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Allelic variations of *Plasmodium vivax* Apical Membrane Antigen -1 (PvAMA-1) in malarious areas of southeastern Iran using PCR-RFLP technique

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Background: Although *Plasmodium vivax* is usually known as benign malaria, some variations of the parasite can result in acute and severe infection. Studies on the genetic variations in *P. vivax* can guide relevant authors to predict the future situation of different strains of the *Plasmodium* in view of treatment, control, vaccine production and drug resistance. In this study we tried to determine some genetic variations in PvAMA-1 antigen among the samples were collected from southeastern Iran.

Methods: About two ml blood samples were collected into EDTA pre-dosed tubes from 36 *P. vivax*-infected patients individually. Previous to the above blood collection process a Giemsa stained thick and thin blood film was prepared from each of the patients. A PCR-RFLP technique was employed using EcoR-1, Pvu-II and Hind3 restriction enzymes to determine the allelic variations of the antigen.

Results: A 1300bp gene of the antigen was selected for the amplification process. Among the total cases identified in this study 90% showed similar bands when exposed to the restriction enzymes. Nine isolates (accession numbers: KF435081-KF435083 and JF682785-JF682790) were identified and registered in Gene bank. Identity among isolates was more than 96% in nucleotide level. Dendrogram clarified a close relationship among the clusters in spite of geographical distribution of the parasite.

Conclusion: This study increased our data about prevalence and variation of PvAMA-1 alleles amongst *P. vivax* isolates in southeastern parts of Iran where besides native population bears considerable Afghan and Pakistani immigrants.

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