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A Major Genetic Mechanism Involved in Resistance to Malaria in Western Amazonia

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KEY WORDS Western Amazon; segregation analysis; Rondônia; malaria; genetic epidemiology; major gene.

ABSTRACT Malaria, the world's most important cause of infectious morbidity and mortality, has a widespread geographical distribution in the tropical region, while its endemicity is very heterogeneous. The Amazonia region, due mainly to its relatively low demographic index, is characterized as an hypo-endemic region. A population of 182 individuals, living in Portuchuelo, State of Rondônia, Brazil, right bank of the Madeira river (8^0 37' S, 63^0 49' W) was surveyed, in order to ascertain data on the epidemiological aspects of malaria and some other infectious diseases. Two main phenotypes involved with *Plasmodium* infection were studied: a) the presence of symptomless infection *i.e*., presence of *Plasmodium*, diagnosed either by traditional thick smear or by PCR amplification of Plasmodium ribosomal DNA in blood samples; b) the reported number of previous malaria episodes. Segregation analysis was applied to both phenotypes. There were no evidences of any type of familial mechanisms acting on the distribution of the symptomless phenotype in this population, since there was no significant familial aggregation. As for the number of malarial episodes, this phenotype showed clear signs of Mendelian inheritance. The most parsimonious model includes a co-dominant major gene with frequency of q = 0.15 and a small multifactorial component (H= 0.08). Due to this frequency and the mode of inheritance, this finding seemed to be independent of the Hb, Fy or G-6-PD polymorphisms.

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