GENE STRUCTURE AND OOKINETE EXPRESSION OF THE CHITINASE GENES OF PLASMODIUM VIVAX AND PLASMODIUM YOELII


After ingestion by mosquitoes, malaria parasites fertilize in the midgut and develop into motile oocinetes, which penetrate the chitin-containing peritrophic matrix and midgut epithelium cells to develop into oocysts. Chitinase activity is critical for oocinetes to penetrate the peritrophic matrix. Recently, genes encoding chitinases were identified in Plasmodium gallinaceum (pgcht1), Plasmodium falciparum (pfcht1), and Plasmodium berghei (pbcht1). Parasites with disrupted pfcht1 or pbcht1 gene loci showed reduced infectivity to the mosquitoes, confirming an important role of chitinase in parasite invasion of the mosquito, presumably at the step of penetrating the peritrophic matrix. We report here the identification of genes encoding chitinase homologues in Plasmodium vivax (pvcht1), Plasmodium knowlesi (pkcht1), Plasmodium yoelii (pycht1), and Plasmodium chabaudi (pcht1), and demonstrate their expression in P. vivax and P. yoelii oocinetes. The predicted primary structure of the catalytic domain of PvCHT1 differs from that of human chitotriosidase, suggesting the possibility that P. vivax chitinase can be a target of blocking parasite transmission to mosquitoes through selective drug inhibition.

Molecular and Biochemical Parasitology 2003; 130(1): 51-4.

GENETIC DIVERSITY AND MULTIPLE INFECTIONS OF PLASMODIUM VIVAX MALARIA IN WESTERN THAILAND

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Using two polymorphic genetic markers, the merozoite surface protein-3α (MSP-3α) and the circumsporozoite protein (CSP), we investigated the population diversity of Plasmodium vivax in Mae Sod, Thailand from April 2000 through June 2001. Genotyping the parasites isolated from 90 malaria patients attending two local clinics for the dimorphic CSP gene revealed that the majority of the parasites (77%) were the VK210 type. Genotyping the MSP3-α gene indicated that P. vivax populations exhibited an equally high level of polymorphism as those from Papua New Guinea, a hyperendemic region. Based on the length of polymerase chain reaction products, three major types of the MSP-3α locus were distinguished, with frequencies of 74.8%, 18.7%, and 6.5%, respectively. The 13 alleles distinguished by restriction fragment length polymorphism analysis did not show a significant seasonal variation in frequency. Genotyping the MSP-3α and CSP genes showed that 19.3% and 25.6% of the patients had multiple infections, respectively, and the combined rate was 35.6%. Comparisons of MSP-3α sequences from nine clones further confirmed the high level of genetic diversity of the parasite and also suggested that geographic isolation may exist. These results strongly indicate that P. vivax populations are highly diverse and multiple clonal infections are common in this malaria-hypoendemic region of Thailand.