A Specific PfEMP1 Is Expressed in *P. falciparum* Sporozoites and Plays a Role in Hepatocyte Infection

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**In Brief**
*P. falciparum* PfEMP1 surface adhesion proteins mediate immune evasion and pathogenesis during asexual blood stage development. Zanghı` et al. find that a strain-specific member of PfEMP1 is expressed at the sporozoite surface. Antibodies against this protein inhibit sporozoite invasion of hepatocytes in a strain-specific manner.

**Highlights**
- Sporozoites expand subtelomeric heterochromatin to silence blood-stage-specific genes
- A strain-specific PfEMP1 is expressed on the surface of sporozoites
- NF54_SpzPfEMP1 is immunogenic in sporozoite-infected human volunteers
- Antibodies against NF54_SpzPfEMP1 block sporozoite infection of hepatocytes

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A Specific PfEMP1 Is Expressed in *P. falciparum* Sporozoites and Plays a Role in Hepatocyte Infection

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**SUMMARY**

Heterochromatin plays a central role in the process of immune evasion, pathogenesis, and transmission of the malaria parasite *Plasmodium falciparum* during blood stage infection. Here, we use ChIP sequencing to demonstrate that sporozoites from mosquito salivary glands expand heterochromatin at subtelomeric regions to silence blood-stage-specific genes. Our data also revealed that heterochromatin enrichment is predictive of the transcription status of clonally variant genes members that mediate cytoadhesion in blood stage parasites. A specific member (here called NF54-var*<sub>sporo</sub>*) of the var gene family remains euchromatic, and the resultant PfEMP1 (NF54_SpzPfEMP1) is expressed at the sporozoite surface. NF54_SpzPfEMP1-specific antibodies efficiently block hepatocyte infection in a strain-specific manner. Furthermore, human volunteers immunized with infective sporozoites developed antibodies against NF54_SpzPfEMP1. Overall, we show that the epigenetic signature of var genes is reset in mosquito stages. Moreover, the identification of a strain-specific sporozoite PfEMP1 is highly relevant for vaccine design based on sporozoites.

**INTRODUCTION**

The most devastating form of human malaria is caused by the protozoan parasite *P. falciparum*, with more than 200 million people infected annually and an estimated 445,000 deaths in 2017 (World Health Organization, 2017). Malaria is transmitted by the bite of an infected *Anopheles* mosquito, which harbors sporozoites in its salivary glands. From the point of injection into the skin, sporozoites migrate via blood vessels to the liver, cross the sinusoidal cell layer separating the blood and the liver, and finally invade hepatocytes where asexual reproduction leads to the release of thousands of merozoites into the bloodstream (Prudêncio and Mota, 2007). Merozoites infect mature red blood cells and, through asexual reproduction, generate daughter merozoites to initiate a new infective cycle. The persistence and pathogenesis of *P. falciparum* during blood stage proliferation relies on the exclusive and successive expression of variant surface adhesion molecules, PfEMP1, expressed at the membranes of infected red blood cells (iRBCs) and mediate cytoadhesion in the microvasculature (Smith, 2014). This immune evasion mechanism, termed “antigenic variation,” depends on monoalectic expression of one of approximately 60 var genes that encode PfEMP1 proteins.

Different epigenetic factors lead to the default transcriptional silencing of all but one var gene via the establishment of facultative heterochromatin (Guizetti and Scherf, 2013). Heterochromatin protein 1 (PH1P1) is a key regulator of facultative heterochromatin in *P. falciparum* (Flueck et al., 2009; Pérez-Toledo et al., 2009),
and conditional depletion of PfHP1 disrupts transcriptional repression of var genes as well as the master regulator of sexual commitment, PfAP2-G (Brancucci et al., 2014). In addition, transcription of a single var gene is associated with antisense transcription of a long non-coding RNA (lncRNA) originating from its intron, a conserved feature shared by all members of the var family (Ralph et al., 2005; Jiang et al., 2013; Amit-Avraham et al., 2015). Thus, the parasite uses multiple layers of epigenetic regulation to ensure monoallelic expression of variant gene families, which creates phenotypic plasticity in genetically identical parasites during blood stage development (Lopez-Rubio et al., 2009; Rovira-Graells et al., 2012).

Although variegated gene expression appears to have evolved as a survival strategy to promote prolonged blood stage infections in humans, it is unknown whether heterochromatin-mediated control of variant gene families is important in other parasite stages, such as the sporozoite stage. Sporozoites have been successfully used to provide immune protection to human volunteers and are a key stage to target for malaria vaccine development (Richie et al., 2015).

To study the organization of heterochromatin in sporozoites, which are relatively low in abundance in the mosquito salivary glands, we developed a robust, low-cell-input chromatin immunoprecipitation followed by massively parallel sequencing (ChIP-seq) protocol. ChIP-seq of PfHP1 revealed a remarkable organization of heterochromatin in sporozoites that differs from that observed in asexual blood stage parasites. Furthermore, our epigenetic analysis predicted the expression of a specific PfEMP1 on the surface of sporozoites. Antibodies raised against this particular PfEMP1 efficiently blocked sporozoite infection of human hepatocytes in a strain-specific manner, demonstrating a previously unknown role of the var gene family in malaria parasite transmission.

**RESULTS**

**Heterochromatin Islands Form Nuclear Clusters in Sporozoites**

In *P. falciparum* blood stage parasites, the maintenance of heterochromatin islands is linked to the physical tethering of these genomic regions to the nuclear periphery, forming 4–7 perinuclear foci (Lopez-Rubio et al., 2009). PfHP1 is a major component of heterochromatin in perinuclear chromosome clusters. To determine whether a similar spatial chromosome arrangement exists in sporozoites, we performed DNA fluorescence in situ hybridization (FISH) using a probe corresponding to the conserved sub-telomeric repeat TARE6 (Telomere-Associated Repeat 6) (Figure 1A) and indirect immunofluorescence using anti-PfHP1 antibodies (Figure 1B). We observed an average of 2–4 TARE6-containing foci per nucleus, which localized to the nuclear periphery and overlapped with PfHP1-containing foci (Figure 1C). These data indicate
a conserved spatial organization of heterochromatin in the nucleus between asexual blood stage parasites and salivary gland sporozoites.

**PfHP1 Genome-wide Distribution in *P. falciparum* Sporozoites**

Previous studies have used ChIP to elucidate the role of histone post-translational modifications (PTMs), histone variants, and other chromatin factors in gene expression during the asexual stage of the human malaria parasite, *P. falciparum* (Lopez-Rubio et al., 2013). In asexual blood stages, PfHP1 and H3K9me3 regulate transcription of clonally variant virulence gene families such as *var* by establishing facultative heterochromatin at promoter regions and gene bodies (Lopez-Rubio et al., 2009; Flueck et al., 2009). These heterochromatic regions span approximately 100 kb, forming so-called heterochromatin islands at sub-telomeric regions and several internal chromosome clusters. Because the number of sporozoites that can be recovered from the infected mosquito salivary gland is low, we developed a robust low input ChIP-seq protocol, which allowed us to use approximately 600,000–800,000 sporozoites per immunoprecipitation (IP). We investigated the genome-wide distribution of heterochromatin by performing ChIP with highly specific antibodies against PfHP1 and the transcriptionally repressive histone H3 modification lysine 9 trimethylation (H3K9me3) (Tables S1 and S2). We observed an enrichment of PfHP1 and H3K9me3 in sub-telomeric regions of all 14 chromosomes, as well as in central chromosome regions of chromosomes 4, 6, 7, 8, and 12 (Figure 2A; Table S2). These regions contain variant gene families and show a similar heterochromatin enrichment in blood stage parasites (Lopez-Rubio et al., 2009). In contrast, ChIP-seq of the transcriptionally activating mark H3K9ac revealed its absence from these heterochromatic loci and enrichment within chromosome regions that primarily contain housekeeping genes (Figures 2A and 2B). Notably, ApiAP2-G, a member of the AP2 DNA-binding protein family that is involved in gametocyte formation, appears to be enriched in PfHP1 and H3K9me3 in sporozoites as it is in asexual blood stage parasites, suggesting a re-setting of the chromatin of this gene after gametogenesis is complete (Figure S1). We conclude that the heterochromatin organization is largely preserved in different life cycle stages.

**Heterochromatin Spreads into Genes Coding for Exported Blood Stage Proteins in Sporozoites**

When comparing the genome-wide PfHP1 pattern in sporozoites to that in asexual blood stage parasites (Figure 3A), we observed an overall similar organization of PfHP1 islands along all 14 chromosomes. We noted, however, a significant sporozoite-specific spreading of sub-telomeric heterochromatin from nearly all chromosome ends toward central chromosomal regions (Figures 3A and 3B). These extended heterochromatic regions of approximately 50 kb are highly enriched in genes encoding parasite proteins that are typically exported to the host erythrocyte during blood stage development, remodeling the erythrocyte to accommodate the parasite’s needs (de Koning-Ward et al., 2016) (Figures 3B and S2). RNA sequencing in sporozoites showed that steady-state mRNA levels of these sub-telomeric genes encoding...
blood-stage-exported proteins have an inverse correlation with H3K9me3/HP1 occupancy (Figure S3; Table S3), linking sporozoite heterochromatin extension to stage-specific gene silencing.

**Heterochromatin Enrichment Predicts Expression of a var Gene in Sporozoites**

In asexual blood stage parasites, a single PfEMP1 is expressed at any given time on the erythrocyte surface, and this expression correlates with low levels of PfHP1 and H3K9me3 within the promoter and gene body of the corresponding var gene. In contrast, the silent var genes are enriched for these heterochromatic marks (Lopez-Rubio et al., 2009). We performed MACS2-based peak enrichment analysis of four independent PfHP1 (Tables S2A and S4A) and three independent H3K9me3 (Table S2B) ChIP-seq sporozoite experiments. All var genes present in the NF54 *P. falciparum* strain were enriched for PfHP1 and H3K9me3 (Table S4A, “Peaks”). Intriguingly, one var gene (PF3D7_0809100) consistently showed the lowest enrichment of PfHP1 within its promoter and gene body (Figure 4A; Table S4A), suggesting that the corresponding PfEMP1 may be expressed in sporozoites. PF3D7_0809100 (subsequently referred to as NF54var<sup>sporo</sup>) is located in the central region of chromosome 8, adjacent to two other var genes and two members of a second clonally variant gene family rif, all of which retain higher levels of PfHP1 and H3K9me3 (Figure 4A). In general, other clonally variant gene families, including rif, Pfmc2TM, and PfACS, which are located proximal to sub-telomeric var genes on 13 of the 14 chromosomes, appear to maintain blood-stage-like heterochromatin patterns: only two of 180 rif genes, one of 13 Pfmc2TM genes, and five of 13 PfACS genes are depleted for PfHP1 and H3K9me3 (Table S5).

Given the major role of PfEMP1 in parasite virulence and immune evasion (Wahlgren et al., 2017), we focused on the expression of var genes in sporozoites. We investigated NF54var<sup>sporo</sup> transcription by performing strand-specific RNA sequencing (RNA-seq) analysis of the sporozoite steady-state transcriptome (Figure S4; Table S3). As shown in Figure 4B (lower panel) and Figure 4C, we did not detect full-length mRNA transcripts for NF54var<sup>sporo</sup> in the sporozoites (Tables S4B and S4C), but only bidirectional intronic promoter activity (Figure 4C, left panel) similar to that observed for silent var genes in the late-stage asexual blood stage parasites (Ralph et al., 2005; Epp et al., 2009). Despite identifying low-level, full-length mRNAs for two other var genes, PF3D7_0711700 and PF3D7_0412400 (Figure 4B, bottom panel; Figure S5; Tables S4B and S4C), these lack antisense noncoding RNAs (ncRNAs) to exon I that has been associated with var gene transcriptional activation and monolecilic expression in asexual blood stage parasites (Figure S5, left panel; and Table S4D) (Ralph et al., 2005; Jiang et al., 2013; Amit-Avraham et al., 2015). For this reason, we consider that var genes PF3D7_0711700 and PF3D7_0412400 may not be expressed in the sporozoite stage.

Since var mRNA transcription and PfEMP1 expression show limited overlap during asexual blood stage development, it is possible that NF54var<sup>sporo</sup> is transcribed at the stage that precedes sporozoites: the oocysts in the mosquito midgut. Indeed, RNA-seq of oocysts (day 8 post-infection of the mosquito)
Figure 4. PfHP1 Occupancy Predicts Transcription of NF54var\textsubscript{sporo} in Sporozoites

(A) ChIP sequencing data show enrichment of PfHP1 (red) and H3K9me3 (blue) over a 55-kb genomic region of chromosome 8 (chromosome coordinates are shown at top) in \textit{P. falciparum} sporozoites. The coverage of the ChIP input DNA is indicated in black, and the MACS2-based peaks (Table S2) are indicated as rectangular boxes underneath the coverage plots. Coverage plots are represented as average RPM over bins of 1,000 nt with the maximum value indicated on the y axis. Data are representative of three or more independent experiments. The \textit{var} gene PF3D7\textsubscript{0809100}, or NF54\textit{var}\textsubscript{sporo}, shows low H3K9me3/PfHP1 enrichment and is highlighted in green.

(B) RNA-seq shows \textit{var} gene transcription across different \textit{P. falciparum} life-cycle stages: asexual-ring-stage parasites 12 hr post-invasion (two replicates at top), mosquito-derived oocysts (three replicates in the middle), and mosquito salivary gland sporozoites (three replicates at bottom). Transcripts corresponding to

(legend continued on next page)
revealed the presence of the full-length transcript of NF54var\textsuperscript{sporo}, which showed the highest RPKM (reads per kilobase of exon per million reads) value of any var gene in three biological replicates (Figures 4B, middle panel, and 4C, right panel; Tables S4B and S4C), indicating that NF54\_SpzPIEMP1 could be synthesized already in late mosquito stages. We observed another full-length var transcript, PF3D7\_1240600; however, in the absence of intron-derived exon I antisense ncRNA, we speculate that this prohibits protein expression (Figure S5, right panel; Tables S4C and S4D). Alternatively, the observed oocyst var transcripts are expressed in individual parasites. Sporozoites expressing NF54var\textsuperscript{sporo} may have a selective advantage in the process of migration to the salivary gland, leading to, predominantly, sporozoites that express NF54\_SpzPIEMP1.

In contrast, RNA-seq data from the parental ring asexual blood stage parasites detected almost no reads mapping to NF54var\textsuperscript{sporo} compared to the predominately transcribed var gene, PF3D7\_1200600 (top panel of Figure 4B; Tables S4B and S4C), suggesting a reset of var gene transcription during the parasite transmission stage.

**A Strain-Specific PfEMP1 Is Expressed on the Surface of Sporozoites**

To determine whether the PIEMP1 protein encoded by NF54var\textsuperscript{sporo} is synthesized in sporozoites, we prepared NF54 sporozoite extracts and performed immunoblotting assays using either an antibody against the conserved intracellular C-terminal ATS (Acid Terminal Segment) domain that reacts with all PIEMP1 proteins (Nacer et al., 2015) or specific antibodies against the extracellular variable domain of NF54\_SpzPIEMP1 (Figure 5A). Anti-NF54\_SpzPIEMP1 antibodies and the anti-ATS reacted with a band corresponding to the predicted molecular weight of NF54\_SpzPIEMP1 (241 kDa in Figures 5B and S6A). These sera detect smaller bands of approximately 70 to 75 kDa that may represent degraded forms of PIEMP1. Furthermore, IFAs of fixed NF54 sporozoites using mouse anti-NF54\_SpzPIEMP1 and ATS antibodies showed a surface membrane-like staining pattern (Figure 5D). Almost all sporozoites (>98%) react with the anti-NF54\_SpzPIEMP1 antibodies. We observed a similar IFA staining pattern in six independent NF54 sporozoite preparations, selecting the selective expression of a member of the var gene family. No surface staining was observed with antibodies against the extracellular domain of the PIEMP1 encoded by var2CSA (PF3D7\_1200600) or the CIDR (cysteine-rich interdomain region) domain of an unrelated central var gene (PF3D7\_0412700), both of which retain H3K9me3/3IP1 enrichment in sporozoites (Figure S6B; data not shown).

Since NF54var\textsuperscript{sporo} is not conserved in other P. falciparum parasite strains (http://www.plasmodb.org) we performed IFA analysis on sporozoites of a genetically distinct strain, the Cambodian clone NF135 (Teirlinck et al., 2013). NF135 reacts with antibodies directed against the major surface antigen of sporozoites, Circumsporozoite protein (CSP) (Figure S6C). However, no cross-reactivity with anti-NF54\_SpzPIEMP1 was observed. Expression of a PIEMP1 was confirmed by using anti-ATS (Figure 5D). These data suggest that an antigenically variant PIEMP1 antigen, possibly with a similar function as that of NF54\_SpzPIEMP1, is expressed on the surface of NF135 *P. falciparum* sporozoites. Moreover, we performed blast on the NF135 proteome (UniProt ID: UP000019114, based on the assembly deposited at GenBank [GEO: AOPS00000000, Broad Institute]). No ortholog of NF54var\textsuperscript{sporo} was detectable in NF135, supporting the hypothesis that anti-NF54\_SpzPIEMP1 antibodies do not crossreact with NF135 sporozoites.

The IFAs on live sporozoites, with intact cell membranes, and the anti-NF54\_SpzPIEMP1 antibody, but not the anti-ATS antibody, stained the surface of sporozoites (Figure 5E). Trypsin treatment of live sporozoites (50 µg/mL) abolished antibody surface reactivity in immunofluorescence and by western blot, confirming that the CIDR domain of NF54\_SpzPIEMP1 is extracellular in sporozoites (Figures 5B and 5E). Together, these results provide evidence of expression of a clonally variant and strain-specific PIEMP1 protein at the surface of sporozoites with a similar orientation to that seen at the membrane of iRBCs.

To study further the specificity of the anti-NF54\_SpzPIEMP1, we incubated NF54 asexual blood stage parasites, with magnetic beads coated with immunoglobulin G (IgG) of anti-NF54\_SpzPIEMP1. After three rounds of selection, we obtained parasites that react (>30%) with anti-NF54\_SpzPIEMP1 (Figure S6C). qRT-PCR analysis on RNA prepared from ring stage parasites before and after panning showed an enrichment for NF54var\textsuperscript{sporo} transcripts of approximately 50-fold (Figure S6D). We demonstrate that the same PIEMP1 can be expressed in two distinct phases of the life cycle.

**Antibodies against NF54\_SpzPIEMP1 Block Sporozoite Infection of Hepatocytes**

In intra-erythrocytic parasites, PIEMP1 proteins are exported across the parasite membrane and the parasitophorous vacuolar membrane to the surface of the erythrocyte, where they serve as adhesion molecules that can bind to a variety of endothelial receptors such as CD36, ICAM, etc., causing malaria pathogenesis by obstructing blood vessels in critical organs such as the brain (Wahlgren et al., 2017). Antibodies against the extracellular PIEMP1 region have been shown to block the rosetting phenotype and/or adhesion to various host endothelial receptors, such as CD36 or CSA.

Because NF54\_SpzPIEMP1 is expressed on the surface of mature sporozoites, we evaluated its potential to interact with
Figure 5. **NF54**_SpzPfEMP1 Protein Is Strain Specific and Exported to the Sporozoite Surface

(A) Schematic representation of the predicted domains of the PfEMP1 encoded by *PF3D7_0809100* and the corresponding antibodies against the semi-conserved ATS region and the polymorphic domains of the NF54_SpzPfEMP1.

(legend continued on next page)
hepatocytes, thus contributing to hepatocyte infection. We pre-incubated freshly isolated salivary gland sporozoites with either the anti-NF54_SpzPfEMP1 mouse antibody (both serum and the purified IgG) against the first 737 amino acids containing the DBL1 and CIDR1 domains (Figure 5A) or the corresponding pre-immune serum before adding the sporozoites to a primary human hepatocyte culture. After 3 days of infection, we observed that the anti-NF54_SpzPfEMP1 serum strongly reduced hepatocyte infection in a dilution-dependent manner, whereas the preimmune mouse serum showed only very low inhibition (Figure 6A). It is noteworthy that the purified anti-NF54_SpzPfEMP1 IgG (1.8 μg/mL) inhibits hepatocyte infection at a level similar to that of the anti-CSP IgG (20 μg/mL) (Figure 6A). Importantly, anti-NF54_SpzPfEMP1 did not block infection with clone NF135, which does not express NF54_SpzPfEMP1 (Figures 5D and 6A), whereas the anti-CSP antibody blocked both strains at levels >90% (Figure 6A).

Lastly, we assessed the immunogenicity of NF54_SpzPfEMP1 during natural infection. Serum of volunteers infected with NF54 sporozoites under chloroquine cover was obtained from a previous clinical trial that demonstrated that protective responses were mainly directed against *P. falciparum* pre-erythrocytic stages (Roestenberg et al., 2009) and was able to inhibit sporozoite invasion into hepatocytes (Peng et al., 2016). HEK293 cells expressing NF4_SpzPfEMP1, SEA-1 (PF3D7_1021800, positive control), or Etramp 14.2 (PF3D7_1476100, negative control) were incubated with serum and then subjected to fluorescence-assisted cell sorting. As shown in Figures 6B and 6C, the serum of one third of the infected volunteers contained significant antibody levels against NF54_SpzPfEMP1 (N-terminal CIDR region from amino acids 1–737), indicating that this PfEMP1 molecule is exposed on the surface of *P. falciparum* parasites before parasite blood stage infection develops.

**DISCUSSION**

Epigenetic regulation of *var* gene transcription and studies on the role of PfEMP1 in malaria pathogenesis have been focused on blood stage parasites (Guizetti and Scherf, 2013; Smith et al., 2013). Here, we present highly reproducible data from multiple NF54 sporozoite preparations that a specific member of the *var* multigene family (~60 members) is expressed in mosquito salivary gland parasites. Although we found that the overall nuclear organization is surprisingly conserved between asexual blood stage parasites and migratory sporozoite stages of *P. falciparum*, our developed ChIP-seq protocol for salivary gland stage sporozoites uncovered several features that provide insight into the biology of malaria transmission to humans. A striking feature is that subtelomeric heterochromatin region extends to genes that are exported into the host cell in asexual stages, adding a new parasite strategy to silence genes that are not used in free-living stages.

Our genome-wide analysis of PfHP1 and H3K9me3 enrichment predicted the expression of a member of the *var* gene family: PF3D7_0809100 or NF54_varsporo. Given that a bulk culture of the NF54 blood stage parasites express *var* genes that are distinct from NF54_varsporo, we propose that an epigenetic resetting of *var* genes occurs during mosquito stage development to select for expression of a specific PfEMP1 on the surface of sporozoites. We detect the NF54_varsporo transcript in late oocyst stage parasites, but this does not exclude the possibility that the resetting occurs at an earlier transmission stage. Regardless of when the epigenetic resetting occurs, our data suggest that, similar to asexual blood stage parasites, sporozoites may maintain monoallelic expression of *var* genes.

Our observation of epigenetic resetting of *var* genes is supported by transcriptional data obtained from blood stage parasites after passage through the mosquito. Studies with human volunteers have shown that *var* gene choice is altered upon mosquito transmission (Bachmann et al., 2016). A recent study reported the presence of a specific *var* gene transcript in sporozoites obtained from *P. falciparum*-infected patients from a malaria-endemic region in Africa; however, the authors did not report whether the corresponding PfEMP1 was produced (Gómez-Díaz et al., 2017). In light of these published data and our results, genetically different parasite strains may express antigenically variant PfEMP1 proteins in sporozoites.

Thus far, the biological role of the PfEMP1 surface adhesion molecule was believed to be restricted to immune evasion in the asexual blood stage. Our IFA data show that all salivary gland sporozoites express NF54_SpzPfEMP1 on their surface in a manner similar to that of iRBCs. It is currently unclear why a particular *var* gene member would be specifically targeted for mosquito stage expression. Structural analysis of NF54_SpzPfEMP1 does not reveal any specific features that would make it a particularly good candidate for expression at the sporozoite plasma membrane. One possibility is that the expression of a particular adhesive property may enhance sporozoite migration and hepatocyte infection. This hypothesis may limit the choice of expressed *var* gene for efficient transmission of parasites. The NF54_varsporo gene has not been studied before, and its adhesive features remain unknown.

Given that all asexual blood stage PIEMP1 proteins studied so far display adhesive properties (Smith, 2014), we hypothesized that NF54_SpzPfEMP1 plays a role in sporozoite interaction with various host tissues and infection of hepatocytes. Indeed, antibodies directed against the DBL and CIDR domains of NF54_SpzPfEMP1 resulted in very potent inhibition of hepatocyte
infection. In the future, genetically modified parasites that either lack the NF54var<sub>apo</sub> var gene or express genetically modified extracellular PfEMP1 domains may help to elucidate the function of NF54_SpzPfEMP1 during the various mosquito stages and, perhaps, even hepatocyte infection.

Our work is highly relevant to vaccine development based on live-attenuated sporozoites. Sterile protection in human volunteers has been reported after challenge with homologous, laboratory-adapted <i>P. falciparum</i> sporozoites (Kublin et al., 2017). Given our discovery that a clonally variant antigen on the surface of sporozoites is expressed in a strain-specific manner, one may speculate that natural protective immune responses target variant sporozoite surface antigens such as PfEMP1. This could impact the efficacy of a sporozoite vaccine in patients from distinct geographic regions, as has been recently reported (Scats et al., 2015). It is noteworthy that PIEMP1 does not exist in rodent models that are often used for sporozoite vaccine evaluation. Thus, prediction of vaccine efficacy in these models does not take into account the expression of <i>P. falciparum</i> species-specific variant molecules.

In conclusion, this study provides evidence for the sporozoite-specific repurposing of the PIEMP1 surface antigen family, the biological function of which was thought to be restricted to immune evasion (antigenic variation) during chronic blood stage infection in the human host. Our discovery of a strain-specific surface antigen may provide a molecular explanation for the reduced protection of human volunteers after challenge with heterologous <i>P. falciparum</i> sporozoites. As our data demonstrate...
an unprecedented role of PIEMP1 proteins in transmission stages and provide insight into the biology of sporozoites during infection of hepatocytes, this work is highly relevant for vaccine design based on sporozoites.

**EXPERIMENTAL PROCEDURES**

**Human Plasma Samples**

Samples were obtained from a previous clinical trial carried out at the Radboud University Nijmegen Medical Center (Nijmegen, the Netherlands), in accordance with principles of good clinical practice and with prior approval from the Central Committee for Research Involving Human Subjects of the Netherlands (NCT00442377). Study subjects (n = 14) were exposed to either infective (n = 9) or non-infective (n = 5) mosquito bites with concurrent chloroquine prophylaxis (Roestenberg et al., 2009).

**Isolation and Purification of *P. falciparum* Sporozoites and Oocysts**

Adult *Anopheles stephensi* females were infected with either *P. falciparum* strain NF54 (originating from West Africa) or strain NF135, clone C10 (originating from Cambodia) as previously described (Ponnudurai et al., 1989; Teirlinck et al., 2013). For each biological replicate, sporozoites were obtained by aseptically dissecting salivary glands of 200–400 infected mosquitoes 14–21 days after an infective blood meal. Pooled salivary glands were homogenized, filtered, and purified using the leading log2 fold changes (i.e., average [root-mean-square] of the largest absolute log2 fold changes) (Robinson et al., 2010). To generate coverage plots, the gene counts normalized for gene length and sequencing depth by calculating RPKM values in the Rlimma package (Ritchie et al., 2015). Coverage plots were visualized using the Integrated Genomics Viewer (Robinson et al., 2011; Thorvaldsdottir et al., 2013).

**ChIP and Next-Generation Sequencing**

ChIP was performed as previously described (Lopez-Rubio et al., 2009), using 5 x 10^6 *P. falciparum* sporozoites (strain NF54) or 10^5 asexual ring stage parasites (strain 3D7, clone G7). For each ChIP experiment, 0.5 μg anti-H3K3me3 (Millipore #07-442), anti-H3K9ac (Millipore #07-352), or anti-PFHP1 (Chen et al., 2016) rabbit polyclonal antibodies was used. To generate Illumina-compatible sequencing libraries, the immunoprecipitated DNA was processed using the MicroPlex Library Preparation Kit (Diagenode) according to the manufacturer’s instructions. As a control, DNA corresponding to the ChIP input or DNA immunoprecipitated using rabbit IgG (Diagenode, #C15410206) was processed. Pooled, multiplexed libraries were subjected to 150-bp single-end sequencing on an Illumina NextSeq 500. The resulting data were demultiplexed using bc2fastq (illumina) to obtain fastq files for downstream analysis. A minimum of two biological replicates was analyzed for each antibody and each parasite stage (Table S6).

**ChIP-Seq Data Analysis**

Quality control of fastq files was performed using the FastQC software (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/). Sequencing reads were mapped to the *P. falciparum* genome (Gardner et al., 2002; PlasmoDB, v.3) with the Burrows-Wheeler Alignment tool (BWA-MEM algorithm) using default parameters (Li and Durbin, 2009). Uniquely mapped reads were filtered for duplicates and an alignment quality Phred score (Q) ≥ 20 using samtools (Li et al., 2009). The ChIP-seq data were normalized over input cells.

**RNA-Seq Library Preparation and Data Analysis**

For RNA-seq library preparation, total RNA from sporozoites, oocysts, or asexual ring stage parasites was extracted using the mirNeasy Mini Kit (QIAGEN) according to the manufacturer’s instructions, including on-column DNase digestion. Total RNA was poly(A)-enriched using the Dynabeads mRNA Purification Kit (Life Technologies) and subjected to strand-specific RNA-seq library preparation using the TrueSeq Stranded mRNA Library Prep Kit (Illumina). The libraries were multiplexed and subjected to 150-bp single-end sequencing on an Illumina NextSeq 500. The resulting data were demultiplexed using bc2fastq (illumina) to obtain fastq files for downstream analysis. A minimum of two biological replicates was analyzed for each parasite stage (Table S6).

As described earlier, quality control of fastq files was performed using FastQC software and sequencing reads mapped to the *P. falciparum* genome (Gardner et al., 2002; PlasmoDB, v.3) with the Burrows-Wheeler Alignment tool (BWA-MEM algorithm) using default parameters. Gene counts (i.e., the number of aligned reads mapping to different genomic loci) were calculated using bedtools (Quinlan and Hall, 2010). Differential gene expression analysis was performed using the R package edgeR (Robinson et al., 2010).

Multidimensional scaling (MDS) plots were also made in edgeR using ‘plotMDS,’ where distances between pairs of RNA samples correspond to the leading log2 fold changes (i.e., average [root-mean-square] of the largest absolute log2 fold changes) (Robinson et al., 2010). To generate coverage plots, the gene counts normalized for gene length and sequencing depth by calculating RPKM values in the Rlimma package (Ritchie et al., 2015). Coverage plots were visualized using the Integrated Genomics Viewer (Robinson et al., 2011; Thorvaldsdottir et al., 2013).

**DNA Fluorescence In Situ Hybridization and Immunofluorescence Imaging**

Sporozoites were fixed in suspension with 4% paraformaldehyde (PFA) in PBS (pH 7.4) overnight at 4°C. After three PBS washes, parasites were resuspended in PBS, and deposited on poly-L-lysine-coated coverslips (Marienfeld Superior). Parasites were permeabilized with 0.1% Triton X-100 for 15 min and subjected to DNA FISH labeling with the TARE6 probe as described previously for blood stage parasites (Mancio-Silva et al., 2008). Immunofluorescent labeling using rabbit anti-PFHP1 antibodies was performed as previously described (Chen et al., 2010). For combined DNA FISH and immunofluorescence, sporozoites were first labeled with rabbit anti-PFHP1 antibodies (diluted 1:2,000 in 3% BSA [Sigma] in PBS) and then with anti-rabbit Alexa Fluor 488 secondary antibodies (Life Technologies). After an additional fixation step with 4% PFA, DNA FISH was performed using a biotinylated locked nucleic acid (LNA) probe (Exiqon) targeting all TARE6 telomeric repeats (5'-Biotin+AC+TAAAC+A+GG+T+CTT+TA+Biotin-3'), which was then detected with streptavidin-conjugated Alexa Fluor 568 secondary antibodies (Life Technologies).

**NF54 SpzPIEMP1 Protein Expression and Antibody Generation**

The DNA sequence encoding the CIDR-alpha of *P. falciparum* was cloned into the Baculo virus transfer vector pAcGP67-A (BD Biosciences). Recombinant CIDR product was expressed by infection of insect High Five cells with recombinant Baculo virus. Antibodies to Baculo-expressed CIDR were raised in Wistar rats by subcutaneous injection as previously described (Bengtsson et al., 2013). All experimental animal procedures were approved by The Danish Animal Procedures Committee (“Dyreforsøgstilsynet”) as described in permit no. 2008/561-1498 and according to the guidelines described in Danish acts LBK 1306 (23/11/2007) and BEK 1273 (12/12/2008). As a control, DNA was sequenced using the MicroPlex Library Preparation Kit (Diagenode) according to the manufacturer’s instructions. DNA sequencing was achieved by the leading log2 fold changes of each chromatin mark was calculated as average reads per million over bins of 1,000 nt using bamCoverage from the package deepTools2 (Ramirez et al., 2016), unless otherwise specified. Correlation of the different biological replicates was determined using the MACS2 software (Zhang et al., 2009) with default settings and a significance cutoff of FDR < 1%, using Benjamini and Hochberg’s correction method. For genome-wide representation of PFHP1, H3K9ac, and H3K9me3 distribution, the coverage of each chromatin mark was calculated as average reads per million over bins of 1,000 nt using bamCoverage from the package deepTools2 (Ramirez et al., 2016), unless otherwise specified. Correlation of the different biological replicates was determined using the MACS2, bedtools (Quinlan and Hall, 2010), and deepTools2. Circular and linear coverage plots were generated using Circos (Krzywinski et al., 2009) and Integrated Genomics Viewer (Thorvaldsdottir et al., 2013), respectively.
performed in compliance with institutional guidelines and European regulations (http://ec.europa.eu/environment/chemicals/lab_animals/index_en.htm). A statement of compliance with the French government’s ethical and animal experiment regulations was issued by the Ministère de l’Enseignement Supérieur et de la Recherche under the number 00218.01.

**Western Blot Analysis**

5 × 10⁵ *P. falciparum* NF54 sporozoites were resuspended in 100 μL 2× NuPAGE sample buffer supplemented with reducing agent (Thermo Fisher Scientific) and incubated at 95 °C for 5 min, after which DNA was sheared. The resulting sporozoite protein extract was resolved on a 3%–8% Tris-Acetate SDS-polyacrylamide gel (NuPAGE) using MOPS SDS Running Buffer (Thermo Fisher Scientific) and transferred to a PVDF membrane. The membrane was blocked for 1 hr with 5% milk in TBS (50 mM Tris, 150 mM NaCl, 0.1% Tween 20). PIEMP1 proteins were detected using guinea pig anti-ATS antibodies (Nacer et al., 2015) or anti-NF54, SpzPEP1 antibodies. PIADolase was detected with anti-PIADolase-HRP (horseradish peroxidase) antibodies (Abcam, ab38905). Primary antibodies were detected by goat anti-guinea pig-HRP (Abcam, ab6908), anti-rat-HRP, or anti-mouse-HRP (GE Healthcare Life Sciences, NA935V and NA931V, respectively) secondary antibodies. HRP signal was developed with SuperSignal West Pico chemiluminescent substrate (Thermo Fisher Scientific, #34080) and imaged with a ChemiDoc XR+ System (Bio-Rad). Images were analyzed using the Fiji image processing package (http://fiji.sc).

**Immunofluorescence Assay**

NF54 or NF135 sporozoites were placed on poly-L-lysine-coated coverslips for 10 min at room temperature (RT) under one of three conditions: live or fixed in 4% PFA and permeabilized with 0.01% Triton X-100. The cells were blocked with 4% BSA in PBS for 30 min at RT and then incubated with primary antibody for 1 hr at RT; dilutions were 1:1,000 for anti-ATS, 1:11,000 for anti-NF54, SpzPEP1, 1:200 for anti-var2CSA (Avril et al., 2011), and 1:15,000 for anti-CSP (Okitsu et al., 2007) antibodies in 3% BSA in PBS. After three washes with PBS, primary antibodies were detected with Alexa Fluor 488- or 568-conjugated secondary antibodies (Life Technologies) diluted 1:1,000 in 3% BSA in PBS. After three final washes in PBS, cells were mounted in Vectashield containing DAPI for nuclear staining. Images were captured using a Delivation Elite imaging system (GE Healthcare). Image processing of at least two independent replicates was performed using the Fiji package (http://fiji.sc). For trypsinization prior to imaging, 10⁶ living sporozoites were treated with trypsin (GIBCO, 50 mg/mL in 200 μL BSA in PBS) and washed with culture medium and fresh red blood cells. In total, three antibody pannings were performed. The enrichment was assessed at each panning by IFA using anti-NF54, SpzPEP1.

**Determination of Serum Response against NF54, SpzPEP1**

Sera isolated from individuals from a previous clinical trial (Roestenberg et al., 2009) were used to probe HEK293 cells transfected for cell-surface expression of *P. falciparum* proteins. For NF54, SpzPEP1, a DNA construct encoding amino acids 1–737 was used for transfection. These HEK293 cells were analyzed by flow cytometry, as previously described (Peng et al., 2016). Serum response was defined as the percentage of transfected cells that show bound serum antibodies (Peng et al., 2016). For sera with positive serum response (>5%), the serum response against var-transfected cells was compared with the serum response against Ettram142-transfected cells (negative control), using the Mann Whitney U test, and was found to be significantly higher.

**Parasite Panning on Antibody-Coated Magnetic Beads**

Sterile Dynabeads Protein G (Life Technologies 10003D) were incubated with 20 μg filtered anti-NF54, SpzPEP1 IgG for 10 min at RT under agitation. The Dynabeads were blocked with 1% BSA for 20 min. iRBCs containing trophozoites and schizonts were isolated by plasmagel enrichment and resuspended in 400 μL PBS at a concentration of 5 × 10⁴ iRBCs per milliliter. The iRBCs and the beads were mixed by gently pipetting and allowed to bind for 1 hr with gentle agitation at 37 °C. After incubation, the beads were washed 8 times with 800 μL sterile PBS to eliminate all unbound cells. Bound cells were resuspended with culture medium and fresh red blood cells. In total, three antibody pannings were performed. The enrichment was assessed at each panning by IFA using anti-NF54, SpzPEP1.

**DATA AND SOFTWARE AVAILABILITY**

The accession number for the ChiP-seq and RNA-seq fastq files generated in this study is NCBI: PRJNA344838. To understand the files, please refer to Table S6.

**SUPPLEMENTAL INFORMATION**

Supplemental Information includes six figures and six tables and can be found with this article online at https://doi.org/10.1016/j.celrep.2018.02.075.

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**AUTHOR CONTRIBUTIONS**


**DECLARATION OF INTERESTS**

The authors declare no competing interests.

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