Possible Roles of the Xenobiotic Transporter P-glycoproteins Encoded by the MDR1 3435 C>T Gene Polymorphism in Differentiated Thyroid Cancers

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Abstract

**Background:** P-glycoprotein (Pgp), encoded by the multidrug resistance 1 (MDR1) gene, is an efflux transporter which plays an important role in pharmacokinetics. The current preliminary study was designed to determine associations between a germ-line polymorphism in the MDR1 gene with differentiated thyroid carcinoma (DTC).

**Materials and Methods:** In the current case-control study, 60 differentiated thyroid cancers (DTC) - 45 papillary TC (PTC), 9 follicular TC (FTC) and 6 well-differentiated tumors of uncertain malignant potential (WDT-UMP) were examined. Results were compared to a healthy control group (n=58) from the same population. Genomic DNA was extracted from peripheral blood with EDTA and the target gene was genotyped by real-time PCR.

**Results:** Carriers of the variant allele of MDR1 exon 26 polymorphism were at 2.8-fold higher risk of DTC than the control group (odds ratio [OR]: 0.3805, 95% confidence interval [CI]: 0.1597-0.9065 (p> 0.046).

**Conclusions:** Presented results suggest that the MDR1 3435TT genotype might influence risk of development of DTC and that the CC genotype might be linked to a poor prognosis. Large-scale studies are now needed to validate this association.

**Keywords:** Differentiated thyroid carcinoma - MDR1 gene - increased T allele frequency in codon C3435T
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(HCA) and polycyclic aromatic hydrocarbons (PAH) and may promote gastrointestinal carcinogenesis, affecting angiogenesis, apoptosis, and invasiveness as claimed by Andersen et al. (2009). Owing to the fact that it controls the efflux of toxic compounds, the Pgp transporter takes crucial role in the process of detoxification and elimination of xenobiotics which in turn is related to cancer risk (Andersen et al., 2009).

By the current case-control study we wished to explore the possible role of the xenobiotic transporter P-glycoprotein polymorphism (encoded by the MDR1 gene) that is also known as the transport dietary carcinogen in the susceptibility of differentiated thyroid cancer.

Materials and Methods

Patients, clinical diagnosis and laboratory assessment

In a total of 60 thyroid cancer patients; 45 papillary thyroid cancer (PTC), 9 follicular thyroid cancer (FTC), 6 well-differentiated tumors of uncertain malignant potential (WDT-UMP) of 11 male (18.3%), 49 female (81.7%) and mean age-min-max: 55.25±3.22(28-75) were included in the current results. The PTC patients were include; 19 (42.2%) cases of conventional, 15 (33.3%) diffuse sclerosing variant, 7 (15.5%) follicular and 4 (8.8%) oncocytic subtypes of PTC patients. The current FTC patients were include; 7 (77.7%) of conventional and 2 (32.3%) of Hurle cell carcinomas histopathologically according to the WHO classification. Patients were genotyped for MDR1 C3435T SNP and compared to the healthy controls that are excluded from any familial cancer history. Results were compared to the 58 healthy control individuals from the same population that published in our previous case-control study (18). The volunteer individuals who has no any thyroid diseases were used as a control group cohort from the same population. There was no thyroid cancer history in those control cohort and their first degree relatives. The current study was performed in Departments of Nuclear Medicine and Medical Genetics of Cumhuriyet University Hospital between 2007-2009 years. All applications were approved and informed consent was obtained from all of the patients and control group individuals.

Mutation analysis

Blood samples with EDTA from 60 thyroid cancer patients that underwent total thyroidectomy were used in the current study. Total genomic DNA was extracted from peripheral blood samples from each individual by both automated Magna Pure Compact (Roche) and Invitrek kit extraction techniques (Invitrek®; Invisorb spin blood, Berlin, Germany) manually. Target MDR1 gene was genotyped by Real Time PCR, LightCycler 2.0 methods (Roche) for all patients. Briefly, LightCycler FastStart DNA Master HybProbes, master mix (water, PCR-grade, MgCl₂, stock solution, Primer mix, HybProbe mix) and DNA template were used for real-time amplification. The protocol consisted of a denaturation step of 30 seconds at 95°C; followed by amplification step of 45 cycles of 5 seconds at 95°C, 5 seconds at 55°C, and 8 seconds at 72°C; and melting curve analysis of 30 seconds at 95°C, followed by 2 minutes at 40°C, 0.1 second (continuous) at 80°C, cooling step of 30 seconds at 40°C. Software programme (LightCycler 2.0, Roche) was used for detection of the mutated and normal genotype profiles of target gene in the current DTC patients.

Statistical analysis

In current results the odds ratio and p-values were used to estimate the risk for C, T alleles frequency of codon 3435 SNP for MDR1 gene in DTC patients. The software SPSS for Windows version 12.0 was used to perform statistical analysis. Mutational variables were analyzed by using Fisher’s exact test. The Mann–Whitney U and chi-square tests were used to analyze differences between the patients and the controls. The estimate risk was examined by multivariate logistic regression analysis. Results were given as the mean (standard deviation [SD]).

Results

In the current case-control study it was aimed to find out the association between germ-line point mutations in MDR1 gene and thyroid carcinomas. By multiplex Real-time PCR technique, we evaluated common SNP 3435 C>T for MDR1 gene in DTC patients and results were compared to the healthy controls (Figure 1). The estimate risk was examined by multivariate logistic regression analysis. Statistically, the TT homozygous genotype of polymorphic 3435 C>T SNP codon was associated with a significance of 2.8 fold increase in risk for DTC patients in the current results.

Clinicopathologic data and follow-up knowledge

Peripheral blood-EDTA samples from healthy controls and DTC patients were examined for genotyping in the current study. In a total of 60 DTC patients [(49F (81.7%) and 11M (18.3%)] of 45 PTC (75%), 9 FTC (15%) and 6 UMP (10%) mean age 55.25±13.22 (28-75) were clinically diagnosed and treated. The subtypes and some clinical characteristics such as; mean age, sex distribution of patients were given in Table 1. The

![Figure 1](image-url)

Figure 1. Shows Melting Peak Profiles of Real Time – PCR for wild (A) and Mutated Genotypes for MDR1 3435 C>T SNPs in the Current DTC Patients. B: Homozygous Mutated TT Alleles, C: Heterozygous CT alleles
The meta-analysis
Hepatic Chinese
Gastric Chinese
Gastric Iranian
Breast Canary Islands(Spain)
Colorectal
The meta-analysis

Table 3. The Latest Literature Findings about Strong Association of T Allele Frequency of MDRI C>T SNP in Distinct Tumoural Types in Human in Different Populations

<table>
<thead>
<tr>
<th>Cancer type</th>
<th>Population</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colorectal</td>
<td>The meta-analysis</td>
<td>He et al., 2013</td>
</tr>
<tr>
<td>Colorectal</td>
<td>North German</td>
<td>Campa et al., 2012</td>
</tr>
<tr>
<td>Breast</td>
<td>Canary Islands(Spain)</td>
<td>Henrikz-Hernandez, 2009</td>
</tr>
<tr>
<td>Gastric</td>
<td>Iranian</td>
<td>Sabahi et al., 2010</td>
</tr>
<tr>
<td>Gastric</td>
<td>Chinese</td>
<td>Li et al., 2011</td>
</tr>
<tr>
<td>Leukemia</td>
<td>Chinese</td>
<td>Qian et al., 2012, 2012</td>
</tr>
<tr>
<td>Ovarian</td>
<td>Japan</td>
<td>Nakajima et al., 2005</td>
</tr>
<tr>
<td>Lung</td>
<td>Turkish</td>
<td>Dogu et al., 2012</td>
</tr>
<tr>
<td>Hepatic</td>
<td>Chinese</td>
<td>Huang et al., 2012</td>
</tr>
<tr>
<td>Other Common(Renal, Breast)</td>
<td>The meta-analysis</td>
<td>Sheng et al., 2012, 2012</td>
</tr>
</tbody>
</table>

* Significant: The status of T allele frequency for MDRI C>T SNP (Table 2). The frequencies of MDRI C>C, C>T, T/T in healthy controls were 41%(70.69%), 12%(20.69%), 5%(8.63%) respectively. Elevated risk for DTC of 2.8 fold was observed in individuals with homozygous TT genotype odds ratio [OR]: 2.849, 95% confidence interval [CI]: 1.578-5.142 (P<0.001) when compared to the healthy control group from the same population.

Multivariate analysis demonstrated the TT genotype, an increased risk of DTC for the 3435 C>T homozygous genotype for the presented results. The results indicated that individuals with homozygous TT genotype had a 14.67% higher risk of having DTC. The current results were also compared to the latest literature findings that showing the strong association of T allele frequency of MDRI gene in distinct tumoural types in different populations (Table 3).

Discussion

The incidence of refractory thyroid cancers including undifferentiated and differentiated cancers are increasing in several populations (Schlumberger et al., 2011). Wide range of genetic factors were reported in thyroid cancer susceptibility (Akdi et al., 2011; Schlumberger et al., 2011). The DTC is the most common malignancy of the thyroid gland and involves some molecular ethiological parameters such as; point mutations in proto-oncogenes of BRAF V600E, KRAS, RET, functional genes of MTHFR, MDRI and epigenetic alterations of several tumor suppressor gene abnormalities (Jasim et al., 2011; Jin et al., 2011; Ozdemir et al., 2012). Differentiated thyroid cancer (DTC) is an important clinical entity in our population which is characterized by important environmental influences, as iodine deficiency (ID) and subsequent supplementation, thyroiditis and occupational exposure. Thyroid cancers of follicular cell origin account for the majority (95%) of all thyroid cancers and represent the most common type of endocrine neoplasia. Morari et al. (2011) have suggested that the detection of NIS gene expression may help characterizing patient’s risk and individuals with a poor response to therapy in DTC (Morari et al., 2011). The polymorphic MDRI gene includes 28 exonic subunits and it is highly variable between different ethnic groups and populations. The genotype and allele frequency of MDRI gene from Turkish subpopulation was found to be significantly different from some other populations such as; Han Chinese, Uygd Chinese, Kazakh Chinese, Indian, Malay, Japanese, Caucasian, and Ashkenazi Jewish (Gumus-Akay et al., 2010). Silent C3435T polymorphism which is located in exon 26 of gene induces a conformational change in P-glycoprotein due to the ribosome stalling during translation (Kroetz et al., 2003). Fung and Gottesman (2009) claimed that the polymorphic P-glycoprotein shows substrate specificity for transporting of Verapamil (Fung and Gottesman, 2009). Wang et al. (2005) reported that the silent MDRI C3435T polymorphism leads to an unstable mRNA molecule and consequently, lower P-glycoprotein activity in the target tissues (Wang et al., 2005). The MDRI/ABCB1 gene seems to play a role in early carcinogenesis by preventing apoptosis in tumor
The MDR1 C3435T polymorphism in exon 26 has been extensively investigated in the variability in cancer risk and therapeutic outcome (Andersen et al., 2009; Jasim et al., 2011; Lu et al., 2011; Manduz et al., 2011). Lots of researchers claim that point mutation in MDR1 causes lower in vitro P-glycoprotein activity, changes substrate specificity, and alters expression due to the following factors: a lower mRNA stability, protein folding and altered ability of tissues to remove toxins and properly metabolize anticancer drugs. That might help explain the initiate and develop of different types of cancer, as well as design appropriate therapies based on the particular genetic composition of the tumors (Kroetz et al., 2003; He et al., 2010). The polymorphic homozygous (T/T) genotype of MDR1 gene showed a significant association with the incidence of gastric (Sabahi et al., 2010) and colorectal cancers (Andersen et al., 2009).

Pharmacogenomics and pharmacogenetics studies have revealed that mutated MDR1 gene is associated with alteration in P-gp expression and function and associated with higher risk of clinical conditions. Rao et al. (2010) have claimed that MDR1 TT genotype might influence the risk to develop an acute lymphoblastic leukemia (ALL) due to the lower activity of eliminating antileukemic drugs such as; anthracyclines, daunorubicin, vincristine, mitoxanthrone that lead to lower intra cellular drug concentrations and a poor prognosis in ALL (Rao et al. 2010). Huang et al. (2011) have reported that P-glycoprotein that is encoded by mutated MDR1 gene may be implicated into the hematotoxicity of benzene. Subjects carrying MDR1 3435 T/T genotype may have a higher risk of benzene poisoning (Huang et al., 2011). Crouthamel et al. (2010) have reported a novel genetic variation of GT1292-3TG, (Cys431Leu) in MDR1 gene in leukemia patients by the accumulation of the intracellular doxorubicin, vinblastine, and paclitaxel (Crouthamel et al., 2010). P-glycoprotein, highly restricts the entry of ivermectin into the brain by an ATP-driven efflux mechanism at the blood-brain barrier. In dogs with a homozygous MDR1 TT mutation though, ivermectin accumulates in the brain and provokes severe signs of neurotoxicosis and even death (Geyer et al., 2009).

Recently, there are lots of crucial reports about MDR1 gene polymorphism and distinct human cancers in the literature (Li et al., 2001; Nakajima et al., 2005; Henriquez-Hernandez et al., 2009; Ni et al., 2011; Campa et al., 2012; Dogu et al., 2012; Qian et al., 2012; Huang et al., 2012; Sheng et al., 2012; Wang et al., 2012; He et al., 2013), (Table 3). We found that the functional SNP of MDR1 gene was associated with DTC risk in the Turkish population. The current preliminary results on MDR1 mutability on thyroid cancer are the first literature findings that showing mutation prevalence of the multidrug resistance MDR1 (ABCB1) gene in DTC.

In the current preliminary study it was aimed to find out the possible linkage between homozygous mutated (T/T alleles) MDR1 gene and DTC. Genomic DNA was extracted from peripheral blood and genotyped by Real Time PCR method. Presented results are the first report the genotype and allele frequency of polymorphic codon 3435 of MDR1 gene in Turkish DTC patients. Preliminary results of the current study showed that homozygous T allele in 3435 C>T codon in MDR1 gene may be associated with high risk of thyroid cancer and may play a pivotal role in the development of DTC in human. Despite some limitations, current results indicated that individuals with homozygous TT genotype had a 14.67% higher risk of having DTC. Furthermore, patients carrying both copies of the variant alleles (TT) showed 2.8 times increased risk of developing DTC than their control counterparts. By the presented case-control results it is possible to claim that the polymorphic xenobiotic transporter P-glycoprotein (encoded by the MDR1 gene) which is also known as the transport dietary carcinogen is associated with susceptibility of DTC.

In conclusion, the codon 3435 C>T transitional polymorphism in exon 26 of MDR1 gene was significantly associated with DTC risk in the current results. Results need to be supported by population based large-scale samples of representative DTC patients.

References


