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Association study of CTLA-4 +49A/G gene polymorphism with recurrent pregnancy loss in the Iranian Azeri Turkish ethnic group

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Background/aim: Recurrent pregnancy loss (RPL) is defined as two or more pregnancy losses. T-regulatory cells play an important role in the feto-maternal interface. Cytotoxic-T-lymphocyte antigen-4 (CTLA-4) is a molecule that downregulates the activation and proliferation of T cells. The objective of the current study was to investigate the possible association of CTLA-4+49A/G gene polymorphism with RPL among patients from the Iranian Azeri Turkish ethnic group.

Materials and methods: The study group/patients consisted of 101 women with the experience of two or more pregnancy losses and the control group consisted of 101 women with at least two live births, without any previous history of pregnancy loss and autoimmune diseases from the same ethnic group. The CTLA-4+49A/G was detected by polymerase chain reaction-restriction fragment length polymorphisms assay.

Results: The distribution of CTLA-4+49A/G genotype was AA, 38.61%; AG, 51.48%; GG, 9.9% in patients and AA, 37.62%; AG, 47.52%; GG, 14.85% in controls (P-value: 0.2). Furthermore, no association in G-allele was observed in the patient and control groups (P-value: 0.5).

Conclusion: The results of the present study suggest that CTLA-4 does not have any association with RPL in the Iranian Azeri Turkish ethnic group.

Key words: CTLA-4, immune system, recurrent pregnancy loss
a key role in response to antigens. On the other hand, when CTLA-4 binds to B7, it commences the JNK (Jun N-terminal kinase) pathway to increase the localization of transcription factor Foxo3, which leads to the prevention of IL-6 production (16).

The CTLA-4 gene, which maps to human chromosome 2q33, has 4 exons and the +49 A/G polymorphism is located at the +49 position of exon 1 (13).

Several studies have been carried out to investigate the association of CTLA-4 polymorphism with several autoimmune diseases such as diabetes and Graves disease (17). It has been suggested that this polymorphism, which leads to a change in codon 17 of leader peptide, reduces membrane CTLA-4 protein expression (18,19).

Given the importance of CTLA-4 in maternal tolerance, we preformed this study to investigate the possible association of +49 A/G gene polymorphism with idiopathic RPL among women from the Iranian Azeri Turkish ethnic group.

### 2. Materials and methods

A hundred and one women with idiopathic RPL (defined by ASRM) and another 101 women with at least two live births and also without any previous history of pregnancy loss and/or autoimmune diseases were involved in this case-control study. The Ethics Committee at Tabriz University of Medical Science approved the study. All participants signed an informed consent form to provide their blood for genotyping.

The standard salting out technique was applied to extract the genomic DNA of blood leukocytes. +49 A/G CTLA-4 gene polymorphism was detected using PCR-RFLP. The 25-µL PCR reaction mixture contained 100 ng of genomic DNA, 10 pmol of each primer, and 1 U of Taq DNA polymerase (Sinagene). The cycling parameters were followed by 3 min initial denaturation at 94 °C; 30 cycles of 30 s at 94 °C, 30 s at 58 °C, 15 s at 72 °C; this was followed by a final extension of 3 min at 72 °C. Next, the amplicons were digested by BbvI(NEB) at 37 °C overnight by RFLP. The digestion of wild-type allele produced a single fragment with 162 bp length, whereas the polymorphic allele produced two fragments of 72 bp and 90 bp. All data were analyzed using SPSS version 21.0 (SPSS Inc., Chicago, IL, USA). In addition, the Hardy–Weinberg equilibrium (HWE) for the genotype frequencies was verified by the chi-square test. Probability values of 0.05 or less were regarded as statistically significant.

### 3. Results

The HWE results for genotype frequencies for both patients and control groups (patients as object and controls as expect groups) showed no significant association. Therefore, it was concluded that the studied population enjoys the HWE. Of all the 202 subjects, 101 patients with RPL as the study group and 101 healthy controls were genotyped for CTLA-4 +49A/G polymorphism. The average age of patients was 28 years. The demographic data and genotype frequencies of both patients and controls are given in the Table. The results were obtained using the chi-square test. The frequencies of AA, AG, and GG genotypes were 37.62%, 47.52%, and 14.85% in the control group and 38.61%, 51.48%, and 9.9% in the patients, respectively. The results showed no significant differences among patients and controls.

### 4. Discussion

Pregnancy is a unique condition in a woman’s reproductive life (4,7). Many factors are suggested to be involved in RPL, including the immune system and its components, which could play an important role in maternal tolerance during pregnancy (6). It has been reported that autoimmune abnormalities such as antiphospholipid, antithyroid, antinuclear, and antisperm antibodies are associated with RPL (20). In such abnormalities cell-mediated immunity

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<table>
<thead>
<tr>
<th>Genotype</th>
<th>Patients n (F)</th>
<th>Controls n (F)</th>
<th>Chi-square</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA</td>
<td>39 (38.61%)</td>
<td>38 (37.62%)</td>
<td>0.020</td>
<td>0.885</td>
</tr>
<tr>
<td>AG</td>
<td>52 (51.48%)</td>
<td>48 (47.52%)</td>
<td>0.316</td>
<td>0.573</td>
</tr>
<tr>
<td>GG</td>
<td>10 (9.9%)</td>
<td>15 (14.85%)</td>
<td>1.141</td>
<td>0.285</td>
</tr>
<tr>
<td>Allele</td>
<td>Patients n (F)</td>
<td>Control n (F)</td>
<td>Chi-square</td>
<td>P value</td>
</tr>
<tr>
<td>A</td>
<td>130 (64.35%)</td>
<td>124 (61.38%)</td>
<td>0.686</td>
<td>0.407</td>
</tr>
<tr>
<td>G</td>
<td>72 (35.64%)</td>
<td>78 (38.61%)</td>
<td>0.303</td>
<td>0.581</td>
</tr>
</tbody>
</table>

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**Table.** Genotypic and allelic distribution of +49 A/G CTLA-4 among patients and controls from the Iranian Azeri Turkish ethnic group.
is increased and the level of regulatory T cells is altered (21). Regulatory T cells (Tregs) are crucial components of humeral immune response, which is important in the initiation and maintaining of pregnancy (1,22). The regulation of Tregs is mediated by antigen independent co-stimulatory signals, which act on the surface of Treg cells (1). The expression of CTLA-4 could be downregulated by activated T cells (15).

This study was planned to investigate the possible association of CTLA-4 A49G gene polymorphism with RPL among women from northwest Iran and mainly originated from the Azeri Turkish ethnic group. The frequency of genotypes and alleles did not show significant differences between the controls and patients.

There are only a few studies that have investigated the polymorphisms of the CTLA-4 gene in maternal tolerance during pregnancy. For instance, a recent study performed in the north Indian population showed no significant association between the CTLA-4 +49 A/G (G allele) and RPL in that population (3). Moreover, Wang et al. investigated the CTLA-4 +49 A/G gene polymorphisms in Chinese women with unexplained spontaneous abortion (SA) and unexplained recurrent spontaneous abortion (RSA). The study showed no significant association between CTLA-4 and RSA (9). However, another study carried out on the Tunisian population showed a significant association between CTLA-4 +49 A/G gene polymorphism and RPL (22). Two other studies by Wang, with larger study groups, showed the association of the studied polymorphism with the immunopathogenesis of RSA in the Chinese population (23,24).

The results of the current study confirm the results of the Chinese and Indian reports and suggest that the +49 A/G CTLA-4 polymorphic region might not affect RPL in the studied population. Although in the Chinese and Indian populations no association was observed between +49 A/G CTLA-4 gene polymorphism and RPL, it is possible that there might be some other SNPs on CTLA-4 that would show an association with RPL. Therefore, studying these SNPs may lead to stronger findings.

Our findings also indicate that, in fact, the frequency of the G allele of the CTLA-4 gene in the study population from northwest Iran is higher than that of the other previously reported populations.

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References


