Concurrent overexpression of RET/PTC1 and TTF1 confers tumorigenicity to thyrocytes

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Abstract

A variant located on 14q13.3 nearest to thyroid transcription factor-1 (TTF1) predisposes individuals to thyroid cancer, but whether this variant is related to the RET/PTC rearrangement associated with human papillary thyroid carcinomas (PTCs) is unknown. The aims of this study were to investigate the effects of RET/PTC1 on the expression of thyroid-specific genes in thyrocytes and their relationship with malignant transformation of the thyrocytes. In the absence or presence of TSH, an extracellular signal-regulated kinase was phosphorylated in FRTL5 cells that stably expressed RET/PTC1, and these cells grew independently of TSH. FRTL (RET/PTC1) cells produced 566% more thyroglobulin mRNA and 474% more Na+/I− symporter mRNA than did the control FRTL (pcDNA) cells. FRTL (RET/PTC1) cells expressed 468% more Ttf1 mRNA than did FRTL (pcDNA) cells, but these two cell types did not differ significantly with respect to Pax8 or Ttf2 mRNA levels. When FRTL (RET/PTC1) cells and FRTL (pcDNA), cells were injected into each of nine nude mice, each mouse developed a single tumor at the site of FRTL (RET/PTC1) cell injection; in contrast, tumor formation never occurred at sites of FRTL (pcDNA) cells injection. Tumors resulting from FRTL (RET/PTC1) cells retained 125I-uptake activity; moreover, the cells invaded into surrounding skeletal muscle. When overexpression of Ttf1 in FRTL (RET/PTC1) cells was silenced, the cells completely lost their tumorigenic potential. Exogenous TTF1 cDNA enhanced the tumorigenicity of BHP18-21v cells, human PTC cells that express RET/PTC1, in nude mice. These results indicated that concurrent overexpression of RET/PTC1 and TTF1 confers tumorigenicity to FRTL5 and BHP18-21v cells in nude mice.

Key Words
- RET/PTC
- thyrocytes
- thyroid transcription factor-1
- tumorigenesis

Introduction

Papillary thyroid carcinomas (PTCs) are the most frequent cancers of the thyroid gland, and they are usually well differentiated given their ability to i) take up iodine, ii) secrete thyroglobulin (TG), and iii) be responsive to thyroid-stimulating hormone (TSH; Nikiforov & Nikiforova 2011).

The RET/PTC rearrangement and the BRAFV600E point mutation are the two most common genetic alterations associated with PTCs; the prevalence of RET/PTC varies from 2.5 to 78% (Zou et al. 1994, Nikiforov et al. 1997), and the prevalence of BRAFV600E varies from 23 to 62% (Xing et al. 2005, Fugazzola et al. 2006).

Rearrangements of the RET gene can cause recombination of sequences encoding the intracellular kinase domain of RET with a heterologous gene and
thereby generate a chimeric oncogene that induces RAS-dependent activation and consequent ERK activation (Melillo et al. 2005). However, constitutive activation of ERK caused by a RET/PTC oncogene may or may not be sufficient to induce all hallmarks of cancer in vivo. Santoro et al. (1996) found that some RET/PTC1 transgenic mice developed thyroid tumors, but others developed only thyroid hyperplasia. Knostman et al. (2007) reported that doxycycline-induced expression of RET/PTC1 led to ERK phosphorylation in mice that carried a doxycycline-regulated RET/PTC1 transgene; however, thyroid lesions were not found in any of these mice.

These results indicate that oncoproteins such as RET/PTC activate the MEK/ERK cascade, which then promotes an initial wave of dramatic cell proliferation that, in turn, initiates tumor development, but subsequent development of a solid cancer requires an additional unknown lesion or alteration (Pritchard et al. 2007).

Gudmundsson et al. (2009) recently conducted a genome-wide association study (GWAS) of thyroid cancer cases; they found that a variant predisposes individuals from European populations to thyroid cancer; this variant is located on 14q13.3 near thyroid transcription factor-1 (TTF1), which is also called NKX2.1 (TTF1) and PAX8 are master regulators of thyroid-specific gene expression. For example, they regulate TG, NIS (SLC5A5), and TSHR; moreover, they play pivotal roles in the development of thyroid glands (Sinclair et al. 1990, Silberschmidt et al. 2011). Therefore, the GWAS findings may be relevant to the pathogenesis of PTCs. However, whether relationships between the variant at 14q13.3 and the genetic alterations in PTCs (e.g., RET/PTC rearrangements) exist is unclear.

To assess whether there are important interactions between the 14q13.3 variant and RET/PTC rearrangements, we expressed RET/PTC1 in FRTL5 cells, functional thyroid epithelial cells, and studied the effects of RET/PTC1 on the expression of thyroid-specific genes with a particular focus on the expression of Ttf1, Ttf2, and Pax8, and their relationship with tumorigenicity of the cells. Further, TTF1 cDNA was introduced into BHP18-21v cells, which are human PTC cells, to examine the effects of TTF1 on tumorigenicity of these cells.

Materials and methods

Cells, tissues, and animals

FRTL5 cells (CRL8395, ATCC, Manassas, VA, USA) were cultured in Ham F12 medium that contained 5% calf serum with or without 10 mU/ml TSH (Sigma–Aldrich, Inc.) (Endo et al. 1990). The cells grew in a TSH-dependent manner and expressed seven thyroid-specific genes—Ttf1, Ttf2, Pax8, Tg, thyroid peroxidase (Tpo), Na+/I− symporter (Nis), and Tsh receptor (Tshr). BHP18-21v cells were isolated from BHP18-21 cells, which are human thyroid papillary cancer cells that express RET/PTC1 (Ohta et al. 1997); BHP18-21v cells were cultured in RPMI-1640 containing 10% FCS, and they expressed Pax8 but not TTF1, TTF2, TG, TPO, NIS, or TSHR. This expression profile is unique to BHP18-21v cells among BHP cell lines; therefore, the BHP18-21v cells we used were free from contamination. BRL-3A cells (CRL-1442, ATCC) were cultured in Ham F12 medium that contained 5% FCS. A 5-bromo-2′-deoxyuridine (BrdU) incorporation assay (BrdU labeling and detection kit, Roche Diagnostics) was used to monitor cell proliferation. Normal human thyroid tissues were obtained from surgical specimens taken from patients with papillary thyroid cancer; each patient gave written informed consent. Male Balb/c nude mice (aged 12 weeks) were obtained fromCLEA Japan, Inc., Tokyo, Japan. Each mouse was specific pathogen free and checked for pathogens once every 2 months. All studies performed were approved by the Animal Research Committee at the University of Yamanashi.

Plasmid construction and transfection

cDNAs were reverse transcribed from mRNA templates that had been isolated from BHP18-21v cells. Using this cDNA sample as template, RET/PTC1 cDNAs were PCR amplified with the following primers: sense, 5′-CTCCCTCCTCCTTTTCCCCAGGC-3′; and antisense, 5′-GCTCGGCCAATGTGACGTTCAC-3′. Amplified cDNAs were first ligated into a pCR2 vector (Invitrogen Co.) and then isolated insert cDNA was ligated into the KpnI/NotI site of pcDNA3.1-hygro (Invitrogen Co.) and an Eco RI insert that contained the full coding sequence (1.4 kb) was ligated into the pcDNA3.1zeo. Plasmid DNA (1 µg) was introduced into FRTL5 or BHP18-21v cells with the Gene Pulser (Gene Pulser Xcell; Bio-Rad) at 250 V-750 µF. Stable transfectants were selected by adding 300 µg/ml hygromycin B (Wako Pure Chemicals, Inc., Ltd., Osaka, Japan) or 100 µg/ml Zeocin (Life Technologies Co.) to the culture medium. TTF1 siRNA was expressed in cells from a pSilencer 4.1-CMV neo construct (Applied Biosystems, Inc.); to generate this TTF1 siRNA construct, two
oligonucleotides – 5′-GATTCACACGACTCCGTTCTCAGTTTCAAGAGAACTGACAACGGAGTCGTGTGCA-3′ and 5′-AGCTTGCACACGACTCCGTTGTCAGTTCTCTTGAAGACTGAGAACGGAGTCGTGTG-3′ (Kolla et al. 2007) – were annealed and ligated into the BamH1/HindIII site of pSilencer 4.1-CMV neo (Applied Biosystems, Inc.) (pSilencer-TR1). The construct or the pSilencer 4.1-CMV neo-negative control was introduced into cultured cells. Stable transformants were selected by adding 300 µg/ml geneticin (Sigma–Aldrich, Inc.) to the culture medium.

Quantitative PCR

The Rotor-Gene Q (Qiagen, Inc.) and 13 TaqMan probes (Applied Biosystems, Inc.) – rat Tg (Rn01458686_A1), rat Nis (Rn01420249_g1), rat Tshr (Rn00563612_A1), rat Ttf1 (Rn01512482_A1), rat Ttf2 (Foxe1) (Rn00594363_s1), rat Pax8 (Rn00579743_A1), rat Gapdh (Rn01775763_g1), human TTF1 (Hs00968940_m1), human TG (Hs00174974_m1), human thyroid peroxidase (TPO) (Hs00892519_m1), human NIS (Hs00166567_m1), human RET (Hs04259657_s1), and human GAPDH (Hs02758991_g1) – were used to perform quantitative PCR. Assays for each gene were carried out in triplicate, and transcript levels of thyroid-specific mRNA were normalized to those of GAPDH (human) or Gapdh (rat). Expression of GAPDH or Gapdh from the samples was within ±2 cycle number of threshold (Ct).

125I-uptake assay and TSH binding activity

The 125I-uptake by FRTL5 cells was measured as described previously (Endo et al. 1996). 125I scintigraphy of the tumors formed in nude mice was performed by injecting Na125I into the peritoneal space (Endo & Kobayashi 2010). Radioactivity was monitored with a BAS2500 image analyzer (Fuji Film Co., Tokyo, Japan). 125I-TSH binding activity in each cell population was measured using 125I-bovine TSH (Cosmic Co., Tokyo, Japan) and methods described by Mizutori et al. (2008).

Statistical analysis

The Student’s t-test and one-way ANOVA were used to assess the statistical differences between groups.

Figure 1

Morphology of FRTL (pcDNA) and FRTL (RET/PTC1) cells. Phase-contrast images of FRTL (pcDNA) cells cultured for 6 days in the presence of 1 mU/ml TSH (A) or absence of TSH (B). Hematoxylin–eosin-stained FRTL (pcDNA) cells cultured in the presence of TSH (C). Phase-contrast images of FRTL (RET/PTC1) cells cultured for 6 days in the presence of 1 mU/ml TSH (D) or absence of TSH (E). Hematoxylin–eosin-stained FRTL (RET/PTC1) cells cultured in the presence of TSH (F). Scale bars, 100 µm.
Results

Effects of RET/PTC1 on the morphology of FRTL5 cells

In the presence of TSH, FRTL5 cells transfected with the empty pcDNAhygro vector (FRTL (pcDNA) cells) were small and round and their cellular borders were well defined (Fig. 1A). When TSH was withdrawn from the medium, these control cells became flattened and the cell borders became obscured (Fig. 1B). We transfected pcDNAhygro-RET/PTC1 into FRTL5 cells and established stable lines (FRTL (RET/PTC1) cells). Quantitative RT-PCR using the plasmid DNA as a standard had revealed that $(4\pm0.6)\times10^5$ copies/µg RNA were transfected into the cells. When compared with FRTL (pcDNA) cells, FRTL (RET/PTC1) cells were enlarged and flattened even in the presence of TSH, and their cellular borders were obscured regardless of the presence or absence of TSH (Fig. 1D and E). FRTL (RET/PTC1) cells and control cells were stained with hematoxylin; the nuclei of the FRTL (RET/PTC1) cells were irregularly shaped and larger than those of FRTL (pcDNA) cells (Fig. 1C and F). The nuclei of FRTL (RET/PTC1) contained more nucleoli than did those of FRTL (pcDNA) cells (Fig. 1F).

Effects of RET/PTC1 on FRTL5 cell proliferation and function

Proliferation of FRTL (pcDNA) cells depends on TSH, and addition of dibutyryl cAMP mimics the effect of TSH (Fig. 2A; Vitti et al. 1983). However, there was no significant difference in growth of FRTL (RET/PTC1) cell cultured in the presence or absence of TSH (Fig. 2A). FRTL (RET/PTC1) cells were able to proliferate even in the absence of TSH; the doubling time of the transformed cells was about 18 h, which was shorter than that of FRTL (pcDNA) cells (24 h). Extracellular signal-regulated kinase (ERK) 1 and ERK2 in FRTL (pcDNA) cells were

Figure 2

Effects of RET/PTC1 on FRTL5 cell proliferation and function. (A) Growth curves of cultures of FRTL5 cells stably transfected with pcDNAhygro (FRTL (pcDNA)) (FRTL, left panel) or with pcDNA-RET/PTC1 (FRTL (RET/PTC1), right panel) in the presence (open circle–open circle) or absence (closed circle–closed circle) of 1 mU/ml TSH or in the presence of closed triangle–closed triangle: 1 mM dibutyryl cAMP. Data are mean ± S.E.M. of three independent experiments. *P<0.01, TSH (+) vs TSH (−). (B) Western blot analysis of ERK phosphorylation. FRTL (pcDNA) cells or FRTL (RET/PTC1) cells were cultured in the absence of TSH for 7 days, and then TSH (1 mU/ml) was added to the culture medium. FRTL (pcDNA) cells before (lane 1) and 3 min after the addition of TSH (lane 2). FRTL (RET/PTC1) cells before (lane 3) and 3 min after the addition of TSH (lane 4). M, molecular weight marker. (C) TSH binding activities of FRTL (RET/PTC1) cells and FRTL (pcDNA) cells. TSH binding activities of FRTL (RET/PTC1) cells (closed circle–closed circle), FRTL (pcDNA) cells (open circle–open circle), or BRL-3A rat liver cells (closed square–closed square) were studied using $^{125}$I-TSH as a tracer. Data are mean ± S.E.M. of triplicate wells of cells. (D) Iodide-uptake activities of FRTL (RET/PTC1) cells (closed circle–closed circle), FRTL (pcDNA) cells (open circle–open circle), or BRL-3A rat liver cells (closed square–closed square) were studied using $^{125}$I-TSH as a tracer. Data are mean ± S.E.M. of triplicate wells of cells.
phosphorylated only after the addition of TSH (lane 2), but both proteins were phosphorylated in the presence and in the absence of TSH in FRTL (RET/PTC1) cells (lanes 3–4) (Fig. 2B). FRTL (pcDNA) cells showed high-affinity TSH binding activity (Ka = 24 μU/ml). FRTL (RET/PTC1) cells also showed high-affinity TSH binding activity, but total binding activity of FRTL (RET/PTC1) cells was about 30% of that of FRTL (pcDNA) cells (Fig. 2C). In spite of the decreased TSH binding activity, 125I-uptake activity of FRTL (RET/PTC1) cells was about 300% of that of FRTL (pcDNA) cells (Fig. 2D).

Effects of RET/PTC1 on the expression of genes encoding thyroid-specific proteins in FRTL5 cells

We used quantitative RT-PCR to measure the expression of thyroid-specific mRNAs, such as Tg, Nis, or Tshr in FRTL (RET/PTC1) cells. When target-gene expression in FRTL (pcDNA) cells was defined as 1.0, expression of Tg and Nis mRNAs in FRTL (RET/PTC1) cells was 5.66 and 4.74 respectively; in contrast, expression of Tshr mRNAs in FRTL (RET/PTC1) cells was 0.26 (Table 1).

Table 1  Effects of RET-PTC1 on the expression of thyroid-specific genes in FRTL5 cells

<table>
<thead>
<tr>
<th>Gene</th>
<th>FRTL5 (pcDNA)</th>
<th>FRTL5 (RET-PTC1)</th>
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<tbody>
<tr>
<td>Tg/Gapdh</td>
<td>1.00</td>
<td>5.66±0.25*</td>
</tr>
<tr>
<td>Nis/Gapdh</td>
<td>1.00</td>
<td>4.74±0.25*</td>
</tr>
<tr>
<td>Tshr/Gapdh</td>
<td>1.00</td>
<td>0.26±0.04*</td>
</tr>
<tr>
<td>Ttf1/Gapdh</td>
<td>1.00</td>
<td>4.68±0.34*</td>
</tr>
<tr>
<td>Ttf2/Gapdh</td>
<td>1.00</td>
<td>0.97±0.24</td>
</tr>
<tr>
<td>Pax8/Gapdh</td>
<td>1.00</td>
<td>1.28±0.34</td>
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</table>

Data are mean±s.e.m. of three independent experiments. *P<0.01.

We then further transfected pSilencer (Ttf1) into FRTL (RET/PTC1) cells and established stable cell lines (FRTL (RET/PTC1)-siTtf1) by selecting with G418. When expression of Ttf1 in FRTL (pcDNA) cells was set to 1.0, the level of Ttf1 mRNA in FRTL (RET/PTC1)-siTtf1 cells was 0.81±0.042 and not significantly different from that in FRTL (pcDNA) cells.

Table 2  Tumor formation after injection of FRTL (RET/PTC1) cells

<table>
<thead>
<tr>
<th>Site of injection</th>
<th>Tumour formation</th>
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<tbody>
<tr>
<td>Subcutaneous left</td>
<td>Developed</td>
</tr>
<tr>
<td>Subcutaneous right</td>
<td>Did not develop</td>
</tr>
</tbody>
</table>

Tumor formation was evident at the site of FRTL (RET/PTC1) cell injection in six of ten mice, but one mouse did not have a tumor form at the site of FRTL (pcDNA) cell injection. By 4 months after injection, each mouse (n=9) had developed a tumor at the site of FRTL (RET/PTC1) cell injection, and the mean of the maximum tumor diameter was 24±4.5 mm (Fig. 3A). By contrast, no tumor formation was evident at sites of FRTL (pcDNA) cell injection even 4 months after injection (Table 2).

Effects of TTF1 on the human thyroid papillary cancer cell line BHP18-21v

BHP18-21v cells are derived from a PTC, and they express RET/PTC1. They also express PAX8 but not TTF1 or TG. Previously, we found that adenovirus-mediated transfer of Ttf1 into BHP18-21v cells induces re-expression of TG and TPO (Furuya et al. 2004). However, expression of TTF1 via this method is transient; therefore, we introduced pcDNAzeo-hTTF1 into BHP18-21v cells to generate BHP18-21v (TTF1) cells that stably express TTF1. We then used BHP18-21v (pcDNA) and BHP18-21v (TTF1)
cells to study the effect of TTF1 on tumorigenicity. Quantitative PCR using the plasmid as a standard revealed that (6.2 ± 0.62) × 10^5 copies/µg RNA of TTF1 (n = 3) were transfected into BHP18-21v (TTF1) cells. When TTF1 expression in normal human thyroid glands was defined as 1.0, TTF1 expression in BHP18-21v (TTF1) cells was 0.84 ± 0.06. Expressions of TG and TPO genes were undetectable in BHP18-21v (pcDNA), but these genes were re-expressed at (0.51 ± 0.06) (n = 3) and (0.28 ± 0.03) (n = 3) respectively in BHP18-21v (TTF1) cells (Fig. 4A). But, TTF1 showed little effect on NIS or TSHR gene expression in stably transfected cells as was observed in the transiently transfected cells BHP18-21v (Ad-TTF1) (Furuya et al. 2004). There was no significant difference in cell growth (Fig. 4B) or in BrdU incorporation (Fig. 4C) between BHP18-21v (pcDNA) and BHP18-21v (TTF1) cells. TTF1 also showed little effect on the morphology of BHP18-21v cells (Fig. 4D and E).

To investigate the effect of co-expression of TTF1 and RET/PTC1 on the tumorigenicity of BHP18-21v cells,

<table>
<thead>
<tr>
<th>Tumorigenicity of FRTL5 cells in nude mice</th>
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<tr>
<td><strong>Ttf1 expression</strong></td>
</tr>
<tr>
<td>FRTL5 (pcDNA)</td>
</tr>
<tr>
<td>FRTL5 (RET-PTC1)</td>
</tr>
<tr>
<td>FRTL5 (RET-PTC1) + pSilenc-TTF1</td>
</tr>
</tbody>
</table>

Data are mean ± s.e.m. of three independent experiments. *P < 0.001 vs FRTL5 (pcDNA).

Expression of TTF1 mRNA in FRTL (pcDNA) cells was set as 1.0.
Figure 4
Effects of TTF1 on thyroid-specific gene expression in, cell growth of and, morphology of BHP18-21v cells. (A) Effects of TTF1 on thyroid-specific gene expression in BHP18-21v cells. pcDNAzeo-hTTF1 was stably transfected into BHP18-21v cells, and expression levels of five thyroid-specific genes (TTF1, Tg, TPO, NIS, and TSHR) in the cells were determined by quantitative PCR. Expression of each gene of interest in human thyroid glands was normalized to that of GAPDH, and these values were set as 1.0 for comparisons with expression in BHP18-21v (pcDNA) cells or BHP18-21v (TTF1) cells. NA, no product could be amplified. (B) Growth curves of BHP18-21v (TTF1) (open circle–open circle: n = 3) cells and of BHP18-21v (pcDNA) cells (closed circle–closed circle: n = 3). (C) Incorporation of BrdU into BHP18-21v (TTF1) (open column) cells or into BHP18-21v (pcDNA) cells (closed column) 48 h after addition of BrdU. Microscopic views of BHP18-21v (pcDNA) cells (D) or BHP18-21v (TTF1) cells (E). Scale bars, 100 μm.
we transplanted BHP18-21v (TTF1) cells into subcutaneous tissues on the right side and BHP18-21v (pcDNA) cells on the left sides of the backs of Balb/c nude mice. After 2 weeks, tumor formation was evident at the site of BHP18-21v (TTF1) cells injection in each of the eight mice, but not one mouse had a tumor form at the site of BHP18-21v (pcDNA) cell injection. After 4 weeks, all mice (n=8) had developed a large solid mass at the site of BHP18-21v (pcDNA) cell injection, and the mean of the maximum tumor diameter was 25±5.5 mm (Fig. 5A and Table 3). At this 4-week time point, three of the eight mice had developed a tumor at the site of BHP18-21v (pcDNA) cell injection, and the mean of the maximum tumor diameter was 8±2.1 mm for these three tumors. Notably, the mean of the maximum tumor diameter was significantly larger (P<0.01) for the BHP18-21v (TTF1) tumors than for the BHP18-21v (pcDNA) tumors. Figure 5A, B, and C shows macroscopic and microscopic views of tumors derived from injected BHP18-21v (TTF1) and BHP18-21v (pcDNA) cells. Histologically, no glandular structure was observed in tumors from BHP18-21v (TTF1) or from BHP18-21v (pcDNA) cells. Notably, BHP18-21v (TTF1) cells had infiltrated into surrounding skeletal muscles within 4 weeks, but BHP18-21v (pcDNA) cells had not.

Table 3  Tumorigenicity of BHP19-21v cell derivatives in nude mice

<table>
<thead>
<tr>
<th></th>
<th>Tumor formation at 2 weeks (mean of maximum diameter of tumors (mm))</th>
<th>Tumor formation at 3 weeks (mean of maximum diameter of tumors (mm))</th>
<th>Tumor formation at 4 weeks (mean of maximum diameter of tumors (mm))</th>
</tr>
</thead>
<tbody>
<tr>
<td>BHP18-21v (pcDNA)</td>
<td>0/8</td>
<td>1/8</td>
<td>3/8 (8.1±2.1)</td>
</tr>
<tr>
<td>BHP18-21v (TTF1)</td>
<td>8/8* (12.3±2.4)*</td>
<td>8/8* (17.8±3.9)*</td>
<td>8/8* (25.0±5.5)*</td>
</tr>
</tbody>
</table>

*P<0.001 vs BHP18-21v (pcDNA).

Discussion

We used FRTL5 cells for this study because these cells express almost every thyroid-specific gene – including Tg, Nis, and Tshr, as well as the thyroid-specific transcription factors, Ttf1, Ttf2, and Pax8 (Santisteban et al. 1987). Expression of RET/PTC1 in FRTL5 cells caused nuclei to become irregularly shaped and cell proliferation to become independent of TSH. These changes indicated that expression of RET/PTC1 was sufficient to cause FRTL5 cells to develop malignant phenotypes.

Additionally, De Vita and colleagues expressed RET/PTC1 in PC Cl cells, another line of rat thyroid
epithelial cells. Pax8 expression was significantly lower in PC CI (RET/PTC1) cells than in the parental PC CI cells, but TTF1 expression was essentially unaltered by RET/PTC1 expression; function of TTF1 might be inactive (De Vita et al. 1998). By contrast, we demonstrated that RET/PTC1 increased the expression of Ttfl, Tg, and Nis in FRTL5 cells, but RET/PTC1 had little or no effect on Ttf2 and Pax8 expression. These results indicated that TTF1 functions in FRTL5 cells. Therefore, the results reported by De Vita et al. seem to conflict with our findings.

FRTL5 and PC CI cells present similar sets of properties, including i) TSH-dependent growth and differentiated functions, ii) iodine-uptake, and iii) Tg and Tpo gene transcription. The transformation of PC CI cells requires a combination of two retroviral oncogenes, but one oncogene is sufficient to fully transform FRTL5 cells; this difference indicates that FRTL5 cells may intrinsically express some oncogenic function that contribute to a fully malignant phenotype, but PC CI cells may lack this function (Fusco et al. 1987). Although the discrepancy between our results and those of De Vita remains unresolved, it might due to a difference in the precancerous condition of PC CI cell and that of FRTL5 cells.

TTF1 is a master regulator of the expression of Tg and NIS (Sinclair et al. 1990, Endo et al. 1997), and increased levels of Tg and Nis in FRTL (RET/PTC1) cells might be due to increased expression of TTF1. Indeed, when FRTL (RET/PTC1) cells were transplanted into the subcutaneous tissue of nude mice, the resulting tumor cells retained 125I-uptake activity, as do some human papillary thyroid cancer tissues. These findings were consistent with the findings that human PTCs that expressed RET/PTC1 maintained Nis gene expression, but those that expressed BRAFV600E did not (Romei et al. 2008).

It is of particular interest that FRTL (RET/PTC1) cells were tumorigenic in nude mice, in spite of the fact that FRTL (pcDNA) cells were not. Further, when TTF1 gene expression was silenced by siTTF1, FRTL (RET/PTC1) cells failed to form tumors in nude mice. Similarly, TF1 was also important to the tumorigenicity of BHP18-21v cells. These cells lacked intrinsic TTF1 expression; however, stable expression of TTF1 from a transgenic expression construct increased Tg and TPO mRNA levels in cultures of these cells; moreover, transgenic expression of TTF1 enhanced tumorigenicity of these cells when they were transplanted into nude mice. These results indicated that the oncoprotein, RET/PTC1, and the thyroid-specific transcription factor, TTF1, might interact and consequently affect the tumorigenicity of PTCs.

Therefore, our present results might provide a new insight into the roles of the oncoprotein, RET/PTC1, and thyroid-specific transcription factor, TTF1, in the pathogenesis of PTCs.

Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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