GENETIC COMPLEXITY OF PLASMODIUM VIVAX PARASITE POPULATIONS IN INDIVIDUAL HUMAN INFECTIONS

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Population of human malaria parasites are known to be genetically diverse with respect to a wide variety of properties antigenic differences in specific protein antigens[1]. In the present study we have attempted to analyse the genetic complexity of individual P. vivax infections by studying the distribution of variants of a single P.vivax schizont protein PV200 using monoclonal antibodies (MAbs) against variant epitopes of this highly polymorphic antigen. We determined the serotype(s) of parasites in individual isolates with respect to the reactivity of these MAbs by the Indirect Immunofluorescence Test, using a double labelling technique with sub-class specific chromophores. In 9 out of 10 isolates of freshly drawn P.vivax infected blood from different individuals, parasites of a single PV200 serotype only were detected; in the 10th isolate parasite population of 3 distinct PV200 serotypes were identified. Thus, most P.vivax infections appeared to consist of a single genetically homogeneous population of parasites within the limits of detection of the technique. Consideration of the prevalence of P.vivax infections in an area of malaria transmission in Southern Sri Lanka and of the densities of oocysts in mosquitoes fed on P.vivax infected individuals indicated that parasite populations would be transmitted many times before encountering parasites of other origins and that the individual populations would tend to reduce to genetic homogeneity during transmission. These expectations are consistent with the high proportion of genetically homogeneous P.vivax isolates observed in this study.

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References:

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