

Genetic polymorphisms in TLR4, CR1 and Duffy genes are not associated with malaria resistance in patients from Baixo Amazonas region, Brazil

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ABSTRACT. The main purpose of this research was to analyze the relation of the genetic polymorphisms frequently expressed by antigen-presenting cells, erythrocytes and malaria susceptibility/resistance with the human malaria infection cases. The sample used consisted of 23 *Plasmodium vivax* (Pv)- and *P. falciparum* (Pf)-infected patients, and 21 healthy individuals as a control group, from the Baixo Amazonas population in Pará, Brazil. The Asp299Gly polymorphisms in the Toll-like receptor 4 (TLR4), and Gly42Asp, Arg89Cys, Ala100Thr, and T-33C in the Duffy gene (FY) were analyzed by restriction fragment length polymorphism-polymerase chain reaction. The Lys1590Glu and Arg1601Gly polymorphisms in the

complement receptor type 1 (CR1) were analyzed by DNA sequencing. According to the results obtained and statistical analysis considering a significance level or $\alpha = 0.01$, we conclude that the low heterozygote frequency (2.27%) for the Asp299Gly mutation, detected in the TLR4 gene, is not related to the Pv and Pf infections in the patients analyzed. Also, the promoter region GATA-1 analysis of the FY gene in the Pv-infected patients showed that the heterozygote frequency for the T-33C mutation (11.36% of the infected patients and 20.45% of the control patients) is not related to infection resistance. Regarding the CR1 gene, the observed heterozygote frequency (9.09%) for the Arg1601Gly mutation in Pf-infected patients when compared to heterozygote frequency in the control group (18.18%) suggests that there is no correlation with infection resistance.

Key words: Malaria; Complement receptor-1; Toll-like receptor; Duffy blood group; Genetic polymorphisms; Brazilian population