Abstract—The p53 tumor suppressor gene plays two important roles in genomic stability: blocking cell proliferation after DNA damage until it has been repaired, and starting apoptosis if the damage is too critical. Codon 72 exon4 polymorphism (Arg72Pro) of the p53 gene has been implicated in cancer risk. Various studies have been done to investigate the status of p53 at codon 72 for arginine (Arg) and proline (Pro) alleles in different populations and also the association of this codon 72 polymorphism with various tumors. Our objective was to investigate the possible association between P53 Arg72Pro polymorphism and susceptibility to colorectal cancer among Isfahan and Chaharmahal Va Bakhtiari (a part of south west of Iran) population. We investigated the status of p53 at codon 72 for Arg/Arg, Arg/Pro and Pro/Pro allele polymorphisms in blood samples from 145 colorectal cancer patients and 140 controls by Nested-PCR of p53 exon 4 and digestion with BstU restriction enzyme and the DNA fragments were then resolved by electrophoresis in 2% agarose gel. The Pro allele was 279 bp, while the Arg allele was restricted into two fragments of 160 and 119 bp. Among the 145 colorectal cancer cases 49 cases (33.79%) were homozygous for the Arg72 allele (Arg/Arg), 18 cases (12.41%) were homozygous for the Pro72 allele (Pro/Pro) and 78 cases (53.8%) found in heterozygous (Arg/Pro).

In conclusion, it can be said that p53Arg/Arg genotype may be correlated with possible increased risk of this kind of cancers in south west of Iran.

Keywords—TP53, Polymorphism, Colorectal Cancer, Iran

I. INTRODUCTION

Colorectal cancer (CRC) also called colon cancer or large bowel cancer, includes cancerous growths in the colon, rectum and appendix [1]. It is the third most common cancer worldwide, the second leading cause of cancer death in the United States after lung cancer and the significant cause of morbidity and mortality in western populations [2]. Colorectal cancer is a complex, multistep and multifactor process, and is thought to result from an interaction between environmental and genetic factors [3]. The risk of developing colorectal cancer is influenced by a number of factors, including sex, age, alcohol consumption, low-fiber or high-fat diet intake hereditary conditions, familial history of colorectal cancer, personal history of colonic polyps, bowel inflammatory diseases and a variety of genetic factors [3]. Among the genetic factors, the TP53 tumor suppressor gene is a suitable candidate for modulating colorectal cancer risk and is one of the most commonly mutated genes in all types of cancer (found in 50% of human cancers) [1], [4]. The p53 gene located on chromosome 17p13 [5]. It contains 11 exons and encodes for a 53 kDa multifunctional DNA-binding protein [6]. The p53 plays a critical role in the prevention of tumor formation; however, it is not required for normal cell growth. p53 can induce cell cycle arrest, DNA repair, differentiation, or apoptosis in response to oncogenic cellular stress including carcinogen induced DNA damage, abnormal proliferative stimulation [7]. In the cell, p53 protein binds DNA, which in turn stimulates another gene to produce a protein called p21 that interacts with a cell division-stimulating protein (cdk2). When p21 is complexed with cdk2 the cell cannot pass through to the next stage of cell division. Mutant p53 can no longer bind DNA in an effective way, and as a consequence the p21 protein is not made available to act as the ‘stop signal’ for cell division. Thus cells divide uncontrollably, and form tumors [2]. p53 gene is the target of point mutations and of small deletions and insertions [8]. These mutations (mostly missense mutations) may damage the normal function of TP53 as a transcription factor, and the induction of repair or apoptosis may be abolished. Consequently, other genetic alterations may accumulate in the cell [9].

To date, several polymorphisms in the wild-type p53 gene locus have been described [10]. At least three of them have been reported to be involved in cancer: the 16-bp duplication in intron 3, MspI restriction fragment length polymorphism (MspI-RFLP) in intron 6 (cc) and an arginine/proline variant at codon 72 in exon 4 [11], [12]. The most important p53 polymorphism is the BstUI-RFLP in codon 72 of exon 4 results in two alleles, the arginine (72Arg: CGC) and proline (72Pro: CCC) isoforms [3], [13]. This polymorphism has been reported to be associated with some tumor types [Pro: bladder cancer, lung cancer; Arg: hepatocellular carcinoma, cervical cancer, human papilloma virus (HPV)-associated cervical cancer]. An alteration of the p53 tumor suppressor gene is also
a mutational event involved in colorectal mucosa carcinogenesis [13], [4].

The Arg72Pro polymorphism is located in a praline rich region (residues 64-92) of the p53 protein, where the 72Pro amino acid constitutes one of five PXXP motifs resembling a SH3 binding domain. The region is required for the growth suppression and apoptosis mediated by SH3 binding domain. The region is required for the growth suppression and apoptosis mediated by the E6 protein of the human papillomavirus and degradation of p53 protein by HPV E6 is correlated with increased risk for HPV-associated cancers [7], [4]. Although the presence of HPV-DNA in colorectal tissues and adenocarcinomas was reported in populations from different regions, the association of p53 codon 72 polymorphism with colorectal cancer taking into account mRNA expression was investigated only once [15]. Therefore, we investigated the association of p53 codon 72 polymorphism with colon cancer cases in south west of Iran by Nested-PCR and RFLP analysis with BstUI restriction enzyme.

II. MATERIALS AND METHODS

Subjects

A total of 145 patients (77 patients (53%) were male and 68 (47%) were female) with colorectal cancer, who attended the clinical hospitals and clinical laboratories from south west of Iran were enrolled into this study. Their age ranged from 18-85 years with a mean of 48.56 years (Table I). Informed consent was obtained from the patients and their blood samples were collected. Blood from 140 people who attended clinical laboratories and were negative for colorectal cancer served as normal control.

DNA extraction from blood samples

Genomic DNA was extracted from the blood samples by using a DNA extraction kit (QIAGEN Ltd., Crawley, UK) in accordance with the manufacturer’s protocol. The extracted DNA was stored at -20°C until further use.

p53 codon 72 polymorphism analysis

Nested-PCR and RFLP analyses were used to genotype the G-to-C p53 polymorphism in codon 72 as described previously.

The amplified fragments from second PCR were purified and digested with BstUI restriction enzyme (Fermentas, Germany) according to the instructions of the manufacturer. Each digestion reaction mixture (30 µl) contained 10 units of BstUI endonucleases and 25 µl of second PCR products and was incubated at 37°C for 2 h. After digestion, the fragments were electrophoresed on 2% agarose gel and visualized by UV light after ethidium bromide staining.

Statistical analysis

Analysis of data was performed using the SPSS version 17.0 computer software (SPSS, Chicago, IL). Chi-square analysis was used to compare categorical variables. A 5% level of significance was used in the analysis and its 95% confidence interval (CI) was calculated to measure the association between P53 Arg72Pro polymorphism in case and control population. Whenever appropriate, the observed number of each genotype was compared with that expected for a population in the Hardy-Weinberg equilibrium by using a goodness of fit $\chi^2$ test.

Gene amplification with Nested-PCR method

The first PCR primers used were D1-F: 5′-GCT CTT TTC ACC CAT CTA CAG- 3′ and D2-R: 5′-TGA AGT CTC ATG GAA GCC AGC- 3′. PCR was performed in a final volume of 25 µl reaction buffer containing 20 ng genomic DNA, 2 mM MgCl2, 25 pmole of each primer (D1-F and D2-R), 1 unit of Taq polymerase, 200 mM dNTP mix. Reaction mixtures were preincubated at 95°C for 5 minutes, followed by 30 cycles at 94°C for 1 minute, 58°C for 1 minute, 72°C for 1 minute and a final extension step at 72°C for 5 minutes. Reaction mixture without DNA template was used as a negative control and that with known DNA template was used as a positive control which yielded PCR products of expected results.

The second PCR primers used were F2-F: 5′-TCC CCC TTG CCG TCC CAA- 3′ and R2-R: 5′-CGT GCA AGT CAC AGA CTT- 3′. Reaction mixtures were as above, except that 2.5µl of product from the first reaction as template DNA and the second primers set were used.

RFLP analysis

The first PCR primers used were D1-F: 5′-GCT CTT TTC ACC CAT CTA CAG- 3′ and D2-R: 5′-TGA AGT CTC ATG GAA GCC AGC- 3′. PCR was performed in a final volume of 25 µl reaction buffer containing 20 ng genomic DNA, 2 mM MgCl2, 25 pmole of each primer (D1-F and D2-R), 1 unit of Taq polymerase, 200 mM dNTP mix. Reaction mixtures were preincubated at 95°C for 5 minutes, followed by 30 cycles at 94°C for 1 minute, 58°C for 1 minute, 72°C for 1 minute and a final extension step at 72°C for 5 minutes. Reaction mixture without DNA template was used as a negative control and that with known DNA template was used as a positive control which yielded PCR products of expected results.

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<table>
<thead>
<tr>
<th>Age group</th>
<th>Male</th>
<th>Female</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>30-40</td>
<td>9</td>
<td>6.21</td>
<td>16</td>
</tr>
<tr>
<td>40-50</td>
<td>16</td>
<td>11.05</td>
<td>29</td>
</tr>
<tr>
<td>50-60</td>
<td>13</td>
<td>8.98</td>
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</tr>
<tr>
<td>60&lt;</td>
<td>35</td>
<td>24.19</td>
<td>61</td>
</tr>
<tr>
<td>Total</td>
<td>77</td>
<td>53.2</td>
<td>145</td>
</tr>
</tbody>
</table>

TABLE I

PREVALENCE OF CLORECTAL CANCER CASES ACCORDING TO RACIAL GROUPS

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<th>Male</th>
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<td>53.2</td>
<td>145</td>
</tr>
</tbody>
</table>
III. RESULTS

Amplified DNA fragments with Arg at codon 72 would contain the polymorphic BstU I site thus the Pro allele was 279 bp, while the Arg allele was restricted into two fragments of 160 and 119 bp. Among the 145 colorectal cancer cases 49 cases (33.79%) were homozygous for the Arg72 allele (Arg/Arg), 18 cases (12.41%) were homozygous for the Pro72 allele (Pro/Pro) and 78 cases (53.8%) found in heterozygous (Arg/Pro). The frequencies of the three P53 genotypes; Arg/Arg, Arg/Arg and Pro/Pro in controls were 60.7%, 20% and 19.3%, respectively.

A representative Nested-PCR and RFLP pattern is depicted in Figure 1. The results on genotype distribution are presented in Table II.

![Image](image_url)

**Table II**

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Cases (N=145)</th>
<th>Controls (N=140)</th>
<th>P-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Arg/Arg</td>
<td>49</td>
<td>71</td>
<td>&gt;0.01</td>
</tr>
<tr>
<td>Arg/Pro</td>
<td>78</td>
<td>69</td>
<td>&gt;0.02</td>
</tr>
<tr>
<td>Pro/Pro</td>
<td>18</td>
<td>85</td>
<td>&gt;0.005</td>
</tr>
</tbody>
</table>

In this regard, an increase in the Arg/Arg genotype and a decrease in Pro/Pro genotype among patients was observed, and have a statistical significance (P<0.01). Comparison of the allele frequencies revealed an increase in the Arg allele among colorectal cancer patients compared to healthy individuals (Table III). However, the difference was not statistically significant (P=0.10). Comparison of the genotype frequencies between colorectal cancer patients and normal controls confirmed the accumulation of Arg/Arg genotype in these patients (33.79% vs. 20%, P<0.01).

### IV. DISCUSSION

The p53 gene is one of the most extensively studied human genes because of its role as a tumor suppressor gene. The overall function of p53 is to maintain genomic integrity as a whole, providing a protective effect against tumorigenesis [13]. Recently, several studies have provided evidence that alterations of p53, either through genetic mutation or allelic polymorphisms, have been described as the most common genetic changes in human cancers, such as cervical cancer, breast cancer, lung and colorectal cancer [7], [13]. In Iran colorectal cancer accounts are approximately 8% of all malignancies [16]. The p53 gene is known to exhibit distinct mutational patterns in various cancer types. The proline/arginine substitution at codon 72 represents a common amino acid polymorphism in the p53 gene, the functional significance of which is unknown [13]. This may be due to the production of a mutant p53 protein that is not capable of inducing apoptosis in response to toxic environmental stimuli [7]. The role of the Arg/Pro polymorphism in colorectal cancer susceptibility has been examined in several studies, which have reported controversial results [17]. This controversy might be due to the fact that the genotype distribution of the p53 codon 72 Arg/Pro polymorphism is varies in different geographic regions and ethnicity [16]. According to the literature, general populations from Latin America, United States and Europe exhibit high frequencies of the Arg allele compared to the Pro one, while lower prevalence's of Arg are found in African and Asian populations [18].

Relevant to this, by nested-PCR, amplification of 4th exon were performed from isolated DNA samples of blood of colon cancer diagnosed in 145 cases and followed by enzyme restriction. As a result, the analysis of the p53 codon 72 genotype revealed 49 cases (33.79%) arginine homozygotes (Arg/Arg), 18 cases (12.41%) proline homozygotes (Pro/Pro) and 78 cases (53.8%) arginine/proline heterozygotes (Arg/Pro). The frequencies of the three P53 genotypes; Arg/Arg, Arg/Arg and Pro/Pro in controls were 60.7%, 20% and 19.3%, respectively. In the present study, the frequency of p53 codon 72 genotypes among the controls and patients non-closely conformed to Hardy-Weinberg equilibrium and we found significant differences in the genotype or allele frequencies between the patients and the control groups. Moreover, the results showed increases in the Arg/Arg genotype and a decrease in Pro/Pro genotype among patients and an increase in the Arg allele.
In agreement with prior studies on breast, stomach and colorectal cancer in Iran we found significant differences in the genotype or allele frequencies between the patients and the control groups [16].

A number of studies have failed to demonstrate the association between the p53 codon 72 polymorphism colorectal cancers. For example, Hamajima et al. analyzed this SNP in 147 colorectal cancer patients, and 241 non-cancer patients, in a Japanese population, and found no significant association between the genotype or allele frequencies and the diseases. However, other studies found the p53 codon 72 polymorphism to be a genetic risk factor for colorectal cancer [12].

The genotype frequencies of TP53 codon 72 in 180 sporadic colorectal adenocarcinomas and 180 healthy individuals from Isfahan province of Iran in 2008 was showed a significant difference between cases and controls for the Arg/Arg genotype compared with (grouped) Arg/Pro and Pro/Pro genotypes. The Arg allele was found more often in patients than in controls. The allele and genotype frequencies of the p53 codon 72 Arg/Pro polymorphism in stomach, colorectal adenocarcinoma and breast cancer patients and compared to the healthy individuals from the population of southern Iran showed non significant differences in the genotype or allele frequencies between the patients and the control groups [19]. Case and control studies conducted in Japan and Turkey failed to find an association between the prevalence of p53 polymorphism and colorectal cancer. In this study the allelic frequencies were concordant between the controls and colorectal cancer cases, reaching a frequency of approximately 0.6 for the Arg allele.

In conclusion, the findings of the present study indicate that TP53 codon 72 polymorphism may be a genetic predisposing factor for colorectal adenocarcinomas and p53 Arg72 protein may be correlated with possible increased risk of this kind of cancers in south west of Iran.

ACKNOWLEDGMENT

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REFERENCES