Mannose-Binding Lectin (MBL) gene polymorphisms in susceptibility to pulmonary tuberculosis among the Lur population of Lorestan Province of Iran

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**ABSTRACT**

**Objective:** Tuberculosis (TB) is caused by infection of Mycobacterium tuberculosis. Host genetic variability is an important determinant of the risk of developing TB in humans. Although the association between MBL polymorphisms and TB has been studied in various populations, the results are controversial. The aim of this study was to investigate mannose-binding lectin (MBL) gene polymorphisms with susceptibility to pulmonary tuberculosis (PTB) in a Lur population of Iran.

**Methods:** In this case-control study, four functional MBL gene polymorphisms (HL, XY, PQ and AB) were genotyped by using PCR Single Strand Conformation Polymorphism (SSCP) technique in a Lur population living in Lorestan Province, consisting of 100 patients with pulmonary tuberculosis (PTB) age and sex matched 100 healthy controls (HCs). Association analyses were performed with the SPSS 21 statistical software.

**Results:** We found that MBL (HH) genotype polymorphism significantly was associated with increased susceptibility to TB (35% in patients vs. 22% in controls, \(P = 0.0417, \text{OR} = 1.909, \%95 \text{CI} = 1.020-3.573\)). Additionally, \(H\) allele showed a significant association with increased risk of TB (56.5% in patients vs. 46% in controls, \(P = 0.0357, \text{OR} = 1.525, \%95 \text{CI} = 1.028-2.262\)). Also, the distribution of \(L\) allele in patients was significantly lower frequency in TB patients compared to controls (43.5% vs. 54%, \(P = 0.0357, \text{OR} = 0.656, \%95 \text{CI} = 0.442-0.973\)). However, the allelic and genotypic frequencies of \(AB\), \(XY\) and \(PQ\) polymorphisms were not significantly different between the patients and the controls. We couldn’t detect any significant differences between haplotypes among TB patients and healthy controls.

**Conclusions:** Our findings demonstrated that \(HH\) genotype and \(H\) allele may increase the susceptibility to pulmonary TB in the Lur population of Iran, although \(L\) allele may decrease the susceptibility to pulmonary TB in this population. We suggest that it is necessary to further more studies with larger sample size and other ethnic population.

**Keywords:** MBL, Pulmonary tuberculosis, Lur population

1. Introduction

Tuberculosis (TB) is caused by the infection of Mycobacterium tuberculosis (MTB) and remains the first leading cause of global death from infectious diseases [1]. Each year > 9 million novel cases are infected by PTB and > 1.7 million succumb to PTB annually [2]. Tuberculosis (TB) is responsible for an estimated 1.5 million deaths in 2014 [3]. Approximately 10% of patients who are infected with MTB are known to progress to clinical disease [4,5]. MTB presumably infects a third of the world’s population [6]. Additionally, the course and duration of disease vary in different individuals [7]. This suggests that individual differences may act upon the susceptibility to tuberculosis and that contact with this microorganism does not always result in infection. These differences may be due to host factors and genetic sensitivity of different individuals to this disease [8,9]. From the anthropological point of view, susceptibility to infectious diseases can be associated with genetic diversities of polymorphic genes like human leukocyte antigen (HLA) [10]. The identification of factors which increase disease susceptibility has potential to inform control strategies.

The host-pathogen interactions and environmental factors may
contribute to TB. Furthermore, Host genetic variability is an important determinant of the risk of developing TB in humans [11,12]. Many studies have reported the association between TB and genetic polymorphisms related to human innate immunity [7]. Unraveling the genetic factor contributing to the pathogenesis of TB may lead to improved treatment and prevention of this disease [13]. One of which is KIR3DS1 gene and it combines with HLA-B Bw4 and IlE80 ligand [14,15]. Also, other studies showed Toll like Receptors (TLRs) [16–20], Interleukin-10 (IL-10) [21], Tumor Necrosis Factor (TNF) [22] and Vitamin D Receptor (VDR) has roles in the susceptibility or resistance to TB [23,24].

Mannose-Binding Lectin (MBL) is a member of the collectin family that recognizes pathogens by its carbohydrate-recognition domains [25]. MBL is an acute-phase serum protein, which is synthesized in the liver and circulates as oligomers complexed with MBL-associated serine proteases (MASPs) [26]. MASPs bind to the sugar moieties on the surface of a pathogen, and then are activated to initiate the lectin serine proteases (MASPs) [26]. MBL is an acute-phase serum protein, which is synthesized in the liver and circulates as oligomers complexed with MBL-associated serine proteases (MASPs) [26]. MBL2 gene polymorphisms and TB.

2. Materials and methods

2.1. Patients and controls

The study was approved by the Ethical Committee of Lorestan University of Medical Sciences and Informed consent was taken from all subjects before blood sampling and questionnaire investigation. All subjects agreed to take part in the study. The patients included in this study were newly diagnosed PTB patients registered in the health center of Khorramabad city of Lorestan Province from January 2016 to January 2017. Cases were 100 unrelated Lur individuals selected with newly diagnosed pulmonary tuberculosis, positive sputum smear and/or culture and significant symptoms of typical PTB, chest radiography consistent with active disease. Then, patients with any autoimmune disease, chronic renal failure and any chronic inflammatory disease were excluded. The control group composed of healthy individuals who matched in age and gender. Controls were 100 unrelated Iranian individuals of the same race and geographic region. None of the controls showed any clinical manifestations of PTB at the time of blood sample collection, and no evidence of prior PTB noted on chest radiography. The healthy control group composed of healthy individuals who matched in age and gender with the patient group. Additionally, all study subjects had parents of the same race.

2.2. Determination of sample size

The sample size was determined by the following factors: the known prevalence MBL genetic polymorphisms in the Iranian population, α and β errors. We used a value of at least 10% for the prevalence of polymorphisms, an α error of 0.05, a β error of 0.2, a 10% expected difference, and match ratio of 1:1. The minimum sample size was estimated to be 100 for the PTB group for the HC group.

2.3. Genotyping

A case-control study was conducted in 100 pulmonary tuberculosis (PTB) patients and 100 healthy controls (HCs). Blood samples were collected from all subjects. We extracted genomic DNA from 5 ml Venous blood samples using the QIAmp kit (Qiagen, Germany) according to the manufacturer's protocol. Polymerase chain reaction (PCR) and single-strand conformation polymorphism (SSCP) technique were used to study the frequencies of MBL gene polymorphisms, that previously suggested by Wu et al. [37] and Chen et al. [40]. MBL gene, the AB, HL, PQ and XY polymorphisms were detected in patients and controls using their genomic DNA. PCR amplifications were performed using purified DNA Mastercycler (BioRad, USA) in 25 µl reaction volumes. Thermocycling parameters were as follows: 94 °C for 4 min and 35 cycles of 94 °C for 30 s, 59 °C for 60 s and 72 °C for 45 s, with a final extension at 72 °C for 5 min. PCR amplification products were analyzed on a polyacrylamide gel to detect alterations in PCR-amplified products. The primer sequences were previously reported [27,39,42] and listed in Table 1. To ensure the validity of result, we also did the DNA sequencing on the 5% representative isolates to check the PCR.

2.4. Statistical analysis

The genotypic and allelic frequencies of AB, HL, PQ and XY polymorphisms were ascertained by direct counting in the PTB patients and control group. Departure from Hardy-Weinberg Equilibrium (HWE) of All polymorphisms frequency was assessed by an exact test in both patient and control groups. Data were managed and analyzed using

Table 1

<table>
<thead>
<tr>
<th>MBL polymorphisms</th>
<th>Sequences of the primers</th>
</tr>
</thead>
<tbody>
<tr>
<td>MBL-AB (+ 230) (rs1800450)</td>
<td>F: 5'-AGTGGACCGAGATGTTAGGACGAGAG-3'</td>
</tr>
<tr>
<td>R: 5'-AGGATCAGGCGAGTTGTCCGAGAG-3'</td>
<td></td>
</tr>
<tr>
<td>MBL-HL (- 550) (rs11003125)</td>
<td>F: 5'-GCTTACCAGGACTCCGTCGTG-3'</td>
</tr>
<tr>
<td>R: 5'-ACTACTAGCGCGAGCCGCGTC-3'</td>
<td></td>
</tr>
<tr>
<td>MBL-PQ (+ 4) (rs7095891)</td>
<td>F: 5'-CTGAGTTAACCCACCTATTTACCAGG-3'</td>
</tr>
<tr>
<td>R: 5'-CTGAGTTAACCCACCTATTTACCAGG-3'</td>
<td></td>
</tr>
<tr>
<td>MBL-XY (- 221) (rs7096206)</td>
<td>F: 5'-GAAGACATTTTATTAGCTTCAGGC-3'</td>
</tr>
</tbody>
</table>

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SPSS 21 program. We calculated differences in the genotypic and allelic frequencies of AB, HL, PQ and XY polymorphisms between the cases group and control group by Chi-square test and Fisher’s exact test [43]. All of the P-values presented in this study are two-sided, and P < 0.05 was used as the threshold of statistical significance. Odds ratios (OR) and 95% confidence intervals (CIs) were calculated to quantify the degree of association between the polymorphisms and tuberculosis [44].

3. Result

A total of 100 cases with smear-positive PTB and 100 healthy controls were recruited to the study. The mean age of cases was (28.83 ± 6.12, range 21–46 years) and the mean age of controls was (26.18 ± 4.35, range 19–53 years). 46 individuals of cases were males and 54 individuals were females, and 58 individuals of controls were males and 42 individuals were females.

The genotype distribution of MBL polymorphisms in all subjects did not deviate from the Hardy-Weinberg equilibrium (P > 0.05). The results of the association between the MBL AB (+ 230) (rs1800450), HL (− 550) (rs11003125), PQ (+ 4) (rs7095891) and XY (− 221) (rs7096206) genotypic and allelic frequencies and the risk of PTB were listed in Tables 2 and 3.

In PTB patients, the HH, HL, LL genotype frequencies of the MBL gene were 35%, 43% and 22%, while these were 22%, 48% and 30% in healthy individuals respectively. The genotypic frequencies of MBL AB, PQ and XY polymorphisms did not have significant difference between the PTB and the controls. Based on the analysis of loci, we found that MBL (HH) genotype polymorphism significantly was associated with increased susceptibility to TB (35% in patients vs. 22% in controls, P = 0.0417, OR = 1.909, %95 CI = 1.020–3.573). Additionally, H allele showed a significant association with increased risk of TB (56.5% in patients vs. 46% in controls, P = 0.0357, OR = 1.525, %95 CI = 1.020–2.262). Also, the distribution of L allele in patients was significantly lower frequency in TB patients compared to controls (43.5% vs. 54%, P = 0.0357, OR = 0.656, %95 CI = 0.442–0.973).

For MBL-HL (rs11003125) polymorphism, the genotype (HH) and H allele increased PTB risk by 1.909-fold and 1.525-fold respectively among patients compared with controls. Also, the L allele decreased PTB risk by 0.656-fold among patients compared with controls (Table 2). The allelic frequencies of MBL AB, PQ and XY polymorphisms did not have significant difference between the patients and the controls (Table 3). The combination of the seven haplotypes found in patients and controls are shown in Table 4. In the present study we couldn’t detect any significant differences between haplotypes among TB patients and healthy controls.

### Table 2

<table>
<thead>
<tr>
<th>MBL Polymorphisms</th>
<th>Genotypes</th>
<th>% of TB patients group</th>
<th>% of healthy controls group</th>
<th>OR</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>MBL-AB</td>
<td>A</td>
<td>69</td>
<td>72</td>
<td>0.866</td>
<td>0.6418</td>
</tr>
<tr>
<td></td>
<td>B</td>
<td>29</td>
<td>27</td>
<td>1.104</td>
<td>0.7528</td>
</tr>
<tr>
<td>MBL-HL</td>
<td>H</td>
<td>35</td>
<td>22</td>
<td>1.909</td>
<td>0.0417</td>
</tr>
<tr>
<td></td>
<td>L</td>
<td>43</td>
<td>48</td>
<td>0.817</td>
<td>0.4777</td>
</tr>
<tr>
<td>MBL-PQ</td>
<td>P</td>
<td>76</td>
<td>69</td>
<td>1.423</td>
<td>0.2676</td>
</tr>
<tr>
<td></td>
<td>Q</td>
<td>21</td>
<td>26</td>
<td>0.757</td>
<td>0.4044</td>
</tr>
<tr>
<td>MBL-XY</td>
<td>X</td>
<td>36</td>
<td>29</td>
<td>1.377</td>
<td>0.2906</td>
</tr>
<tr>
<td></td>
<td>Y</td>
<td>59</td>
<td>64</td>
<td>0.809</td>
<td>0.4675</td>
</tr>
</tbody>
</table>

* Significant difference (P < 0.05), n = 100.

4. Discussion

Tuberculosis is an infectious disease caused by Mycobacterium tuberculosis. However, a relatively small proportion of people infected with Mycobacterium tuberculosis will develop TB [45–48]. Host genetic factors can determine differences in the susceptibility and/or resistance to infections, as well as in the clinical patterns of diseases. The host immune response against MTB is mediated by cellular immunity [11]. Recently, MBL2 gene polymorphisms have been reported to be associated with the risk of TB. However, the results were inconsistent and inconclusive MBL gene may be involved in genetic susceptibility to TB. They are rapidly degraded and exist as lower order oligomers, which have a lower binding capacity to mannos and do not activate complement [49]. MBL has been shown to bind with lipoparabinomannan, one component of Mycobacterium tuberculosis, and promote opsonophagocytosis [50,51]. Low serum level of the protein may contribute to the susceptibility to TB. In previous studies, there is no research reported that the association between MBL gene and PTB susceptibility in the Lur population of Iran.
We for the first time studied the correlations between MBL gene polymorphisms $\text{AB} (+ 230)$ (rs1800450), $\text{HL} (-550)$ (rs11003125), $\text{PQ} (+ 4)$ (rs7095891) and $\text{XY} (-221)$ (rs7096206) and PTB susceptibility in this population. In our study we showed that $\text{MBL} (\text{IH})$ genotype and the $\text{H}$ allele are involved in the susceptibility to TB development in a Lur population of Iran. A significant association was found for $\text{L}$ allele to resistant against the pulmonary tuberculosis. The genotypic and alleleic frequencies of $\text{MBL} \text{AB}, \text{XY}$ and $\text{PQ}$ polymorphism showed no correlations with PTB susceptibility By contrast, our study did not replicate previous studies of associations between MBL polymorphisms and susceptibility to PTB.

The relation between MBL gene polymorphisms and susceptibility to TB has been studied in different populations. The effect of low MBL levels on TB has been controversial. Some studies reported low MBL levels as associated with protection against the disease, whereas others estimated a relation with increased susceptibility [52]. Denholm et al. suggested that there was no significant association between $\text{MBL}$ gene polymorphism and pulmonary TB infection [52]. Studies showed that $\text{MBL-AB}$ polymorphism, affect the serum level as well as configuration and function of MBL more significantly than other [25]. In China, the $\text{MBL-AB}$ gene polymorphism is more common than the other [39]. Alagarasu et al. [53] and Selvaraj et al. [54], have previously suggested that $\text{BB}$ genotype may be associated with susceptibility to TB, since they observed a significant increase in the frequency of $\text{BB}$ genotype in TB patients than controls. Additionally, Capparelli et al. [33], reported higher frequencies of the $\text{BB}$ genotype among patients (22.3% vs. 3.5% in controls) in an Italian population. Our results are inconsistent with some previous studies, a possible explanation could be their ethnic differences.

On other hand, some studies have shown that MBL deficiency protects against disease caused by $\text{M. tuberculosis}$ [39,52,55,56]. $\text{MBL2}$ variants, either structural alleles (codons 54) in Gambian children [57] and South African adults [58], or full promoter haplotypes responsible for low MBL production, have been shown to be protective against tuberculosis. Seborg et al. [13] demonstrated a significantly decreased frequency of individuals with the low-expressing $\text{MBL}$ genotype in Caucasian patients compared to control subjects. The same tendency was also observed in patients of other ethnic origin. The authors hypothesized that heterozygosity for $\text{MBL2}$ variant alleles, responsible for low serum levels of MBL, was associated with protection against clinical TB. Studies in Danish patients [13] and Turkish children [42] showed no association between $\text{MBL2}$ polymorphisms at the codons 54 and susceptibility to TB. A large study in India showed that a significantly increased genotype frequency of $\text{MBL}$ mutant homozygotes was seen in pulmonary TB patients as compared with that in control subjects [59].

Our results showed similar outcome as a study that carried out in PTB patients of Chines. In Wu et al. study, the $\text{MBL} (\text{HH})$ and ($\text{HL}$) genotype was associated with susceptibility to TB, although in our study $\text{MBL} (\text{HL})$ genotype were not associated with susceptibility to pulmonary tuberculosis [37]. In daCruz et al. study, the $\text{BB}$ genotype frequency distribution was similar between patients and controls, but the $\text{B}$ allele, as well as the $\text{AB}$ genotype, was significantly more frequent in TB patients than healthy controls; the homozygous AA genotype, responsible for higher levels of circulating MBL proteins, was more frequent in controls than in TB patients [34]. In a Araújo et al. study, have studied the $\text{AB} \text{MBL2}$ variant in TB patients and healthy controls in a population from the Amazon region (Northern of Brazil), without finding any evidence of association between this polymorphism and TB [60]. Shi et al. study reported for the $\text{MBL2}$ codon 54 $\text{AB}$ gene polymorphism, significant association was found in the dominant model ($\text{OR} = 1.52, 95\% \text{CI} : 1.22–1.88$), homozgyote comparison ($\text{OR} = 2.10, 95\% \text{CI} : 1.08–4.09$), and $\text{B}$ vs. $\text{A}$ ($\text{OR} = 1.45, 95\% \text{CI} : 1.20–1.75$). The results suggested that individuals with $\text{B}$ allele may have an increased risk of TB as compared with wild type $\text{AA}$ homozygotes in Chinese population. In their study no significant association was found between $\text{MBL2} + 4 \text{PQ}$ gene polymorphism and the risk of TB. They suggests that individuals carrying the $\text{MBL2}$ codon 54 $\text{B}$ allele may have an increased risk of TB as compared with $\text{AA}$ homozygous, whereas $\text{MBL2} + 4 \text{PQ}$ gene polymorphism is possibly not associated with TB in Chinese population [38].

TB is a multifactorial disease and its susceptibility depends not only upon host genetic aspects, but also on mycobacteria characteristics and on interactions with environmental factors. In addition, different genetic backgrounds and environmental factors may also influence the results. There is no doubt about the difficulty in comparing results from studies conducted in different populations, even when the same allele or haplotype are analyzed and the same study design is used. These paradoxical findings could be due to the Ethnic difference, different between genotyping technique, criteria for sample inclusion and exclusion and the small sample size of this study and could be caused by gene-environment interaction, gene-gene interaction, and gene-agent interactions [61,62].

5. Conclusions

Our comprehensive analysis of $\text{MBL}$ polymorphisms suggests that $\text{MBL} (\text{IH})$ genotype, $\text{H}$ and $\text{L}$ allele associate with PTB risk in the Lur population of Iran. For better understanding of the association between these polymorphisms and the risk of TB, larger sample size and more studies, especially those investigating haplotypes as well as gene-gene and gene-environment interactions, are required in the future. Further studies are required to determine how $\text{MBL}$ polymorphisms influence susceptibility to Mycobacterium tuberculosis infection.

Conflict of interest statement

The authors declare no conflict of interest.

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