SHORT REPORT

Does apolipoprotein E polymorphism influence susceptibility to malaria?

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Outcome of infection varies greatly among people, and in the case of three very different viruses, it is determined by apolipoprotein E (*APOE*) genotype. *APOE* might affect outcome of malaria infection also, since apoE protein and the protozoon (like the viruses) share cell entry mediators (heparan sulphate proteoglycans and/or specific apoE receptors). *APOE* polymorphisms give rise to protein variants that differ in binding strength to these mediators; thus, the extent of competition between apoE and protozoon for cell entry, and hence magnitude of protozoan damage, might depend on apoE isoform. Genotypes of infants infected with malaria were examined. It was found that *APOE* ε2 homozygotes became infected at an earlier age than those carrying the other genotypes, the difference being statistically significant. Parasite densities, all of which were low, did not differ significantly. This effect, although based on small numbers, suggests that *APOE* ε2 may be a risk factor for early infection.

Malaria affects about 200-300 million people at any one time and more than one million, mostly children, die as a result each year. The age at which primary infection occurs varies greatly; some infants are infected at or very soon after birth whereas others become infected later.[1 2] This depends in part on the intensity of malaria transmission but genetically determined differences between people may also influence risk of infection. Numerous genetic factors have been shown to influence the outcome of malaria infection,[3] but none has been shown to affect the risk of infection per se. If a genetic factor involved in susceptibility to infection, or in severity of response to infection, were to be identified, this would contribute to our understanding of the mode of infection and pathogenesis of the disease and might contribute to the development of preventive measures to protect those who are most at risk.

One possible host factor that might affect susceptibility to infection is apolipoprotein E (*APOE* for gene, apoE for protein). There are three main *APOE* alleles (*APOE* ε2, ε3, and ε4) encoding three main isoforms (apoE2, 3, and 4), which differ in primary structure at two sites, apoE3 having cysteine at residue 112 and arginine at 158, apoE4 having arginine and apoE2 having cysteine at both sites. ApoEs transport lipids in the blood and are involved in repair of tissue damage.[4]

Several studies have shown that *APOE* determines the extent of damage in the case of certain diseases caused by viruses. Firstly, *APOE* governs the outcome of infection with herpes simplex virus type 1 (HSV1); *APOE* ε4 and *APOE* ε2 are risk factors for herpes labialis and herpes simplex encephalitis, respectively.[5–7] Moreover, possession of an *APOE* ε4 allele and presence of HSV1 in brain is a strong risk factor for Alzheimer's disease.[5 6] Secondly, carriage of *APOE* ε4 is a risk factor for dementia and peripheral neuropathy in pre-AIDS HIV infected subjects,[8] and, finally, *APOE* ε4 is strongly protective against severe liver damage caused by hepatitis C virus (HCV).[9]

One of the possible mechanisms of the virus-apoE interactions might relate to viral entry. ApoE enters cells via members of the low density lipoprotein receptor (LDLR) family and/or heparan sulphate proteoglycans (HSPG) on the cell surface.[4] The viruses HSV-1, HIV, and HCV also use one or other of these entry mediators.[10–12] Differences in apoE isoform binding to the receptors (which are cell type dependent) have been noted, and so the extent of viral spread and hence of damage might well depend on the specific isoform(s) of the host (as well as on the tissue involved). The malaria sporozoite (the form in which the protozoon invades hepatocytes in the liver, the initial target organ) also uses a member of the LDLR family as well as HSPG to enter hepatocytes,[13 14] suggesting that *APOE* might also influence the outcome of infection with this parasite. Further, a recent study has shown that a small heparin oligosaccharide, one which binds specifically to apoE, blocks interaction of the malarial circumsporozoite protein with human hepatoma (HepG2) cells in culture.[15] The extent of sporozoite entry into liver and/or its spread in that organ could be affected by the apoE isoform of the host, since the affinities of the isoforms for receptors on HepG2 cells in culture differ greatly, that of apoE4 being much greater than that of apoE2 and apoE3.[16 17] Thus, in the case of apoE4 carriers, there could be less sporozoite entry than in those carrying the other alleles.

In the present study, we have examined *APOE* genotypes of a birth cohort of Ghanaian infants, being raised in an area of stable, perennially endemic *Plasmodium falciparum* malaria transmission, to find if there is any association with their risk of becoming infected with malaria at different ages. We have sought also the possibility of an association of *APOE* genotype with parasite density in blood. Overall, mean time to infection differed significantly between genotypes and was significantly shorter in *APOE* ε2 homozygotes, indicating that *APOE* genotype affects risk of malaria infection. Interestingly, the frequency of the *APOE* ε2 allele in the Ghanaian population was unusually high, perhaps suggesting that this allele is under positive selection. However, these findings must be interpreted with caution as they are based on a small number of affected infants.

METHODS

Study area and cohort

The study was conducted in Prampram (population 8000), approximately 50 km east of Accra on the south coast of Ghana, in an area of coastal savanna. Malaria transmission in the area is perennial (although with some seasonal variation), stable, and of low to moderate intensity (5-10 infectious bites per person per year).[18] *P falciparum* accounts for 98% of all detected infections. Informed consent was obtained from all volunteers and ethical approval for all procedures was obtained from the ethical review committee of the London

Table 1 Mean time (in weeks) to infection by allele type/combination

Allele combination	Sample size	Number censored*	Mean time (weeks) to infection	95% confidence limits
All infants	110	14	48	41 to 55
ε2/ε2	4	0	13	0 to 26
ε2/ε3	15	3	45	31 to 59
ε2/ε4	9	1	55	26 to 85
ε3/ε3	44	5	51	40 to 62
ε3/ε4	32	3	43	29 to 56
ε4/ε4	6	2	66	45 to 87
ε2 absent	82	10	49	41 to 58
ε2 present	28	4	44	31 to 57
ε3 absent	19	3	51	32 to 69
ε3 present	91	11	48	40 to 55
ε4 absent	63	8	48	39 to 57
ε4 present	47	6	48	37 to 59

*Number of children infection free at termination of study.

School of Hygiene and Tropical Medicine, the institutional review board of the Noguchi Memorial Institute of Medical Research, University of Ghana, and the Ghanaian Ministry of Health. After giving informed consent, a consecutive sample of 110 mothers and their newborn infants was recruited into the study. A heparinised heel prick blood sample was obtained from each child on the day of delivery, at 2, 4, and 6 weeks of age, and then every four weeks. The child's axillary temperature was measured and a health questionnaire was completed by the mother every two weeks. If the child was febrile (temperature ⩾37.5°C), a blood film was made and examined immediately so that anti-malarial chemotherapy could be instituted if necessary. All children with fever and a parasite positive blood film were treated with a full course of chloroquine. As blood films from clinically well children were not read until some weeks later, asymptomatic infections were not treated. As free treatment was provided by study staff and was continuously available, we believe that very few infections were treated without our knowledge. Antimalarial chemoprophylaxis was not available to pregnant women in Prampram during the study period and thus transfer of antimalarials across the placenta, or via breast milk, was estimated to be minimal. Infants did not receive malaria prophylaxis.

Parasite detection

Giemsa stained thick blood films were examined by oil immersion microscopy. The number of parasitised erythrocytes per 300 leucocytes was counted and the number of parasites per µl of blood calculated was based on an average leucocyte count of 13 000/µl in children under 1 year of age.[19] Slides were classified as negative only after a minimum of 1000 leucocytes had been counted; the minimum parasite density that could reliably be detected by microscopy was 40 parasites/µl.

To improve the sensitivity of parasite detection, DNA was extracted from the red cell pellet[20] and amplified using primers to the multicopy, subtelomeric *7H8/6* gene of *P falciparum*, as described previously.[1] This method had a resolution of approximately one parasite per µl,[1] offering greater than 10-fold sensitivity over microscopy alone.

Examination of *APOE* genotype

DNA prepared from the red cell pellet contained also human DNA extracted from white blood cells trapped in the pellet, and so it was usable for determination of *APOE* genotypes. This was done using the method of Wenham *et al*.[21]

Statistical analysis

The ages (in weeks) at which infection was detected were evaluated using the Kaplan-Meier survival analysis method in conjunction with the log rank test. This is a statistical procedure for estimating time to event models in the presence of differing follow up times and "censored" cases (that is, in this context, of infants who remained infection free at the termination of the study). Mean times to infection were compared between *APOE* genotypes.

The maximum parasite counts detected in each infected infant were compared using one way analyses of variance. As these counts were very positively skewed, a natural logarithmic transformation was applied to normalise the data distribution. Geometric mean maximum parasite densities were also compared between *APOE* genotypes and allele frequencies.

In the presentation of results, all summary statistics are accompanied by their 95% confidence limits.

RESULTS AND DISCUSSION

Infection occurred in 96 (87.3%) of the 110 infants during the study period. The mean time to infection was 48 weeks (95% confidence interval 41 to 55). Among the 110 children for whom an *APOE* genotype was obtained, the allele frequencies were 14.5%, 61.4%, and 28.5% for ε2, ε3, and ε4, respectively. Overall, mean time to infection differed (statistically) significantly between genotypes (log rank test: $\chi^2(5)=15.69$, $p=0.008$), indicating that *APOE* genotype affects risk of malaria infection. A more detailed evaluation showed that the latter result was the result of the mean time to infection being significantly shorter for infants with a ε2/ε2 genotype compared to all other genotypes, but the differences between the remaining five genotypes were all non-significant (log rank test: $\chi^2(4)=2.94$, $p=0.568$). However, this result must be interpreted with great caution as only four infants had an ε2/ε2 genotype. Calculation of the expected frequency of *APOE* ε2 homozygotes in this population, using the Hardy-Weinberg distribution, gives a value of only 2.6%, so clearly to evaluate our findings a much larger study would be needed to yield an adequate number of these homozygotes.

A secondary analysis was carried out based on the presence of a particular type of allele (table 1). No significant relationship was found between mean time to infection and the presence of a ε2 allele (log rank test: $\chi^2(1)=0.48$, $p=0.491$), the presence of a ε3 allele (log rank test: $\chi^2(1)=0.10$, $p=0.755$), or the presence of a ε4 allele (log rank test: $\chi^2(1)<0.01$, $p=0.985$). Thus, if APOE ε2 does confer a risk, possibly by affecting entry of sporozoites into the liver, it does so only in homozygotes.

To find if the number of maturing liver schizonts (and thus parasite density in the blood) depended on *APOE* genotype, we

Table 2 Geometric mean maximum parasite count levels by allele type/combination

Allele combination	Sample size	Geometric mean max parasite count	95% confidence limits
All infants	96	198	126 to 309
ε2/ε2	4	72	1 to 3647
ε2/ε3	12	303	117 to 783
ε2/ε4	8	229	43 to 1218
ε3/ε3	39	249	115 to 541
ε3/ε4	29	128	53 to 310
ε4/ε4	4	277	15 to 4994
ε2 absent	82	192	111 to 332
ε2 present	28	217	100 to 470
ε3 absent	19	179	61 to 525
ε3 present	91	202	122 to 333
ε4 absent	63	237	130 to 433
ε4 present	47	155	77 to 309

Table 3 *APOE* allele frequencies of various African populations[22] and the UK[23]

		APOE allele frequencies (%)		
	No*	ε2	ε3	ε4
Ghana, Prampram	110	14.5	61.4	24.1
UK	119	7.3	77.9	14.8
Central African Rep, Aka Pygmies	70	5.7	53.6	40.7
Nigeria, West Africans (Bariba, Berba)	97	10.3	74.2	15.5
Nigeria, West Africans	781	6.4	68.4	25.2
Nigeria, West Africans	357	2.7	66.7	29.7
Sudan, Sudanese	103	8.3	62.6	29.1
Ethiopia, Amhara, Oromo	164	3.0	81.1	15.8
Morocco	100	6.5	85.0	8.5
South Africa, Khoi San	247	7.7	55.3	37.0
South Africa, Tswana speaking	100	14.5	57.0	28.5

*Total number of subjects in the study.

examined parasite density. In most of the infants, the density was very low, being detectable by PCR but not reliably so by microscopy. Values were mainly in the range of tens or hundreds of infected red blood cells per microlitre, with relatively few in the low thousands and only one very high value, 60 000/µl. Table 2 shows the (geometric) mean maximum parasite counts for each of the genotypes. The average parasite density was slightly lower for those infants who were *APOE* ε2/ε2 homozygotes, but overall the differences between the subgroups were not statistically significant ($F(5,90) = 0.580$, $p=0.715$). Similarly, maximum parasite counts were not significantly affected by the presence of an ε2 allele ($F(1,94) = 0.055$, $p=0.815$), the presence of a ε3 allele ($F(1,90) = 0.036$, $p=0.849$) or the presence of a ε4 allele ($F(1,90) = 0.883$, $p=0.350$).

Thus, our preliminary data suggest that *APOE* may affect susceptibility to malaria infection, in contrast with the previous findings on HSV1, HCV, and HIV,[5–9] which show that *APOE* does not influence susceptibility but instead influences the extent of damage caused by these agents. Whether the severity of disease caused by malaria infection is determined by *APOE* genotype remains to be discovered, by comparing genotypes of subjects with advanced disease with those found here for mild disease.

The high overall *APOE* ε2 allele frequency of our group of infants is noteworthy (table 3). All allele frequencies were calculated using values for all the 110 infants investigated; since the survey was a prospective cohort study and the infants comprised a random sample of the population, allele frequencies can be taken as population values. The value of 14.5% for *APOE* ε2 is substantially higher than almost all the other known values for sub-Saharan African populations (Pygmies, Nigerians (apart from group 3), Sudanese, Ethiopian, and South African Khoi San), but almost identical to the Tswana speaking South Africans (table 3). The Prampram *APOE* ε4 allele frequency of 24.1 is substantially lower than the values for Pygmies, group 3 Nigerians, Ethiopians, and South African Khoi San, but very similar to the Tswana value, while both the *APOE* ε2 and ε4 allele frequencies of the Prampram infants are much higher than those for UK subjects (table 3).

In summary, this study points to a possible correlation between susceptibility to malaria infection and homozygous carriage of the *APOE* ε2 allele, in that *APOE* ε2 homozygous infants became infected with malaria earlier than other children; this was accompanied by a relatively high frequency of the *APOE* ε2 allele in the study population. One interpretation of these data might be that early malaria infection is beneficial in the long term, as has been suggested by epidemiological studies,[24 25] perhaps allowing children to acquire protective immune responses while being relatively protected from severe malaria by passively transferred maternal antibodies or by physiological factors.[26] Clearly, further studies of the role of *APOE* in susceptibility to malaria are warranted using a larger numbers of infants, and in particular identifying more infants with an ε2/ε2 combination in order to improve the precision of the estimates of both time to infection and maximum parasite

counts. Also, it would be of interest to examine the *APOE* genotypes of older children or adults with much more severe disease, including cerebral malaria, to find out if *APOE* does in fact determine susceptibility to severity of damage caused by the protozoon.

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