Association of a Single Nucleotide Polymorphism in the C-Reactive Protein Gene (-286) with Susceptibility to Plasmodium falciparum Malaria

Association of a Single Nucleotide Polymorphism in the *C-Reactive Protein* Gene (–286) with Susceptibility to *Plasmodium falciparum* Malaria

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The role of inflammation in malaria pathogenesis is not fully understood, although C-reactive protein (CRP) may have a negative influence on host immunity to infections. An upstream polymorphism, –286 (C > T > A), in the *CRP* gene is known to influence CRP levels. In this study, a cohort of 192 Sudanese donors, followed for malaria infection for 9 years, had their *CRP* –286 gene locus genotyped by pyrosequencing. The number of malaria episodes experienced by each individual over the study period was used as an index for malaria susceptibility. The prevalence of the *CRP* alleles A, C and T were 21%, 52% and 27%, respectively. Importantly, the A-allele, unlike the C- and T-alleles or *CRP* genotypes, was significantly associated with an increased number of malaria episodes, $P = 0.007$. The proportion of A-allele carriers among donors not known to have had malaria during the study period was 18%, whereas it was 43% and 63% among donors who had experienced 1–4 and ≥5 malaria episodes, respectively, over the same period ($P = 0.002$). Furthermore, the A-allele was associated with higher parasite counts. In conclusion, the *CRP* –286 A-allele was associated with an increased susceptibility to uncomplicated *Plasmodium falciparum* malaria.

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INTRODUCTION:

Malaria imposes an unlimited burden in communities, notably in sub-Saharan Africa and other equatorial regions (1). Over time, malaria infections have left imprints in the human genome that evolved into single nucleotide polymorphisms (SNPs) of genes involved in protection/susceptibility to malaria (2). The role of inflammation in malaria pathogenesis is not well understood (3).

C-reactive protein (CRP), a nonspecific acute-phase protein, is a classic marker for inflammation. CRP is found in plasma in trace amounts in healthy individuals, and increases in concentration 100- to 10,000-fold during acute inflammation and in disease situations including infections (4,5). CRP is produced predominantly by the liver and its production is induced by the proinflammatory cytokine interleukin 6 (IL-6) (6,7).

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Recent studies suggest that CRP acts through FcγR to reduce inflammation and protect against certain autoimmune diseases (8). Structurally, the CRP has a sequence homology (shared domains) to the FcγR binding regions of IgG (9). Furthermore, CRP has high affinity to the R131-allele product of the *FcγRIIa* gene (10), an allele that has been associated with protection against malaria (11). Thus, CRP could be a natural competitor for antimalarial IgG binding to phagocytic and other FcγR-containing cells. Interestingly, both *CRP* and *FcγR* genes are located on chromosome 1.

Although the pathological role of CRP in cardiovascular diseases has been thoroughly investigated (12), its role in parasitic infections, more specifically in ma-

laria, has been less investigated (13). The involvement of CRP in human defense against infection is partially due to its capacity to bind to phosphorylcholine in membranes of microorganisms (14,15). In malaria, the secretion of CRP is induced by proinflammatory cytokines secreted by host monocytes/macrophages (16), and strong correlations have been found between CRP levels and parasitemias (17). Furthermore, apparently healthy African children were found to have higher levels of CRP compared with children in Europe (18) and Papua New Guinea (13), which might indicate chronic malarial parasitization of the former population.

The *CRP* gene is highly polymorphic, with SNPs identified at several loci; however, the trialleleic –286 (C > T > A) SNP (rs3091244) is strongly associated with the plasma CRP concentration (19). The A-allele was found to be associated with higher basal levels of CRP (20). The distribution of *CRP* genotypes and alleles are geographically and ethnically different. Previous studies showed that the A-allele is more common in African than in white populations (21), and would thus be expected to confer a survival advantage for the inhabitants of malaria endemic areas. We examined three SNPs; –286 C > T > A, –717 T > C and +1444C > T in material obtained from Daraweesh village in eastern Sudan. The –286 SNP was found to be different in ethnic groups with varying susceptibility to malaria (22); thus, it was selected for further analysis in this study.

MATERIALS AND METHODS

Study Area and Population

This study was carried out in Daraweesh village (the total population was >550 individuals in 2005), eastern Sudan, between 1991 and 2005. The inhabitants are descendant of the Fulani tribe from Higher Volta (Burkina Faso) in West Africa. The ethnicity in Daraweesh has been maintained by a high rate of intermarriage. In Daraweesh, malaria transmission is seasonal, starts in September, peaks in October or November and declines in January to a baseline of few sporadic cases, a pattern that continues to August. The malaria incidence is markedly unstable; severe epidemics occur in flood years, whereas in drought years malaria cases are almost absent. In Daraweesh more than 98% of the malaria infections were due to *Plasmodium falciparum*. An individual in the village is unlikely to experience more than one malaria episode in the same season (23,24).

Table 1. The frequencies of the *CRP* –286 (C > T > A) genotypes carriers, characterization of the genotype carriers and association of the genotypes with the frequency of malaria episodes over 9 years of follow-up in Daraweesh village.

CRP genotype	Frequency (n)	Age in years in 2005 (median, 25–75%)	Sex, M/F	Proportions of Hb AS (n)	Malaria episodes (median, 25–75%)
AA	0.052 (10)	27.0 (11.0–43.0)	1/9	10.0% (1)	1.5 (0.0–2.00)
AC	0.193 (37)	24.0 (12.8–46.8)	12/25	16.2% (6)	2.0 (1.00–3.00)
AT	0.125 (24)	19.5 (13.5–36.5)	7/17	20.8% (5)	2.0 (1.00–3.00)
CC	0.302 (58)	21.5 (13.0–32.0)	19/39	19.0% (11)	1.0 (0.00–2.00)
CT	0.245 (47)	16.0 (9.3–29.8)	23/24	17.0% (8)	1.0 (0.00–2.00)
TT	0.083 (16)	17.0 (11.0–23.5)	5/11	12.5% (2)	2.0 (0.00–2.00)
Total	(192)	19.0 (12.0–34.5)	67/125	17.2 (33)	1.5 (0.00–2.50)
Range		6–78			0–7
P values		$P = 0.382$[a]		$P = 0.964$[b]	$P = 0.076$[a]

[a]Kruskal–Wallis one-way analysis of variance on ranks.
[b]Chi-square test.

Study Design

The Daraweesh project was a total population longitudinal study begun in 1991, aiming to document seasonal incidence of malaria in the village, with a cohort-based component for study of the natural immune response to malaria. The study design has been thoroughly described (23,25). Malaria infection was documented by active and passive surveillances during the malaria season. Data used in this study were obtained over a 9-year period between 1991 and 2005. This study used longitudinally collected data for 3 parameters: the number of malaria episodes, the parasite density and the temperature. For consistency in execution and method, we used the parasite density data obtained in the period between 1993–1996, when the density was scored semiquantitatively (+, + +, + + + and + + + +) and in 1998–1999, when parasite count was used. However, during both periods heavy malaria transmission occurred in the area. The plasma samples used in this study were obtained in May 2005 from 192 donors. All donors had no malaria infection at the time of sampling, demonstrated by polymerase chain reaction (PCR) analysis of the samples. The number, age and sex of the patients are shown in Table 1.

Longitudinal Clinical and Parasitological Data

Clinical examination and malaria diagnosis. Malaria was defined as fever with measurable temperature of ≥37.5°C or a recent history of fever and microscopically detectable asexual *P. falciparum* parasitemia of any count. Individuals complaining of fever or symptoms suggestive for malaria were clinically examined, then oral temperature (in young children axillary temperature) and body weight were measured; thereafter, a blood smear was taken. Thin and thick blood films were stained with Giemsa and examined microscopically for detection of both sexual and asexual stages of *P. falciparum* parasites, using the WHO standard procedure (26). Slides were read and revised by expert microscopists using light microscopy. Malaria patients were mostly treated with chloroquine alone (10-10-5 mg/kg/day, over 3 d); however, in the last two malaria seasons,

in addition to chloroquine, dihydroartimisinin and sulphadoxine/pyrimethamine were used. For clinical and parasitological follow-up, passive and active surveillances were carried out and the overall morbidity and mortality during the study period were documented as previously described (23,25). Individuals in Daraweesh are less likely to develop more than one malaria episode in the season, because only <8% of the recrudescent parasites show new genotypes (24). Chemoprophylaxis and bed-nets were not used in the village.

The consent of the village leaders was obtained and individual informed consent was obtained from donors or parents. The finger prick and venous blood sample donation were entirely voluntary; however, for young children the consent was sought from the parents/guardians. Ethical permission for the study was granted by the ethics committees of the University of Khartoum and Ministry of Health, Sudan, and national clearance from the Sudanese Ministry of Health was obtained.

Blood Samples

Blood samples (3 mL collected in EDTA-coated vacutainers) were obtained from 192 donors. The donors included most of the villagers who were available at the time of the survey. The sampling was done before the malaria transmission season, in May 2005, at a time when all donors were asymptomatic and their blood smears were negative for malaria parasite. The blood was centrifuged for 15 min at 250*g*, and the buffy coat was separated and stored at –20°C.

DNA Preparation

DNA was extracted from blood with Chelex-100. Briefly, around 25 μL of peripheral blood was incubated at 4°C in 1 mL of 0.5% Saponin in phosphate-buffered saline overnight, and then washed in 1 mL phosphate-buffered saline at 4°C for 15–30 min. The pellets were boiled in 200 μL of 5% Chelex-100 in water for 15 min, and after centrifugation at 8,000*g* for 3 min the DNA was collected in supernatants and stored at –20°C.

CRP Genotyping with Pyrosequencing

The –286 C > T > A *CRP* polymorphism (rs3091244) was analyzed by the pyrosequencing method (22). PCR primers were designed to amplify the –286 C > T > A polymorphism, using the forward and reverse primer (MWG-Biotech AG, Ebersberg, Germany). The PCR amplification was performed in a 40-μL reaction using 8 μL of genomic DNA, 20 μL iProof™ High-Fidelity Master Mix (BIO-RAD Laboratories, Hercules, CA, USA), and 1.5 μL of each primer (10 pmol/μL). The PCR was carried out in an Eppendorf Mastercycler® (Eppendorf AG, Hamburg, Germany) using a 30-s denaturation at 98°C followed by 35 cycles with 98°C for 10 s, 59°C for 20 s and 72°C for 15 s. The final extension was at 72°C for 5 min. The sequencing primer was 5′-GTG CAC CCA GAT GGC-3′ (MWG-Biotech AG), and the nucleotide dispensation order was GCACGTACAGT. Sequencing was carried out as instructed by the protocol using the PSQ™ 96MA pyrosequencing apparatus.

Statistical Analysis

Sigma Stat software was used for data analysis. Kruskal–Wallis one-way analysis of variance on ranks was used for comparison of age, parasite count and number of malaria episodes between the different *CRP* –286 allele/genotype carriers. Proportions and rates were tested by Chi-square test or Fisher exact test and correlations were performed by using Pearson product moment correlation.

RESULTS

Longitudinal Clinical Data

The age of the donors ranged between 6 and 78 years, with a median (25–75%) age of 19 (12–34.5 years) at the time of blood sampling in May 2005. There were no significant age differences between the carriers of the different *CRP* –286 genotypes ($P = 0.382$, Kruskal–Wallis one-way analysis of variance on ranks). Although females predominated in this study (male/female ratio 67:125), the sex ratios were comparable between the groups. The number of malaria episodes experienced by each individual over the study duration was not correlated with the donor age at the time of sampling ($r = –0.103$, $P = 0.154$). However, when the analysis was limited to individuals born at least 1 year before the beginning of the study in 1991, there was an inverse relationship between age (year of birth) and number of malaria episodes ($r = –0.266$, $P = 0.003$, n = 121), that is, older individuals had a lower number of malaria episodes.

Selection of SNP for Analysis in the *CRP* Gene

There are several SNPs in the *CRP* gene that could be investigated. However, in a previous study, at least 30 SNPs were identified, 9 of which were found to correlate with plasma CRP levels, but there was strong linkage disequilibrium between these SNPs. With stepwise selection, the trialleleic (C > T > A) SNP –286 (rs3091244) remained strongly associated with plasma CRP concentration, independent of other polymorphisms (19). In our previous study, we examined the –286 SNP in addition to another two polymorphisms, –717 T > C (rs2794521) and +1444C > T (rs1130864). Because the prevalence of –286 SNP, unlike that of the latter two polymorphisms, was significantly different in sympatric ethnic groups with varying susceptibility to malaria in Sudan (22), this SNP was selected for further analysis.

The *CRP –286* Genotypes and Frequency of Malaria Episodes

The frequencies of the six *CRP* genotypes (AA, AC, AT, CT, CC and TT) in Daraweesh are shown in Table 1. The lowest and highest frequencies were AA, 0.052 (n = 10) and CC, 0.302 (n = 58), respectively. The number of malaria episodes (median, 25–75%) experienced by the carriers of the above genotypes were comparable, $P = 0.076$, (Table 1).

CRP –286 C- > T- > A-Alleles and Frequency of Malaria Episodes

The frequencies of *CRP* –286 alleles in decreasing order were; C-allele (52.08%), T-allele (26.8%) and A-allele (21.1%). During the 9 years of study, comparison of the number of malaria episodes (median, 25–75%) between A-allele carriers, (n = 71) 2, 1–3, and non–A-allele carriers (n = 121) 1, 0–2, showed that the difference was strongly statistically significant ($P = 0.007$) (Figure 1). The number of malaria episodes was comparable between the C-allele (n = 50) 2, 1–3 and non–C-allele carriers (n = 142) 1, 0–2, $P = 0.205$. Similarly, between the T-allele (n = 87) 2, 0–3.0 and non–T-allele carriers (n = 105) 1, 0–2, $P = 0.688$. Although only 18.2% (10 of 55) of the patients who did not develop malaria during the follow-up were A-allele carriers, 63% (5 of 8) of the donors who had experienced the highest number of malaria episodes (≥5 episodes) were A-allele carriers. Approximately 43% (56 of 129) of the donors who had experienced between 1 to 4 malaria episodes were A-allele carriers (Figure 2). The overall differences in the proportions between the A- and non–A-allele carriers in all ranks of infections (0 to ≥5 episodes) were significant, $P < 0.002$.

CRP Genotypes/Alleles, Parasite Density and Oral Temperature

The parasite count (malaria seasons 1998–1999 [n = 140]) did not differ between the carriers of the different *CRP* genotypes ($P = 0.384$), but there were statistically significant higher parasite counts among A-allele carriers (n = 65) (2460.0, 455.5–9680.8 parasites/μL of blood [median, 25–75%]) compared with the non–A-allele carriers (n = 75) (983.0, 244.8–4950.0), $P = 0.039$. The parasite counts were comparable between the C-allele carriers and non–C-allele carriers ($P = 0.898$) and between the T-allele carriers and non–T-allele carriers ($P = 0.279$) (Figure 3). However, using the semiquantitative parasite density scoring (malaria seasons 1993–1996), we found no significant differences between the *CRP* phenotype carriers (n = 156) ($P = 0.310$), or between C-, T-, or A-allele carriers and the corresponding noncarriers ($P = 0.612$, $P = 0.580$, $P = 0.395$, respectively). Similarly, there were no differences in oral temperature between the different *CRP* –286 phenotypes/allele carriers (data not shown). There was no association between the parasite count and oral temperature ($r = –0.0008$, $P = 0.992$ [n = 171]), although there was a positive correlation between the oral temperature and the semiquantitative scoring of parasite density ($r = 0.279$, $P < 0.001$ [n = 360]).

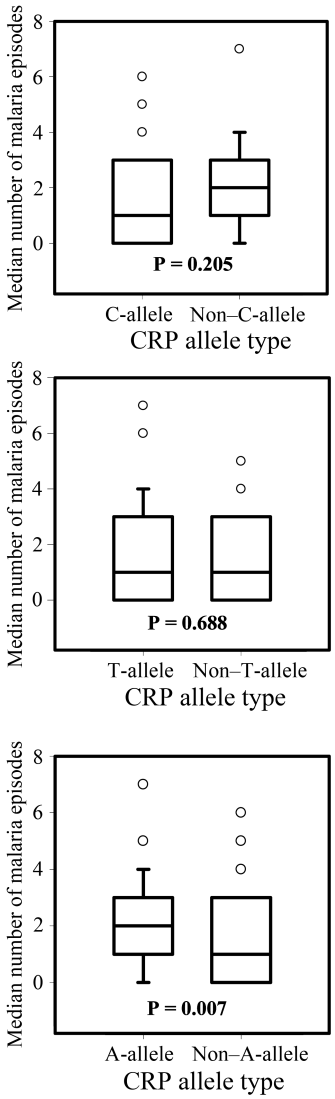

Figure 1. The median number (25–75%) of seasonal malaria episodes experienced by Daraweesh inhabitants during 9 years of surveillance. Comparisons were set between the *CRP* –286 C-allele (A), T-allele (B) and A-allele (C) carriers and the noncarriers of corresponding alleles. There was a strongly significant difference in the number of malaria episodes between the A-allele carriers and the non–A-allele carriers ($P = 0.007$), but not between the pairs of carriers and noncarriers of the other two alleles.

Number of Malaria Episodes and Distribution of *CRP* Genotypes/Alleles between Carriers and Noncarriers of Sickle Hemoglobin

The sickle hemoglobin (Hb AS) carriers (n = 33) experienced a similar number of malaria episodes ([median, 25–75%] 2.0, 0.0–2.25) as the Hb AA carriers (1.0, 0.0–2.75 [n = 159]), $P = 0.944$, even when the analysis was limited to individuals born before the year 1991 ($P = 0.834$). Although only one of the AA genotype carriers (10%, 1 of 10) was a carrier of Hb AS, the proportions of the latter among the other *CRP* genotype carriers were not significantly different (range 12.5–20.8%), $P = 0.964$. The frequency of the Hb AS trait was comparable between the *CRP* –286 A-allele (16.9%, 12/59) and non–A-allele (17.3%, 21/100) carriers ($P = 0.906$); similarly, Hb AS was not associated with C- or T-alleles (data not shown).

DISCUSSION

The overwhelming effect of malaria on man over history has imposed evolutionary alterations of the human genome (27), particularly of genes involved in defense mechanisms, to decrease the disease burden. In this study, we found that the *CRP* –286 A-allele was associated with remarkably increased susceptibility of the Sudanese donors to malaria. This could be one reason for the low prevalence of the A-allele in this area. The *CRP* –286 A-allele influence on malaria susceptibility in this cohort was stronger than the effect of Hb AS, the latter known to be associated with reduced malaria burden. Furthermore, although A-allele carriers account for only 18% of the malaria-resistant individuals (not

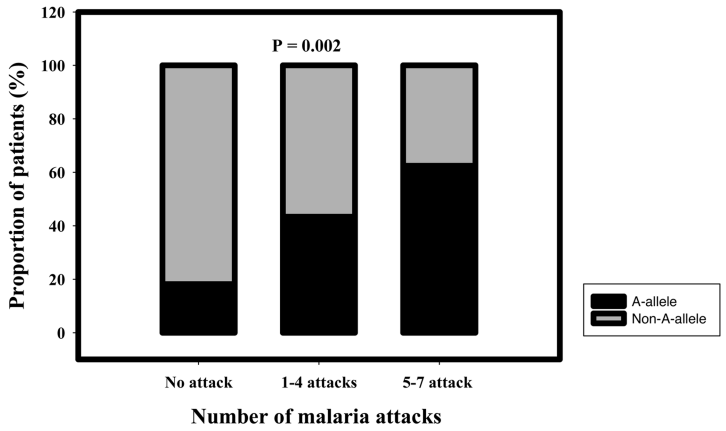

Figure 2. Proportion of A-allele carriers (18%, 43% and 63%) among donors reported to have had no malaria episode (no attack), 1–4 malaria episodes (1–4 attacks) or 5–7 episodes (≥5 attacks), respectively. The number of the malaria episodes was based on 9 years of surveillances in Daraweesh village. The differences in the proportions of the A-allele between the three groups was significant, $P = 0.002$, Chi-square test.

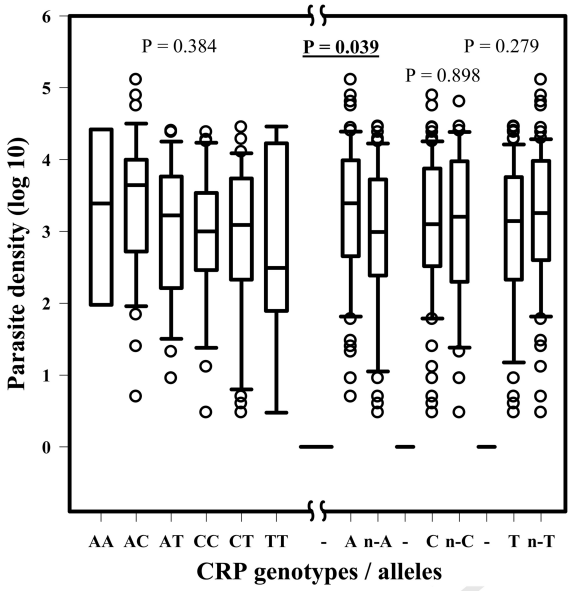

Figure 3. As shown in this figure, there were no significant differences in the parasite counts (in acute and recrudescent infections taken together) between carriers of the different *CRP* –286 genotypes, AA, AC, AT, CC, CT and TT, in Daraweesh (malaria seasons 1998 and 1999), $P = 0.384$. However, the parasite count was significantly higher among the A-allele carriers compared with the non–A-allele carriers ($P = 0.039$), but there were no significant differences between the C- and T-allele carriers compared with the non–C- and non–T-allele carriers, respectively. The break in the *x*-axis separates the genotypes from the alleles of the *CRP* gene.

known to have had malaria in 9 years), they accounted for 63% of the most susceptible individuals in the village. This might be the first report that strongly indicates a role for a *CRP* polymorphism and probably of inflammation in malaria susceptibility. However, the effect of the CRP on susceptibility to malaria might be equally due to modulation of immunity, independently of inflammation.

The dual role of host immunity in protection from as well as in pathogenesis of malaria is known (28). In contrast, the role of inflammation in malaria protection and pathogenesis is not well defined. The implication of plasma CRP levels and inflammation in pregnancy-associated anemia in the tropics has been reported (29), otherwise the literature lacks data relating inflammation or CRP with malaria pathogenesis. Unlike acquired immunity, inflammation is a nonspecific response to different diseases and there are no specific units for measurement of inflammation. However, CRP is one of the best markers for inflammation (6). Polymorphisms in the promoter region of the *CRP* gene (–286 C > T > A) affect the plasma CRP level, and the A-allele has been found to be associated with high CRP concentrations (19, 20).

In this study, the A-allele compared with the non–A-allele carriers had the tendency to have higher parasite density when they developed a new malaria attack or upon recrudescence of parasitemia. The association of CRP level with malaria infection has been previously reported (17,18,30). However, the unique observation in this study is that the association of the A-allele with parasitemia was based on several infections in the same individual and included the parasite density following treatment failure. There was no association, however, between the *CRP* genotypes/alleles or the parasite density and body temperature. This result is in line with our observation that high parasitemia does not always parallel malaria symptoms, including fever.

Taken together, the above findings are suggestive of a strong association between CRP and susceptibility to malaria. Possible explanations for this association are (a) inflammation constitutes part of malaria pathogenesis and CRP plays a role in the inflammatory process; (b) CRP modulates host humoral immunity (it has been suggested that CRP binds FcγR in immune cells,

thereby interfering with the immune response to the malaria parasite by inhibiting the binding of malaria-specific IgG antibodies [9]) or (c) CRP modulates the host cellular immunity by altering the proinflammatory (IL-6)/antiinflammatory (IL-10) cytokine balance (16). These effects are not mutually exclusive, however, and are mediated by structurally normal CRP, that is, the SNP is in the noncoding promoter sequence. Thus, what matters is the plasma CRP level, regardless of the causative polymorphism. Additional evidence for the role of CRP in malaria susceptibility was our finding that the A-allele is less frequent in the Fulani ethnic group compared with the neighboring sympatric tribes (22). The Fulani are known to be relatively less susceptible to malaria than their neighbors in different countries in West Africa (31,32). The Daraweesh Fulani are originally from Burkina Faso, in West Africa.

Interestingly, the *CRP* –286 A-allele but not the AA genotype was associated with increased malaria susceptibility, a situation similar to the role of sickle hemoglobin, for which the Hb AS but not the Hb SS genotype is associated with protection from malaria (33). That situation may be explained by the fact that mutations/polymorphisms are developed to overcome certain risks, but the same mutations might incur a fitness cost in the host. Thus, when both alleles are affected the cost might outweigh the benefit. Furthermore, we found no difference in the number of malaria episodes experienced by the Hb AA and Hb AS carriers and the distribution of Hb AS was not different between the different *CRP* –286 genotypes/allele carriers. However, the number of Hb AS carriers was small in this study. Similar studies should be performed to investigate different endemic settings and other functional noncoding and structural coding *CRP* gene mutations.

In conclusion, in this longitudinal cohort-based study in Daraweesh, we found a strong association between increased malaria susceptibility and *CRP* –286 A-allele carriage. In addition, A-allele carriers had significantly higher parasitemia compared with non–A-allele carriers. Consequently, these data suggest a strong association between inflammation and malaria pathogenesis, an association that is greater than previously described.

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DISCLOSURE

The authors declare that they have no competing interests as defined by *Molecular Medicine*, or other interests that might be perceived to influence the results and discussion reported in this paper.

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