Plasmodium falciparum malaria: association of sickle cell trait in the reduction of parasite density in symptomatic Fulani tribe living in sympatry in Mali, West Africa

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**Background:** Mutation of the b-chain of the globin gene due to a single base pair mutation A→T in the genome sequence has been associated with protection from severe malaria outcome. Differences in malaria susceptibility have been accorded to asymptomatic Fulani and other sympatric ethnic groups in Burkina Faso and Mali with Fulani being less parasitized, infected and more responsive to *Plasmodium falciparum* antigens.

**Methods & Materials:** In this study, we have examined symptomatic individuals of different ethnicity (123 Fulani and 254 Dogon) in Mali, genotyped for haemoglobin S and also assessed their antibody levels to crude asexual blood-stage antigen.

**Results:** We found that Fulani individuals with HbAA had a statistically significantly higher parasite density when compared with their HbAS counterparts [OR 1.9 (95% CI, 1.6-2.3, P < 0.001)]. The results also showed that parasite density in Dogon tribe were statistically higher than that of the Fulani tribe, irrespective of their haemoglobin status. We also found a significantly inverse correlation with parasite density and age of HbAS Fulani individuals \( R^2 = 0.549, P = 0.0018 \). No correlation between anti-malarial antibodies and haemoglobin AA or AS was observed.

**Conclusion:** Sickle cell trait could be another contributing factor to the immuno-genetic differences observed in Fulani living in sympatry with other ethnic groups in West Africa.

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Diagnosis of Mycoplasma pneumoniae infection in children by using serology and polymerase chain reaction in community-acquired lower respiratory tract infections

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**Background:** Mycoplasma pneumoniae plays a significant role in lower respiratory tract infections (LRTIs) in children. The aim of this study was to investigate the role of *M. pneumoniae* in community-acquired LRTIs in children, with use of both serological tests and PCR analysis.

**Methods & Materials:** A total of 100 patients 6 months to 12 years of age with acute lower respiratory tract infections were enrolled for this study. These patients were investigated clinically and radiologically. Sera were used for detecting IgM and IgG antibodies to *M. pneumoniae* by ELISA. PCR to amplify fragments in the 16srDNA gene of *M. pneumoniae* was conducted employing throat swab samples.

**Results:** In the present study, there were 61(61%) male and 39(39%) female children had LRTIs but no statistical significant association was found between sex of the patient and incidence of *M pneumoniae* infection. \( p = 0.42 \). Eighteen(60%) patients were positive for *M pneumoniae* in the age group of ≤5 years and 12(40%) patients of ≥5 years of age were positive for *M. pneumoniae* but this difference was found to be statistically significant. \( p = 0.02 \). The clinical and radiological profile across *M. pneumoniae* positive and negative cases were comparable. Serological evidence of acute infection was observed in 28(28%) patients. PCR was positive in throat swab samples of 6(6%) patients; 4(66.6%) patients with serologically proven and 2(33.3%) serological unproven. Together, serology and/or PCR detected thirty (30%) patients *M pneumoniae* infection.

**Conclusion:** In conclusion, our data underline the role of *M. pneumoniae* in children with community-acquired LRTIs, even in children aged < 5 years.

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