EXPERIMENTAL STUDY

PAX8 and peroxisome proliferator-activated receptor gamma 1 gene expression status in benign and malignant thyroid tissues

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Abstract

Objective: Genetic alterations involving the thyroid transcription factor PAX8 and the peroxisome proliferator-activated receptor gamma 1 (PPARγ1) genes have been described in thyroid neoplasms. We investigated in a series of thyroid samples, including 14 normal, 13 hyperfunctioning tissues, 26 follicular adenomas, 21 follicular and 41 papillary carcinomas, both the frequency of the PAX8-PPARγ1 rearrangement and the expression of the PAX8 and PPARγ transcripts.

Methods: Using RT-PCR followed by sequencing PCR products, PAX8-PPARγ1 translocation was not detected in benign tissues nor in papillary carcinomas and was detected in 4 (19%) of 21 follicular carcinomas and in one (4%) of 26 follicular adenomas.

Results: Specific real-time quantitative RT-PCR (Q RT-PCR) methods detected high levels of PPARγ transcripts in follicular carcinomas presenting the rearrangement. Interestingly, the level of PPARγ transcripts was significantly decreased in papillary carcinomas in comparison with those found in benign adenomas and follicular carcinomas. Finally, PAX8 gene expression was decreased in both papillary and follicular thyroid carcinomas, and in these tumors to the same extent in the presence or absence of the rearrangement. These alterations in both PPARγ and PAX8 gene expression may explain the poorly differentiated histotype of follicular carcinomas harboring the translocation. Immunohistochemistry showed that nuclear PPARγ staining was weak in normal tissues, adenomas, papillary carcinomas and in some follicular carcinomas, and strong in the follicular carcinomas positive for the PAX8-PPARγ1 translocation, but also in some follicular tumors in which no translocation could be evidenced.

Conclusion: These observations confirm that the PAX8-PPARγ1 translocation characterizes a subset of thyroid follicular carcinomas but is not a specific marker of carcinoma and that its frequency is lower than that initially reported. Finally, immunohistochemistry is not a reliable method for the specific detection of the translocation, that can be specifically evidenced by Q RT-PCR.

Introduction

Follicular cell-derived thyroid tumors include benign adenomas, papillary and follicular carcinomas, two entities considered as differentiated carcinomas, and anaplastic carcinomas (1). Genetic abnormalities found in these tumors have been largely substantiated (2), and chromosomal rearrangements are typical features of differentiated thyroid carcinomas (3). The RET/PTC oncogene, generated by the fusion of the tyrosine-kinase domain of the RET gene and the 5’ domain of various genes was detected in papillary carcinomas and with a high frequency in radiation-associated carcinomas (4); NTRK1 rearrangement was also found in papillary carcinomas (2, 3). Chromosomal imbalances are frequent in follicular neoplasms, with gains at chromosomes 7 and 5 and deletions at 3p (5, 6). In these tumors, the t(2;3) (q13;p25) rearrangement results in the fusion of the DNA binding domains of the thyroid transcription factor PAX8 to DNA binding, ligand binding, RXR dimerization and transactivation domains of the peroxisome proliferator-activated receptor gamma 1 (PPARγ1) (7). PPARγ belongs to the nuclear hormone receptor superfamily and plays a critical role in the differentiation of adipocytes and in the regulation of fat metabolism (8, 9). Although their precise mechanism of action remains unknown, the anti-proliferative effects of PPARγ agonists have been demonstrated in tumor cell lines, including those established from thyroid carcinomas (10–13). Furthermore, changes in expression, mutations and polymorphism within the PPARγ gene have been depicted in various malignancies (10, 14–16). PAX8, a member of the paired domain-containing gene family, plays a key role in thyroid cell differentiation (17). In the adult thyroid gland,
PAX8 regulates the expression of major thyroid genes and its expression is more profoundly decreased in carcinomas than in adenomas (18).

The PAX8-PPARγ1 fusion oncogene appears to act through a dominant negative effect on the transcriptional activity of the wild-type PPARγ1. The frequency of the rearrangement in follicular carcinomas ranges from 10 and 63% among series, depending on the number of tumors tested and the method used (7, 19–27). The PAX8-PPARγ1 rearrangement was also detected in some follicular adenomas but these could be early minimally invasive follicular carcinomas (19–21). This observation suggests that the PAX8-PPARγ1 rearrangement is not a reliable marker of malignancy and is not sufficient per se for carcinogenesis (20, 21). In contrast, the rearrangement was not found in Hürthle cell tumors, papillary carcinomas and in hyperplastic thyroid tissues (7, 19, 20, 22, 25).

In the present report, we analyzed a large series of benign hyper- and hypofunctioning thyroid tissues, and of papillary and follicular carcinomas for the presence of papillary and follicular carcinomas by RT-PCR followed by sequencing. We then developed a real-time quantitative RT-PCR (Q RT-PCR) to quantify the presence of the PAX8-PPARγ1 fusion oncogene by RT-PCR followed by sequencing. We then developed a real-time quantitative RT-PCR (Q RT-PCR) to quantify the expression level of PAX8 and PPARγ genes, and an immunohistochemical method to evaluate PPARγ protein expression. Polymorphisms at codons 12 and 449 that have been reported to be associated with some malignant tumors have also been analyzed in these samples.

Materials and methods

Tissue samples

Thyroid tissue samples were selected after histological analysis and classified according to World Health Organization recommendations (1). They included hyperfunctioning tissues, including Graves’ thyroid tissues and toxic adenomas (n = 13), benign hypofunctioning follicular adenomas (n = 26), and papillary (n = 41) and follicular (n = 21) thyroid carcinomas. Among follicular carcinomas, 15 were poorly differentiated (either microfollicular, insular or Hürthle cell carcinoma) including 14 widely invasive and one minimally invasive. The other six were well differentiated macrofollicular carcinomas, including five minimally invasive and one widely invasive. The clinical features of follicular thyroid carcinoma patients are presented in Table 1. Briefly, follicular carcinomas occurred in 10 males and 11 females with a mean age of 50 years. According to the TNM classification (Table 1), seven tumors were classified as stage I, four as stage II, one as stage III, and nine as stage IV (28). Finally, normal thyroid tissues (n = 14) obtained from patients with a unifocal papillary carcinoma, were used as calibrators. All specimens were frozen at −80°C in isopentane and stored in liquid nitrogen before RNA extraction. All patients, except those with Graves’ disease or toxic adenoma were euthyroid at the time of surgery as shown by a normal serum thyrotropin (TSH) level. Informed consent was obtained from all patients.

RT-PCR for detection of PAX8-PPARγ1 translocation

Total RNA was isolated from tissue samples using a DNA/RNA Extraction Midi Kit according to the manufacturer’s instructions (Qiagen, Hilden, Germany). The quality of RNA was controlled by conventional gel electrophoresis, stained with ethidium bromide; 28S and 18S bands were visualized under UV illumination. The quantification yield was assessed by spectrophotometry. RNA (1 μg) was reverse transcribed with Moloney murine leukemia virus reverse transcriptase at 42°C for 45 min in a 20-μl volume reaction, in the presence of random primers. Two microliters reversed-transcribed mixture (cDNA 0.1 μg) were amplified by PCR for detection of PAX8-PPARγ1 translocation. PCR reaction was assessed with forward primer for exon 7 of PAX8 (5′-GCAACCTTCGACTCA-CCAG-3′) and reverse primer for exon 1 of PPARγ1 (5′-CATTACCGAGATCCACGG-3′), as previously described (7). PCR products of the four positive samples were separated using 2% agarose gel electrophoresis (SeaPlaque GTG Agarose, FMC Bioproduct, Rockland, ME, USA). Each band was purified with QIAquick Gel Extraction Kit (Qiagen) according to the manufacturer’s instructions. These purified products were directly sequenced using Big Dye Terminator Cycle Sequencing Kit (Applied Biosystems, Foster City, CA, USA). All samples were also tested with the primers described by Nikiforova et al. (23).

Determination of mRNA level of PPARγ and PAX8 using real-time quantitative PCR

Determination of the PPARγ and PAX8 gene expression was performed in all thyroid tissue samples. Oligonucleotide primers and Taqman probes specific for PPARγ and PAX8a were designed to be intron spanning using the computer program Primer Express (Applied Biosystems) and GenBank databases. Their sequences are presented in Table 2. For PPARγ, the primers and the probe were located in exons 5–6. The analysis did not allow us to distinguish between fusion oncogene transcripts and wild-type PPARγ transcripts.

Real-time quantitative PCR was set up in 96-sample tubes/assay using a cDNA equivalent of 20 ng total RNA per tube as previously described (29). To normalize for the differences in the amount of total RNA added to the reaction, amplification of 18S ribosomal RNA was performed as an endogenous control. A pool of 5 normal thyroid tissues was used as a calibrator (1 × sample) for determining the relative expression of PAX8 and PPARγ genes in tissues as previously
Table 1 Clinical, pathological and molecular features of patients with a follicular thyroid carcinoma.

<table>
<thead>
<tr>
<th>Patient number</th>
<th>Age (years)</th>
<th>Gender (M/F)</th>
<th>TNM stage</th>
<th>Histotype</th>
<th>Invasion</th>
<th>t(PAX8-PPAR(g))</th>
<th>PPAR(g) mRNA ((x)-fold)</th>
<th>PPAR(g) protein staining (% positive cells/intensity)</th>
<th>Follow-up</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>50 F</td>
<td>T2N0M0 II</td>
<td>Microfollicular</td>
<td>Widely</td>
<td>Absent</td>
<td>&lt;3</td>
<td>No staining</td>
<td>3.6 years Alive</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>20 F</td>
<td>T1N0M0 I</td>
<td>Macrofollicular</td>
<td>Minimally</td>
<td>Absent</td>
<td>&lt;3</td>
<td>&gt;80% / +++++</td>
<td>7 years Alive</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>36 F</td>
<td>T2N0M0 I</td>
<td>Macrofollicular</td>
<td>Minimally</td>
<td>Absent</td>
<td>&lt;3</td>
<td>&lt;20% / +</td>
<td>5 years Alive</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>63 M</td>
<td>T4N1M1 IvC</td>
<td>Microfollicular</td>
<td>Widely</td>
<td>Absent</td>
<td>&lt;3</td>
<td>&lt;20% / ++++</td>
<td>3 months Dead</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>30 M</td>
<td>T2N0M0 I</td>
<td>Microfollicular</td>
<td>Widely</td>
<td>Present</td>
<td>14.5</td>
<td>60–80% / +++++</td>
<td>5 years Alive</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>52 F</td>
<td>T1N0M0 I</td>
<td>Macrofollicular</td>
<td>Minimally</td>
<td>Absent</td>
<td>&lt;3</td>
<td>60–80% / +++++</td>
<td>5.5 years Alive</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>70 M</td>
<td>T4aNxM1 IvC</td>
<td>Hürthle cell carcinoma</td>
<td>Widely</td>
<td>Absent</td>
<td>&lt;3</td>
<td>20–40% / +</td>
<td>3 years Alive</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>59 F</td>
<td>T4aN0M1 IvC</td>
<td>Insular</td>
<td>Widely</td>
<td>Absent</td>
<td>&lt;3</td>
<td>No staining</td>
<td>6 months Dead</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>51 F</td>
<td>T3N0M0 III</td>
<td>Microfollicular</td>
<td>Widely</td>
<td>Present</td>
<td>9</td>
<td>20–40% / ++++</td>
<td>4 years Alive</td>
<td></td>
</tr>
<tr>
<td>10</td>
<td>66 F</td>
<td>T4aN0M0 IvA</td>
<td>Insular</td>
<td>Widely</td>
<td>Absent</td>
<td>&lt;3</td>
<td>60–80% / +</td>
<td>3.5 years Alive</td>
<td></td>
</tr>
<tr>
<td>11</td>
<td>33 M</td>
<td>T3N0M0 I</td>
<td>Macrofollicular</td>
<td>Minimally</td>
<td>Absent</td>
<td>&lt;3</td>
<td>20–40% / +</td>
<td>3.5 years Alive</td>
<td></td>
</tr>
<tr>
<td>12</td>
<td>51 M</td>
<td>T4aN1aM1 IvC</td>
<td>Insular</td>
<td>Widely</td>
<td>Absent</td>
<td>&lt;3</td>
<td>No staining</td>
<td>1 year Dead</td>
<td></td>
</tr>
<tr>
<td>13</td>
<td>65 F</td>
<td>T2N1aM1 IvC</td>
<td>Insular</td>
<td>Widely</td>
<td>Absent</td>
<td>&lt;3</td>
<td>&lt;20% / +</td>
<td>1.5 years Dead</td>
<td></td>
</tr>
<tr>
<td>14</td>
<td>32 M</td>
<td>T3N1aM1 II</td>
<td>Microfollicular</td>
<td>Widely</td>
<td>Absent</td>
<td>&lt;3</td>
<td>&lt;20% / +</td>
<td>4 years Alive</td>
<td></td>
</tr>
<tr>
<td>15</td>
<td>63 M</td>
<td>T3N0M0 II</td>
<td>Macrofollicular</td>
<td>Minimally</td>
<td>Absent</td>
<td>&lt;3</td>
<td>40–60% / +</td>
<td>14 years Alive</td>
<td></td>
</tr>
<tr>
<td>16</td>
<td>52 F</td>
<td>T3N1M1 IvC</td>
<td>Microfollicular</td>
<td>Widely</td>
<td>Absent</td>
<td>&lt;3</td>
<td>60–80% / ++++</td>
<td>4.5 years Dead</td>
<td></td>
</tr>
<tr>
<td>17</td>
<td>58 M</td>
<td>T3N0M0 II</td>
<td>Macrofollicular</td>
<td>Widely</td>
<td>Absent</td>
<td>&lt;3</td>
<td>20–40% / +</td>
<td>9 years Dead</td>
<td></td>
</tr>
<tr>
<td>18</td>
<td>45 M</td>
<td>T4aN1M1 IvC</td>
<td>Microfollicular</td>
<td>Widely</td>
<td>Absent</td>
<td>&lt;3</td>
<td>&lt;20% / +</td>
<td>6 years Alive</td>
<td></td>
</tr>
<tr>
<td>19</td>
<td>77 F</td>
<td>T3N1M1 IvC</td>
<td>Insular</td>
<td>Widely</td>
<td>Absent</td>
<td>&lt;3</td>
<td>No staining</td>
<td>10 months Dead</td>
<td></td>
</tr>
<tr>
<td>20</td>
<td>40 F</td>
<td>T3N0M0 I</td>
<td>Microfollicular with papillary structures</td>
<td>Widely</td>
<td>Present</td>
<td>22</td>
<td>60–80% / ++++</td>
<td>6 years Alive</td>
<td></td>
</tr>
<tr>
<td>21</td>
<td>37 M</td>
<td>T2N0M0 I</td>
<td>Microfollicular</td>
<td>Minimally</td>
<td>Present</td>
<td>31</td>
<td>40–60% / ++++</td>
<td>3 years Alive</td>
<td></td>
</tr>
</tbody>
</table>

1\(t(PAX8-PPAR\(g\))\): status of tumors for PAX8-PPAR\(g\) translocation detected with RT-PCR assay; PPAR\(g\) mRNA: expression level of PPAR\(g\) mRNA by real time quantitative PCR; PPAR\(g\) protein staining: immunohistochemical evaluation for PPAR\(g\) protein took into consideration both the percent of positive cells and the staining intensity. TNM Stage: T, primary tumor; T1, ≤2 cm; T2, >2 cm to ≤4 cm; T3, >4 cm; T4, extension beyond thyroid capsule; T4a, tumor of any size with extension beyond the thyroid capsule and invades any of the following: subcutaneous soft tissues, larynx, trachea, oesophagus, recurrent laryngeal nerve; T4b: tumor invades prevertebral fascia, mediastinal vessels, or encases carotid artery. N, regional lymph node metastases; N0, absence; N1, lymph node metastases; N1a, metastases in pretracheal and paratracheal including prelaryngeal and delphian lymph nodes; N1b, metastases in other unilateral, bilateral or contralateral cervical or upper mediastinal lymph nodes; M, distant metastases; M0, absence; M1, distant metastases; Stage I: age < 45 years any T, any N, M0 or age ≥ 45 years T1, N0, M0; Stage II: age < 45 years any T, any N, M1 or age ≥ 45 years T2, N0, M0; Stage III: age ≥ 45 years T3, N0, M0 or any T1-3, N1a, M0; Stage IVa: age ≥ 45 years T1-3, N1b, M0 or T4a, any N, M0; Stage IVb: age ≥ 45 years T4b, any N, M0; Stage IVc: age ≥ 45 years any T, any N, M1 (28).
**Detection of the PPARγ variants**

In order to test whether a particular PPARγ polymorphism is associated with the occurrence of benign or malignant thyroid tumor, DNA from the tumoral tissues was analyzed. Fragments encompassing the two sites of PPARγ polymorphism, namely P12A in the unique PPARγ2 exon and H449H in the 6th common exon, were generated from DNA by PCR as previously reported (31, 32). The P12A (CCA → GCA) polymorphism was analyzed by using BstUI digestion followed by 3% agarose gel electrophoresis. Two microliters PCR product were digested by 6 U restriction endonuclease PmlI (New England Biolabs) and 8 C overnight followed by a 3% agarose gel electrophoresis. The expected products after digestion with BstUI were 270 bp for normal homozygote, 227 and 107 bp for heterozygote and 267 bp for H449H (CA) polymorphism is associated with the occurrence of benign or malignant thyroid tumor, DNA from the tumoral tissues was analyzed. Fragments encompassing the two sites of PPARγ polymorphism, namely P12A in the unique PPARγ2 exon and H449H in the 6th common exon, were generated from DNA by PCR as previously reported (31, 32). The P12A (CCA → GCA) polymorphism was analyzed by using BstUI digestion followed by 3% agarose gel electrophoresis. Two microliters PCR product were digested by 6 U restriction endonuclease PmlI (New England Biolabs) and 8 C overnight followed by a 3% agarose gel electrophoresis. The expected products after digestion with BstUI were 270 bp for normal homozygote, 227 and 107 bp for heterozygote and 267 bp for H449H homozygote.

**Immunohistochemistry for PPARγ protein**

Immunohistochemistry was performed on formalin-fixed paraffin-embedded 5-μm sections of normal, benign and malignant thyroid tissues, with the DAKO LSAB System procedure (DAKO, Carpenteria, CA, USA). Briefly, sections were deparaffinized by serial passages in xylene and in alcohol. After blocking endogenous peroxidase activity, microwave/pressure cooker pretreatment was performed in 1 mM EDTA buffer (pH 8). Sections were then incubated for 30 min at room temperature with a mouse monoclonal antibody anti-PPARγ which recognizes the carboxyl terminus of the protein (Santa Cruz Biotechnology, Santa Cruz, CA, USA). They were washed three times in Tris–HCl 1× buffer for 5 min each time and incubated with a peroxidase-conjugated antibody for 15 min (peroxidase anti-rabbit/mouse DAKO EnVision System cod. K4003). After three further washes, peroxidase staining was revealed in diaminobenzidine tetrahydrochloride (Polysciences Inc., Warrington, PA, USA) with 0.1% hydrogen peroxide in Tris buffer 0.01 mol/l (pH 7.2). Sections were counterstained with hematoxylin, dehydrated and mounted. Negative controls were obtained by performing the same procedure on tissue sections without the anti-PPARγ antibody incubation step. Immunohistochemical evaluation was assessed by taking into consideration both the percentage of positive cells (noted as percentage of stained cells) and the intensity of staining (noted from + to ++++ + ).

**Results**

**Detection of the PAX8-PPARγ1 rearrangement in human thyroid tissues**

No PAX8-PPARγ1 translocation was detected in normal tissues, hyperfunctioning tissues and in classical papillary carcinomas with characteristic nuclear features. Among the 21 follicular carcinomas analyzed, the presence of the PAX8-PPARγ1 rearrangement was detected in only four samples (19%) (Fig. 1). Among the 26 hypofunctioning adenomas analyzed, a translocation was also detected in one sample (4%). In positive patients, RT-PCR revealed amplification fragments of different sizes. Sequencing of the PCR products from follicular carcinomas showed four transcripts generated by the fusion of different exons of PAX8 (exon 7, exons 7–8, exons 7–8–9 and exons 7–9) with exon 1 of PPARγ1. Three positive carcinomas were microfolicular carcinomas, two being widely invasive and one minimally invasive (Table 1). The remaining one displayed a peculiar histological feature with papillary structures but without the characteristic ‘papillary nuclei’. The positive adenoma was an atypical adenoma with a hypercellular and microfollicular pattern, limited by a capsule of variable thickness but without complete invasion. The transcripts were generated by the fusion of exons 7 or 7 and 8 with exon 1 of PPARγ1.

All these results were confirmed by an independent PCR based on protocols described by Nikiforova et al. (23) (data not shown).

**Determination of PPARγ and PAX8 gene expression in thyroid tissues**

The mRNA levels of the two genes were determined by Q RT-PCR (Fig. 2). PPARγ gene expression was detected

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**Table 2** Sequences of primer pairs and TaqMan probes.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Genbank</th>
<th>Primers and probe</th>
</tr>
</thead>
<tbody>
<tr>
<td>PPARγ1</td>
<td>GI2605496</td>
<td>Sense GCA GGA GCA GAG CAA AGA GG</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Antisense CCA GGA ATG CTT TTG GCA TAC</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Probe FAM-CCA TCC GCA TCT TTCA GG GCT TC-TAMRA</td>
</tr>
<tr>
<td>PAX8A</td>
<td>X69699</td>
<td>Sense CAA CAG CAC CCT GGA CCA C</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Antisense AGG GTG AGT GAG GAT CTG CC</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Probe FAM-CTG ACC CCT TCC AAC ACG CCA CTG-TAMRA</td>
</tr>
</tbody>
</table>

FAM, 6-carboxy-fluorescein; TAMRA, 6-carboxy-tetramethyl-rhodamine.

In order to exclude potential contamination by the adipose tissue, which also expresses PPARγ transcripts, a leptin Q RT-PCR method was used (30).
in all tissues examined, and its level appeared variable: it was in the normal range in hyperfunctioning tissues and in follicular adenomas without the translocation, whereas it was significantly decreased, by about tenfold, in papillary carcinomas. In contrast, PPARγ mRNA values were in the normal range in follicular carcinomas without the translocation and were increased by 8- to 31-fold in tissues presenting the PAX8-PPARγ1 translocation. PAX8A gene expression was similar in normal, hyperfunctioning and hypofunctioning benign thyroid tissues. In contrast, PAX8A gene expression was significantly decreased in papillary and follicular carcinomas, and the transcript levels were decreased to the same extent in samples presenting or not the translocation. Q RT-PCR leptin assay did not show any contamination by adipose tissue (data not shown).

**PPARγ polymorphism in benign and malignant thyroid tumors**

There was no association between the PPARγ variant frequencies and the three groups of patients bearing a hypofunctioning adenoma, a papillary carcinoma or a follicular carcinoma (data not shown). However, the limited size of our series does not permit us to totally rule out the hypothesis that an isoform may predispose to a particular benign or malignant tumor.

**PPARγ protein expression in thyroid tissues**

Immunohistochemistry with an antibody directed against the wild-type PPARγ displayed a weak nuclear staining in normal, benign tissues and in papillary carcinomas. In the 17 follicular carcinomas in which no translocation was found, nuclear staining was absent in four samples, was weakly positive in eight samples (intensity: + to ++, in 20–40% of cancer cells) and was diffusely positive and intense in five samples (intensity: +++ to ++++, in 40–60% of cancer cells). In the four follicular carcinomas and in the hypofunctioning follicular adenoma with the PAX8-PPARγ1 translocation by RT-PCR in follicular thyroid tumors. Lanes 1 to 4 correspond to follicular thyroid carcinomas and lane 5 corresponds to the follicular thyroid adenoma. RT-PCR revealed amplification fragments of predicted size: (a) 407 bp corresponding to fusion of PAX8 exons 7–8–9 to PPARγ1 exon 1; (b) 305 bp corresponding to fusion of PAX8 exons 7–8 to PPARγ1 exon 1; (c) 217 bp corresponding to fusion of PAX8 exons 7 plus 9 to PPARγ1 exon 1 and (d) 108 bp corresponding to fusion of PAX8 exons 7–8 and 7 to PPARγ1 exon 1. RT-PCR negative controls are presented in the last lane (−).

**Figure 2** Box plots for PPARγ and PAX8A gene expression levels according to histology (N, normal; HFT, hyperfunctioning tissues; FTA, hypofunctioning follicular thyroid adenomas; FTC, follicular thyroid carcinomas; PTC, papillary thyroid carcinomas). The box shows the limits of the middle half of the data, the line inside the box represents the median. Whiskers are drawn to represent the standard span of the 5th/95th percentile. Solid circles correspond to tumors with PAX8/PPARγ translocation, and open circles correspond to tissue samples without translocation.
translocation, a strong nuclear staining (intensity: ++ to ++++) was observed in 40–80% of tumor cells (Fig. 3).

**Correlation with clinical features**

No relationship was found between the presence of the PAX8-PPARγ1 rearrangement and the clinical status of the patients, including the age, the TNM stage, the 131I uptake and the outcome (Table 1).

**Discussion**

In the present report, the status of both PAX8 and PPARγ1 gene expression was examined in a large series of normal, benign and malignant thyroid tissues by means of a rapid and semi-automated real-time Q RT-PCR method. Both types of transcripts were detected in all normal thyroid tissues examined.

Analysis was first focused on follicular carcinomas because the PAX8-PPARγ1 rearrangement had previously been implicated in their pathogenesis (7). Using a conventional RT-PCR method followed by sequencing of amplified products, 19% of the follicular carcinoma samples presented the PAX8-PPARγ1 rearrangement. This is in agreement with other studies showing that the frequency of the translocation is lower than initially reported (20–24). We also found the translocation in one of the 26 hypofunctioning adenomas studied. This is also in agreement with previous studies in which the translocation was found in a low percentage of atypical adenomas. Indeed, this atypical adenoma, like the positive adenomas in the previous series may in fact be a minimally invasive follicular carcinoma treated at an early stage. Thus, our results also confirm the specificity of the PAX8-PPARγ1 rearrangement for the follicular histotype of thyroid tumors and its absence in papillary carcinomas. However, the rearrangement was found in both minimally and widely invasive follicular cancers.

It has been suggested that immunohistochemistry could be a sensitive, specific and rapid tool for the detection of this translocation (7). In fact, the anti-PPARγ antibody provided a strong nuclear staining in all tumors presenting the PAX8-PPARγ1 rearrangement. However, staining was strong also in some samples in which no translocation was found and was detected in the majority of follicular carcinoma cells, corresponding to the expression of either the wild-type PPARγ protein or to a rearrangement with another fusion gene (27). Therefore, due to its lack of specificity, this method cannot be used alone for the detection of the PAX8-PPARγ1 translocation (26). Although the experimental design of our Q RT-PCR method did not allow us to distinguish between wild-type PPARγ and fusion oncogene transcripts, our analysis clearly demonstrates that high levels of PPARγ transcripts were found only in the follicular tumors presenting the PAX8-PPARγ1 rearrangement as detected by RT-PCR and in which a strong immunostaining was also observed. This observation suggests that PPARγ Q RT-PCR could be a convenient method for detecting the PAX8-PPARγ1 rearrangement. Interestingly, PAX8 gene expression was not different in thyroid tissues either positive or negative for the presence of the translocation. This might be explained by the strong expression of PAX8 in thyroid tissue, as compared with a weak PPARγ expression, that acts as a promoter of the expression of the chimeric gene.

The level of PPARγ transcripts was significantly lower in papillary carcinomas than in benign adenomas and follicular carcinomas. Using a semi-quantitative RT-PCR and immunohistochemistry, Aldred et al. (24) also detected a down-regulation of PPARγ gene expression in all tumors tested, including follicular carcinomas. Reports on PPARγ gene expression in thyroid tumoral cell lines are contradictory, with either an up-regulation (11) or a down-regulation (12). Altogether, the relevance of these observations remains to be
investigated, as it would be of interest to determine whether two different processes, a decrease in gene expression in papillary carcinomas and a dominant negative suppressor effect in follicular carcinomas bearing the PAX8-PPARγ1 rearrangement, contribute or not to the same action on the oncogenic process.

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