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Plasmodium vivax population structure in malaria endemic area of southern Iran

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Malaria is an important parasitic disease that consider as a threat of public health in worldwide. *Plasmodium vivax* causes malaria infection mainly in Asia, South America and Oceania. In Iran, as member of east Mediterranean region office (EMRO), *Plasmodium vivax* and *Plasmodium falciparum* are responsible of malaria that occur mainly in south and southeast of the country. This area has common borders with Pakistan and Afghanistan. *Plasmodium vivax* accounts as agent of more than 90% of malaria cases in Iran. The access to enough information about population structure of *Plasmodium vivax* is necessary for developing malaria vaccine and epidemiological studies. The present study was conducted to determine population genetic diversity of *Plasmodium vivax* in southeast of Iran. Blood was taken from symptomatic malaria patients. The nested PCR were performed to amplify the two merozoite antigens of *Plasmodium vivax*. The products of PCR were sequenced. The MEGA 5 and DNASP software were used for the genetic analysis. The nucleotide sequences were deposited in world gene bank. The findings of present study showed genetic diversity in *Plasmodium vivax* population in the hypo-endemic area for malaria in Iran.

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