High Prevalence of BRAF Gene Mutation in Papillary Thyroid Carcinomas and Thyroid Tumor Cell Lines

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ABSTRACT

The RAS-RAF-MEK-ERK-MAP kinase pathway mediates the cellular response to extracellular signals that regulate cell proliferation, differentiation, and apoptosis. Mutation of the RAS proto-oncogene occurs in various thyroid neoplasms such as papillary thyroid carcinomas (PTCs), follicular thyroid adenomas and carcinomas. A second genetic alteration frequently involved in PTC is RET/PTC rearrangements. Recent studies have shown that BRAF, which is a downstream signaling molecule of RET and RAS, is frequently mutated in melanomas. This study tests whether BRAF is also mutated in thyroid tumors and cell lines. We analyzed BRAF gene mutation at codon 599 in thyroid tumors using mutant-allele-specific PCR and in 10 thyroid tumor cell lines by DNA sequencing of the PCR-amplified exon 15. We found that BRAF was mutated in 8 of 10 thyroid tumor cell lines, including 2 of 2 papillary carcinoma cell lines, 4 of 5 anaplastic carcinoma cell lines, 1 of 2 follicular carcinoma cell lines, and 1 follicular adenoma cell line. BRAF mutation at codon 599 was detected in 21 of 56 PTC (38%) but not in 18 follicular adenomas and 6 goiters. BRAF mutation occurred in PTC at a significantly higher frequency in male patients than in female patients. To test whether BRAF mutation may cooperate with RET/PTC rearrangements in the oncogenesis of PTC, we tested whether BRAF-mutated PTCs were also positive for RET/PTC rearrangements. Immunohistochemical staining was conducted to evaluate RET/PTC rearrangements by using two different anti-RET antibodies. Surprisingly, we found that a large number of BRAF-mutated PTCs (8 of 21) also expressed RET, indicating that the RET proto-oncogene is rearranged in these BRAF-mutated PTCs. These observations suggest that mutated BRAF gene may cooperate with RET/PTC to induce the oncogenesis of PTC.

INTRODUCTION

Thyroid cancer is the most common endocrine neoplasm in the United States. Tumors derived from thyroid epithelial cells display diverse neoplastic phenotypes, including benign follicular adenomas, well-differentiated papillary and follicular carcinomas, and aggressive anaplastic carcinomas (1). Both genetic and epigenetic alterations are involved in the initiation and progression of thyroid carcinomas. Mutation of the thyroid hormone receptor gene (2) or proto-oncogenes (3–5) and all three proto-oncogenes (KRAS, HRAS, and NRAS) are found in both benign and malignant thyroid neoplasms (6–18). Mutation and activation of these genes play an important role in the early steps of thyroid tumor progression (19). In contrast, rearrangement and point mutation of the protein tyrosine kinase receptors, RET and TRK, are not found in benign follicular adenomas but are restricted to PTCs (19)–(24). TP53 tumor suppressor gene mutations are not present in benign adenomas nor in papillary carcinomas but are present in poorly differentiated and anaplastic carcinomas (25–28). Epigenetic alterations of tumor suppressor genes P15INK4B and P16INK4A through aberrant DNA methylation that silences gene expression is common in primary thyroid tumors and is an early event in thyroid tumorigenesis (29). p27, a potential tumor suppressor gene that belongs to the Kip/Cip cyclin-dependent kinase inhibitor family, is not mutated in thyroid tumors, but its expression is retained in the cytoplasm, which eliminates its effect in blocking cell cycle progression (30).

Davies et al. (31) recently reported that somatic missense BRAF mutation occurs in 66% of malignant melanomas and at low frequencies in many human cancers, including ~11% of colon cancers, 14% of borderline ovarian cancers, and 0.5% of sarcomas. Mutations are restricted to the kinase domain of the BRAF gene at multiple sites located in exons 11 and 15. However, >80% of these mutations are attributable to a single-base thymidine substitution at the nucleotide position 1796 with adenosine, which leads to the conversion of valine at codon 599 to glutamic acid. These investigators did not find BRAF mutation in 33 breast, 23 prostate, 14 lung, and 19 head and neck squamous cell carcinomas, and 15 gliomas. It appears that BRAF mutations tend to occur in tumors that harbor RAS mutations at a higher frequency. Because RAS oncogenes are mutated in ~30% of spontaneous thyroid tumors (6, 32), it is possible that BRAF may be mutated in thyroid neoplasms at high frequency too. Here, we report that BRAF mutation at V599E occurred in 21 of 56 papillary thyroid carcinomas (38%). However, BRAF mutation at this site was not detected in any of 18 FTAs examined. These observations suggest that BRAF mutation may be involved in the oncogenesis of papillary thyroid carcinomas but not involved in the formation of benign FTAs.

MATERIALS AND METHODS

Tumor Specimens and Patient Information. Paraffin-embedded tumor blocks from thyroidectomy specimens of patients with thyroid neoplasms were retrieved for analysis of BRAF gene mutation upon approval by the Institutional Review Board of Rush Presbyterian St. Luke’s Medical Center. A total of 80 specimens, all with adequate clinical and pathological information, was studied. These included 56 papillary carcinomas, 18 follicular adenomas, and 6 benign nodular goiters. The presence of metastases was determined by reviewing the patients’ medical records, pathology reports, and subsequent clinical courses. Patients were staged using the tumor-node-metastasis system and classified according to the presence of extrathyroidal extension, cervical nodes, and distant metastases. Nontumor tissue blocks (lymph nodes, parathyroid, and thyroid) from 20 patients with BRAF-mutated PTC were sectioned and used for genomic DNA extraction followed by PCR analysis of BRAF mutation.

Cell Lines. Ten thyroid tumor cell lines were used in this study (Table 1). One follicular adenoma (KAK-1), 1 papillary carcinoma (KAT-10), and 3 anaplastic (KAT-4, KAT-18, and SW1736) carcinoma cell lines were originally established in Dr. Ain’s laboratory and have been described previously (33). The other 5 thyroid tumor cell lines, including 1 papillary (NPA87), 2 follicular (WRO82 and MRO87), and 2 anaplastic carcinomas (ARO81 and DRO90), were kindly provided by Dr. G. F. Juillard at University of California at Los Angeles. All thyroid tumor cell lines were grown in complete RPMI 1640 containing 10% fetal bovine serum.

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3 The abbreviations used are: PTC, papillary thyroid carcinoma; FTA, follicular thyroid adenoma; IHC, immunohistochemistry; MMA, mutant-allele-specific amplification; mAb, monoclonal antibody.
Genomic DNA Extraction and PCR Amplification of Exon 15 of the BRAF Gene and Exons 1 and 2 of the NRAS Gene. Genomic DNA from paraffin-embedded tissues were extracted using a standard protocol. Briefly, one set of slides was stained with H&E and examined microscopically by a pathologist with expertise in thyroid disease. Tumor areas were marked and matched with a dewaxed but unstained set of slides. Tumor areas were dissected from unstained slides and transferred into an Eppendorf tube followed by proteinase K digestion at 56°C overnight and DNA extraction with a standard protocol. Briefly, genomic DNA extraction from thyroid tumor cell lines and blood of one patient was conducted by using Qiagen genomic DNA extraction kit following the manufacturer’s instructions. DNA concentration was quantitated by A260 absorbance in a spectrophotometer. Exon 15 of the BRAF gene was amplified with two primers in the introns flanking it. The sequence of the forward primer is 5'-TGTAATGGGCTGCTGATAGGA-3' and the sequence of the reverse primer is 5'-GGCCTCACCTCTATGGTG-3'. Genomic DNA (100 ng/sample) was used as the template to amplify exon 15. The PCR reaction was set with an initial denaturation of 2 min at 94°C and subsequent denaturation for 30 s at 94°C, annealing for 45 s at 55°C, and extension for 45 s at 72°C. Thirty-five cycles were used to apply the PCR product with the expected size of 215 bp. Exon 1 of the NRAS gene was similarly amplified with a forward primer (5'-GACTGATACAAACCTGGTTG-3') and a reverse primer (5'-GGGCTCCACCTCTATGGTG-3'); exon 2 of the NRAS gene was amplified with a forward primer (5'-GGTGAAAACCTGGTTGTTGG-3') and a reverse primer (5'-ATACACAGAGGAGGCTTGG-3'). BRAF and NRAS mutations were detected using sequencing the PCR products at the CRC-DNA sequencing facility of the University of Chicago.

**RESULTS**

**BRAF Gene Mutation in Thyroid Tumor Cell Lines.** We first analyzed BRAF gene mutation in 10 thyroid tumor cell lines by sequencing the PCR-amplified exon 15 of the **BRAF** gene. As shown in Fig. 1 and Table 1, 2 anaplastic thyroid carcinoma cell lines, AR081 and DRO90, harbored a homozygous **BRAF** mutation at the nucleotide position 1796 where an adenosine was replaced by a thymidine, leading to the substitution of valine at 599 with glutamic acid. In the other 6 thyroid tumor cell lines (Table 1; 1 follicular adenoma, 2 anaplastic, 2 papillary, and 1 follicular carcinoma cell lines), only one allele of the **BRAF** gene was mutated at this site (Fig. 1 and Table 1). No mutation at T1796 was detected in an anaplastic cancer cell line (KAT18) and a follicular carcinoma cell line (WRO82; Fig. 1 and Table 1). No other point mutation within exon 15 was detected. Overall, our results show that 8 of 10 thyroid tumor cell lines originally established in two laboratories (Dr. Guy J. F. Juillard, University of California at Los Angeles; Dr. Kenneth B. Ain, University of Kentucky Medical Center) contained **BRAF** gene mutation at the T1796 nucleotide position. This suggests that **BRAF** may be mutated at high frequency in thyroid neoplasms.

**Somatic BRAF Mutation in Thyroid Neoplasms.** We sought to analyze **BRAF** mutation in benign follicular adenomas and papillary thyroid carcinomas using PCR-based MASA to detect the hot-spot **BRAF** mutation at the T1796 site. A PCR primer with two mismatches at the 3'-end was used to amplify mutant **BRAF**, whereas a control primer derived from wild-type **BRAF** gene that amplifies both wild-type and T1796 mutant **BRAF** was used as a control. We first tested the feasibility of this method to detect **BRAF** mutation at the T1796 site in well-characterized thyroid tumor cell lines. As shown in Fig. 1B, the **BRAF** exon 15 was amplified by using the mismatched primer in 4 **BRAF**-mutant thyroid tumor cell lines (DRO90 and AR081 with homozygous mutation; NPA87 and MRO87 with heterozygous mutation) but not in 2 wild-type cell lines (WRO82 and KAT18). A PCR reaction that amplifies **BRAF** exon 15 was included as a positive control. **BRAF** exon 15 was amplified in all samples. These results suggest that screening of **BRAF** mutation using this MASA-PCR is specific, and this approach can be used to rapidly screen **BRAF** mutation at codon 599 in a large number of tumor samples.

We next analyzed **BRAF** mutation in microdissected thyroid tumor tissues by using MASA. As shown in Fig. 2A, **BRAF** mutation at...
T1796 was detected in 21 of 56 papillary carcinomas but not detected in 18 benign follicular adenomas and 6 nodular goiters. All negative DNA samples were reanalyzed for BRAF mutation by PCR reaction with 40 cycles, no BRAF mutation was found. Nine of 21 positive samples were randomly selected for DNA sequencing to confirm BRAF mutation. All 9 samples were positive with BRAF mutation. Shown in Fig. 2B are three representative DNA sequences of BRAF-mutated samples, two of which had almost equal peak areas of A and T nucleotides, indicating a high homogeneity of tumor cells in these two microdissected sections. A third sample had a smaller A peak than T peak, reflecting heterogeneity of tumor cells and nontumor cells in the microdissected section. Nevertheless, these sequencing data additionally suggest that BRAF mutation detected by MASA is reliable and specific.

To test whether BRAF mutation in these PTC is somatically acquired, MASA-PCR was carried out to analyze BRAF mutation using the genomic DNA from normal tissues such as lymph nodes, parathyroid, or thyroid, which were separately embedded in paraffin tissue blocks. There was no BRAF mutation detected in all 20 normal tissues derived from patients with BRAF-mutated PTC (data not shown). One patient with BRAF-mutated PTC also developed melanoma at the time of thyroidec-tomy and thus was highly suspicious of a germ-line BRAF mutation. However, direct sequencing of PCR-amplified exon 15 of the BRAF gene derived from normal tissue confirmed that there was no germ-line BRAF mutation. In another patient with BRAF-mutated PTC, genomic DNA from peripheral blood was used in MASA-PCR to analyze for BRAF mutation. Again, no germ-line BRAF mutation was present in this patient. Thus, we concluded that BRAF mutation in all 21 PTC cases was somatic. Higher Frequency of BRAF Mutation in Male Patients than in Female Patients with PTC. We analyzed whether BRAF mutation correlated with patient age, gender, and tumor stage. Interestingly, we found that BRAF mutation occurred in 9 of 14 male PTC patients and in 12 of 42 female patients (Table 2). Statistical analysis revealed that BRAF mutation occurred at a significantly higher frequency in male patients than in female patients (P < 0.05). In addition, we found that BRAF mutation occurred in 15 of 33 PTC patients older than 40 years old and in only 6 of 23 PTC patients younger than 40 years old. BRAF mutation in patients with PTC tended to occur at a higher frequency in older patients than in younger patients, but this was not a significant difference (P > 0.05). We did not find that BRAF mutation was associated with tumor volume (Table 2). BRAF was mutated at a higher rate in PTC with invasive and metastatic potential (Table 2) than in the noninvasive tumors, but again, this was not statistically significant (P > 0.05).

Overlapping of BRAF Mutation with other Genetic Alterations in PTC. RET/PTC rearrangements frequently occur in papillary thyroid carcinomas. To test whether BRAF mutation concurs with RET/PTC rearrangements, we conducted IHC to determine the status of RET/PTC rearrangement. IHC analysis using an anti-RET rabbit serum revealed that RET/PTC expression was abundantly present in the cytoplasm of the tumor cells in a BRAF-mutated specimen (Fig. 3A, inset) and a PTC with wild-type BRAF but not in the neighboring normal thyroid follicular cells (Fig. 3A). Similar results were obtained when an anti-RET mAb was used (Fig. 3, C and D). Normal mouse IgG and normal rabbit serum included as negative controls did not show any positive signal (data not shown). All samples analyzed for RET/PTC expression using anti-RET rabbit serum were additionally tested for RET/PTC expression by IHC with an anti-RET mAb. We found that RET/PTC expression was consistent in 85% of the specimens. The samples graded as having RET/PTC expression with either method were considered as RET/PTC positive.

We next analyzed whether RET/PTC rearrangements were overlapping with BRAF mutation in PTC. As shown in Table 3, we found that 21 of 56 PTCs (38%) were RET/PTC positive. Among them, 13 of 35 PTCs (37%) with wild-type BRAF were RET/PTC positive. Unexpectedly, we found that 8 of 21 BRAF-mutated samples (38%) were also RET/PTC positive, suggesting that BRAF mutation and RET/PTC rearrangements are overlapping in a large number of PTC.

All three RAS oncogenes (NRAS, KRAS, and HRAS) were equally mutated in thyroid neoplasms. In this study, we selectively analyzed NRAS mutation in BRAF-mutated PTC to determine whether BRAF and NRAS mutations were overlapping. Exons 1 and 2 of the NRAS gene were amplified individually, and the PCR products were directly
sequenced to monitor NRAS mutation at codons 12 and 13 in exon 1 and at codon 61 in exon 2. As shown in Table 3, we did not find any NRAS mutations in all 21 BRAF-mutated specimens, indicating that there is no overlapping in NRAS and BRAF mutations in these PTC. Because KRAS and HRAS mutations were not analyzed in this study, we could not exclude the possibility that KRAS and HRAS mutation might be overlapping with BRAF mutation. However, a recent study by Kimura et al. (39) demonstrated that 28 BRAF-mutated PTCs did not contain any form of mutated RAS genes.

**DISCUSSION**

Recent studies have demonstrated that BRAF mutation at codon 599 comprises ~80–90% of all mutations detected in several types of tumors, in particular in melanomas and colon cancers (31, 40). Several other sites in the kinase domain of BRAF in exons 11 and 15 can also be mutated but with much lower frequency (31, 40). Our present study using MASA demonstrated that BRAF mutation at the hot-spot codon 599 occurred in 21 of 56 papillary carcinomas (38%). While our manuscript was being revised, Kimura et al. (39) reported that BRAF mutation occurs in 28 of 78 PTCs (35.8%) and that all mutations are located at codon 599. Thus, these observations collectively suggest that the rate of BRAF mutation in PTC is the second highest to that in melanomas (>60%; Refs. 31, 41, 42) and is much higher than other cancers such as colorectal adenocarcinomas (5–10%; Refs. 31, 40, 43) and lung cancers (1.8%; Ref. 44).

Although our present study revealed that BRAF was mutated in 38% of PTC at codon 599, we did not find BRAF mutation at this site.
in any of 18 follicular adenomas studied. Statistical analysis revealed that BRAF was differentially mutated in these two different types of thyroid neoplasms (Table 1; \( P = 0.006 \)). Consistent with this observation, Kimura et al. (39) reported that no BRAF mutation was detected in 14 FTAs, as well as in 10 follicular thyroid carcinomas. These observations are in sharp contrast to previous studies showing that the upstream activators of BRAF, the \( RAS \) genes (HRAS, KRAS, and NRAS), are mutated in both benign FTAs and papillary thyroid carcinomas (10, 45, 46). It is not clear why BRAF is only mutated in papillary thyroid carcinomas but not in FTs, whereas \( RAS \) is mutated in both benign and malignant thyroid neoplasms. Nevertheless, a higher BRAF mutation rate in carcinomas than in adenomas was also observed in another type of tumor: Rajagopalan et al. (40) reported that BRAF is mutated in 30 of 276 clinical colon cancers (11%) but is mutated in only 2 of 54 colon adenomas (3.8%); Similarly, Yuen et al. (43) reported that BRAF is mutated in 11 of 215 colorectal adenocarcinomas (5.1%) and in 3 of 108 (2.8%) sporadic adenomas.

The RET proto-oncogene is rearranged in ~40% of spontaneous PTC when analyzed by IHC staining and/or reverse transcription-PCR followed by Southern hybridization (36–38) and with a much higher rate in radiation-associated PTC (56–84%) as well as in pediatric PTCs (70%; Ref. 47). A few prior studies demonstrated that combined RET/PTC rearrangements or \( TSHR \) and \( RAS \) mutation can occur in papillary thyroid carcinomas (18, 46, 48–50). For example, Bounacer et al. (48) reported that combined \( RAS \) mutation and RET/PTC rearrangements are detected in 2 of 28 radiation-associated thyroid tumors. In another study, Sugg et al. (50) analyzed genetic alterations in 20 PTCs and found one of them harboring both NRAS mutation and a \( RET/PTC3 \) rearrangement. In this study, we tested whether BRAF mutation would occur together with RET/PTC rearrangements in PTC.

To our surprise, IHC analysis revealed that a large number (8 of 21) of BRAF-mutated PTC-expressed RET, indicating that the RET proto-oncogene is rearranged in these tumors. This observation is totally unexpected not only because it contradicts recent studies showing that BRAF mutation at codon 599 does not overlap with RET/PTC rearrangements nor with \( RAS \) mutation (39) in PTC, as well as in other malignancies such as melanomas and colorectal adenocarcinomas (31, 40, 43) but also because two combined genetic alterations in the same signaling pathway appear to be redundant and therefore to be unnecessary. Nevertheless, based on our observation that 38% of the 21 BRAF-mutated PTCs also harbored RET/PTC rearrangements, we speculate that RET/PTC may cooperate with mutated BRAF to induce clinically overt PTC (24). In fact, both mutant BRAF gene and RET/PTC have a relatively low oncogenic potential. For example, the oncogenic potential of mutant BRAF gene is ~50-fold lower than V12 HRAS when tested in NIH3T3 cells (31), whereas RET/PTC is unable to fully transform the rat thyroid PC Cl3 cells (e.g., unable to grow in soft agar and to develop tumorigenicity in athymic mice) but can cooperate with \( RAS \) oncogenes to fully transform PC Cl3 cells (24). It is possible that BRAF may cooperate with RET/PTC to fully transform thyroid epithelial cells, leading to the progression of occult malignancies such as melanomas and colorectal adenocarcinomas (31, 40, 43).

### Table 2. BRAF gene mutation in thyroid neoplasms

<table>
<thead>
<tr>
<th>Tumor type</th>
<th>No.</th>
<th>Positive (%)</th>
<th>( P )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Follicular adenoma</td>
<td>18</td>
<td>0 (0%)</td>
<td></td>
</tr>
<tr>
<td>Papillary carcinoma</td>
<td>56</td>
<td>21 (38%)</td>
<td>0.006</td>
</tr>
<tr>
<td>Tumor stage (PTC)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>( T_1 )</td>
<td>10</td>
<td>4 (40%)</td>
<td>&gt;0.05</td>
</tr>
<tr>
<td>( T_2 )</td>
<td>35</td>
<td>13 (37%)</td>
<td></td>
</tr>
<tr>
<td>( T_3 )</td>
<td>11</td>
<td>4 (36%)</td>
<td></td>
</tr>
<tr>
<td>Age (PTC)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;40 years</td>
<td>23</td>
<td>6 (26%)</td>
<td></td>
</tr>
<tr>
<td>&gt;40 years</td>
<td>33</td>
<td>15 (46%)</td>
<td>0.233</td>
</tr>
<tr>
<td>Gender (PTC)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>14</td>
<td>9 (64%)</td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td>42</td>
<td>12 (27%)</td>
<td>0.038</td>
</tr>
<tr>
<td>Node metastasis (PTC)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>13</td>
<td>7 (54%)</td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>44</td>
<td>14 (32%)</td>
<td>0.288</td>
</tr>
</tbody>
</table>

### Table 3. Overlapping of BRAF mutation with other genetic alterations in PTC

| BRAF mutation | No. of tumors | RET/PTC positive | \( NRAS \) mutation
<table>
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<tr>
<th></th>
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</thead>
<tbody>
<tr>
<td>Yes</td>
<td>21</td>
<td>8 (38%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>No</td>
<td>35</td>
<td>13 (37%)</td>
<td>ND(^ab)</td>
</tr>
<tr>
<td>Total</td>
<td>56</td>
<td>21 (38%)</td>
<td>ND(^ab)</td>
</tr>
</tbody>
</table>

\(^a\) Exons 1 and 2 of the \( NRAS \) gene were PCR amplified individually and sequenced to detect \( NRAS \) mutation at codons 12, 13, and 61.

\(^b\) ND, not done.
microcarcinomas, which have a very high rate of RET/PTC rearrangements (>70%), into clinically overt papillary thyroid carcinomas. Bearing in mind that concomitant BRAF mutation and RET/PTC rearrangements were not confirmed in a similar study recently published by Kimura et al. (39), this double-hit model should be taken with caution.

Detailed mutation analyses in a variety of tumors by Davies et al. (31) demonstrated that BRAF is generally mutated at a higher frequency in tumor cell lines than that in their corresponding tumor samples. For example, these investigators reported that BRAF is mutated in 7 of 40 colon cancer cell lines (18%), 5 of 59 sarcoma cell lines (9%), 4 of 38 glioma cell lines, and 4 of 131 lung cancer cell lines. In contrast, BRAF mutation is only detected in 4 of 33 colon cancers (12%), 1 of 182 sarcomas (0.5%), and none of the 15 gliomas and 14 lung cancers (31). Our present study demonstrated that BRAF was mutated overall in 8 of 10 thyroid tumor cell lines (80%), including one follicular adenoma cell line, whereas BRAF was only mutated in 38% of papillary thyroid carcinomas. The higher BRAF mutation rate in tumor cell lines than in their corresponding tumor specimens may be attributable to: (a) the cell lines from the original tumors with BRAF mutations may be selectively established because of an advantage in cell growth (31) and an antiapoptotic effect (51); (b) established cell lines are homogenous, whereas microdissected tumor sections contain many normal cells such as stromal cells, endothelial cells, and infiltrating immune cells. Therefore, a low percentage of tumor cells in a specimen may lower the sensitivity of the methods used to detect BRAF mutation, resulting in a false negative result; and (c) BRAF mutation in cell lines may be gained during long-term in vitro cell culture.

The molecular mechanisms by which BRAF is mutated at high frequency in melanoma and papillary thyroid carcinomas are not known. Davies et al. (31) proposed that BRAF mutation in melanoma is somehow related to features of melanocyte biology. This supposition is based on the observations that besides the RAS signaling pathway, BRAF in melanocytes can be directly activated by cyclic AMP, a secondary messenger regulated by binding of α-melanocyte stimulating-hormone, and other proopiomelanocortin-derived peptides to their melanocortin receptor I (52, 53). This alternative BRAF activation pathway plays a critical role in controlling melanocyte proliferation and differentiation, particularly in response to UVB radiation (52, 53). Interestingly, in thyrocytes, thyroid-stimulating hormone strongly activates cyclic AMP and promotes thyrocyte cell proliferation (54–57). Therefore, it is likely that mutation of BRAF in melanocytes and thyrocytes may be related to cyclic AMP, although how exactly cyclic AMP results in BRAF gene mutation remains elusive. In colon cancer, Rajagopalan et al. (40) reported that BRAF mutation is associated with the deficiency of mismatch repair. Although it is not clear whether mismatch repair activity is also compromised or deficient in papillary thyroid carcinomas, β-catenin, another gene frequently mutated in colon cancer because of the deficiency of mismatch-repair, is also mutated in papillary thyroid carcinomas (58). Therefore, it is possible that BRAF mutation in papillary thyroid carcinomas may, in part, result from the defective DNA mismatch repair.

Another interesting observation in this study is that among 8 mutant thyroid tumor cell lines, 6 were heterozygous (Table 2). The other two cell lines (ARO81 and DRO90) were either homozygous because of gene conversion or hemizygous because of the loss of a second allele of the BRAF gene. Similar to this observation, Rajagopalan et al. (40) found that 2 of 28 colon adenocarcinomas with BRAF mutation at residue 599 were not heterozygous. The underlying mechanism for this nonheterozygous BRAF gene mutation and its role in triggering cell transformation and tumorigenesis remain to be defined.

In summary, our present study demonstrates that BRAF was mutated at a high frequency in papillary thyroid carcinomas but not in follicular adenomas and that a large number of BRAF-mutated PTCD also harbored RET/PTC rearrangements. These observations provide a molecular basis for the oncogenesis of PTC and suggest that PTC and FTA may be developed through the mutation of different oncogenes within the same signaling pathway. It will be interesting to find out whether quantitative and/or qualitative differences in the RAS/BRAF-signaling pathway determine the type of thyroid neoplasm.

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