PROTECTIVE EFFICACY OF THE RTS,S/AS02 PLASMODIUM FALCIPARUM MALARIA VACCINE IS NOT STRAIN SPECIFIC

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Abstract. RTS,S/AS02 is a recombinant protein malaria vaccine that contains a large portion of the C-terminal of the circumsporozoite protein (CSP) sequence fused to hepatitis B virus surface antigen. It has been shown to induce significant protection to challenge infection with a homologous parasite strain in American volunteers. In a recently completed trial in semi-immune Gambian adults, vaccine efficacy against natural infection was 34% (95% confidence interval = 8–53%, P = 0.014) during the malaria season following vaccination. Breakthrough P. falciparum parasites sampled from vaccinated subjects and from controls were genotyped at two polymorphic regions of the CSP gene encoding T cell epitopes (csp-th2r and csp-th3r) to determine if the vaccine conferred a strain-specific effect. The overall distribution of CSP allelic variants was similar in infections occurring in vaccine and control groups. Also, the mean number of genotypes per infection in the RTS,S/AS02 group was not reduced compared with the controls.

INTRODUCTION

Several prototype Plasmodium falciparum vaccines have undergone preliminary testing in naturally exposed human populations, including circumsporozoite protein (CSP) vaccines against the pre-erythrocytic stage of the infection.4 Trials of CSP vaccines have generally not shown good levels of protection.2–4 However, encouraging results have been obtained with a recombinant protein vaccine known as RTS,S/AS02. This comprises most of the P. falciparum CSP sequence fused to hepatitis B virus surface antigen (HBsAg) co-expressed as a fusion protein in yeast and formulated with the adjuvant AS02.5 An initial trial in naive individuals showed that RTS,S/AS02 conferred a high degree of protection against experimental P. falciparum sporozoite challenge with parasites of the NF54 strain (3D7 clone) used to produce the vaccine.5,6 Subsequent trials in naive individuals have given similar degrees of protection.6–8 Evaluation of the efficacy of RTS,S/AS02 against natural parasite challenge has recently been undertaken in phase III trials in Gambian semi-immune adults with rabies vaccine as the comparator.9 Overall, vaccine efficacy against infection during the malaria transmission season following vaccination was 34% (95% confidence interval [CI] = 8–53%, P = 0.014).9 Vaccine efficacy was 71% (95% CI = 46–85%) during the first nine weeks of surveillance, but subsequently decreased to 0% (95% CI = −52–34%) in the last six weeks.

To evaluate whether RTS,S/AS02 has a protective effect only against parasites with a CSP sequence similar to that of NF54, parasites from breakthrough infections in control and vaccine groups have been characterized at two highly polymorphic epitope sequences encoded within the CSP gene, csp-th2r and csp-th3r. In addition, we investigated whether vaccination with RTS,S/AS02 led to a reduction in the mean number of P. falciparum genotypes per infection, as has been described previously in trials with the SPf66 malaria vaccine conducted in Tanzania and in The Gambia.10,11

MATERIALS AND METHODS

Study area, population, and design. The aim of the vaccine trial was to evaluate the efficacy, safety, and immunogenicity of RTS,S/AS02; the primary endpoint of efficacy was first infection with P. falciparum. Details of the study area and design have been previously reported.12 Briefly, adult male volunteers 18–45 years of age were recruited from six villages in Basse in the Upper River Division of The Gambia in 1998. Volunteers were given either three doses of RTS,S/AS02 or rabies vaccine over a five-month period (February to August) before the malaria transmission season (August to December). Pyrimethamine/sulfadoxine (Fansidar;® F. Hoffmann LaRoche, Basel, Switzerland) was given two weeks before the third dose of vaccine to clear blood stage infections. Starting two weeks after administration of the third dose of vaccine, volunteers were visited daily by field workers who were posted to each of the six villages for 15 weeks during the transmission season. Each week and whenever a volunteer had symptoms compatible with malaria, two thick blood films were made and three drops of blood were spotted onto glass fiber membranes for parasite genotyping. Only the first parasite-positive samples for each subject were used in genotyping for allelic specificity of RTS,S/AS02 at the csp-th2r and csp-th3r loci and for measurement of the multiplicity of infection (MOI) at three unrelated loci.

Written informed consent was obtained from adult males participating in the trial. The study was approved by the Joint Gambia Government/Medical Research Council Ethics Committee, an Independent Data Safety Monitoring Committee, and collaborating partners’ Institutional Review Boards. The trial, which was conducted according to International Conference of Harmonisation (ICH) Good Clinical Practice guidelines, was monitored by the World Health Organization and GlaxoSmithKline Biologicals.

Genotyping of CSP polymorphic epitope sequences. Extraction of DNA and amplification by the polymerase chain reaction (PCR) of a 319-base pair fragment of the CSP gene were performed as described previously.15 Samples of DNA were amplified routinely in a single round PCR. However, samples with low parasitemia were amplified in a second round PCR using fresh primers, Tag DNA polymerase (BIOTAQ™ Bioline, London, United Kingdom), and 1 μl of PCR CSP gene product from the first PCR. PCR products were subsequently tested by sequence-specific oligonucleotide probing, a tech-
nique that was designed specifically for these investigations. The overall allele frequencies at both regions of the csp sequence (th2r and th3r) were determined by counting each allelic type detected in an isolate and dividing it by the total number of alleles detected in the samples analyzed. When more than one allele was present in an isolate, it was necessary to score the results based on the relative intensity of hybridization of the probes to each allele. In this way, it was possible to determine the major allele, i.e., the allelic form that gave the strongest hybridization signal (minor alleles hybridized weakly but specifically to their respective probe). Allele frequencies at csp-th2r and csp-th3r loci at the trial site had been characterized in 1997 before the start of the study.12

Genotyping of other markers to assess multiplicity of infection. The same set of DNA samples was analyzed for diversity at other genetic markers that contain polymorphic repeat sequences. The markers tested were within the merozoite surface protein 1 (msp1), msp2, and glutamate-rich protein (glurp) genes. An allele-specific, nested PCR was used for the discrimination of msp1 block 2 and msp2 allelic families, and the allelic variants present within the RII repeat region of glurp were detected by semi-nested PCR.13 PCR products were resolved by electrophoresis through Metaphor™ (FMC BioProducts, Rockland, ME) agarose gels in 0.5× TBE buffer, stained with ethidium bromide, and visualized by ultraviolet transillumination. Bands corresponding to parasite allelic forms were distinguished by their size and counted and the number of genotypes for msp1, msp2, and glurp loci determined for each isolate. In addition, the overall MOI for each isolate was then determined as the highest number of alleles observed at any of the loci.

Statistical analyses. To test if RTS,S/AS02 vaccine efficacy was allele-specific, we compared the frequency of the csp-th2r*03 and csp-th3r*03 alleles (vaccine type) in breakthrough infections in the vaccine and control groups using the chi-square test. The Wilcoxon test14 was used for two-group comparisons and the Cuzick15 non-parametric linear trend test was used when the groups were ordered (parasite density and time). Poisson regression was used to produce estimates of the ratio of control to RTS,S/AS02, which was estimated using the primary analysis concentrated on the effects of vaccination with RTS,S/AS02 on the frequency of the NF54-like allele in breakthrough infections when present either alone or with other alleles. Fifteen alleles were detected at csp-th2r locus (Figure 1a). No new types were detected. At the csp-th3r locus, 10 alleles were detected (Figure 1b), and a small number of new alleles were detected with low frequencies in both groups (<5%), but these were not characterized further. The csp-th2r*03 allele (vaccine type for th2r sequence) was present in nine of 77 infections in subjects in the RTS,S/AS02 group (12%) and in 28 of 80 infections in subjects in the control group (35%) (Figure 1a). These proportions are higher than the allele frequencies because some infections contained more than one parasite genotype.

Analysis of MOI. One hundred fifty-seven DNA samples were genotyped at the polymorphic loci msp1, msp2, and glurp (all samples were successfully amplified at the three loci). A high degree of genetic diversity was observed. Overall MOI was significantly higher in the RTS,S/AS02 group than in the controls, 4.90 and 4.23, respectively (P = 0.05) (Table 1). The ratio of control to RTS,S/AS02, which was estimated using

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**Table 1**

<table>
<thead>
<tr>
<th>MOI</th>
<th>msp1</th>
<th>msp2</th>
<th>glurp</th>
<th>Overall</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vaccine group†</td>
<td>RTS,S/AS02 (n = 77)</td>
<td>3.86 (1.85)</td>
<td>4.25 (2.11)</td>
<td>2.61 (1.50)</td>
</tr>
<tr>
<td>Controls (n = 80)</td>
<td>3.54 (1.86)</td>
<td>3.45 (2.01)</td>
<td>2.11 (1.44)</td>
<td>4.23 (1.94)</td>
</tr>
<tr>
<td>Time to first infection‡</td>
<td>0–59 days (n = 49)</td>
<td>3.20 (1.54)</td>
<td>3.31 (1.62)</td>
<td>2.33 (1.48)</td>
</tr>
<tr>
<td></td>
<td>60–76 days (n = 54)</td>
<td>3.69 (1.83)</td>
<td>3.76 (2.01)</td>
<td>2.13 (1.54)</td>
</tr>
<tr>
<td></td>
<td>77–111 days (n = 54)</td>
<td>4.15 (2.05)</td>
<td>4.41 (2.41)</td>
<td>2.61 (1.42)</td>
</tr>
<tr>
<td>Parasite density/μL</td>
<td>&lt;10 (n = 46)</td>
<td>3.43 (1.87)</td>
<td>3.13 (1.76)</td>
<td>1.91 (1.38)</td>
</tr>
<tr>
<td></td>
<td>10–99 (n = 60)</td>
<td>3.88 (1.83)</td>
<td>4.12 (2.06)</td>
<td>2.55 (1.53)</td>
</tr>
<tr>
<td></td>
<td>≥100 (n = 51)</td>
<td>3.71 (1.88)</td>
<td>4.16 (2.27)</td>
<td>2.53 (1.46)</td>
</tr>
</tbody>
</table>

* msp = merozoite surface protein; glurp = glutamate-rich protein. Standard deviations for the MOI are in parentheses.
† 161 subjects who received 3 doses of vaccine developed parasitemia; 157 of 161 primary infections were genotyped.
‡ Time to infection and parasite density were grouped to give three groups with approximately equal numbers of infections in each group. P values were obtained using the non-parametric trend test. Median time to infection was 82 days in the RTS,S/AS02 group and 73 days in the rabies group.

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Of 306 volunteers who were enrolled in the trial, 250 received all three doses of vaccine (131 RTS,S/AS02 and 119 controls) and were followed-up for 15 weeks. One hundred sixty-one volunteers had at least one episode of asexual parasitemia and DNA from 157 (98%) of these individuals was successfully amplified by PCR and characterized at several loci (77 from subjects in the RTS,S/AS02 group and 80 from those in the controls). Forty-nine samples had low parasitemias (<10 parasites/μL), and for some of these it was necessary to perform two rounds of PCR amplification before genotyping at the csp-th2r and csp-th3r loci could be performed. Age distribution, pre-vaccination anti-CSP and anti-HBsAg antibody concentrations were similar in the two vaccine groups at enrolment and at the start of surveillance.

Genotyping at the csp-th2r and csp-th3r loci. The overall allele frequencies were similar to those described previously for a population sample in the trial site before vaccination.12
Poisson regression and adjusting for effects of time period and village by including these variables as factors in the model, was 0.96 (95% CI 0.81–1.13) for msp1, 0.84 (95% CI 0.71–0.99) for msp2, 0.80 (95% CI 0.65–0.99) for glurp, and 0.88 (95% CI = 0.76–1.03) overall. The MOI increased during the transmission season and was higher at the end of the season than at the beginning (Table 1); however, there was no interaction between the effect of the vaccine group and the time to infection.

The MOI varied significantly between villages in the study area and correlated positively with parasite density. No association was seen between MOI and age.

**DISCUSSION**

This study demonstrates that RTS,S/AS02 protected Gambian semi-immune adults against *P. falciparum* infections in a
non-allele-specific manner. Genotyping of breakthrough parasites at the csp-th2r and csp-th3r epitopes showed that allelic frequency of the vaccine-type allele sequences were similar in both vaccine and control groups, although the vaccine had a marked effect on the incidence of infection. Frequencies of all other csp allelic types were similar in the two groups.

If RTS,S/AS02 had an allele-specific effect, a reduction in the prevalence of the csp-th2r*03 and csp-th3r*03 alleles should have been observed. Given the prevalence of the csp-th3*03 allele (35%) and the sample size in each group, the study had 99% power to detect a two-fold allele-specific effect of RTS,S/AS02. Since the prevalence of the vaccine type at th2r (csp-thr2*03) was 16%, the study had 60% power to detect a two-fold effect at that locus. Thus, the statistical power was very high for th3r and reasonably high for th2r, so the lack of an allele-specific effect is well supported.

Studies of immune responses elicited by vaccination with RTS,S/AS02 suggest that protection may be mediated, at least in part, by antibodies against the NANP(n) repeat region of CSP, a conserved region among all _P. falciparum_ parasite strains. In the RTS,S/AS02 group, anti-CSP antibody levels to the NANP(n) repeat region were 20 times higher after the third dose than those in the control group and these levels correlated with efficacy among the vaccinees.

The vaccine also induced strong T cell responses as determined by proliferation and cultured ELISPOT (Millipore, Watford, England) to many peptides in the th2r and th3r epitopes of _csp_, although, given the small numbers studied for these responses it has yet to be examined whether these responses were associated with protection. Our decision to analyze csp-th2r and csp-th3r epitopes for correlation with protection was based partly on the absence of real T cell protective epitopes, and partly on existing suggestive data, that these two epitopes might be protective.

The T cell responses to peptides within the conserved CST3 region apparently correlated with protection. This and the conserved NANP(n) antibody epitope might explain why there was no specific effect on the frequency of any allelic type of _csp_ in vaccinees compared with controls.

Having established that RTS,S/AS02 vaccine did not have any effect on the distribution of alleles at the csp-th2r and csp-th3r loci, the possibility that it reduced the genetic complexity of infection (MOI) as assessed by typing of unrelated parasite strains was investigated. This approach was prompted by reports that children vaccinated with another malaria vaccine (SPf66) in Tanzania and The Gambia had a marked effect on the incidence of infection. Frequencies of all other _csp_ allelic types were added another dimension to the understanding of the molecular mechanisms involved in conferring protection against a specific parasite strain. This study has clearly demonstrated that the effect of RTS,S/AS02 vaccine is not allele-specific. The non-allelic protective efficacy of RTS,S/AS02 vaccine should encourage the testing of this vaccine in transmission settings where the NF54 strain is not the predominant type. Molecular typing should become an integral part of the evaluation of future malaria vaccine trials in which vaccines that might be anticipated to have a strain specific effect is used.

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REFERENCES:

7. Kester KE, McKinney DA, Tornieporth N, Ockenhouse CF,


