FRA-1 Expression in Hyperplastic and Neoplastic Thyroid Diseases

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ABSTRACT

The fra-1 gene overexpression has been shown to represent a general event in thyroid cell transformation in vitro and in vivo. Moreover, inhibition of FRA-1 protein synthesis by stable transfection with a fra-1 antisense construct significantly reduces the malignant phenotype of the transformed thyroid cells, indicating a pivotal role of the fra-1 gene product in the process of cellular transformation. In the attempt to define the potential use of FRA-1 protein detection in the diagnosis of thyroid diseases, we analyzed Fra-1 expression by a combination of immunohistochemistry and reverse transcription-PCR (RT-PCR) assay in 174 samples of thyroid nodules (22 nodular hyperplasias, 102 follicular adenomas, 34 papillary carcinomas, 12 follicular carcinomas, and 4 anaplastic carcinomas) representative of the spectrum of thyroid tumor pathology. FRA-1 protein was abundant in all of the carcinoma samples (50/50, 100%), with an intense staining in the nucleus and the cytoplasm. Positive staining was also found in most of the adenomas (90 of 102; 88%), but in this case, the staining was restricted to the nucleus. Similar results were obtained from the analysis of thyroid goiters; however, the number of positive cases is lower than adenomas (8 of 22; 36%); moreover, the staining was not observed in all of the cells. Conversely, no FRA-1

Received 4/13/00; revised 6/22/00; accepted 7/6/00.

INTRODUCTION

The FRA-1 protein is a member of the AP-1 complex that is formed by the three Jun family members (c-Jun, JunB, and JunD) and four Fos family members (c-Fos, FosB, Fra-1, and Fra-2; Refs. 1–5). Each of these Fos-related proteins is a transcription factor that can dimerize with Jun family proteins through a leucine zipper domain and bind through a conserved basic region to very similar or identical DNA motifs. The DNA element recognized by all of these heterodimers is an AP-1 site with core sequence TGACTCA (6–8). However, the Fos proteins cannot dimerize among themselves and have no intrinsic specific DNA binding activity (9).

Modification in AP-1 activity has been often correlated with cell transformation (8). In fact, c-jun knock-out mice-derived cells are resistant to ras-mediated transformation (10). Moreover, fra-2-c-jun heterodimers play a crucial role in chicken fibroblast transformation (11). Mouse JunD antagonizes transformation by ras (12), and c-fos expression is required for malignant progression of skin tumors (13). We have demonstrated recently that thyroid neoplastic transformation induced by the v-ras-Ki and v-mos oncogenes is associated with a drastic increase of AP-1 activity, which reflects multiple compositional changes (14). The main effect is represented by a dramatic fra-1 gene induction. Although no specific biological effect was observed after fra-1 gene overexpression, the inhibition of the FRA-1 protein synthesis by stable transfection with a fra-1 antisense construct significantly reduces the malignant phenotype of the transformed thyroid cells, indicating a pivotal role of the fra-1 gene product in the process of cellular transformation (14). Our recent results showing that the induction of the fra-1 gene is present even in cells transformed with several oncogenes (E1A gene of adenovirus, RET/PTC, v-raf, v-abl, Middle T of polyoma, v-src, and others) and in human thyroid carcinoma cell lines of different histotype indicate that the fra-1 gene expression induction is a general event in the process of thyroid carcinogenesis (15). Moreover, in rat fibroblasts fra-1 exhibits oncogenic potential because its overexpression has been shown to be unable to induce morphological transformation, but capable to stimulate anchorage-independent growth (16).
fra-1 gene expression is subject to positive control by AP-1 activity (15, 17); however, AP-1-induced expression of fra-1 depends on regulatory sequences located not only in the promoter region but also in the first intron. Because fra-1 gene expression is prevented by the block of the HMGI-C protein synthesis, the possibility that fra-1 gene expression is directly or indirectly regulated by the expression of the HMGI proteins should also be taken into account. The presence of five consen-
sus binding sites for members of the HMG-box family (18) in indirectly regulated by the expression of the HMGI proteins.

Thyroid nodules are frequently found in the general popula-
tion. The large majority of them are benign, and 5–10% are eventually diagnosed as carcinomas only after surgical removal of the lesion. Evaluation of the potential of molecular markers in the diagnosis of thyroid nodules is therefore justified. In this context, we analyzed FRA-1 expression by immunohistochem-
istry and RT-PCR in nodular lesions of the thyroid gland to assess its possible role as a diagnostic tool.

The results presented here show the expression of the FRA-1 protein in all of the thyroid carcinomas analyzed. Eighty-

MATERIALS AND METHODS

Tissue Samples. Tissue sections for immunohistochem-

Thyroid Cell Lines. The FRO cell line was derived from a human anaplastic thyroid carcinoma (19, 20). They were grown in DMEM plus 10% FCS. HTCP-2 cells were established from a human anaplastic thyroid carcinoma (19, 20). They were grown in DMEM plus 10% FCS. HTC-2 cells were established as described (21). Briefly, single 6–8-mm tissue sections, cut from paraffin blocks, were stirred for 20 min in 1.5-ml tubes with 1 ml of xylene. After centrifugation, the pellet was washed with 0.5 ml of ethanol and air-dried. The dried pellet was resuspended in 200 ml of 6 mg/ml proteinase K (Sigma Chemical Co., St. Louis, MO), 1 m guanidinium thiocyanate, 25 mM 2-mercapto-
ethanol, 0.5% Sarkosyl, and 20 mM Tris-HCl (pH 7.5) and incubated at 37°C for 18 h. RNA was then extracted with phenol and precipitated with ethanol following a standard procedure (23). Fine needle aspiration samples were washed twice with 1× PBS and then processed for RNA extraction following the same procedure. One-fifth of RNA of total RNA, digested with DNase, was reverse transcribed using random exanucleotides as primers (100 nm) and 12 units of AMV reverse transcriptase (Life Technologies, Inc.), and subsequent PCR amplification was performed as reported previously (24). Two hundred ng of cDNA were amplified in a 25-μl reaction mixture containing Taq DNA polymerase 0.06 mM diaminobenzidine and 0.06 mM diaminobenzidine solution containing 0.06 mM diaminobenzidine and 2 mM hydrogen peroxide in 0.05% PBS (pH 7.6) for 5 min, and after chromogen development, slides were washed, dehydrated with alcohol and xylene, and mounted with coverslips using a permanent mounting medium (Permount). Micrographs were taken on Kodak Ektachrome film with a photo Zeiss system.

The antibodies used in this study were rabbit polyclonal raised against the epitope corresponding to amino acids 3–22 mapping at the NH2 terminus of FRA-1 of human origin. They are specific for FRA-1 and non-cross-reactive with the other members of the fos family. The immunostained samples were blindly read by two independent individuals (G. C. and G. T.). RT-PCR Analysis of fra-1 Gene Expression. RNA was extracted from paraffin-embedded blocks on 37 cases that were analyzed in parallel for FRA-1 expression by immunohisto-

RT-PCR primers (100 mM ) and 12 units of AMV reverse transcriptase to serve as internal control for the amount of cDNA tested. GAPDH was added to each reaction after 20 cycles of PCR amplification was performed for 30 cycles (94°C for 30 s, 55°C for 2 min, and 72°C for 2 min). The specific primers for fra-1 were: forward, 5'-GTCATTGCTAGGATAACCAAC-3'; and reverse, 5'-GTCATTGCTAGGATAACCAAC-3'. The amplified products were separated by 1.5% agarose electro-

Slides were then incubated overnight at 4°C in a humidified chamber with the primary antibodies diluted 1:100 in PBS and subse-

The GAPDH-specific primers were: forward, 5'-CAATGTCGAACTGATATGGCTGTTG-3' corresponding to the nucleotides 194–214; and reverse, 5'-TGACCACTGACGTACCTAG-3' corresponding to the 336–356 nucleotides. The product of the
reaction was analyzed on a 2% agarose gel and then transferred by electroblotting to GeneScreen plus nylon membrane (Du-
Pont, Boston, MA). DNA was fixed to the membranes by air
drying and UV cross-linking, and then membranes were hybrid-
ized with a GAPDH probe. DNA was fixed to the membranes by air
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ized with a GAPDH probe. A PhosphorImager screen was
briefly exposed to the membranes, and the screen was then
scanned on a Molecular Dynamics PhosphorImager. The images
recorded by the PhosphorImager were analyzed by volume
integration with the ImageQuant software. The relative level of
fra-1 expression was assessed by comparison with the level of
GAPDH in the same sample.

Table 1 FRA-1 protein expression in human thyroid tumors

<table>
<thead>
<tr>
<th>Histological type of thyroid specimens</th>
<th>No. of positive cases/no. of cases analyzed by immunohistochemistry</th>
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*RT-PCR was performed on selected cases that were also analyzed by immunohistochemistry. The cases positive by RT-PCR were also positive by immunohistochemistry.

The goiter samples positive for RT-PCR were also positive by immunohistochemical analysis. Conversely, the other five cases were negative for both the assays.

**RESULTS**

**Immunohistochemical Analysis of fra-1 Gene Expression.** Detection of FRA-1 protein by immunohistochemical analysis allows a rapid and sensitive screening of thyroid pathological tissues and is amenable to regular use as a routine diagnostic test. This technique was therefore chosen for FRA-1 protein analysis using antibodies raised, in our laboratory, against a FRA-1-specific peptide. To find the best experimental conditions, FRO cells and tumors induced by injecting the FRO cell line into athymic mice were used as positive controls (20). The FRO cell line was chosen because of its high expression of the Fra-1 protein by Western blot analysis (15). No staining was observed with human thyroid cells (HTC-2 cells; Fig. 1A; Ref. 21), whereas a positive nuclear staining was obtained with FRO cells (Fig. 1B) and FRO-induced tumors (Fig. 1C).

The results of the immunohistochemical study of 186 thy-
rind specimens are summarized in Table 1. No staining was
observed in normal thyroid tissue (Fig. 2). Conversely, strong
immunoreactivity was detected in all of the thyroid carcinomas
analyzed (Fig. 2). The positivity appears in the nucleus, but it is
also present, although slightly weaker, in the cytoplas.
This result is consistent with previous published data that showed
FRA-1 protein localization in the nucleus and the cytoplasm of
the COS cells (25). Eighty-eight % of follicular adenomas and
36% of the goiters were positive for FRA-1. However, in these
cases, the immunoreactivity was always restricted to the nuclei.
Moreover, in goiters the nuclear staining was not observed in all
of the cells. In Fig. 2, we show some examples of the immu-
nohistochemical assay. No positive signal was detected in nor-
mal thyroid (Fig. 2A) and in one goiter (Fig. 2F), whereas an
intense nuclear and a weaker cytoplasmic staining was clearly
observed in a papillary carcinoma (Fig. 2C) and in a follicular
carcinoma (Fig. 2E). Fig. 2, G and H, shows the immunostaining
of one positive goiter and one positive adenoma, respectively;
the immunoreactivity is present only in the nuclei. For each
case, sections were stained without the primary antibody, and in
all cases, these controls were negative (Fig. 2D). No staining
was also observed when the neoplastic tissues were analyzed
after the FRA-1-specific antibodies had been preincubated with
the FRA-1 control peptide (Fig. 2B). In Fig. 3, we show that
fra-1 detection was specific for the neoplastic cells, because no

**Fig. 1** Immunohistochemical analysis of FRA-1 protein in normal thyroid cells, in FRO (anaplastic carcinoma) cells, and in FRO-induced tumors. A, HTC 2 cells; B, FRO cells; C, tumors induced by the injection of the FRO cells into athymic mice.

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the FRA-1 control peptide (Fig. 2B). In Fig. 3, we show that
fra-1 detection was specific for the neoplastic cells, because no
staining was observed in the normal follicles present in the same field.

**RT-PCR Analysis of fra-1 Gene Expression.** To quantitate the levels of the fra-1 gene expression and validate the immunohistochemical data, we analyzed 37 samples (4 normal thyroids, 8 goiters, 10 adenomas, and 15 carcinomas) for the fra-1 mRNA levels by a semiquantitative RT/PCR assay. The results are summarized in Table 1. Fig. 4 shows a representative RT-PCR assay. Normal thyroid was negative for the fra-1 gene expression (Lane 1). Three adenomas (Lanes 3, 4, and 5) of four (Lane 2) were positive. Conversely, all of the malignant tumors showed a significant fra-1 expression (from Lanes 6 to 15). In thyroid malignant neoplasias, the expression was higher (at least 4–5-fold) in comparison with benign lesions. The fra-1 gene expression in goiters was slightly lower than that observed in adenoma samples (data not shown). Therefore, these data support the immunohistochemical findings.

**Analysis of FNABs.** FNAB has become an integral part of the preoperative evaluation of thyroid nodules. To evaluate the applicability of fra-1 gene expression analysis to FNABs samples, we studied four cases of follicular adenoma and four of thyroid carcinoma (two papillary carcinomas and two follicular carcinomas). The results, shown in Table 2 and Fig. 5, are consistent with the immunohistochemical findings. The fine
needle biopsies from patients carrying a carcinoma showed expression of the fra-1 gene (Lanes 5, 6, 7, and 8), whereas the fine needle biopsy from normal thyroid (Lanes 1 and 9) was negative. Two adenoma samples were positive for the fra-1 gene expression (Lanes 3 and 4), and one scored negative (Lane 2). No amplification product was achieved when a carcinoma RNA sample was analyzed in absence of reverse transcriptase (data not shown).

DISCUSSION

Thyroid tumors include a wide spectrum of lesions with different phenotypic characteristics and biological behavior: benign adenomas, differentiated carcinomas, and anaplastic carcinomas (26). We have demonstrated previously that the chromatic proteins belonging to the group of the high mobility proteins are expressed at high levels in neoplastically transformed thyroid cells in culture and in human carcinomas, whereas they were not detected in normal thyroid and goiters and are present in 20% of adenomas (19, 20). Recently, the analysis of the AP-1 complex in thyroid cells transformed by MPSV and KiMSV revealed the induction of fra-1 in transformed thyroid cells. This induction was abolished by blocking the HMGI protein synthesis, suggesting a regulation of the fra-1 gene by the HMGI proteins (14). Rat and human thyroid carcinoma cell lines showed expression of the fra-1 gene, which was absent in normal rat thyroid cells and in human thyroid tissue (15). In addition, the inhibition of FRA-1 protein synthesis by stable transfection with a fra-1 antisense RNA vector significantly reduced the malignant phenotype of transformed thyroid cells, indicating a pivotal role for the fra-1 gene product in the process of cellular transformation (14). Recent data showing immunohistochemical evidence of FRA-1 protein expression in

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<td>Normal thyroid</td>
</tr>
<tr>
<td>Follicular neoplasm</td>
<td>Follicular adenomas</td>
</tr>
<tr>
<td>Follicular neoplasm</td>
<td>Follicular carcinomas</td>
</tr>
<tr>
<td>Suspicious for papillary carcinoma</td>
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</tr>
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</table>

* After surgical removal of the thyroid nodule.

* Cytologic samples from the contralateral lobe in one patient with follicular adenoma and one patient with follicular carcinoma.
The expression of the fra-1 gene in human adenomas is consistent with the results regarding in vitro thyroid cell transformation. In fact, we showed that fra-1 was expressed in all of the rat thyroid transformed cell lines, even in those that did not show a fully malignant phenotype, such as PC E1A, PC PTC, and PC Harvey (15).

In conclusion, fra-1 gene activation appears to be an early event in the process of thyroid carcinogenesis, and its detection may represent, together with the analysis of other markers, a useful tool in the diagnosis of human thyroid neoplastic diseases.

ACKNOWLEDGMENTS

We thank Annamaria De Bernardi for editing the manuscript.

REFERENCES


Unpublished results.


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