Plasmodium vivax MSP-3ß Gene as a Genetic Marker for the Parasite Detection in Comparison with Ssrrna Gene

A Shahbazi¹, H Mirhendi²,*A Raeisi³

¹Dept. of Parasitology, School of Medicine, Tabriz University of Medical Sciences, Tabriz Research Center of Infectious Diseases And Tropical Diseases, Iran

(Received 16 Jan 2010; accepted 20 May 2010)

Abstract

Background: The importance of accurate diagnosis of all of major diseases cannot be underestimated and efficient laboratory testing is vital to identifying and treating life-threatening illnesses including malaria. In this study, we compared the potential of one of merozoite surface protein genes, *PvMSP-3β*, for detection of *Plasmodium vivax* in blood samples by PCR with routinely used marker, ssrRNA gene.

Methods: One hundred P. vivax microscopy-positive blood samples were simultaneously tested with two genetic markers, including $PvMSP-3\beta$ gene and ssrRNA gene by PCR and nestedPCR method, respectively, and their sensitivity and specificity in detection of P. vivax was compared.

Results: An important difference was seen in sensitivity between the 2 genetic markers, 100% in case of ssrRNA gene vs. 95% of $PvMSP-3\beta$ gene. The specificity of the two markers was same (100%). Microscopic diagnoses of thick and thin blood smears was used as "golden standard" method.

Conclusion: Due to critical importance of accurate detection of the parasite in malarious area, the $PvMSP-3\beta$ gene cannot be a suitable marker for detection of P. vivax in blood sample by PCR. More investigations are needed to find other valid markers.

Keywords: PvMSP-3B, Plasmodium vivax, Ssrrna, Iran

Introduction

Plasmodium vivax causes most of the malaria morbidity in endemic regions of Central and South America, North Africa, and Asia (1). The broad and continuous occurrence of vivax malaria in some countries creates significant social and economic losses (2). Total malaria cases in Iran in 2005, were 18966, and about 88% of them caused by P. vivax (3). In the recent years the economy of four malaria endemic provinces of Iran (Sistan and Bluchestan, Hormozgan, Kerman and Booshehr) has sustained heavy losses during the malaria epidemics, and malaria control activities imposes a grave disbursement to the socio-economic development programs (3).

Prompt and accurate diagnosis is one of the most important aspects of effective management of any disease and a major strategy of the Global Malaria Control Strategy (4). Although, the careful ex-

amination of a well prepared and well stained blood film by an expert microscopist remains currently the "golden standard" for detecting and identifying malaria parasites (5), but there are several documents indicating misdiagnosis of malaria in different laboratories of health system in Iran (6-8), and there is an important need for applying an alternative method to control and confirm of the diagnostic results in malaria control system. Among several genetic markers that have been described for *P. vivax* detection and genetic diversity assessment, the small subunit ribosomal ribonucleic acid (ssrRNA) gene is the most familiar and is used in majority of studies in the world (5-9).

In this study, we assessed the value of a new marker, merozoite surface protein-3ß gene of *P. vivax*, for detection of the vivax malaria in comparison with molecular diagnosis with ssrRNA marker.

²Dept. of Medical Parasitology and Mycology, School of Public Health, Tehran University of Medical Sciences, Iran ³Disease Management Center, Ministry of Health, Tehran, Iran

Materials and Methods

One hundred symptomatic patients attending the malaria clinics in southeast of Iran from August to September 2005 were recruited in the study. Sample collection was approved by the Ethical Committee of Tehran University of Medical Sciences and through informed consent of patients. After primary detection of the disease through microscopic method by specialized staff, approximately 1000 µl of venous blood was collected in EDTA from P. vivax microscopy-positive samples. In Molecular Laboratory (Isfahan University of Medical Sciences, Isfahan, Iran) the microscopic diagnosis was rechecked by specialized laboratory staff, and parasite DNA was extracted by phenol-chlorophorm method (9). Primarily, samples were processed by nested PCR using plasmodium genus specific (primary PCR) and p. vivax species-specific primers for the small subunit ribosomal ribonucleic acid (ssrRNA) gene of P. vivax (9). Then, samples were tested by PCR for $PvMSP-3\beta$ gene with specific primers: forward (5'-AACTTGAGAAACGGATG-3')/ reverse (5'-TGCGAGTGTTTTATGCG-3'), which amplify a small $PvMSP-3\beta$ fragment and bind at positions 102-118 and 1943-1961 of the Belem $PvMSP-3\beta$ coding sequence (10). The polymerase chain reaction (PCR) was performed with an initial denaturation of 2.5 min at 95° C, followed by 35 cycles of 30 Sec at 95° C, 56 °C for 30 sec and 68° C for 2.5 min (10).

For negative control we used 5 genomic DNA prepared from healthy individuals with no history of malaria living in non-malarious areas of the country and 4 genomic DNA prepared from *P. falciparum* positive samples maintained through permanent culture in malaria laboratory of department of Medical Parasitology and Mycology (School of Public Health of Tehran University of Medical Sciences). In the case of positive control, because of restrictions in laboratory maintenance of *P. vivax* isolates and lack of such an isolate, we used four positive PCR productions (Their positiveness had been proved through previous studies).

In this study, the golden standard was microscopic diagnosis of Geimsa-stained thick and thin blood smears by expert microscopist (5).

Results

All of samples diagnosed by microscopic examination of thick and thin blood smears and positive controls were positive through nested PCR by primers of ssrRNA gene. Negative controls were negative in this process. In PCR process with primers of $PvMSP-3\beta$ gene, 5 samples were negative. All of negative controls were negative and positive controls were positive with primers of $PvMSP-3\beta$ gene. Different types of $PvMSP-3\beta$ gene, based on the size of PCR products were observed (Fig. 1).

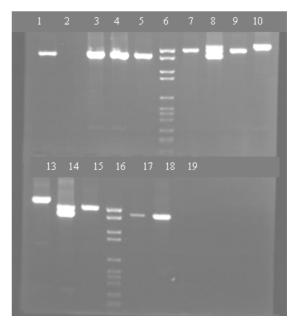


Fig. 1: PCR products of the msp-3β gene of Plasmodium vivax isolates. The gene had different genotypes with different sizes ranging from 1400 to 2400 bp. Lane 2 was microscopically positive and lane 19 was microscopically negative samples. Lanes 6 and 16 contain DNA marker 6 (Roche)

Dissuasion

Laboratory diagnosis of malaria currently is performed by detection of parasites by light microscopy of Geimsa-stained thick and thin blood smears. This procedure is cheap and simple, but is a laborintensive procedure, which requires well-trained personnel (8). When parasitaemia is very low, the data of microscopy diagnosis is limited, and in some cases biased, by the inability to devote the necessary amount of time to the examination of blood smears (8).

Greater sensitivity and specificity of PCR method in comparison with thick blood films examination method have been shown by many studies. High sensitivity and specificity of PCR method, at low parasitaemia, has been reported earlier (11-17). The method described by Snounou et al. (9) is the most common one. The sensitivity of *Plasmodium* detection by PCR method is about 10 parasites per 5 micro liter of blood or 1 parasite in 200 microscopic fields (18).

In this study, we assessed the sensitivity and specificity of different genetic markers for detection of merozoite surface protein- 3ß of P. vivax. Merozoites are surrounded by a layer of proteins (merozoite surface proteins or MSPs) organized into a structurally complex coat (19). $PvMSP-3\alpha$, $PvMSP-3\beta$ and $PvMSP-3\gamma$ are members of a multi-gene family of related MSPs (19-21). The three encoded proteins share only 35-38% identity and 48-58% similarity in pairwise comparisons. All of them contain similar structures including signal sequences and are expressed on the merozoite surface, although they lack transmembran domains or GPI attachment sites (19). $MSP-3\beta$ gene encodes merozoite surface protein dominated by alanine-rich central domains strongly predicted to form coiledcoil tertiary structure, perhaps contributing to the structural complexity of the surface coat. The function of this gene is unknown, although immune evasion has been raised as one possibility (20).

In this study, we observed that the sensitivity of PCR with primers of PvMSP-3 β gene was 95% versus 100% with primers of ssrRNA gene of P. vivax and golden standard microscopic method. The specificity of both methods in comparison with golden standard microscopic method was the same (100%). Due to importance of prompt and accurate diagnosis as the key to effective malaria management, which is one of the main

interventions of the Global Malaria Control Strategy and the first strategy in National strategy plan for malaria control of Iran (4), we can say that the sensitivity of $PvMSP-3\beta$ gene detected in our study, is not adequate for malaria control program in the malarious areas of the country, although this marker can detect different types of the parasite (10, 22). Previously, we showed that, $PvMSP-3\beta$ could be considered as a useful polymorphic locus for $P.\ vivax$ population study in field setting (22), and the types of the parasite can be detected based on the various sizes of the PCR product of this marker (Fig.1).

Although the sensitivity of $PvMSP-3\beta$ marker in the diagnosis of parasite is less than ssrRNA, but for amplification of related part of $PvMSP-3\beta$ we did not follow the nested PCR procedures and we did it only by PCR method that was a major saving in time and cost in comparison with ssrRNA amplification (9).

In conclusion, detection of patients with low-grade parasitaemia and in carriers without any parasite in blood is vital for malaria laboratory diagnosis. Additionally, as there is no national standard malaria microscopic diagnosis quality control system in Iran and since it is only limited to occasionally issued circulars, and, whereas there are several documents indicating misdiagnosis of malaria in different laboratories of health system (6-8), it seems that the *ssrRNA* gene of *P. vivax*, would be useful until unknown future and more investigations is needed to introduce a more sensitive and specific marker.

Ethical Consideration

All Ethical issues (such as informed consent, conflict of interest, plagiarism, misconduct, co-authorship, double submission, etc) have been considered carefully.

Acknowledgments

This study was supported by Disease Management Center of Ministry of Health, Iran. Manager and staff of Isfahan Health Research Center are highly appreciated.

References

- 1. Cui L, mascorro CN, Fan Q, Rzomp KA, Khuntirat B, Zhou G, Chen H, Yan G, Sattabongkot J (2003). Genetic diversity and multiple infections of *Plasmodium vivax* malaria in western Thailand. *Am J Trop Med Hyg*, 68: 613-19.
- 2. Gomez JC, Mc Namara DT, Bockarie JM, Baird JK, Carlton JM,Zimmerman PA (2003). Identification of a polymorphic *Plasmodium vivax* microsatellite marker. *Am J Trop Med Hyg*, 69(4): 377-79.
- 3. Annual reports of Malaria Department of Diseases Management Center of MOH, 2006.
- 4. Raeisi A, Shahbazi A, Ranjbar M, Shoghli A, Vatandoost H, Faraji L (2004). National strategy plan for malaria control (Iran) 2004-2008. *Seda Press*, p 28.
- 5. Payne D (1988). Use and limitations of light microscopy for diagnosing malaria at the primary health care level. *Bulletin of World Health Organization*, 66: 621-26.
- 6. Zakeri S, Mamaghani S, Mehrizi AA, Shahsavari Z, Raeisi A, Arshi S, Dinparast-Djadid N (2004). Molecular evidence of mixed *P. vivax* and *P. falciparum* infections in northern Islamic Republic of Iran. *Eastern Mediteranian Health Journal*, 10(3): 336-42.
- 7. Ebrahimzadeh A, Fouladi B, Fazaeli A (2007). High rate of detection of mixed infections of *Plasmodium vivax* and *Plasmodium falciparum* in South-East of Iran, using nested PCR. *Parasitology International*, 56: 61-4.
- 8. Zakeri S, Talebi NS, Zare A, Djadid ND (2002). Detection of malaria parasites by nested PCR in south-eastern, Iran: Evidence of highly mixed infections in Chahbahar district. *Malaria Journal*, 1:2.
- Snounou G, Pinheiro L, Goncalves A, Fonseca L, Dias F, Brown KN, Rosario VE (1993). The importance of sensitive detection of malaria parasites in the human and insect hosts in epidemiological studies, as shown by the

- analysis of field samples from Guinea Bissau. *Trans R Soc Trop Med Hyg*, 87: 649-53.
- 10.Rayner JC, Huber CS, Feldman D, Ingravallo P, Galinski MR, Barnwell JW (2004). *Plasmodium vivax* merozoite surface protein P_v *MSP-3\beta* is radically polymorphic through mutation and large insertions and deletions. *Infection, Genetics and Evolution*, 4: 309-19.
- 11. Brown AE, Kain KC, Pipithkul J, Webster HK (1992). Demonstration by the polymerase chain reaction of mixed *plasmodium falciparum and plasmodium vivax* infections undetected by conventional microscopy. *Trans R Soc Trop Med Hyg*, 86: 609-12.
- 12. Sethabutr O, Brown A, Panyim S, Kain KC, Webster HK, Echeverria P (1992). Detection of *Plasmodium falciparum* by polymerase chain reaction in a field study. *J Infect Dis*, 166:145-148.
- 13. Wataya Y, Arai M, Kubochi F, Mizukoshi C, Kakutani T, Ohta N, Ishii A (1993). DNA diagnosis of falciparum malaria using a double PCR technique: a field trial in the Solomon Islands. *Mol Biochem Parasitol*, 58: 165-68.
- 14. Khoo A, Furuta T, Abdullah NR, Bah NA, Kojima S, Wah MJ (1996). Nested polymerase chain reaction for detection of *plasmodium falciparum* infection in Malaysia. *Trans R Soc Trop Med Hyg.* 90:40-41.
- 15. Black J, Hommel M, Snounou G, Pinder M (1994). Mixed infections with *plasmodium* falciparum and plasmodium malariae and fever in malaria. Lancet. 30:1095.
- 16. Roper C, Elhassan IM, Hviid L, Giha H, Richardson W, Babiker H, Satti GM, Theander TG, Arnote DE (1996). Detection of very low level *plasmodium falciparum* infections using the nested polymerase chain reaction and a reassessment of the epidemiology of unstable malaria in Sudan. *Am J Trop Mew Hyg*, 54(4): 325-31.
- 17. Singh B, Cox-Singh J, Miller AO, Abdullah MS, Snounou G, Rahman HA (1996). Detection of malaria in Malaysia by nested polymerase chain reaction amplification of dried blood

- spots on filter papers. *Trans R Soc Trop Med Hyg*, 90(5): 519-21.
- 18. Warrel DA, Gilles HM. *Essential Malariology* (2002). Oxford University Press Inc. PP: 54-9.
- 19. Galinski MR, Corredor-Medina C, Povoa M, Crosby J, Ingravallo P, Barnwell JW (1999). *Plasmodium vivax* merozoite surface protein-3 contains coiled-coil motifs in an alanine-rich central domain. *Mol Biochem Parasitol*, 101: 131-47.
- 20. Galinski MR, Ingravallo P, Corredor-Medina C, Al-Khedery B, Povoa M, Barnwell JW (2001). *Plasmodium vivax* merozoite sur-

- face proteins- 3β and 3γ share structural similarities with *P. vivax* merozoite surface protein- 3α and define a new gene family. *Mol Biochem. Parasitol*, 115: 41-53.
- 21. Shahbazi A, Raeisi A, Nateghpour M, Mirhendi H, Mohebali M, Asmar M (2008). Polymorphism of merozoite surface protein-3α gene of *Plasmodium vivax* in isolates of Iran. *Iranian J Parasitol*, 3(2): 15-20.
- 22. Shahbazi A, Nateghpour M, Mirhendi H, Mohebali M, Raeisi A, Asmar M(2007). Diversity of merozoite surface protein-3β gene of *Plasmodium vivax* isolates from Iran. *Iranian J Publ Health*, 36(4): 1-5.