Mutational Analysis of CTLA4 Gene in Pakistani SLE patients

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Abstract—The main aim is to perform mutational analysis of CTLA4 gene Exon 1 in SLE patients. A total of 61 SLE patients fulfilling “American College of Rheumatology (ACR) criteria” and 61 controls were enrolled in this study. The region of CTLA4 gene exon 1 was amplified by using Step-down PCR technique. Extracted DNA of band 354 bp was sequenced to analyze mutations in the exon-1 of CTLA-4 gene. Further, protein sequences were identified from nucleotide sequences of CTLA4 Exon 1 by using Expasy software and through Blast P software it was found that CTLA4 protein sequences of Pakistani SLE patients were similar to that of Chinese SLE population. No variations were found after patients sequences were compared with that of the control sequence. Furthermore it was found that CTLA4 protein sequences of Pakistani SLE patients were similar to that of Chinese SLE population. Thus CTLA4 gene may not be responsible for an autoimmune disease SLE.

Keywords—American College of Rheumatology criteria, autoimmune disease, Cytotoxic T Lymphocyte Antigen-4, Polymerase Chain Reaction, Systemic Lupus Erythematosus

I. INTRODUCTION

MHC region genes are known as a prominent genetic factor of autoimmune diseases in both animal models and in humans. In humans, number of MHC genes has been identified and one of the most studied is Cytotoxic T lymphocyte associated antigen 4 gene (CTLA4), which is located on chromosome 2. This gene consists of four exons and the size spans to 6,175 bases. It is identified as the fourth cDNA that are particularly expressed in Cytotoxic T Lymphocytes. This molecule is very much similar to CD28 molecule. CD28 as well as CTLA4 play a dynamic role in autoimmune disorders [1]. So the main objective of this study is to perform mutational analysis of CTLA4 gene Exon 1 in SLE patients.

II. SUBJECTS AND MATERIALS

The human studies reported in this manuscript were approved by the “Ethical Committee of the School of Biological Sciences”, University of the Punjab, Lahore, Pakistan. Samples described in this work are part of a larger study on lupus patients coming to different hospitals of Lahore for the treatment. The study population covered different areas of Punjab; mainly Lahore, Gujranwala, Sialkot, Raheem-Yar Khan, Gujrat and district Kasur. Of the 61 SLE patients, fifty-five (90.16%) were females and six (9.83%) were males. The female versus male ratio was 9.16:1. Mean age at diagnosis was 30.163 years (Range: 11-68 years). Muscudonate involvement was found in lupus patients such as malar rash 6 (9.84%), discoid rash 11 (18.03%), photosensitivity 11 (18.03%). Various syndromes were overlapping with SLE and the most common one was Rheumatoid arthritis (19 patients: 31.14 %) but cases of Sjogren’s syndrome (10 patients: 16.39 %), Scleroderma (2 patients: 3.27%), Secondary Antiphospholipid syndrome (2 patients: 3.27%), and of Budd-Chiari Syndrome (1 patients: 1.63%) were also found along with SLE. Renal involvement was found in 32.78% patients characterized by proteinuria and red cell cast. Blood samples drawn by venepuncture from each patient and control were collected in a EDTA vial. An informed written consent was taken from all subjects recruited in the study as well as from the matched controls. Genomic DNA (Fig. 1) was purified from peripheral blood by using Genomic DNA purification kit (Fermentas, Cat # K0512-Germany). The concentration of DNA was estimated by taking A260/A280 ratio with the help of spectrophotometer (Cecil, CE 7200). Absorbance ratio A260/A280 1.8 or above was taken as pure preparation.

PCR was performed by Step-down PCR technique in order to get rid of non-specific bands and achieved the band of our interest that is of 354 bp (Fig. 2).
The region of “CTLA4 gene exon 1” that was amplified is as follow:

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GCTTCTGTGTGACATGTGAAATCTCTTCTGGGATCAAAGCT
ATCTATATAAGGTCAGGATTCGCTTCTGGGATTCAACACATTTCA
AGCTTCAAATCCGGAGGATCTGCTACTCTCTGAAAGACCTGA
ACACCGCCTCAAAAGGATCTGCTAAGGAGTCCCTGACCTGCTTTT
CTTCTTCTTCTATCCCTGCTTCTGCAAAG
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Procedure of Step-down PCR

The PCR reaction was performed in a total volume of 50 μl using 250 ng of genomic DNA, 10 pmol of each of the primer mixture and 2X PCR mixture. CTLA-4 gene exon 1 was amplified with the primers designed by entering the selected portion of CTLA-4 exon 1 in Primer 3 Software. Step-down PCR conditions consisted of an initial 95 ºC denaturation for 5 minutes followed by 35 cycles of denaturation at 95 ºC for 30 seconds, then annealing step and finally elongation at 72 ºC for 30 seconds followed by final extension at 72 ºC for 3 minutes. The difference lies in the annealing temperature; in the beginning annealing temperature was higher than the melting temperature of the primers that was 60 ºC; then there was fewer and steeper decline in the PCR annealing temperature that was up to 52 ºC. Genomic DNA was subjected to 35 cycles of amplification according to “Step-down PCR” protocol in a peQLab advance primus 96 thermal cycler, USA. The DNA fragment of 352 bp was analyzed on a 2% agarose gel. Low-range DNA ladder (Fermentas Cat # R0631) was used to verify results.

III. RESULTS

Extracted DNA of band 354 bp was sequenced to analyze mutations in the exon-1 of CTLA4 gene. “Chromas” software was used to convert the instrumental data in to a nucleotide base order and “Edit Seq” software to analyze the resulting nucleotide sequence. Particularly, we were interested in CTLA4 gene polymorphism of exon 1 at +49. According to “Genbank”, the standard sequence of CTLA4 gene includes adenine (A) at +49. If there is any A to G polymorphism at position +49 in CTLA4 Exon 1 then there should be threonine to alanine substitution in the leader peptide. But no variations were found after patients sequences (TABLE 1) were compared with that of Chinese SLE population.

<table>
<thead>
<tr>
<th>Sample #</th>
<th>Accession #</th>
<th>Patient description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sample 02-P7</td>
<td>HM545121</td>
<td>SLE</td>
</tr>
<tr>
<td>Sample 59-P8</td>
<td>HM545122</td>
<td>SLE + Budd-chiari syndrome</td>
</tr>
<tr>
<td>Sample 24-P14</td>
<td>HM545123</td>
<td>SLE + Lupus nephritis</td>
</tr>
<tr>
<td>Sample 03-P16</td>
<td>HM545124</td>
<td>SLE + Skin involvement</td>
</tr>
<tr>
<td>Sample 26-P30</td>
<td>HM545125</td>
<td>SLE overlapping Scleroderma</td>
</tr>
<tr>
<td>Sample 05-P36</td>
<td>HM545126</td>
<td>SLE + Antiphospholipid syndrome</td>
</tr>
</tbody>
</table>

IV. DISCUSSION

Number of polymorphisms in the CTLA4 gene has been identified that are genetically linked to several autoimmune disorders, namely systemic lupus erythematosus, grave’s disease, rheumatoid arthritis, type 1 diabetes, celiac disease, autoimmune thyroid disease, and multiple sclerosis [2]. There are more than 100 known single nucleotide polymorphisms in the CTLA4 gene. In humans, CTLA4 gene has been proposed to play a vital role in autoimmune pathogenesis [3]. SLE patients have been genotyped for allelic determinants at four polymorphic sites in the CTLA-4 gene. Three polymorphisms were in the promoter region while one is within the exon 1 at position +49 (A/G). CTLA4 exon 1 49G allele coding for position 17 Ala has been shown to be significantly associated with autoimmune diseases. In Chinese population, no statistical difference was found in both exon 1 and promoter gene polymorphism between SLE patients and controls [4]. In the present study, adenine deletion at 49bp could not be considered because the peak was quite wide (Fig. 3) so the experiment was repeated to confirm results but no such mutations were found.
In the present study, CTLA4 gene Exon 1 was studied in SLE patients. Amplification of 356 bp fragment from CTLA4 gene supposed to be carried 49 A/G polymorphism but no such SNP was found in CTLA4 gene Exon 1 of SLE patients thus the results matched with Chinese population. After sequencing, alignment of six different sequences was done by the use of multiple sequence alignment tool “Seaview”. These nucleotide sequences were not only similar to CTLA4 gene Exon 1 but also to Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Haplorrhini.

Further, protein sequences were identified from nucleotide sequences of CTLA4 Exon 1 by using “Expasy software” and through “Blast P” software it was found that CTLA4 protein sequences of Pakistani SLE patients were similar to that of Chinese SLE population. HM545121 was a linear DNA of 216 bp, its protein sequence was similar to Cytotoxic T lymphocyte associated protein 4 and its product was “MACLGFRHKQLNLATRTWP”. HM545122 and HM545123 contained frameshifts relative to similar CTLA4 protein. In case of HM545122, coding region contain frameshifts that were present around nucleotides 168, 175 and 195 while in HM545123 frameshift was present around nucleotide 164 that result in different translations from similar proteins in the database. Therefore in both cases the CDS was converted in to misc_features and the translation was removed. HM545124 was a linear DNA of 190 bp and after translation the product was “MACLGFRHKQLNLATRTWPCT”. HM545125 and HM545126 had a linear DNA of 216 bp and 230 bp respectively and their translated products were “MACLGFRHKQLNLATRTWP” and “MACLGFRHKQLNLATRTWPCT” (TABLE 2).

V. CONCLUSION

No CTLA-4 gene Exon 1 mutations were found in Pakistani SLE patients with “Sjogren’s syndrome” or SLE patients with “Budd-Chiari syndrome” and “Scleroderma”. One of the major reasons is that SLE is a complex genetic disorder and multiple genes are involved so the effects of this gene may be weak and thus go undetected experimentally. Another reason for the conflicting results with other populations may include differences in the ethnic groups and the age at the onset of the disease. Thus CTLA4 gene is not responsible for SLE.