 ELISA plates/Dynatech), and incubated at 4°C overnight. Plates were washed 3 times with PBS-0.05% Tween 20 (PBS/T) before adding 200 µL of blocking solution (2% skimmed milk in PBS/T) and then incubated for 3 hours at ambient temperature before washing 3 times with PBS/T. Serum samples were added in duplicate and incubated overnight at 4°C. Following washing 6 times with PBS/T, 50 µL of horseradish peroxidase-conjugated rabbit anti-human IgG (DAKO) diluted 1/5,000 in PBS/T was added and incubated for three hours at room temperature. The plates were again washed 6 times with PBS/T and OPD substrate solution (100 µL/well) was added and left at room temperature for 10 to 15 minutes for the assay to develop. Twenty-five microlitres of H<sub>2</sub>SO<sub>4</sub> (2M) were added to stop the reaction and the plates were read at 492 nm in an ELISA reader. The cut-off value of the assay was determined by calculating the arithmetic mean of the absorbance of negative control samples obtained from European individuals who had never been exposed to malaria and adding three standard deviations to that value (mean OD +3SD). Using standard positive (Brefet4 pool [19], 0 and negative controls (European pool), the positive-negative threshold baseline was constructed using OD values obtained upon ELISA and was used for calculation of the observed antibody titres as described previously [20]. The titre values were log<sub>10</sub> transformed to symmetrise them for regression analysis.

Ethical clearance

The study was given ethical clearance from the Institution Committee on Ethics of the Mali School of Medicine Pharmacy and Dentistry at the University of Bamako. Community informed consent was obtained before the beginning of the study. Individual oral consent was also obtained for each examination or blood collection from adults or the parents or guardians of children. The ethical clearance was obtained through the Institutional Review Board of the Malian School of Medicine Pharmacy and Dentistry at the University of Mali. Treatment for malaria and other illnesses detected during the course of the study was provided to the study population at no cost to participants. Community permission was obtained according to the procedures described by Diallo et al., in CID 2005 [14]. Individual written consent was then obtained for each exam or blood collection from the adult or from the child’s parent or care-givers.

Statistical analysis

All clinical and meta-data were double-entered from a case-report form, and underwent range checks, where any outlier was checked with written records and site staff. Mann-Whitney-Wilcoxon sum-rank tests were used to assess overall ethnic differences with continuous background (e.g. age in months) and phenotypic (e.g. immunological titres) variables. Similarly, Pearson’s χ<sup>2</sup> independence tests were applied to categorical variables (e.g. age group, parasite positivity). Genotypic deviations from Hardy-Weinberg equilibrium (HWE) were assessed using a χ<sup>2</sup> statistical test. SNPs were excluded from analysis if they had at least 10% of genotype calls missing or there was significant deviation from HWE (p<0.0001). The SNP association analysis for the (binary) malaria and clinical phenotypes used a logistic regression model including age group and season as covariates. The AMA1, MSP1, MSP2, CSP assay results were logarithmically (base 10) transformed in order to obtain Gaussian distributions approximately (see Figure S1). The association analysis for continuous (log<sub>10</sub> transformed) immunological titre phenotypes used linear regression models, which included age group and season as covariates. In all regression models, SNP data were included by fitting a series of genetic models (additive, dominant, recessive, heterozygous advantage, and general), and the minimum p-value reported. Performing multiple statistical tests leads to inflation in the occurrence of false positives. In our setting a Bonferroni correction would be too conservative because many of the SNPs are from a chromosome 5 region and the same genes. We applied a permutation approach that accounted for the correlation between tests, and estimated that a p-value cut-off of 0.003 to ensure a global significance level of 5%. All association analyses were performed on each ethnic group separately. The Fst metric [21] was used to assess the degree of genetic differentiation (0 = no differentiation, 1 = complete differentiation) between the Fulani and Dogon ethnic groups. All analyses were performed using the R statistical software (http://www.r-project.org).

Results

The study enrolled 939 participants of which 53.8% were Dogon and 46.2% are Fulani (Table 1). Data from each ethnic group was reasonably matched for age, gender and seasonal distribution (all p-values at least 0.05). However, there was a significantly higher number of O blood individuals (known to be protective against malaria [9]) in the Fulani (56.5%) compared to Dogon (43.7%). Similarly, there was a higher frequency of the HbC A allele in the Dogon (3.8%) compared to the Fulani (0.6%) (P<0.001), and less clinical malaria cases in the Fulani (6.9% vs. Dogon 12.5%, P=0.02). All immunoassays showed greater median (geometric mean) levels in the Fulani (Table 1,
Figure S2), with all being statistically significant (P<0.001) in overall analysis, except total IgE (P=0.02). Multivariate analysis of immunoassays adjusting for age and season, did not change this result. Measures of infection rate, including hyperparasitemia (p<0.005) and parasite density (P <0.005) were significantly higher in Dogon compared to Fulani. Malaria parasite positivity was marginally lower among the Fulani (16.5%) than among the Dogon (21.6%). The proportion of persons with enlarged spleen was significantly (P < 0.001) higher in the Fulani (30.7%) than in the Dogon (8.8%) (see Table 1). Similar results were obtained after adjusting for age, gender and season (data not shown).

We compared the study characteristics between rainy and dry seasons (Table S3). As expected, parasite positivity was higher in the rainy season (30.6% versus 0.0%). There was ~70% reduced prevalence of spleen enlargement in the dry season (odds ratio (OR) 0.305, 95% CI 0.209-0.447, P<10^{-5}, adjusting for ethnicity and age). CSP, AMA1 and IgE titres show no differences between seasons, but MSP1 and MSP2 were significantly lower during the dry season (P<10^{-5}, adjusting for ethnicity and age). There were modest (Spearman) correlations between the AMA1, CSP, MSP1, and MSP2 immunoassay measurements (median: 0.439, min. 0.266, max. 0.525), and less between these assays and total IgE (median: 0.163, min. 0.148, max. 0.190) (Table S4). There were low percentages of missing genotype data in each ethnic group (median 5%). Using the 126 SNPs with low missing genotype data and with minor allele frequency of at least 2%...
the degree of population differentiation between the ethnic groups was small ($F_{st}$; median 0.013, range 0.000-0.428). The rs3211938 polymorphism (CD36-aa325Y/stop [22]) had the maximum $F_{st}$ (G allele frequency: Dogon 0.680 vs. Fulani 0.477), with four others greater than 0.1 (rs2243250, IL4, $F_{st}=0.229$; rs542998, RTN3, $F_{st}=0.150$; rs2243251, IL4, $F_{st}=0.140$; rs10775349, ADCY9, $F_{st}=0.105$) (see Table S5 for all results).

There were no strong effects of immunological variables on clinical outcomes ($P<0.03$) (see Table S6, adjusted for age and season) across each ethnic group. Increasing age was associated with reduced risk of parasite positivity ($P<10^{-6}$), but not with spleen enlargement ($P=0.133$). We then considered the role of the polymorphisms on malaria outcomes, spleen enlargement and parasite positivity in each ethnic group (adjusted for age and season) (see Figure 1, Table 2 for significant results, Table S7 for all results). The rs3091336 (IL3) polymorphism was associated with asymptomatic and any malaria in the Dogon (Asymptomatic OR 4.543, 95% CI 1.900-10.864, $P=0.0007$), whilst the rs2304081 (SLC22A4) SNP was associated with these phenotypes in the Fulani ethnic group (Any malaria OR 0.334, 95% CI 0.175-0.635, $P=0.0004$). For clinical malaria, only significant associations were found in the Fulani (rs17047661 (CR1), OR 5.327, 95% CI 1.973-16.376, $P=0.0008$; rs2075820 (NOD1), OR 0.364, 95% CI 0.188-0.704, $P=0.001$). The rs1128127 polymorphism (DERL3 gene) in the Dogon group was the only SNP associated with spleen enlargement (OR 0.437; 95% CI 0.257-0.741, $P=0.0014$). Whilst there were five polymorphisms associated with parasite positivity: (i) rs17047661 (CR1, Fulani OR 2.874, 95% CI 1.505-5.487, $P=0.0008$); (ii) rs2304081 (SLC22A4, Fulani OR 0.277, 95% CI 0.120-0.639, $P=0.001$); (iii) rs3212227 (IL12B, Dogon OR 2.475, 95% CI 1.399-4.381, $P=0.0014$); (iv) rs569108 (MS4A2, Dogon OR 0.466, 95% CI 0.288-0.755, $P=0.0011$); and (v) rs10775349 (ADCY9, Fulani OR 2.471, 95% CI 1.355-4.506, $P=0.0027$). A combined analysis (adjusting for ethnicity) identified no polymorphisms associated with spleen enlargement, but one with parasite positivity (rs3212227, IL12B, GT genotype vs. other OR 1.930, 95% CI 1.230-2.7219, $P=0.0027$). These effects did not change markedly with adjustment for immunological assay data (results not shown).

The effect of the candidate genetic polymorphisms on the immunological assays was considered (adjusted for season and age, Figure 2, Table 3 for significant results, Table S8 for all results). The associations detected ($P<0.003$) include: (i) CSP (rs2251746, FCER1A gene, Dogon; rs3148, IL3, Fulani; rs1800629 (TNF-308), Dogon; rs3093662, TNF, Dogon), (ii) AMA1 (rs739718, IL5, Dogon), (iii) MSP1 (rs2304081, SLC22A4; rs2077022, IRF1; rs739718, IL5; rs2239704, LT; rs1799964, TNF; all Fulani hits), (iv) MSP2 (rs5743809, TLR6, Dogon; rs35415145, IL3, Fulani; rs1799964, TNF, Fulani; rs1012356, IL22, Dogon), and (v) total IgE (rs31481, IL3, Fulani; rs20541, IL13, Dogon; rs5498, ICAM1, Fulani). A combined analysis (adjusted for age, season and ethnicity) revealed the following polymorphisms: (i) CSP (rs2251746, FCER1A, CC genotype vs CT/TT slope 1.466, 0.555-2.377, $P=0.0016$; rs17772565, RAD50, CT vs. other slope=-0.194, -0.320--0.067, $P=0.0026$; rs1800629, TNF, GG/GA vs. AA, 0.263, 0.094-0.432, $P=0.0023$), (ii) MSP1 (rs2304081, SLC22A4, AA/AG vs. GG, 0.350, 0.154-0.546), and (iii) total IgE (rs20541, IL13, TT vs. TC/CC, -0.209, -0.346-0.072, $P=0.0028$). There were no putative associations for AMA1 and MSP2 in this combined analysis.

**Discussion**

This study considers two sympatric ethnic groups (Fulani and Dogon) living in close proximity in Mali. Using standardized and robust genetic and immunological assays, we found that the Fulani ethnic group had significantly higher levels of total IgE against crude malaria antigens relative to the Dogon ethnic group. This confirms results from other studies in Burkina Faso comparing the Fulani and Mossi ethnic groups [6,7]. In our study, the Fulani had higher levels of spleen enlargement than the Dogon, a result in line with previous findings in The Gambia and Burkina Faso [4,6,7,11]. The higher total IgE and antigenic (AMA1, CSP, MSP1 and MSP2) responses and the lower parasite rate displayed among the Fulani ethnic group, suggests a higher protection against *P. falciparum* in Fulani compared with the Dogon, and potentially other sympatric ethnic groups (consistent with [6,7]). This difference in protection was observed despite the fact that the two ethnic groups were apparently exposed to similar malaria transmission dynamics. Both groups are known to have different historic and geographic origins and other sociocultural differences [8]. We identified that the Fulani tribe had a higher prevalence of O blood group, which has an established protective effect potentially through reduced *P. falciparum* rosetting, which has been identified in other genetic studies in Mali [9,23] and Kenya [23]. There was a difference in the genotypic profile at the HbC polymorphism between the ethnic groups (AG/AA genotype: Dogon 7.6%, Fulani 0.9%), in keeping with those reported in Burkina Faso (6.7). We also found strong allele frequency differences between ethnic groups in the rs3211938 (CD36, under recent positive selection in Ghana [24]), rs2243250 and rs2243251 (IL4, associated with malaria susceptibility [25]; observed previously in the Gambia and other West African populations [26]), rs542998 (RTN3) and rs10775349 (ADCY9) (both identified in a recent Tanzanian case-control study [27]).

CD36 (Platelet glycoprotein IV) has been consistently found to be a major ligand for adhesion of iRBC expressing PfEMP-1 [28,29], and it enhances phagocytosis and host clearance of the parasite in the spleen, but its exact role in the pathogenesis of malaria remains unresolved [30]. IL4 is an anti-inflammatory cytokine involved in the regulation of the adaptive immunity [31]. This cytokine is mainly produced by activated Th2 cells, and induces proliferation and differentiation of activated B cells and enhances the expression of MHC class II and the IgE low affinity receptor (CD23) on resting B cells. In a study performed in the same ethnic groups and region, the IL4-590 (T vs. C alleles) was associated with higher parasite prevalence in Fulani (compared to Dogon). Our data are also consistent with the reported high correlation between the IL4 polymorphism
and IgE production in asymptomatic individuals belonging to the Fulani groups [32,33].

We identified genetic loci associated with CSP (FCER1A; IL3; TNF), AMA1 (IL5), MSP1 (SLC22A4, IRF1, IL5, LTA, TNF), MSP2 (TLR6, IL3, TNF, and IL22), and total IgE (IL3,
Table 2. Genetic association tests for malaria and clinical phenotypes by ethnic group.

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<tbody>
<tr>
<td>rs17047661 (CR1)</td>
<td>G A</td>
<td>23.6</td>
<td>27.6</td>
<td>35.6</td>
<td>51.7</td>
<td>0.887 (0.453, 1.735) 0.706  5.327 (1.733, 16.376) 0.0008</td>
</tr>
<tr>
<td>rs2075820 (NOD1)</td>
<td>A G</td>
<td>29.2</td>
<td>33.9</td>
<td>47.1</td>
<td>28.3</td>
<td>Additive G 1.232 (0.747, 2.031) 0.238  0.364 (0.188, 0.704) 0.001</td>
</tr>
<tr>
<td>rs3091336 (IL3)</td>
<td>G A</td>
<td>25.9</td>
<td>37.8</td>
<td>20.6</td>
<td>27.6</td>
<td>GG/AG vs. AA 4.543 (1.900, 10.864) 0.0007  1.553 (1.004, 2.400) 0.049</td>
</tr>
<tr>
<td>rs2304081 (SLC22A4)</td>
<td>G A</td>
<td>1.6</td>
<td>1.2</td>
<td>18.3</td>
<td>8.3</td>
<td>AA/GA vs. GG 0.782 (0.149, 4.100) 0.767  0.342 (0.167, 0.700) 0.002</td>
</tr>
<tr>
<td>rs3091336 (IL3)</td>
<td>G A</td>
<td>25.9</td>
<td>35.0</td>
<td>20.6</td>
<td>26.9</td>
<td>GG/AG vs. AA 3.692 (1.579, 8.634) 0.002  1.699 (1.026, 2.810) 0.03</td>
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<tr>
<td>rs2304081 (SLC22A4)</td>
<td>G A</td>
<td>1.6</td>
<td>2.0</td>
<td>18.3</td>
<td>7.9</td>
<td>AA/GA vs. GG 1.507 (0.446, 5.093) 0.51  0.334 (0.175, 0.635) 0.0004</td>
</tr>
<tr>
<td>rs112812 (DERL3)</td>
<td>A G</td>
<td>49.0</td>
<td>30.8</td>
<td>43.3</td>
<td>45.2</td>
<td>Additive G 0.437 (0.257, 0.741) 0.0014  0.948 (0.683,1.316) 0.7496</td>
</tr>
<tr>
<td>rs17047661 (CR1)</td>
<td>G A</td>
<td>24.1</td>
<td>28.8</td>
<td>35.8</td>
<td>45.8</td>
<td>GG/AG vs. AA 1.096 (0.637,1.893) 0.7371  2.874 (1.505,5.487) 0.0008</td>
</tr>
<tr>
<td>rs3091336 (IL3)</td>
<td>G A</td>
<td>1.4</td>
<td>2.4</td>
<td>17.4</td>
<td>6.3</td>
<td>GG/AG vs. AA 2.360 (0.556,10.014) 0.2427  0.277 (0.120,0.639) 0.0010</td>
</tr>
<tr>
<td>rs2304081 (SLC22A4)</td>
<td>G A</td>
<td>34.4</td>
<td>40.2</td>
<td>29.8</td>
<td>30.3</td>
<td>GG/GT vs. TT 2.475 (1.399,4.381) 0.0014  1.260 (0.700,2.269) 0.4397</td>
</tr>
<tr>
<td>rs569108 (MS4A2)</td>
<td>A G</td>
<td>21.8</td>
<td>15.4</td>
<td>13.2</td>
<td>15.5</td>
<td>Additive G 0.466 (0.288,0.755) 0.0011  0.907 (0.515,1.600) 0.7364</td>
</tr>
<tr>
<td>rs10775349 (ADCY9)</td>
<td>C G</td>
<td>12.5</td>
<td>13.7</td>
<td>40.8</td>
<td>44.3</td>
<td>GC vs other 1.746 (0.893,3.416) 0.1043  2.471 (1.355,4.508) 0.0027</td>
</tr>
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</table>

* for a AA/GA vs. GG; Odds ratios (OR), 95% confidence intervals (CI) and p-values based on fitting logistic regression models adjusting for age group and season

It is important to highlight some study limitations. First, it was not possible to assess ethnic differences in seroprevalence from the antibody titre data, as there was not a control population for normalization [46]. Second, we measured total IgE, but it may be more useful to derive parasite-specific outcome in the future. Third, whilst our analyses included information on age, ethnicity, antibody levels and genetic variation, other informative data such as the use of routine immunization against other diseases (e.g., tuberculosis), duration and type of exposure were unavailable. Fourth, the number of genetic polymorphisms considered (n=166) was small in relation to a genome-wide association setting and therefore other potential candidates could not be identified. Fifth, no information about pregnant women susceptibility/resistance to malaria and their offspring at the early stage of life is available for either ethnic group. Finally, confirmation of associations in independent cohorts is required, and follow-up functional work would be needed to elucidate the underlying mechanisms.

These potential limitations notwithstanding, our study confirms and provides additional insights into the reduced malaria susceptibility in the Fulani ethnic group. An unresolved issue is whether pregnant Fulani women compared to Dogon are more resistant to malaria. In general, further understanding of the mechanisms underlying the reduced susceptibility of the Fulani to malaria could provide essential information for the rational design of malaria vaccines, monitoring of their trial, or implementation of therapeutic strategies to improve public health.
Conclusion

Our study showed that during the high and low transmission seasons the Fulani tend to be less susceptible to *P. falciparum* malaria infection not only in parasite positivity but also in parasite density than the Dogon. The results of our study suggest that immunogenetic factors may be responsible for the observed differences in malaria–related phenotypes between

![Figure 2](image-url)
the Fulani and Dogon ethnic groups. These factors may be helpful in understanding the precise mechanisms of resistance in the nomadic Fulani population. This study was performed in a rural setting and identifies some human genetic factors that are involved in malaria susceptibility and resistance, and thus strengthens previous observations.

Supporting Information

Table S1. List of 166 Single Nucleotide Polymorphisms (SNPs).

<table>
<thead>
<tr>
<th>SNP, Gene</th>
<th>Alleles</th>
<th>Ref. Alt.</th>
<th>Dogon</th>
<th>Fulani</th>
<th>Comparison</th>
<th>Effect size (95% CI)</th>
<th>p-value</th>
<th>Effect size (95% CI)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>CSP</td>
<td>rs2251746, FCER1A</td>
<td>T C</td>
<td>4.9</td>
<td>13.1</td>
<td>CC vs TC/TT</td>
<td>2.601 (1.109, 4.093)</td>
<td>0.0006</td>
<td>0.933 (-0.229, 2.096)</td>
<td>0.1155</td>
</tr>
<tr>
<td></td>
<td>rs3148, IL3</td>
<td>G A</td>
<td>8.8</td>
<td>6.4</td>
<td>AA vs AG/GG</td>
<td>-0.264 (-1.141, 0.612)</td>
<td>0.5548</td>
<td>2.196 (0.153, 3.340)</td>
<td>0.0002</td>
</tr>
<tr>
<td></td>
<td>rs1800629, TNF</td>
<td>A G</td>
<td>13.4</td>
<td>2.1</td>
<td>GG/GA vs AA</td>
<td>0.274 (0.098, 0.449)</td>
<td>0.0023</td>
<td>0.031 (-0.191, 0.253)</td>
<td>0.7855</td>
</tr>
<tr>
<td></td>
<td>rs3909662, TNF</td>
<td>G A</td>
<td>6.4</td>
<td>8.5</td>
<td>AG vs other</td>
<td>0.38 (0.158, 0.611)</td>
<td>0.0009</td>
<td>0.017 (-0.209, 0.243)</td>
<td>0.8806</td>
</tr>
<tr>
<td>AM1</td>
<td>rs739718, IL5</td>
<td>T C</td>
<td>31.6</td>
<td>21.0</td>
<td>CC vs TC/TT</td>
<td>0.163 (-0.163, 0.489)</td>
<td>0.3266</td>
<td>-0.924 (-1.437, -0.411)</td>
<td>0.0004</td>
</tr>
<tr>
<td></td>
<td>rs2304081, SLC22A4</td>
<td>G A</td>
<td>1.8</td>
<td>15.7</td>
<td>AG/AA vs GG</td>
<td>0.066 (-0.420, 0.552)</td>
<td>0.7907</td>
<td>0.387 (0.165, 0.610)</td>
<td>0.0007</td>
</tr>
<tr>
<td></td>
<td>rs2670722, IRF1</td>
<td>G T</td>
<td>43.9</td>
<td>40.4</td>
<td>Additive T</td>
<td>0.001 (-0.134, 0.135)</td>
<td>0.9930</td>
<td>0.226 (0.080, 0.371)</td>
<td>0.0023</td>
</tr>
<tr>
<td></td>
<td>rs739718, IL5</td>
<td>T C</td>
<td>31.6</td>
<td>21.0</td>
<td>CC vs TC/TT</td>
<td>0.162 (-0.194, 0.516)</td>
<td>0.3713</td>
<td>-1.091 (-1.778, -0.404)</td>
<td>0.0019</td>
</tr>
<tr>
<td></td>
<td>rs2239704, LTA</td>
<td>G T</td>
<td>32.0</td>
<td>47.5</td>
<td>TT/GT vs GG</td>
<td>0.005 (-0.180, 0.191)</td>
<td>0.9573</td>
<td>-0.371 (-0.591, -0.151)</td>
<td>0.0010</td>
</tr>
<tr>
<td></td>
<td>rs1799964, TNF</td>
<td>T C</td>
<td>14.4</td>
<td>19.0</td>
<td>CT vs CC/TT</td>
<td>-0.075 (-0.288, 0.137)</td>
<td>0.4864</td>
<td>0.355 (0.141, 0.569)</td>
<td>0.0012</td>
</tr>
<tr>
<td>MSP2</td>
<td>rs5743809, TLR6</td>
<td>T C</td>
<td>6.0</td>
<td>4.8</td>
<td>CC vs TC/TT</td>
<td>1.562 (0.664, 2.460)</td>
<td>0.0007</td>
<td>-0.570 (-2.167, 1.027)</td>
<td>0.4842</td>
</tr>
<tr>
<td></td>
<td>rs35415145, IL3</td>
<td>C T</td>
<td>1.7</td>
<td>3.0</td>
<td>CT vs other</td>
<td>0.020 (-0.411, 0.451)</td>
<td>0.9267</td>
<td>-0.520 (-0.842, -0.197)</td>
<td>0.0016</td>
</tr>
<tr>
<td></td>
<td>rs1799964, TNF</td>
<td>T C</td>
<td>14.4</td>
<td>19.0</td>
<td>CT vs other</td>
<td>-0.038 (-0.218, 0.143)</td>
<td>0.6825</td>
<td>0.267 (0.102, 0.432)</td>
<td>0.0015</td>
</tr>
<tr>
<td></td>
<td>rs1012356, IL22</td>
<td>T A</td>
<td>48.1</td>
<td>41.5</td>
<td>AA/AT vs TT</td>
<td>-0.294 (-0.467, -0.121)</td>
<td>0.0009</td>
<td>0.009 (-0.154, 0.191)</td>
<td>0.9160</td>
</tr>
<tr>
<td>Total IgE</td>
<td>rs3148, IL3</td>
<td>G A</td>
<td>8.8</td>
<td>6.4</td>
<td>AA vs AG/GG</td>
<td>-0.006 (-0.506, 0.494)</td>
<td>0.9811</td>
<td>0.955 (0.428, 1.483)</td>
<td>0.0004</td>
</tr>
<tr>
<td></td>
<td>rs20541, IL13</td>
<td>C T</td>
<td>27.6</td>
<td>7.6</td>
<td>TT vs CT/CC</td>
<td>-0.251 (-0.399, -0.103)</td>
<td>0.0009</td>
<td>1.034 (0.292, 1.777)</td>
<td>0.0063</td>
</tr>
<tr>
<td></td>
<td>rs5498, ICAM1</td>
<td>A G</td>
<td>13.7</td>
<td>22.9</td>
<td>Additive G</td>
<td>0.013 (-0.073, 0.100)</td>
<td>0.7675</td>
<td>0.109 (0.045, 0.172)</td>
<td>0.0008</td>
</tr>
</tbody>
</table>

Effect sizes (slopes), 95% confidence intervals (CI) and p-values based on fitting linear regression models adjusting for age group and season.

Table S7. Genetic association tests for malaria and clinical phenotypes by ethnic group.

Table S8. Genetic association tests for malaria and Immuno-Assay by ethnic group.

Figure S1. Transformed titre values and correlations.

Figure S2. Transformed antibody levels by age group* and ethnicity.

Acknowledgments

We thank the participants and Manteourou communities who made this study possible; and the healthcare workers who assisted with this work. We thank also Prof Carmen Fernandez, Professor of Immunology, Stockholm University, for her guidance during the first draft of the manuscript.

Table 3. Genetic association tests for (log_{10} transformed) immunoassay titre phenotypes by ethnic group.
Author Contributions

Conceived and designed the experiments: BM AD KR DK MTB OKD. Performed the experiments: BM AD VD AT N. Silva SC PR PC. Analyzed the data: OT KR N. Sepulveda TGC. Contributed reagents/materials/analysis tools: KR DK MalariaGEN MTB OKD. Wrote the manuscript: BM AD OT N. Sepulveda KR TGC MTB OKD.

References


4. Greenwood BM, Groenendaal F, Bradley AK, Greenwood AM, Shenton PR PC. Analyzed the data: OT KR N. Sepulveda TGC. Contributed reagents/materials/analysis tools: KR DK MalariaGEN MTB OKD. Wrote the manuscript: BM AD OT N. Sepulveda KR TGC MTB OKD.


