Association of Arg194Trp, Arg280His and Arg399Gln Polymorphisms in X-ray Repair Cross-Complementing Group 1 Gene and Risk of Differentiated Thyroid Carcinoma in Iran

Pezhman Fard-Esfahani^{*1}, Armaghan Fard-Esfahani², Shima Fayaz¹, Bahareh Ghanbarzadeh³, Parinaz Saidi¹, Reyhaneh Mohabati¹, Seyed Kazem Bidoki³ and Mina Majdi²

¹Dept. of Biochemistry, Pasteur Institute of Iran, Tehran; ²Research Institute for Nuclear Medicine, Tehran University of Medical Sciences, Tehran; ³Dept. of Biochemistry and Genetics, Payam-e-Noor University of Tehran, Tehran, Iran

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ABSTRACT

Background: X-ray repair cross-complementing group 1 (*XRCC1*) gene is a DNA repair gene and its nonsynonymous single nucleotide polymorphisms (SNP) may influence DNA repair capacity which has been considered as a modifying risk factor for cancer development. **Methods:** A case-control study was conducted to investigate impact of three frequently studied polymorphisms (*Arg194Trp*, *Arg280His* and *Arg399Gln*) on developing differentiated thyroid carcinoma (DTC). **Results:** Increased risks for DTC were shown in homozygous (odds ratio [OR]: 3.66, 95% confidence interval [CI]: 0.38-35.60) and in dominant trait (OR: 1.22, 95% CI: 1.64-2.32) of *Arg194Trp* genotype. Also, for *Arg280His* genotype, an increased risk for DTC was shown in dominant trait (OR: 1.42, 95% confidence interval [CI]: 0.76-2.68), while a mildly reduction of risk for DTC (OR: 0.77, 95% [CI]: 0.50-1.17) was estimated in dominant *Gln* genotype of *Arg399Gln*. Considering combinatory effects of *Arg194Trp* and *Arg280His* genotypes on DTC, the calculated OR and 95% CI for being heterozygous for one of *Arg194Trp* or *Arg280His* genotypes were 1.57 and 0.90-2.74, respectively. **Conclusion:** Genotyping of codons 194, 280 and 399 in *XRCC1* gene may use in risk assessment of DTC. *Iran. Biomed. J.* 15 (3): 73-78, 2011

Keywords: Endocrine related cancer, DNA repair gene, X-ray repair cross-complementing group 1 (*XRCC1*) gene, Differentiated thyroid carcinoma (DTC)

INTRODUCTION

xogenous and endogenous mutagens damage DNA, which may result in uncontrolled cell proliferation or programmed cell death. To protect the integrity of genome, some DNA repair systems have been developed in variety of organisms from bacteria to mammals. A few pathways of DNA repair operate on specific types of damaged DNA. Among them, base excision repair (BER) operates on nil lesions [1] and more than 20 gene products are related to BER [2]. The X-ray repair crosscomplementation group 1 (XRCC1) protein plays an important role in BER [3]. The XRCC1 is a multidomain protein, and is required for the efficient repair of single strand breaks and damaged bases in DNA [3, 4]. This protein is essential for mammalian viability because XRCC1 deficiency in mice results in

embryonic lethality. As DNA damage may result in somatic mutations and subsequent stimulation of DNA repair processes, it can be considered that polymorphisms of DNA repair genes may alter cell repair function capacity and lead to carcinogenesis [5]. The XRCC1 gene is located on chromosome 19q13.2 and 17 exons of this gene encode a protein with 633 amino acids [6]. A number of single nucleotide polymorphisms (SNP) have been reported in the Ensembl database. Among them, Arg194Trp (rs1799782), Arg280His (rs25489) and Arg399Gln (rs25487) are highly studied and caused nonconservative changes [7]. Some studies have shown a significant association between these variants and risk of different types of human cancer [8, 9]. These findings suggest that non-conservative changes may result in DNA repair capacity, although there are inconsistent reports in favor of cancer types and

different populations [10, 11]. Rationally, it seems non-conservative that *Arg194Trp*, *Arg280His* and *Arg399Gln* substitutions may attribute to cancer susceptibility.

Thyroid carcinomas are the most frequent endocrine malignancies which among these thyroid carcinomas, more than 90 percent are differentiated thyroid carcinomas (DTC). Pathologically, DTC include papillary, follicular, and Hürthle cell carcinoma [12]. To date, exposure to ionizing radiation is the only known risk factor for thyroid cancer [13]. However, there are evidences that some gene variants including DNA repair genes influence on DTC susceptibility. *XRCC1* is one of the candidate genes which its variant relationship with thyroid cancer has not been extensively studied [14].

In the present case-control study, the genotype frequency distributions of three common *XRCC1* SNP (*Arg194Trp*, *Arg280His* and *Arg399Gln*) are compared in DTC patients and thyroid cancer-free controls using usual statistical methods.

MATERIALS AND METHODS

Cases and controls. The cases were thyroid cancer patients with DTC pathologic diagnosis after surgical excision. The controls were individuals who were thyroid cancer free. The sample volumes are indicated in Table 1. Both cases and control groups were admitted to Research Institute for Nuclear Medicine of Shariati Hospital during the period of September 2008-2009 and signed a consent form for genetic tests. Individuals with cervical lymph node involvement, any other cancer history, heavy smokers, radiation exposure history and alcohol users were excluded from the research. Controls were frequency matched to cases based on age and sex.

Genotype analysis. Peripheral blood was collected in tubes containing EDTA and genomic DNA was extracted from leukocytes by previously described method in literature. *XRCC1* codons 194 and 399 were determined using PCR-RFLP as described previously [11, 15]. Briefly, the primers used for *XRCC1* codon 194 were GCCAGGGCCCCTCCTTCAA and TACC CTCAGACCCACGAG; and for codon 399 were TCCTCCACCTTGTGCTTTCT and AGTAGTCTGC TGGCTCTGGG. The PCR reactions for two polymorphisms were the same. Each 25 µl reaction contained 10 pmol of each primer, 2.0 mM MgCl₂, 200 mM each dNTP, 1 unit of *Taq* DNA polymerase (CinnaGen Smart *Taq*, Iran) and 50-250 ng of genomic DNA. The PCR conditions for codon 194 were 95°C **Table 1.** Arg194Trp (**A**), Arg280His (**B**) and Arg399Gln (**C**): demographic and genotype frequencies of case and control subjects.

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Variable		DTC (n = 15	Controls (n = 187)		
v ur lubic	n	%	P ^a	<u></u> n	%
Sex			0.596		
Male	34	21.7		45	24.1
Female	123	78.3		142	75.9
Age			0.137		
<= 50	131	83.4		144	77.0
> 50	26	16.6		43	23.0
Arg194Trp			0.477		
Arg/Arg	136	86.6		166	88.8
Arg/Trp	18	11.5		20	10.7
Trp/Trp	3	1.9		1	0.5
Trp allele frequency		7.6	0.357		5.9
(B)		DTC (n = 170	<u>.</u>	Cor (n -	ntrols - 193)
(B) Variable		DTC (n = 170)) P ^a	Coi n = n	ntrols = 193) %
(B) Variable		DTC (n = 170 %)) <u> </u> <u> </u>	Con (n = n	ntrols = 193) %
(B) Variable		DTC (n = 170 %)) <u>P</u> ^a 0.826	Con 	ntrols = 193) %
(B) Variable Sex Male Female	n 38 132	DTC (n = 170 % 22.4 77.6)) <u>P</u> ^a 0.826	Con (n = n 45 148	atrols = 193) % 23.3 76.7
(B) Variable Sex Male Female	n 38 132	DTC (n = 170) % 22.4 77.6)) <u>P</u> ^a 0.826 0.173	Con (n = n 45 148	ntrols = 193) % 23.3 76.7
(B) Variable Sex Male Female Age <= 50	n 38 132	DTC (n = 170 % 22.4 77.6 82.9)) <u>P^a</u> 0.826 0.173	Con (n = n 45 148 149	ntrols = 193) % 23.3 76.7 77 2
(B) Variable Sex Male Female Age <= 50 > 50	n 38 132 141 29	DTC (n = 170 % 22.4 77.6 82.9 17.1)) <u>P^a</u> 0.826 0.173	Con (n = 145 148 149 44	ntrols = 193) % 23.3 76.7 77.2 22.8
(B) Variable Sex Male Female Age <= 50 > 50 Arg280His	n 38 132 141 29	DTC (n = 170 % 22.4 77.6 82.9 17.1)) <u>P</u> ^a 0.826 0.173 0.411	Con (n = 145 148 149 44	ntrols = 193) % 23.3 76.7 77.2 22.8
(B) Variable Sex Male Female Age <= 50 > 50 Arg280His Arg/Arg	n 38 132 141 29 146	DTC (n = 170 % 22.4 77.6 82.9 17.1 85.88)) <u>P^a</u> 0.826 0.173 0.411	Con (n = 45 148 149 44 173	ntrols = 193) % 23.3 76.7 77.2 22.8 89.64
(B) Variable Sex Male Female Age <= 50 > 50 Arg280His Arg/Arg Arg/His	n 38 132 141 29 146 23	DTC (n = 170 % 22.4 77.6 82.9 17.1 85.88 13.53)) P^a 0.826 0.173 0.411	Con (n = 45 148 149 44 173 18	ntrols = 193) % 23.3 76.7 77.2 22.8 89.64 9.33
(B) Variable Sex Male Female Age <= 50 > 50 Arg280His Arg/Arg Arg/His His/His	n 38 132 141 29 146 23 1	DTC (n = 170 % 22.4 77.6 82.9 17.1 85.88 13.53 0.59)) P ^a 0.826 0.173 0.411	Con (n = 145 148 149 44 173 18 2	ntrols = 193) % 23.3 76.7 77.2 22.8 89.64 9.33 1.04

(C)

Variable		DTC (n = 155	Controls (n = 190)		
	n	%	P ^a	n	%
Sex			0.700		
Male	34	22		45	23.7
Female	121	78		145	76.3
Age			0.131		
<= 50	130	83.9		147	77.4
> 50	25	16.1		43	22.6
Arg280His			0.401		
Arg/Arg	78	50.3		83	43.7
Arg/Gln	60	38.7		87	45.8
Gln/Gln	17	11		20	10.5
Gln allele frequency		30.3	0.385		33.4

^aP<0.05 is significant



Fig. 1. High resolution melting of *XRCC1* gene in 25 samples. RR-, RH- and HH-type curves are shown as RR, RH and HH, respectively. Small box shows difference graphs.

for 2 min; $35 \times (95^{\circ}\text{C} \text{ for } 30 \text{ s}, 57^{\circ}\text{C} \text{ for } 30 \text{ s} \text{ and } 72^{\circ}\text{C}$ for 45 s); 72°C for 7 min and for codon 399 were 95°C for 2 min; $35 \times (95^{\circ}\text{C} \text{ for } 30 \text{ s}, 61^{\circ}\text{C} \text{ for } 30 \text{ s} \text{ and } 72^{\circ}\text{C}$ for 45 s); 72°C for 7 min . PCR products of codon 194 (485 bp) and codon 399 (517 bp) were digested by *Pvu*II and *Bcn*I restriction enzymes (Fermentas, Switzerland), respectively. Using submarine electrophoresis, the DNA fragments were separated in 2% agarose gel and visualized by ethidium bromide. The expected fragments for codon 194 were 485 bp (194Arg) and 396 plus 89 bp (194Trp) as well as for codon 399 were 384 and 133 bp (399Arg) and 517 bp (399Gln).

For Arg280His genotyping, we developed a high resolution melting (HRM) technique and confirmed the 280His alleles by RLFP. A 125-bp fragment of XRCC1 gene containing codon 280 was proliferated using CCC CAG TGG TGC TAA CCT AAT and CTT CTC CTC GGG GTT TGC C primers. The PCR-HRM reactions carried out in 10-µl reactions using Type-it HRM PCR Kit (Qiagen, Germany) contained 10 pmol of each primers and 20-50 ng genomic DNA. The thermocycling program was 95°C for 5 min; 45× (95°C for 30 s, 60°C for 30 s and 72°C for 10 s); 72°C for 4 min, followed by Pre-HRM heteroduplex enrichment (95°C for 10 s; 65°C for 5 min) and HRM protocol was ramp from 75°C to 95°C, rising by 0.05°C each step and waiting for 2 s in each step. As it was the first time that PCR-HRM used for genotyping of Arg280His change in XRCC1 gene, for confirmation, all samples showed 280His allele were subjected to RsaI restriction enzyme treatment.

XRCC1 codons 194, 280 and 399 genotypes and DTC risk was analyzed by two-sided Chi-squared tests. In each codon we calculated the relative risk of the homozygous patients (Trp/Trp for codon 194, His/His for codon 280 and Gln/Gln for codon 399), heterozygous patients (Arg/Trp for codon 194, Arg/His for codon 280 and Arg/Gln for codon 399) compared with the wild type Arg/Arg genotypes (all three codons) for amino acid substitutions. Moreover, the recessive and dominant effects of the mentioned substitutions were estimated (codon 194: Trp/Trp versus Arg/Trp + Arg/Arg and Trp/Trp + Arg/Trp versus Arg/Arg, respectively; codon 280: His/His versus Arg/His + Arg/Arg and His/His + Arg/His versus Arg/Arg, respectively; codon 399: Gln/Gln versus Arg/Gln + Arg/Arg and Gln/Gln + Arg/Gln versus Arg/Arg, respectively). In addition, relative risks of having combinatory heterozygous form of three codons were calculated. The relative risk was expressed as odds ratio (OR) with 95% CI using logistic regression analyses.

Based on observed genotypes, the haplotype analysis was performed using PHASE program [16] for reconstruction of haplotypes. The frequencies of haplotypes were compared by chi-squared tests and the relative risks were estimated.

RESULTS

Sex distributions of case and control subjects in addition to detailed genotype analysis results for the *194Trp*, *280His* and *399Gln* are demonstrated in Table 1.

Statistical analysis. The relationship between the



Fig. 2. RFLP of samples treated by *Rsa*I restriction enzyme. Lane 1, untreated; lanes 2, 3, 5, 6, 9 and 10, 280RH; lanes 4, 7, 8, 11, 12 and 13, 280RR; M, 100 bp DNA ladder. Gel: agarose 3.5%.

Genotyping of *194Trp and 399Gln* was done by PCR-RFLP method (Fig. 1), while PCR-HRM and PCR-RFLP was used for *280His* codon (Fig. 2).

According to the Hardy-Weinberg equilibrium model, the frequencies of observed genotypes of the controls did not deviate significantly from those expected (194Trp: $\chi^2 = 0.217$, df = 1, P>0.05; 280His: $\chi^2 = 3.382$, df = 1, P>0.05; 399Gln: $\chi^2 = 0.159$, df = 1, P>0.05).

In Arg194Trp, Arg280His and Arg399Gln genotypes, the differences in genotype frequency distributions between DTC cases and controls were not significant (P = 0.477, P = 0.411 and P = 0.401, respectively). Calculated OR are presented in Table 2. For the Arg194Trp change, a 3.6-fold increase in risk for DTC was estimated in homozygous Trp genotype. Also, when considering Trp as recessive trait, the risk was in concordance with it (3.62 fold). By separating Arg194Trp genotypes into groups with and without the Trp allele, the OR was calculated as 1.32 in favor of having DTC. In case of Arg280His change, the dominant His genotype was associated with increased DTC (OR: 1.42, 95% [CI] 0.76-2.68). Finally, in *Arg399Gln* change, the dominant *Gln* genotype was borderline associated with reduction of DTC. Sex and age adjusted OR showed the same trend as the crude OR for all alleles.

Association between carrying different combinatory forms of heterozygous alleles and DTC were estimated and stated as OR. Considering combination of *Arg194Trp* and *Arg280His* heterozygous genotypes, the association between "being heterozygous in only one site" was borderline significant (OR 1.57, 95% [CI] 0.90-2.74, P = 0.111). The other data were not significant and not shown.

The retrieved haplotype frequencies and OR are shown in Table 3. The OR were calculated by comparison of each haplotype with the most frequent one (CGG) in controls. No significant risk association between XRCC1 haplotypes and DTC cases was found.

DISCUSSION

For the first time in Iran, the role of *XRCC1 gene* polymorphisms in relation with DTC was examined in a case-control study.

The impact of changes in DNA repair genes including *XRCC1* gene has been studying in growing studies to elucidate possible susceptibility to various types of cancers [17, 18]. There are significant heterogeneities among studies due to cancer type, population and site of SNP [19-21]. There are only few studies which assessed *XRCC1* gene polymorphism relations with thyroid carcinomas. In a case-control study [22], a significant increased risk of DTC for the *Arg194Trp* homozygous polymorphic genotype was calculated ([OR: 10.4, 95% CI: (1.0-105.5), while for *Arg194Trp* heterozygous polymorphic genotype, the OR was estimated as: 1.4, 95% [CI] (0.9-2.1). These results are in concordance with those of our survey

Table 2. Crude and adjusted odd ratio (OR) and confidence interval (CI) of case and control subjects for Arg194Trp, Arg280His and Arg399Gln alleles

Arg5990th alleles.				
Variable	Crude OR (95% CI), <i>P</i> value ^a	Sex-adjusted OR (95% CI), <i>P</i> value ^a	Age-adjusted OR (95% CI), <i>P</i> value ^a	
Arg194Trp				
Trp/Trp vs Arg/Arg	3.66 (0.38-35.60), 0.226	3.52 (0.37-34.46), 0.437	3.34 (0.34-32.54), 0.137	
Trp/Trp + Arg/Trp vs Arg/Arg ^b	1.22 (0.64-2.33), 0.545	1.21 (0.64-2.31), 0.732	1.21 (0.64-2.33), 0.276	
Trp/Trp vs (Arg/Arg + Arg/Trp) ^c	3.62 (0.37-35.19), 0.229	3.53 (0.36-34.28), 0.416	3.35 (0.34-32.58), 0.131	
Arg280His				
His/His vs Arg/Arg	0.59 (0.05-6.60), 0.12	0.58 (0.05-6.43), 0.82	0.55 (0.05-6.18), 0.44	
His/His + Arg/His vs Arg/Arg ^b	1.42 (0.76-2.68),0.275	1.42 (0.75-2.68), 0.547	1.42 (0.76-2.69), 0.214	
His/His vs (Arg/Arg + Arg/His) ^c	0.57 (0.05-6.29), 0.634	0.56 (0.05-6.22), 0.87	0.53 (0.05-5.85), 0.34	
Arg399Gln				
Gln/Gln vs Arg/Arg	0.90 (0.44-1.85), 0.784	0.90 (0.44-1.85), 0.951	0.89 (0.43-1.83), 0.270	
$(Gln/Gln + Arg/Gln) vs Arg/Arg^b$	0.77 (0.50-1.17), 0.219	0.76 (0.50-1.17), 0.419	0.77 (0.50-1.18), 0.154	
Gln/Gln vs (Arg/Arg + Arg/Gln) ^c	1.05 (0.53-2.08), 0.895	1.05 (0.53-2.08), 0.920	1.03 (0.52-2.09), 0.314	

^a*P*<0.05 is significant, ^bdominant T allele , ^crecessive T allele

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Hanlotyne ^a	Freque	ncy (%)	DTC		
парютурс	DTC Control		OR (95% CI)	P value	
CGG	43.6	38.4	1.0 (Ref)		
CAG	19.9	22.3	0.79 (0.37-1.65)	0.526	
CAA	15.5	20.7	0.66 (0.30-1.45)	0.308	
CGA	13.1	12.4	0.93 (0.38-2.26)	0.874	
TGG	5.6	4.7	1.05 (0.29-3.85)	0.942	
TGA + TAG + TAA	2.3	1.5	1.35 (0.17-11.05)	0.779	

Table 3. XRCC1 haplotype frequency and risk association.

^a Haplotypes follow the SNP: XRCC1 Arg194Trp, Arg280His and Arg399Gln

(Table 4). In the same research, the calculated OR for *Arg399Gln* homozygous and heterozygous were 0.5, 95% [CI] (0.3-0.8) and 0.8, 95% [CI] (0.6-1.0), respectively, demonstrating a decreased risk of DTC for *Arg399Gln* genotypes. Again, the data is in the same direction with our results. Increased risk for DTC is also shown with *Arg194Trp* [23] and *Arg399Gln* genotypes in another case-control study [24]. For *Arg280His* genotype, we found a trend toward having DTC in dominant trait (OR: 1.42, 95% [CI] (0.76-2.68) which is in opposite side of the results from both mentioned studies.

Although the haplotype analysis showed no significant results, the combined relative genetic risk of dominant trait of SNP showed some trends toward having DTC: OR $_{Arg194Trp}$ X OR $_{Arg280His}$ X OR $_{Arg399Gln}$ = 1.22 X 1.42 X 0.77 = 1.33.

All mentioned SNP studied here were missense mutations and we expected impaired function of protein. Although we found an increased risk effect of *Arg194Trp* and *Arg280His* alleles for developing DTC, a minor protective effect of *Arg399Gln* genotype was found for this type of carcinoma. The latter result is in contrast with our hypothesis.

The results are not significant, s are not conclusive, probably because of small sample size or other unknown phenomena in developing thyroid carcinomas. Clearly, larger population samples from different populations and following meta-analysis assays will give better estimation of above SNP' association with DTC.

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