Introduction

Malaria is an infectious disease caused by protozoan parasites. More than half of the world's population in approximately 100 countries is exposed to malaria with about one million deaths annually [1-3]. Iran is located in the Eastern Mediterranean region, where about 45% of the population live with the risk of having both falciparum and vivax malaria. The malaria endemic areas of Iran are located in the south-eastern part of the country, bordered in...
the south by the Persian Gulf and the Gulf of Oman and to the east by Afghanistan and Pakistan. The south-eastern part of Iran consists of the Sistan and Bluchistan province, the Hormozgan province and the tropical part of Kerman province with a combined population of approximately three millions and is considered to be a "refractory malaria region". Annual Parasite Incidence (API) was reported to be 8.74 per 1,000 population [1]. High frequency of some traits in malaria endemic areas suggested the strong selective pressure of malaria on human genome. These traits consist of: thalassemia, HLA antigens, and G6PD deficiency which are common in many areas, and have been shown to be related with the reduced susceptibility to severe malaria and the G6PD deficiency is indicated to be more important than others. This gives the selective advantage against severe malaria since prevalence of the G6PD deficiency has had 5% to 25% increase in comparison with other areas in malaria endemic area. The glucose 6-phosphate dehydrogenase is X-chromosome linked expressing in all tissues. This is the first enzyme of pentose phosphate pathway with 5-carbon sugar ribose and NADPH synthesized by coupled oxidation /reduction reactions. Moreover this enzyme is highly polymorphic in humans by which more than 160 different mutations have been identified so far. In addition, genetic variations in several other genes, including TNFα, MBL and NOS2 have been identified. The tumor necrosis factor-alpha (TNFα) is a key cytokines with an important role in pathogenesis of severe infectious diseases. The genetic susceptibility to severe form of malaria (cerebral malaria) is associated with TNFα promoter polymorphisms and high circulating levels of cytokines. Nonetheless the level of nitric-oxide (NO), which is related to polymorphisms in NOS2 gene, could play an important role in severity of many diseases including malaria. Mannose-binding lectin (MBL) is thought to play an important role in the innate immune defense. The ligands of MBL are high in mannose and N-acetylg glucosamine oligosaccharides that presented on a variety of microorganisms. At present study, we investigate the frequency of common polymorphisms in NOS2 (1 polymorphism), MBL2 (3 polymorphisms), TNFα (3 polymorphisms) genes and G6PD(4 variants) which is related to protection against malaria in 315 healthy samples with G6PD deficiency and 10 samples of malaria patients without G6PD deficiency in five provinces (Fars, Khuzestan, Esfahan, Yazd and Kerman) [13,31].

Methods

Study population and area: We collected 315 samples from non related healthy subjects with G6PD deficiency and 10 samples from patients who were hospitalized with the sign of malaria and their blood smears showed presence of the parasite. All samples were collected from Fars (34 samples), Khuzestan (100 samples), Esfahan (62 samples), Yazd (55 samples) and Kerman (64 samples) provinces of IRAN which comprised 30% of disease incidence of country. Informed consent was obtained from the subjects before sampling. All of the 315 samples had G6PD deficiency using dye reduction test.

DNA extraction: Genomic DNA was extracted from white blood cells using standard methods of DNA extraction (Phenol Cholorophorm and southing out).

DNA polymorphism analysis: All collected samples including the Mediterranean, Chatham, Cosenza, Aures and A-(376,202) variants were evaluated by DNA amplification with specific primer and digestion with restriction enzyme endonuclease (Table1). Amplification of DNA samples from Mediterranean, Chatham, Cosenza, A-(376,202) and Aures variants were 583bp, 208bp, 548bp, 295bp, 108bp and 352bp, respectively. To detect the genetic polymorphism of the NOS2-954 a 680-bp fragment of NOS2 promoter region was amplified. To detect TNFα
polymorphisms a 117-bp fragment of promoter region was amplified and next to detect MBL2 polymorphisms a 340-bp fragment amplified. PCR amplification was done using 2 μl of DNA in a total volume of 50 μl reaction mixture containing appropriate primers (Table 1). The amplified products were analyzed on 10% agarose gel and visualized with ethidium bromide staining. Eight micro liters of each amplified product was digested with 15 μl of reaction mixture containing 1U of appropriate restriction enzyme (Table 1). Inactivation of enzyme was performed with proteinase K after 1-12 hours incubation and the digestion solutions analyzed on 12% acrylamide gel and later visualized with silver-nitrate staining.

Statistical analysis: the two-sample kalmogorov-smiranov test was used to compare the distribution of host genetic variants in individuals with and without malaria.

<table>
<thead>
<tr>
<th>Polymorphism and Variants</th>
<th>Primer sequence</th>
<th>Annealing temperature (°C)</th>
<th>Restriction Enzyme</th>
</tr>
</thead>
<tbody>
<tr>
<td>G6PD-med</td>
<td>Med-F 5′CCCCCGAGGAAATCTAAAGGGGT-3′ Med-R 5′-GAGAAGTGACCCCTCGAGGTTGACT-3′</td>
<td>61</td>
<td>MboII</td>
</tr>
<tr>
<td>G6PD-ChaG1003A</td>
<td>Chat-F 5′CAA GGA GCC CAT TCT CTC CCT T 3′ ChatR5′-TTTCCACATAGGAGCAGACGGTGCACAA</td>
<td>60</td>
<td>BstXI</td>
</tr>
<tr>
<td>G6PD-CozG1367C</td>
<td>Coz-F 5′-GCA GGC AGT GGC ATC AGC AAG-3′</td>
<td>64</td>
<td>Bsu36I</td>
</tr>
<tr>
<td>G6PD A- (G202A)</td>
<td>Coz R 5′-GGG AAG GAG GGT GGC CGT GG-3′ A202 F 5′-GCTGCAAGGGGATGACCCTTG-3′</td>
<td>56</td>
<td>Nla III</td>
</tr>
<tr>
<td>G6PD A- (A375G)</td>
<td>A202 R 5′-CCTGAAGGAGGGTCACCTCTTGGT-3′ A373 R 5′-CTGTCGTCTGTTTGTGTCTGTCG-3′ A373R: 5′ GGCCAGGCTGCAACGAGAAAGG3′ CAGCCACCTCAACCAACAGACT-3′ 5′-CCGACGTCGCCATGCTGGG-3′</td>
<td>61</td>
<td>FokI</td>
</tr>
<tr>
<td>G6PD A-</td>
<td>TNFa-308G→A</td>
<td>58</td>
<td>Bgl II</td>
</tr>
<tr>
<td>G6PD Aures</td>
<td>TNFa-244G→A</td>
<td>58</td>
<td>NcoI</td>
</tr>
<tr>
<td>TNFa-238G→A</td>
<td>TNFa-1 and TNFa-2</td>
<td>58</td>
<td>HpyF31I</td>
</tr>
<tr>
<td>MBL 54G→A</td>
<td>MBL1 5′-CAGGCAGTTTCTCTGGAAGG-3′ MBL2 5′-GCACCCAGATTGTAGAGACAGAG-3′</td>
<td>60</td>
<td>BspRI</td>
</tr>
<tr>
<td>MBL 57G→A</td>
<td>MBL1 and MBL2</td>
<td>60</td>
<td>MboII</td>
</tr>
<tr>
<td>MBL IVS-I-5G→A</td>
<td>MBL1 and MBL2</td>
<td>60</td>
<td>HinfI</td>
</tr>
<tr>
<td>NOS2-954G→C</td>
<td>NOS2 1 5′-TGTTGGAGCGGTGAGATCAAGGT-3′ NOS2 2 5′-CTCATCAAAAGGTGGCCGAGAG-3′</td>
<td>62</td>
<td>Eco31I</td>
</tr>
</tbody>
</table>

Table 1: The polymorphisms and variants with specific primers and restriction enzymes.

Results
All the 315 subjects were screened through PCR-RFLP analysis for TNFa-244G→A, TNFa-308G→A, TNFa-238G→A, NOS2-954G→C, MBL54G→A, MBL 57G→A, MBL IVS-I-5G, G6PD-med, G6PD-ChaG, G6PD-CozG, G6PD A- (G202A), G6PD A- (A375G) and G6PD Aures. The frequency of NOS2-954G→A showed that 127 out of 315 (40.31%) healthy samples had GG genotype, 167 samples (53.01%) GC and 21 samples (6.66%) CC. All the 10 samples from malaria patients showed GG genotype. In TNFa-308, 217 out of 315 (68.8%) samples showed GG genotype, 98 samples (31.11%) AG genotype and 2% had AA. For TNFa-244, 298 of samples (94.60%) showed GG genotype and 5 samples (1.62%) AG genotype and 1% had AA.
none had AA. All malaria patients showed GG genotype in this region. In TNFα-238, 292 of samples (92.69%) showed GG genotype, 21 samples (6.66%) AG genotype and 2 of the samples (0.63%) AA genotype and all of malaria patients had GG genotype in this region. In MBL54, 238 samples (75.55%) had GG genotype, 77 samples (24.44%) AG genotype and 2 samples (0.6%) AA genotype. 2 samples of malaria patients (20%) had AG genotype and 80% GG genotype. In MBL 57, 300 samples (95.23%) had GG genotype, 15 samples (4.76%) AG genotype and 2 samples (0.63%) AA genotype. eight samples (80%) of malaria patient GG genotype and 20% AG genotype. in MBL IVS-I-5G A, All 315 samples showed (100 %) GG genotype and all malaria patients showed GG polymorphism. In studying of
G6PD variant indicated that Mediterranean mutation in Fars, Khuzestan, Esfahan, Yazd and Kerman provinces was 79.4%, 58%, 83/8%, 64% and 63% respectively. Also, Chatham mutation was 8.8%, 8%, 4.5%, 3.6% and 0% respectively. Finally, other four mutations analyzed were Cosenza, A-202(G→A), A-367(A→G) and Aures (T→C) in which none had these mutations.

Difference between distribution of each genotype variants in healthy and patients objects was studied by two-sample kalmogorov-smirnov test, to find the relation between these genotype and protection against malaria. Only distribution of NOS2-954C (p=0.002 by two-sample kalmogorov-smirnov test) supported this theory.

**Discussion**

Malaria is known to be a dangerous and tremendously successful pathogen that is responsible for 300 million cases of infection with and one million deaths annually [3,4]. Plasmodium falciparum is the causative agent
Polymorphism analysis of malaria in more than one million children in Africa. Other species of this parasite, *p. vivax*, *p. Malariae*, *p. Ovale*, can also infect humans. The genetic diversity of the parasite, generated by its sexual stage, provides the organism with many opportunities to maximally adapt to host defenses and continue transmission. Due to the length of exposure time, and significant effects on morbidity and mortality by infection, it has exerted a strong selective pressure on the human genome, and causes mutations in human genes which promote survival in areas where malaria is endemic [33]. Protection against this microorganism is provided with the polymorphisms generated in the human genome after many generations [32]. Large numbers of these polymorphisms have been found in genes which codes erythrocytes protein and cytokines. The relation between some human traits and severity of malaria infection, has been well documented [34]. These traits mainly found in red blood cell disorders like sickle cell anemia, thalassemia and other traits like G6PD deficiency [35,36]. The protection against malaria is suggested to be related to polymorphisms in more than 30 genes [1]. Investigations have indicated that a number of variants are involved including those of the major histocompatibility complex and a cytokine-gene cluster on Chromosome 5q31-q33 [38, 39].

The TNFα codes by TNF genes located in MHC class III nearby MHC class I and II, and is a pro-inflammatory cytokine that plays an essential role in the protection against many infections including malaria, but also fatal when produced in excess [41, 42]. A study on Burkina Faso families revealed the linkage of mild malaria to the MHC region genes with a peak close to TNF [43]. Variaty of polymorphisms in promoter region of TNF gene are related to severity of infectio. It has revealed that Gambian childrens who harbor homozygous TNF-308A allele are more susceptible to cerebral malaria [9]. Other studies in Gabon, Serilanka and kenia suggested individual who carries this allele are more susceptible to recurrence of
plasmodium infection or death [45,46]. The TNF-376A play role in binding to transcription factor, OCT-1 and susceptibility to the cerebral malaria, and the TNF-238A is related to susceptibility to the malarial anemia. Nevertheless, results about the role of TNF polymorphisms in protection against malaria are conflicting [9, 47].

Several findings suggested single nucleotide polymorphisms (SNPs) in 5′ regulatory site of TNF gene and in coding region of FCGR2A are associated with susceptibility to plasmodium falciparum Malaria [9,49,50,52]. The tumor necrosis factor alpha (TNF) have role in many inflammatory responses and also play an important role in pathogenesis of many infectious diseases such as plasmodium falciparum Malaria [10]. Transcription of TNF gene is complex and well regulated [55], and it has revealed that SNPs in 5′ regulatory region of this gene are related with variety of infectious and inflammatory diseases [56,57]. SNPs in -1031, -857, -376 (1800750,G>A), -308 and -238 are located in regulatory region of TNF gene and associated with TNF production as well as protection against Malaria in different populations [50,52,49,60,61]. Taking this, it seems important to discover TNF special responses. A study on polymorphisms of TNF-enhancer and gene for FcγRIIa correlate with the severity and diversity of falciparum malaria in the ethnically diverse Indian population [61]. This differences has been also reported in 17 regions of Africa and Burkina Faso [62,21,25].

In our study three polymorphisms in promoter region of TNFα gene were analyzed based on the two-sample kalmogorov-smiranov test.

Comparison of genotype frequency for the TNFα polymorphisms, between healthy people and malaria patient revealed no significant difference (p>0.01).

Several studies suggested that the presence of the different variant alleles in the MBL gene is associated with an increased tendency for infections [7,27,28]. According to two-sample kalmogorov-smiranov test, no association in frequency distribution of MBL variant alleles and susceptibility to malaria infection was found. A study among Gambian children also, has shown no relation between MBL deficiency and malaria [29]. Another study among young Gabonese children has found a weak correlation between the MBL deficiency and severe malaria [23]. This study also suggested the MBL deficiency may not be associated with malaria, but it could be a risk factor for severe malaria in children who lack well developed protective acquired immune responses [30].

Nitric oxide has been determined to possess antiparasitic activity [31], and our results shown an association between NOS2-954GC alleles and susceptibility to malaria (p=0.002 by two-sample kalmogorov-smiranov test). A study among Gabonian individuals shown heterozygous carriers for NOS-G954C are protected against malaria as effectively as sickle cell trait [8]. Another study showed no significant difference in multiplicity of infection between
children who were heterozygous for NOS2-954C and those with wild type alleles [23].

We found that the G6PD Mediterranean, was the most common G6PD deficient variant in these five provinces, which accounts for 69.56% of the 315 analyzed samples. Similar to other parts of Iran[13,23], in the majority of the people in these provinces, favism is most probably due to Gd-Med, which may suggest a common origin for the populations in Iran and the Mediterranean. It should be emphasized also that G6PD Mediterranean frequency reached 91.2% in Kermanshah province [23]. Our data showed that on the average, in Iranian population, the Chatham mutation was the next one in five provinces, and accounts for 4.95%[23]. Although the origin of the Iranian population is rather uncertain, but the closer similarity of the mutational spectrum to Italian (80-84% for Mediterranean, 20% for Chatham and 1.9% for Cosenza) rather than Middle East population may indicate a common ancestra origin [7-25,3-34].

Acknowledgments

This work supported by grants from the National Research Center for Genetic Engineering and Biotechnology (NRCGEB) and Tehran University of Medical Sciences and health services, Tehran, Iran.

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