

Genetic variations of the dihydrofolate reductase gene of *Plasmodium vivax* in Mandalay Division, Myanmar

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[Parasitol Res.](#) 2005 Jul;96(5):321-5. Epub 2005 May 28.

Abstract

Dihydrofolate reductase (DHFR; EC1.5.1.3) is a known target enzyme for antifolate agents, which are used as alternative chemotherapeutics for chloroquine-resistant malaria. Mutations in the dhfr gene of *Plasmodium vivax* are thought to be associated with resistance to the antifolate drugs. In this study, we have analyzed genetic variations in the dhfr genes of clinical isolates of *P. vivax* (n=21) in Myanmar, to monitor antifolate resistance in this country. Sequence variations within the entire dhfr gene were highly restricted to codons from 57 to 117, and the GGDN tandem repeat region. Double (S58R and S117N/T) or quadruple mutations (F57L/I, S58R, T61M, and S117N/T), which may be closely related to the drug resistance, were recognized in most of the isolates (20/21 cases). Our results suggest that antifolate-resistant *P. vivax* is becoming widespread in Myanmar, as it also is in the neighboring countries in Southeast Asia. It appears that the drug resistance situation may be worsening in the country.