in Ghana. A total of 803 dried blood spots (DBS) on filter paper were collected from symptomatic children, aged 6 months to 14 years, with *Plasmodium falciparum* mono-infection in the coastal savanna (Cape-Coast) and the forest (Begoro) zones of Ghana from 2014 to 2017. The study leveraged the high specificity and relatively low-cost of targeted next generation sequencing using molecular inversion probes for targeting and sequencing on the illumina MISEQ platform for sequencing of *Plasmodium falciparum* Apical Membrane Antigen 1 (PfAMA1) gene. The result showed high genetic diversity in PfAMA1 in Ghanaian samples with a total of 164 PfAMA1 haplotypes and a haplotype diversity of 0.993. The overall nucleotide diversity of the PfAMA1 sequences was 0.015. There was no significant genetic differentiation between the two study populations in Ghana. Parasite isolates from the two ecological zones in Ghana showed a moderate level of genetic differentiation with sequences from Thailand (Fst=0.054) and low differentiation with sequences from Kenya (Fst=0.004). The results also showed balancing selection which might have contributed to the high diversity in PfAMA1. Seventy three percent of the infections were monochlonal with an overall complexity of infection of 1.30. This study provides new data on genetic diversity of PfAMA1 gene in Ghana and gives valuable information or the development of an effective PfAMA1-based malaria vaccine, thus strengthening the importance of investigating genetic diversity of *P. falciparum* and evolutionary history of parasite populations in the field of malaria vaccine development.

**RELATEDNESS BETWEEN MALARIA PARASITES: PORTABLE INSIGHTS ACROSS SETTINGS**

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Increasingly, genetic surveillance of malaria parasites is being used in near-elimination settings to describe patterns of importation and monitor drug resistance. Studies of parasite relatedness based on identity-by-descent (IBD) have generated demographic insight on a temporal-spatial scale relevant for disease control. However, questions remain about what data should be collected and the requirements for reliable inference of relatedness, with most efforts to date being relatively ad hoc. Using a globally diverse set of published data sets of single-genotype *Plasmodium falciparum* and *Plasmodium vivax* parasite samples, we demonstrate the superior portability of IBD-based relatedness estimates relative to those based on allele sharing (i.e. identity-by-state). Under a hidden Markov model framework, we characterize the number and type of genetic markers required for specified error around relatedness estimates, demonstrating that reliable inference can be made using genetic markers without requiring whole genome sequences. Using the parametric bootstrap, we demonstrate how confidence intervals around estimates can aid interpretation across results based on vastly different data types. Finally, we show how concepts from transport theory can be adopted for a more generalized approach to demographic inference. These results provide a basis for statistically informed prospective study design and surveillance strategies. Given a robust foundation, analyses of genetic data from the surveillance of malaria parasites can achieve portability across different data types, accommodating the diversity of different experimental approaches extant in the field and allowing insights from meta-analyses to move the field forward.

**PROTECTION AGAINST MALARIA IN HETEROZYGOUS GIRLS FOR G6PD DEFICIENCY IN ANGOLA**

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G6PD deficiency has become more prevalent in malaria endemic regions because genetic variants can confer protection against *Plasmodium*. However, these conclusions are still in debate. The aim of this work is to evaluate the prevalence of G6PD deficiency in an African holoendemic region for *Plasmodium falciparum*, estimating the genotype and phenotype of the enzyme, and evaluating the risk of malaria associated with the G6PD genotype. A prospective longitudinal cohort study, involving 1692 children selected in the maternity ward and monitored over quarterly medical consultations for two years. The G202A and A376G genotypes were determined through Real Time PCR methods. For enzyme activity, we applied the NeoUSA kit for Neonatal G6PD deficiency screening to measure the NADPH produced calorimetrically in the kinetic mode. The prevalence of the A-allele was 19.4%, with 19% hemizygous boys and 4.5% A-homozygous girls. Enzyme deficiency, measured by enzyme activity, was highly prevalent (32.7% in males and 30.5% in females). The average enzymatic activity was also low for A-hemizygous boys (1.66U/ gHb) and for homozygous girls (0.97U/gHb). Heterozygous girls would seem to hold some protection against malaria, when compared to the other genotypes, mainly A-/A- (χ²=14.35, p=0.014). The prevalence of G6PD deficiency among children in Bengo is high. Heterozygous girls, as proposed elsewhere, may be the driving force for positive selection. This data may serve for the ministry of health in taking safe and appropriate decisions regarding the usage of potentially unsafe drugs for G6PD deficient individuals.

**HUMAN ANTIBODIES TO AN EPITOPE IN PVDBP BLOCK ADHESION OF PLASMODIUM FALCIPARUM PLACENTAL PARASITES VIA CRYPTIC EPITOPIES IN VAR2CSA**

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During Plasmodium falciparum infection in pregnancy, parasites express the PfEMP1 surface antigen VAR1CSA that mediates sequestration of infected red blood cells (iRBCs) to the placenta. Vaccines that target the DBL domains within VAR1CSA are currently in clinical trials and the goal is to elicit antibodies that will block sequestration by interfering with the interaction of VAR1CSA and chondroitin sulphate A (CSA) in the placenta. We are pursuing a novel strategy to develop a vaccine against *P. falciparum* placental malaria that is based on cross-reactivity between PvDBP from *P. vivax* and cryptic epitopes within VAR1CSA. This approach is based on our previous findings that a monoclonal antibody (mAb) raised against PvDBP cross-reacts with VAR1CSA and blocks *P. falciparum* adhesion to CSA in vitro. Also, we discovered that human antibodies to VAR1CSA can be acquired outside of pregnancy and arise from exposure to PvDBP. Here, we identified an epitope within PvDBP that is the target of the mAb and showed that a peptide of this epitope completely blocks antibody recognition of VAR1CSA. To determine whether this same epitope is involved in cross-reactivity of human antibodies to VAR1CSA, we affinity-purified antibodies specific to this epitope from pools of sera from Colombian men and children. These purified antibodies recognized VAR1CSA by ELISA, and strongly blocked adhesion of *P. falciparum* iRBCs to CSA in vitro. Furthermore, sera from multigravid African women or from rabbits immunized with VAR1CSA do not recognize the epitope from PvDBP, demonstrating that the epitope in VAR1CSA is cryptic. Together, these findings identify key epitopes in PvDBP elicited by natural exposure to *P. vivax* and mouse immunization that cross-react with cryptic epitopes in VAR1CSA.