

## ***Plasmodium vivax* diversity in Indian context**

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India greatly contributes to the global malaria incidence. The existence of various vector species, congenial environment for the propagation of both; vector and the parasite, the malaria susceptible human host all make India the best opportune hotspot for persisting malaria disease. In Southeast Asian malaria incidences; contribution of India is about 60%. In India two major human malaria parasites *Pfalciparum* and *P.vivax* are widely distributed. *P.vivax* causes the most widespread malaria in the country with equal frequency as *Pfalciparum* and is the reason for high morbidity in its host. The disease severity of *P.vivax* is the emerging scenario in the country. Severe and fatal vivax malaria is an emerging recognized entity challenging the perception of *P.vivax* as benign disease making it pertinent to understand the emergence of severe *vivax* malaria. The chronicity of the malaria disease is attributed to the variant surface antigens (VSAs) encoded by the multigene families of *Plasmodium*. *P. vivax* genome also contains a multigene superfamily *vir* (variant interspersed repeats), present in the subtelomeric region which might have a possible role in immune evasion like the *var* gene in *P. falciparum*.

From five different epidemiological regions of the country 148 blood samples were collected to study the existing diversity of *vir* genes in natural infections. Sequence analysis of *vir* genes in field isolates showed immense diversity between them and also revealed the presence of synonymous and non-synonymous mutations in amino acid sequences. The results indicate that *vir* genes in different *P. vivax* populations in India are highly divergent both within and between isolates. By taking the presence of single nucleotide polymorphisms (SNPs) into consideration, basic population genetic structure was deduced. Minimum Evolution phylogenetic analysis was used to conclude that there was a random distribution of samples which was not region specific.

Detailed knowledge of the genetic variation among the *vir* genes will help in understanding the evolutionary aspects of *vir* genes and may also provide tools with which to design an effective vaccine. This is the first population based study from India of *P. vivax vir* genes, hypothesized to have a possible functional role in malaria pathogenesis.

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