

Ras oncogenes polymorphism in Turkish thyroid cancer patients

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Abstract

Molecular mutations to proto-oncogene sequences may be involved in the pathogenesis of human thyroid neoplasm. Problems on oncogenes and tumor supressor genes activation in cell circle could cause tumor. Many oncogenes and tumor suppressing genes exist in varying percentages in various types of thyroid cancers. Ras, Gsp, Ret or Trk oncogenes can be involve in thyroid tumors. Members of the Ras gene family (H-ras, K-ras, and N-ras) are signal transferring proteins. These genes codes for 21 kDa GTP binding proteins. We studied 24 thyroid cancer and 77 control for ras gene point mutations in two different codons (12 and 13) using a restriction fragment length polymorphism technique. According to enzyme digesting, no c-K-ras gene codon 12/13 and N-ras gene codon 12 point mutation were observed in any of the samples we studied.

Key words: ras gene, thyroid cancer, mutation, RFLP

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Introduction

Mutations in the genes controlling cell growth and differentiation are considered to be the main cause of cancer (Bos, 1989). The most common cancer in Turkey is lung cancer. Thyroid cancer is not very common in general; however some people are affected in Black Sea and Central region of Turkey. The number of thyroid cancer patients in Trabzon is 6 in 2002 and 22 in 2003 (Tuncer, 2007). This type of cancer is characteristic of a group of malignant tumors related to thyroid gland. There are different types of thyroid cancer which are papillary, follicular, medullar and anaplastic (Donis-Keller, 1993). Radiation exposure, chronic goiter, family history, and environmental factors could cause thyroid cancer (De Groot, 1996).

The thyroid gland is located in the throat, below the larynx. It is made of two lobes. The thyroid gland secretes very important hormones that regulate so many metabolic processes, such as growth and energy expenditure. Women population slightly more affected than men. Approximately 10 % of thyroid cancers are present in patients younger than 21 years of age, representing 3 % of all cancers of children and adolescents, with predominance in females 2:1 in relation to males. Thyroid cancers goup in this age are usually papillary (90 %), bilateral, multifocal and bigger in size compared to adults (Monte etal., 2007). Anaplastic carcinoma is the most aggressive and malignant form of thyroid cancer. The most common type of thyroid carcinoma is papillary carsinom. The most frequent mutations in papillary carcinomas are point mutations of the BRAF, Ras genes and RET/PTC rearrangement (Nikiforov, 2008).

The Ras-Raf-Mek-MAP kinase-signaling pathway is activated in human carcinomas, particularly in adenocarcinomas. The pathway is responsible for transmition of mitogenic signal to the nucleus. The constitutive activation of the pathway is thought to reason of uncontrolled cell division (Fukushima et al., 2003). There are three human RAS genes which are N-Ras, H-Ras, and K-Ras. The ras gene family encode membrane-associated guanine nucleotide-binding

Table 1. Primer used in PCR

Primer	Nucleotide sequences 5'- 3'
c-K-ras (first round amplification)	F: GAAGCTTATGTGTGACATGTCTA
	R: AGGCACTCTTGCCTACGTCA
c-K-ras codon 12 (Hphl)	F: CCTGGTGAAAATGACTGAAT
	R: AGGCACTCTTGCCTACGTCA
c-K-ras codon 13 (HaeIII)	F: GCCTGCTGAAAATGACTGAA
	R: CGTCAAGGCATCTTGCCTAGG
N-ras (first round amplification)	F: TAAAGTACTGTAGATGTGGCT
	R: TCACCTCTATGGTGGGATCAT
N-ras codon 12 (BstNI)	F: CAAACTGGTGGTGGTTGGACCA
	R: AGTGGTCCTGGATTAGCTGGAT

proteins (p21°°) (Ginesa *et al.*, 2003). Mutations in codon 12, 13, or 61 of gene of guanine nucleotide-binding proteins, convert these genes into active oncogenes (Bos, 1989)

In order to find biomarkers for thyroid cancer, it is necessary to study the mechanism of cancer progression. Mutations in cellular *ras* gene have been reported in various thyroid cancer types. In tumors, the point mutations which have been identified have been localized to codon 12, 13 or 61 of three *ras* genes (Leon *et al.*, 1987).

In this study, we evaluate the frequency of RAS mutations in thyroid carcinoma by PCR-RFLP method.

Materials and methods

DNA isolation

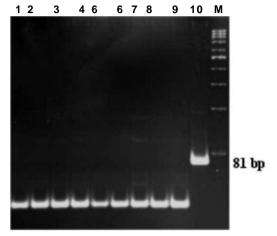
In this study total 111 DNA samples were isolated from 34 patients with histologically verified thyroid cancer (Ankara Numune Education and Investigation Hospital in Turkey) and 77 control group blood samples. DNA isolation from blood samples was isolated as described by Maniatis et al. (1989). 30 ml RBC lyses buffer was added to 9 ml blood sample and shaked gently. The mixture was incubated on ice for 20 min and centrifugeted at 4000 rpm for 20 min at 4°C. The supernatant was removed 25 ml RBC lyses buffer was added and this process was repeated till all the red cells were removed. 20 ug/ml proteinase K, 10 % SDS (final concentration 0.5 %) and 2,5 volume STE were added and incubated overnight at 56°C in a water bath. 1:1 phenol: chloroform: Isoamylalcohol (25:24:1) was

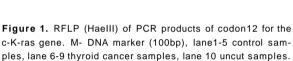
added and shaked by hand for 10 min. Then the mixture was incubated on ice for 20 min and centrifugeted at 4000 rpm for 20 min at 4°C. Upper phase was transferred into a new tube, 1:10 volume 2 M sodium acetate (pH 5.2) and 95 % ethanol (2 fold of total volume) were added and shaked gently until the DNA was precipitated, incubated overnight at -20°C. DNA was centrifugeted at 4000 rpm for 20 min at 4°C. Supernatant was removed; DNA was washed in 500 ul 70 % ethanol and dissolved in 0.5-1 ml TE-buffer overnight at 37°C in a water bath.

PCR Amplification and RFLP

The procedure to detect any mutation at codon 12 and codon 13 of the c-K-ras gene and N-ras gene has been described by Capella et al. (1996). DNA sequences of the first coding exon of the c-K-ras gene were amplified using the primers 5' GAAGCTTATGTGTGACATGTCTA 3' and 5' AAGGATCCTGCAGTAATATGCA 3' for 15 cycles (92°C for 1 min and 4 s; 50°C for 35 s; 72°C for 1 min and 25 s; PCR 1). Then 1 ml of the amplified product was reamplified by means of nested PCR using primers in Table1 for 30 cycles (92°C for 15 s; 50°C for 15 s; 72°C for 30s; PCR 2). PCR was performed (Biometra, Germany) using 1 mg genomic DNA, 2.5U Taq polymerase (Fermentas) 0.2 mM each dNTP, 10 mM Tris-HCl (pH 8.8), 50 mM KCl, 2 mM MgCl2, 0.1 % Triton X-100, and 20 pmol primers in total volume 50 ul.

Codon 12 and 13 mutations were detections by digesting 70 bp amplified fragment with Hphl and Haelll, respectively. A similar approach was used to detect mutations at codon 12 of the N-ras gene. The





first round amplification was performed in the same conditions as for the c-K-ras gene using the primers described in Table 1. Codon 12 mutations were detections by digesting 81 bp amplified fragment with Bstnl. A 10-ul aliquot of amplified material is taken for restriction enzyme digestion using Hphl, HaellI and BstNI (GeneMark) and respective buffer for 2 hr at 37°C in a total volume of 20 ul. After enzymatic digestion, the digested fragments were subjected to electrophoresis in a 12% polyacrylamide gel electrophoresis and stained with ethidium bromide (Fig 1-3).

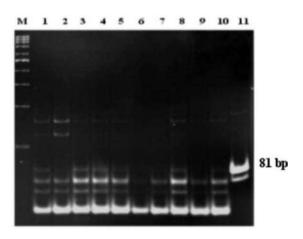


Figure 2. RFLP (Hphl) of PCR products of codon13 for the c-K-ras gene. M- DNA marker(100bp), lane1-5 control samples, lane 6-10 thyroid cancer samples, lane 11 uncut samples.

Results and discussion

In this study, we examined 111 samples with thyroid tumors and without tumors. DNA samples were analyzed for mutations at codons 12/13 of c-K-ras gene and codons 12 of N-ras using Nested Polymerase Chain Reaction and Restriction Fragment Polymorphism (PCR-RFLP). Selective amplification of the region around the studied codons of the ras oncogene was performed by PCR. At two stages PCR reaction, amplification products size were 81 bp for c-K-ras gene and 71 bp for N-ras gene. The Amplfication

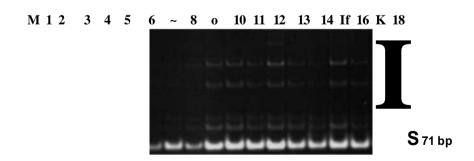


Figure 3. RFLP (BstNI) of PCR products of codon12 for the N-ras gene. M- DNA marker(100bp), lane1-8 control samples, lane 9-17 thyroid cancer samples, lane 18 uncut samples.

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products were digested with restriction enzymes Hph1 and HaeIII for c-K-ras (Figure 1-2) and $Bstn\$ for N-ras gene (Figure 3). According to enzyme digesting, no mutation at codon 12 and codon 13 was observed. Similarly, Bouras et~al.~ (1998) were found any point mutations at the same codon for 128 thyroid tissue samples.

Mutations in all three families of ras oncogenes have been detected in both benign and malignant thyroid tumors (Du Villard et al., 1995; Manenti et al., 1994). Mutations of the ras (Ha-, Ki-, N-ras) protoncogene have been reported in 20-60 % of thyroid tumors, particularly in follicular types (Namba et al., 1990; Wright et al. 1989) and more frequently in iodine-deficient areas (Shi et al., 1991). For this reason, ras mutations have been suggested as an important prognostic marker for thyroid cancer (Karga et al., 1991, Shi et al., 1991; Namba et al., 1990, Shi et al., 1991). The reason we could not find any mutations could be that the number of patients studied is low. We need to increase the number of patients for future studies.

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