

The Expression of the High Mobility Group I(Y) mRNA in Thyroid Cancers: Useful Tool of Differential Diagnosis of Thyroid Nodules.

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Objective : Thyroid nodule is frequent and occurs in about 5% of the general population. In contrast, thyroid cancer is much less frequent and occurs in about 5-10% of thyroid nodules. Distinguishing between benign and malignant lesions is an important task that is best accomplished by fine needle aspiration. Recently, Chiappetta et al. reported that the expression of the high mobility group (HMG) I(Y) proteins correlates with the malignant phenotype of human thyroid neoplasia, and suggested that the detection of the HMG I(Y) proteins might be a valid tool for an easy and sensitive discrimination assay between benign and malignant neoplastic thyroid disease.

Methods : we evaluated the expression of the HMG I(Y) mRNA in 39 frozen thyroid tissues from patients with thyroid nodule by semiquantitative RT-PCR.

Results : The expression of the HMG I(Y) mRNA was low in all of 10 normal thyroid tissues. In all of 3 adenomatous goiters, 6 follicular adenomas and 2 Hurthle cell adenomas, the HMG I(Y) mRNA expression level was low. In 11 of 13 papillary carcinomas and all of 5 follicular carcinomas, the HMG I(Y) mRNA expression level was high.

Conclusion : These results indicate that there is a correlation between the expression of HMG I(Y) and the malignant phenotype of thyroid cancer, suggesting that these proteins may be useful as a marker in thyroid cancer.

Key Words : HMG I(Y), thyroid cancer

INTRODUCTION

Thyroid tumor in a human is one of the most common endocrinologic diseases and occurs in about 5% of the population¹⁾. Thyroid cancer occurs in about 5-10% of thyroid nodules²⁾. Distinguishing between benign and malignant lesions is an important task that is best accomplished by fine needle aspiration. But the reported accuracy of cytologic diagnosis ranges from 70-90%³⁾, largely depending on the experience of the

person performing the biopsy and that of the cytopathologist interpreting it. In addition, follicular carcinoma cannot be differentiated with follicular adenoma by fine needle aspiration. Therefore, a new diagnostic technique is warranted.

Investigations regarding the activation and/or inactivation of oncogenes, tumor suppressor genes and growth factors have not yet revealed consistent differences between the benign and malignant tumors^{4,5)}.

High mobility group (HMG) I(Y) proteins are a class of low-molecular mass, non-histone nuclear proteins characterized by their high content of basic and acid amino acids and binding to the DNA minor groove at AT rich sequences^{6,7)}. HMG I(Y) proteins are required for induction of the human IFN- γ gene by viruses⁸⁾ and for the regulation of the TNF- α ⁹⁾ and rRNA genes¹⁰⁾. The

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expression of these proteins correlates with the neoplastic transformation in several systems. There is a correlation between an elevated expression of the HMG I(Y) proteins and the appearance of a highly malignant phenotype in rat thyroid differentiated cells, as well as in thyroid and skin experimental tumors^{11,12)}. Moreover, a correlation was found between the ability of rat prostatic cell lines to metastasize and the expression of the HMG I(Y)¹³⁾, and between the elevated expression of the same protein and progressive transformation of mouse mammary epithelial cells¹⁴⁾. Furthermore, expression of HMG I(Y) in high grade human prostate cancer was found by in situ hybridization¹⁵⁾. Recently, Chiappetta et al.¹⁶⁾ demonstrated that HMG I(Y) proteins are expressed in human thyroid carcinomas and thyroid carcinoma cell lines, but not in adenomas, goiters and normal thyroid tissues and cells.

Our study evaluated the expression of HMG I(Y) mRNA and its clinical implication in 39 frozen thyroid tissues from patients with thyroid nodule by use of semiquantitative RT-PCR.

MATERIALS AND METHODS

1. Subjects

The study involved 39 thyroid tissues that were obtained from Dankook University Hospital from March 1995 to March 1997. The thyroid tissues that we used were as follows: normal thyroid tissue (n=10), adenomatous goiter (n=3), follicular adenoma (n=6), Hurthle cell adenoma (n=2), papillary carcinoma (n=13) and follicular carcinoma (n=5). The normal tissues were obtained from operations on patients with thyroid nodules. The tissues were frozen in liquid nitrogen and stored frozen until RNA extraction was performed.

2. RNA isolation and RT-PCR

Total RNA was extracted from *the* thyroid tissue using Ultraspec RNA Isolation System (Biotex Lab. INC. USA) according to the manufacturer's recommendations. 4 μ l of total RNA was mixed with 3.0 μ l 10X Buffer, 3.0 μ l 2mM μ l dNTP, 3.0 μ l 10pmol/ μ l HMG I(Y) primer, 1.5 μ l 10pmol/ μ l β -actin, 1.5 μ l 100mM DTT, 0.3 μ l 40 units RNase inhibitor, 0.3 μ l 10 units AMV- reverse transcriptase, 0.1 μ l 5 units/ μ l Taq polymerase and 13.3 μ l DEPC-treated distilled water and simultaneously performed reverse transcription and PCR with Perkin

Elmer DNA Thermal Cycler(Model 9600). The condition of RT-PCR was as follows: reverse transcription-42 for 45 minutes. PCR(24 cycles)-denaturation, 95 for 30 seconds, annealing, 58 for 30 seconds, extension, 72 for 45 seconds. Sequences of the sense and antisense HMG I(Y) were as follows: 5'-TGC CAA CAC CTA AGA GAC CTC G-3' (sense), 5'-AAA GCT GTC CAG TCC CAG AAG C-3' (antisense). These primers were designed on the basis of the cDNA sequence of the HMG I(Y) gene exon 6 and exon 8. The expected size of the amplified product was 234bp. As a control, β -actin was used. Primer sequences of the β -actin were as follows: 5'-CAC TGT GTT GGC GTA CAG GGT-3' (sense), 5'-TCA TCA CCA TTG GCA ATG AG-3'. The expected size of the amplified product was 154bp. After amplification, the PCR products were separated by electrophoresis on a 2.0% agarose gel containing ethidium bromide. Negative controls included the substitution of RNA with distilled water. The HMG I(Y) mRNA was quantified to the amount relative to β -actin with Viber Lourmat Darkroom CN-UV/WL image analyser(C.B.S. Scientific Co., USA) and Bio-1D software.

3. Nucleotide Sequencing

PCR products were sequenced using an ABI Prism Automated DNA Sequencer(model 310, PE Applied Biosystems, USA)and the ABI Prism BigDye Terminator cycle Sequencing Ready Reaction Kit(Perkin-Elmer Co., USA).

4. Statistical analysis

The difference of HMG I(Y) expression between benign and malignant tumors was analyzed using Student t-test. P value less than 0.05 was considered significant. All statistical analyses were performed using a commercially available personal computer program SPSS.

RESULTS

Table 1 and Figure 1 show the distribution of the HMG I(Y) mRNA expression in various thyroid tissues. The ratio of HMG I(Y) to β -actin is high in papillary and follicular adenoma and Hurthle cell adenoma. If we take *the* cutoff value that differentiates between benign and malignant tumors as 1.5, the expression of HMG I(Y) was low in all of 10 normal thyroid tissues, 3 adenomatous goiters, 6

follicular adenomas and 2 Hurthle cell adenomas. On the other hand, in 11 of 13 papillary carcinomas and all of 5 follicular carcinomas, the HMG I(Y) expression level was high(Fig. 1). There was a strong association between HMG I(Y) expression and a diagnosis of carcinoma($p < 0.0001$).

Table 1. HMG I(Y) expression in various thyroid tissues

Histology	samples	expression levels* (range)
Normal thyroid	10	$0.90 \pm 0.46(0.28-1.46)$
Adenomatous goiter	3	$0.61 \pm 0.22(0.35-0.75)$
Follicular adenoma	6	$0.85 \pm 0.18(0.70-1.12)$
Hurthle cell adenoma	2	$1.10 \pm 0.10(1.03-1.17)$
Papillary carcinoma	13	$2.19 \pm 0.54(1.44-3.14)$
Follicular carcinoma	5	$2.78 \pm 0.69(2.26-3.94)$

*; expression levels mean ratio of HMG I(Y) -actin

Figure 2 shows an example of RT-PCR. In normal tissues, lane 6 shows low expression of HMG I(Y), but lane 9 shows a considerable amount of HMG I(Y) expression which is similar to papillary carcinoma(the ratio of HMG I(Y) -actin is 1.32). The expression of HMG I(Y) relative to -actin is low in adenomatous goiter(lane 4) and follicular adenoma(lane 3), but high in papillary carcinomas(lanes 1, 2, 7, 8) and follicular carcinomas(lanes 5, 10). The products of HMG I(Y) and -actin were confirmed by sequencing(data not shown). There was a nonspecific band between -actin and HMG I(Y), because -actin and HMG I(Y) were amplified in the same tube.

DISCUSSION

Because of previous reports that no presence of HMG I(Y) proteins is detected in normal thyroid cells¹⁶⁾, we firstly performed RT-PCR with only HMG I(Y), but there was abundant expression of HMG I(Y) mRNA in not only malignant tumors but also in normal and benign tumor tissues. So, we performed semiquantitative RT-PCR that -actin was coamplified as a control. At first, we separately performed RT-PCR with each protein, and confirmed the amplified bands. Then we simultaneously amplified both proteins and compared the relative amount of expression. As a result, we confirmed that malignant tumor had a higher expression of HMG I(Y) than normal or benign tumor tissues. This result is compatible with a

previous report¹⁶⁾. The mechanism by which HMG I(Y) can influence transcription is still incompletely understood. HMG I(Y) has previously been shown to facilitate the binding of certain transcription factors to DNA^{8,17-19)}. This feature of HMG I(Y) could be explained by at least two mechanism. First, since HMG I(Y) can bend DNA, this could promote binding transcription factor to A/T-rich DNA sites²⁰⁾. Second, direct protein-protein interactions between HMG I(Y) and transcription factors may promote the binding of the latter to their cognate DNA-binding sites^{21,22)}. But the HMG I(Y) gene does not behave like a classical transforming oncogene since, when transfected in normal thyroid cells, it did not cause their transformation, thus suggesting that its expression is necessary but not sufficient to achieve the transformed phenotype²³⁾.

In contrast to previous results by Northern blotting, Western blotting, immunohistochemistry¹⁶⁾ or in situ hybridization¹⁵⁾, normal tissues and benign tumors had a considerable amount of HMG I(Y) mRNA. This result means that HMG I(Y) may regulate the development and differentiation of normal thyroid cells in the cell cycle and its increased expression is correlated with malignant phenotype.

The expression of HMG I(Y) mRNA in two cases of papillary carcinoma was low. But even in these cases, the expression of HMG I(Y) mRNA was higher than normal thyroid tissues from the same patients (ratio of HMG I(Y) -actin in normal tissues: papillary carcinoma; 0.728:0.926, 0.631:1.465). In this study, although the cases were too small, all follicular carcinomas had a higher expression of HMG I(Y) than normal or benign tumor tissues. So, detection of HMG I(Y) might be extremely useful in the differential diagnosis between follicular adenoma and follicular carcinoma, but further evaluation with more cases is warranted.

In conclusion, HMG I(Y) mRNA expression level was high in thyroid carcinomas, but not in normal and benign tumor tissues. These results indicate that increased HMG I(Y) expression is correlated with thyroid carcinogenesis and these proteins may be useful as a marker in thyroid cancer.

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- Fig. 1.** The distribution of the HMGI(Y) mRNA expression in normal tissues and thyroid tumors. The dotted line is a cutoff value that differentiates between benign and malignant tumors.
- Fig. 2.** RT-PCR analysis of the HMGI(Y) gene expression in normal and neoplastic thyroid tissues. M; PhiX174/Hae III marker, Lanes 6, 9; normal tissues, Lane 4; adenomatous goiter, Lane 3; follicular adenoma, Lanes 1, 2, 7, 8; papillary carcinoma, Lanes 5, 10; follicular carcinoma
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