Clinical, genetic, and immunohistochemical characterization of 70 Ukrainian adult cases with post-Chornobyl papillary thyroid carcinoma

Andrii Dinets1,2,3, Mykola Hulchiy3, Anastasios Sofiadis1,2, Mehran Ghaderi4, Anders Höög4,5, Catharina Larsson1,2 and Jan Zedenius4

1Department of Molecular Medicine and Surgery, Karolinska Institutet and 2Center for Molecular Medicine, Karolinska University Hospital, CMM, L8:01, SE-17176 Stockholm, Sweden, 3Kyiv City Teaching Endocrinological Center, 01034 Kyiv, Ukraine, 4Department of Oncology-Pathology, Karolinska Institutet, 17176 Stockholm, Sweden and 5Department of Pathology-Cytology, Karolinska University Hospital, 17176 Stockholm, Sweden

(Correspondence should be addressed to A Dinets at Department of Molecular Medicine and Surgery, Karolinska Institutet; Email: andrii.dinets@ki.se; C Larsson at Department of Molecular Medicine and Surgery, Karolinska Institutet; Email: catharina.larsson@ki.se)

Abstract

Background: Increased incidence of papillary thyroid carcinoma (PTC) is observed as a consequence of radiation exposure in connection to the Chornobyl nuclear plant accident in 1986. In this study, we report a cohort of adult Ukrainian patients diagnosed with PTC from 2004 to 2008 following exposure at the age of 18 years or younger.

Methods: In total, 70 patients were identified and clinically characterized. The common BRAF1799T>A mutation was assessed by pyrosequencing, the RET/PTC1 and RET/PTC3 (NCOA4) rearrangements by RT-PCR, and the expression of Ki-67 (MIB-1 index), BCL2, cyclin A, and cyclin D1 by immunohistochemistry.

Results: In total, 46/70 (66%) cases carried a BRAF mutation and/or a RET/PTC rearrangement. A BRAF mutation was detected in 26 tumors, RET/PTC1 in 20 cases, and RET/PTC3 in four cases. In four of these cases, BRAF mutation and RET/PTC rearrangement were coexisting. The BRAF mutation was underrepresented among PTCs with accompanying chronic lymphocytic thyroiditis (CLT) compared with PTCs without this feature (12 vs 44%). MIB-1 proliferation index determined by double staining with leukocyte common antigen was low (mean 0.8%; range 0.05–4.5%). Moreover, increased expression of cyclin A was observed in PTCs with a tumor size >2 cm compared with PTCs ≤ 2 cm (1.2 vs 0.6%). BCL2 and cyclin D1 showed frequent expression but without associations to clinical characteristics or amplification of the CCND1 locus.

Conclusions: Our results suggest that this cohort has frequent BRAF mutation, RET/PTC rearrangement, and low proliferation index. Furthermore, BRAF1799T>A was underrepresented in PTCs with CLT, and cyclin A expression was associated with increased PTC tumor size.

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Introduction

Papillary thyroid carcinoma (PTC) is the most common type of endocrine cancer comprising up to 80% of all malignant thyroid tumors (1). Increased incidence of PTC was observed among Ukrainian children who were exposed to radioactivity after the Chornobyl (Chernobyl) nuclear plant accident in 1986 (2, 3). Specific molecular and genetic features of such childhood PTC have been described (4). Today, it is known that PTC may also develop in adult individuals who were younger than 18 years at the time of the accident and who lived within the contaminated area (5, 6). Molecular changes in such PTC have not been widely studied, and it is presently unclear whether they have similar and/or distinct molecular characteristics compared with PTC in other populations.

PTC commonly exhibits a hotspot BRAF (v-raf murine sarcoma viral oncogene homolog B1) mutation or activation of the RET or NTRK genes through different translocations that lead to abnormal tyrosine kinase activity (4, 7). The common BRAF mutation involves a thymine to adenine transversion at position 1799 (1799T>A) in exon 15, which results in an activating missense substitution of valine to glutamic acid at codon 600 (V600E) (4). The frequency of BRAF mutation in PTC varies between studies from very low frequencies up to 80% (8, 9, 10), and their presence is reported to have prognostic implications (8). However, a low prevalence of BRAF mutation was reported...
Materials and methods

Patients and tissue samples

The 70 cases included in the study were identified from patients surgically treated for a PTC from 2004 to 2008 in Kyiv City Teaching Endocrinological Center, Ukraine. The standard surgical approach used for these patients was total thyroidectomy followed by central lymph node dissection. All patients in the cohort had been exposed to radioactivity from the accident at the Chornobyl nuclear power station in Ukraine in 1986, as determined from the patients’ addresses and the geographical pattern of the radioactive fallout. However, data about radiation dosages are not available. At the time of the accident, all patients were 18 years of age or younger and lived near the most heavily contaminated regions Kyiv, Chernihiv, or Zhitomyr.

Clinical data were retrieved from medical records, and archival formalin-fixed paraffin-embedded (FFPE) tumor tissue samples were collected for all cases. The tumors were initially classified as primary PTC, classical type, at routine histopathological examination in Kyiv City Teaching Endocrinological Center, whereby presence or absence of coexisting chronic lymphocytic thyroiditis (CLT) was also noted. The diagnosis, presence/absence of CLT, as well as the absence of large lymphocytic infiltrates of the PTC stroma were subsequently confirmed at histopathological revision by one of the authors (A H). In addition, specimens of normal thyroid tissue (n = 4), goiter (n = 1), and follicular thyroid adenoma (n = 1) were collected at the same institution and included as references in the immunohistochemistry and fluorescence in situ hybridization (FISH) analysis. Samples were collected, and the study was conducted with ethical permission obtained from the local ethics committees.

Control samples for pyrosequencing constituted 11 PTC samples with BRAF T1799A mutation status confirmed by Sanger sequencing as previously reported for ten of the cases by Sofiadis et al. (29), as well as three parathyroid adenomas. These samples had been collected as fresh frozen samples at the Karolinska University Hospital, Sweden, with informed consent and ethical approval.

Pyrosequencing of the BRAF 1799T>A mutation

Genomic DNA (gDNA) was extracted from FFPE sections using a commercially available kit (Qiagen), quantified with a Nano Drop 1000 Spectrophotometer (Thermo Fisher Scientific Inc., Wilmington, DE, USA) and commercially synthesized (bio-rad, Hercules, CA, USA). The primer sequences for pyrosequencing were as follows: forward 5'-GGCCAAAATTTATGTACATGGGAA-3', reverse 5'-CCCTCCATGGCTTGCTGTAGT-3' (5'-biotinylated) and sequencing 5'-CCACTCCATGGAGATT-3'. PCRs were performed using HotStar Taq DNA polymerase kit (Qiagen) under the following cycling conditions: 95 °C for 15 min. 35 cycles × (94 °C for 30 s, 58 °C for 30 s, and 72 °C for 30 s) and final extension at 72 °C for 10 min. PCR products were
visualized in 2% agarose gel stained with GelRed (Biotium, Hayward, CA, USA). Subsequently, 30 µL biotinylated PCR product was captured to filtered probes using PyroMark Q24 vacuum prep workstation, flushed, and released to Q24 plates with annealing solution according to the protocol recommended by the manufacturer. Plates with annealed samples were processed in a PyroMark Q24 and the results were analyzed using Pyromark Q24 Software 2.0 (Qiagen). Pyrosequencing of additional DNA samples from PTC cases with a \( \text{BRAF} \) 1799T>A mutation or wild-type status previously determined by standard Sanger sequencing was done as positive and negative controls respectively (29). The accuracy of the pyrosequencing was evaluated by analysis of 11 PTCs for which the \( \text{BRAF} \) 1799T>A mutation determined by Sanger sequencing was verified. Furthermore, the sensitivity was demonstrated by detection of the mutation in gDNA diluted one, five, and ten times from one \( \text{BRAF} \) 1799T>A mutation carrying PTC. The specificity of the method was determined by detection of the wild-type \( \text{BRAF} \) sequence only in the three parathyroid adenomas. The cutoff level for \( \text{BRAF} \) 1799T>A was 10%.

**Real-time PCR detection of RET/PTC1 and RET/PTC3 fusion transcripts**

Total RNA was isolated from all samples using RNA isolation kit for FFPE tissue (Qiagen), according to the protocol recommended by the manufacturer. cDNA was synthesized from 100 ng total RNA using high-capacity cDNA RT kit with random primers (Applied Biosystems) according to the manufacturer’s description. Amplification of cDNA was performed by RT-PCR in a StepOnePlus PCR instrument using TaqMan Universal PCR master mix (Applied Biosystems). Primers and probes for \( \text{RET/PTC1} \) and \( \text{RET/PTC3} \) were synthesized according to Rhoden et al. (30). The phosphoglycerate kinase 1 gene (PGK1) served as endogenous control. Two PTC samples with previously reported expression of \( \text{RET/PTC1} \) or \( \text{RET/PTC3} \), respectively (14), were included as positive controls, and replacement of cDNA template with water constituted the non-template control. RT-PCRs, including negative and positive controls, were performed in duplicate under standard conditions: 50 °C for 2 min followed by 95 °C for 10 min and 45 cycles×(95 °C for 15 s, 60 °C for 1 min). Analysis of RT-PCR results was based on the evaluation of amplification curves for each sample in comparison with positive controls (31).

**Immunohistochemistry**

MIB-1 index and expression of BCL2, cyclin A, and cyclin D1 were analyzed on macroarray tissue slides of the 70 PTCs as well as control thyroid samples by immunohistochemistry using a previously described protocol (29). The following primary antibodies were used for antigen detection: monoclonal mouse anti-Ki-67 (clone MIB-1; Dako, Stockholm, Sweden) at dilution 1:300; monoclonal mouse anti-CD45 (leukocyte common antigen, LCA) at 1:50 (clone 2B11+PD7/26; Dako); monoclonal mouse anti-BCL2 (clone 124; Dako) at 1:100; monoclonal rabbit anti-cyclin D1 (clone Sp4; Dako) at 1:250; and monoclonal mouse anti-cyclin A at 1:300 (clone E6E; Novocastra, Leica Biosystems, Newcastle, UK). Macroarrays were prepared by joining and re-embedding of four to nine tissue samples in novel FFPE blocks. For immunohistochemistry, 5 µm paraffin sections were deparaffinized, rehydrated, and treated in preheated citrate buffer pH 6.0 (Dako) at 95–99 °C for 20 min in a microwave oven. After incubation in 0.3% hydrogen peroxide for 30 min and blocking in 1% BSA with 0.01% sodium azide for 1 h at room temperature, endogenous biotin was blocked using the Avidin/Biotin Blocking Kit (SP-2001; Vector Laboratories, Burlingame, CA, USA). Primary antibody diluted in 1% BSA was incubated overnight at 4 °C followed by the biotinylated secondary antibody horse antimiouse IgG at 1:700 (BA-1000/BA-2000, Vector Laboratories) for 45 min. Slides were subsequently incubated with the avidin–biotin–peroxidase complex (Vectastain Elite Kit; Vector Laboratories) for 45 min and diaminobenzidine tetrahydrochloride for 6 min and counterstained with hematoxylin for 3 min. Slides analyzed in parallel with omission of the primary antibody served as negative controls and showed expected absence of staining in all cases. Positive controls constituted of tissue sections from anonymous normal tissues of stomach, large and small bowels, as well as lymphoid tissue, which revealed expected staining patterns in accordance with information provided by the antibody manufacturers. Anti-cyclin A, anti-cyclin D, and anti-BCL2 were separately incubated. MIB-1 was incubated separately as well as co-incubated with anti-LCA to allow optimal differentiation between proliferating leukocytes and proliferating tumor cells.

**Evaluation of immunohistochemistry**

Slides were evaluated in a Zeiss Axioskop microscope (Carl Zeiss, Jena, Germany) equipped with Zeiss Plan-Neofluar objective lenses, and images were captured using a ProgRes C12 Plus camera and the ProgRes Capture Pro 2.5 software program (Jenoptik, Jena, Germany). For each case, the total number of PTC cells was estimated (×16 objective magnification), and the scoring was based on 1500–2000 cells. Non-PTC cells were identified at microscopy and excluded from the scoring of PTC cells. MIB-1 proliferation index and cyclin A expression were determined by counting all positive PTC cells in the areas where the number of immunoreactive nuclei was the highest (hotspot) and by calculating the proportion of positive nuclei. For cyclin D1, only nuclear staining was considered and the proportion of positive PTC cells estimated at 16 objective magnification.
microscopical evaluation. Cytoplasmic staining pattern was observed for BCL2 and the proportion of positive PTC cells was estimated at microscopical evaluation.

**Fluorescence in situ hybridization**

Dual color FISH analysis was performed to evaluate possible regional amplification of the cyclin D1 locus (CCND1) on FFPE sections from the 70 PTC cases. A FISH probe kit (Abbott, Scandinavia) containing a Spectrum Orange-labeled CCND1 probe (11q13) and a Spectrum Green-labeled CEP11 probe for the D11Z1 alpha centromere satellite repeat was used (11p11.11-q11). FISH was carried out using the Histology FISH Accessory Kit (Dako) according to the recommendations of the manufacturer. Visualization and scoring of FISH signals were performed in a Zeiss Axiosplan 2 imaging epifluorescence microscope (Carl Zeiss) using an ×60 objective. For each case, a minimum of 200 interphase nuclei were scored, including only representative PTC cells with nonoverlapping nuclei and two bright green CEP11 signals. The rationale for this selection was to avoid misscoring of overlapping or sectioned nuclei (32). Sections of an anonymous breast carcinoma with validated CCND1 amplification were analyzed in parallel as positive controls.

**Statistical analyses**

Statistical calculations were performed using the data analysis software Statistica version 10.0 (StatSoft Scandinavia AB, Uppsala, Sweden). The Mann–Whitney U test was applied to compare the results in sample groups. Spearman rank order correlation test was performed to analyze possible relations between studied parameters. Results with P values <0.05 were regarded as statistically significant.

**Results**

**Clinical description of the post-Chernobyl PTC cohort**

The cohort consists of 70 patients who were exposed to radioactivity from the Chernobyl accident in 1986 as children or teenagers (≤18 years) and who were subsequently operated on for a primary PTC from 2004 to 2008. Clinical characterization of patients and tumors was based on medical records and histopathological revision of PTC slides as summarized in Table 1. The mean age of patients was 10.4 years at the time of the Chernobyl accident and 30.4 years at the time of surgery. Female patients were overrepresented 6.8 times compared with male patients (87 vs 13%). For 52 patients, the size of PTC was ≤2 cm in maximum diameter, whereas 18 patients had a PTC >2 cm. Metastases to local lymph nodes were detected at the time of diagnosis in 19 cases (27%). However, distant metastases were not observed. In 16 of the 70 PTC tumors, coexisting CLT was observed (referred to as PTC/CLT), whereas 54 cases did not show this feature (PTC only). Cases with PTC only and PTC/CLT did not differ significantly concerning gender, age at exposure and surgery, tumor size, or metastasis. Similarly, no statistically significant difference was observed when tumor size was compared with gender, age, metastasis, or presence of CLT.

**Frequent occurrence of the common BRAF mutation and/or RET/PTC rearrangements**

All 70 cases were screened for the common BRAF mutation in exon 15 using pyrosequencing (Fig. 1). In total, 26 (37%) tumors exhibited a base substitution 1799T>A predicted to result in the V600E missense mutation (Table 2). Comparison of BRAF mutation status with clinical characteristics did not reveal any significant associations for the parameters gender, sex, age, or lymph node metastasis. However, 24 of the 26 BRAF mutated cases had been classified as PTC only while two cases were of PTC/CLT type. Hence, BRAF mutations were 3.5 times less frequent in the PTC/CLT group (2/16; 12%) compared with PTC only (24/54; 44%) (P = 0.02). The cutoff level of 10% was applied to classify cases as positive or negative. Overall, positive cases exhibited proportions of mutant allele, which varied between 12 and 44%. The proportion of mutant alleles was not found to be different between PTC-only cases (mean 28%, range 12–44%) and the two PTC/CLT cases (18 and 34%).

The presence of a RET/PTC1 or RET/PTC3 rearrangement was assessed by analysis of amplification curves
staining with LCA to facilitate the distinction between proliferative lymphocytes and tumor cells (Fig. 3). All 70 PTC cases were positive, while normal thyroid tissues included in the FFPE macroarrays of the PTC cohort were completely negative (Table 3). The mean MIB-1 index for the entire cohort determined by combined MIB-1/LCA immunohistochemistry was 0.8% (range 0.05–4.5%). For comparison, MIB-1 index was also determined by regular counting of MIB-1-stained slides, applying visual distinction between proliferating lymphocytes and proliferating tumor cells. This analysis showed that 65/70 PTCs were positive with a mean MIB-1 index of 1.5% (median 1.0%, range 0–7.5%). Comparison of MIB-1 index with clinical characteristics did not reveal statistically significant associations for the MIB-1/LCA- or MIB-1-based analyses.

**Expression of cyclin A in relation to size of PTC**

Cyclin A expression was determined by scoring of immunohistochemical nuclear expression (Fig. 4A and B). In normal thyroid tissue, no staining was observed (Table 3). In the PTC cohort, the mean level of cyclin A expression was 1.5% (median 1.0%, range 0–4.5%). For comparison, cyclin A expression was 0.8% (median 0.4%, range 0–7.5%). Comparison of cyclin A index with clinical characteristics did not reveal statistically significant associations for the MIB-1/LCA- or MIB-1-based analyses.

### Table 2 Summary of genetic and immunohistochemical findings in the 70 cases of post-Chornobyl PTCs studied. Cutoff level for positive cases was 0% for all antibodies.

<table>
<thead>
<tr>
<th>Parameter studied</th>
<th>Observation in 70 PTCs</th>
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</thead>
<tbody>
<tr>
<td><strong>BRAF 1799T&gt;A mutation</strong></td>
<td>No. with wild-type 44 (63%) No. with 1799T&gt;A 26 (37%)</td>
</tr>
<tr>
<td><strong>RET/PTC1 rearrangement</strong></td>
<td>No. with RET/PTC1 20 (29%) No. without rearrangement 50 (71%)</td>
</tr>
<tr>
<td><strong>RET/PTC3 rearrangement</strong></td>
<td>No. with RET/PTC3 4 (6%) No. without rearrangement 66 (94%)</td>
</tr>
<tr>
<td><strong>BRAF and RET/PTC</strong></td>
<td>No. with 1799T&gt;A and RET/PTC1 3 (4%) No. with 1799T&gt;A and RET/PTC3 1 (1%)</td>
</tr>
<tr>
<td><strong>MIB-1 proliferation index (MIB-1 only)</strong></td>
<td>Mean proportion positive nuclei 1.5% Median proportion positive nuclei 1.0%</td>
</tr>
<tr>
<td><strong>MIB-1 proliferation index (MIB-1+anti-LCA)</strong></td>
<td>Mean proportion positive nuclei 0.8% Median proportion positive nuclei 0.7%</td>
</tr>
<tr>
<td><strong>Cyclin A immunohistochemistry</strong></td>
<td>Mean proportion positive cells 0.7% Median proportion positive cells 0.4% No. of positive cases 64 (92%)</td>
</tr>
<tr>
<td><strong>Cyclin D1 immunohistochemistry</strong></td>
<td>Mean proportion positive nuclei 27% Median proportion positive nuclei 20% No. of positive cases 68 (97%)</td>
</tr>
<tr>
<td><strong>BCL2 immunohistochemistry</strong></td>
<td>Mean proportion positive cells 48% Median proportion positive cells 50% No. of positive cases 53 (78%)</td>
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**MIB-1 proliferation index**

Proliferation index was determined using MIB-1 immunohistochemistry and counting of cells with positive nuclei (Fig. 3 and Table 2). Lymphocytes used as internal controls showed strong nuclear staining in more than 50% of the cells. Given the frequent occurrence of lymphocytes in the PTC specimens, including 16 cases with PTC/CLT, we performed double
Expression was 0.7% positive cells ranging from 0 to 3.9%. Six PTC cases were negative with lack of immunoreactive PTC cells. Among the 64 tumors with cyclin A expression, 48 cases showed $\leq1\%$ positive cells and 16 exhibited 1–4% positive cells according to the previously published recommendations of classification (33). When compared with the clinical characteristics, we found that the expression of cyclin A differed significantly according to the size of the PTC. Specifically, expression of cyclin A was higher in PTCs $>2$ cm than in PTCs $\leq2$ cm ($P=0.004$; mean 1.2 vs 0.6% respectively). No other association between cyclin A expression and clinical parameters was noted.

**Frequent expression of cyclin D1 without associated CCND1 amplification**

Cyclin D1 was evaluated concerning both protein expression and regional amplification of the CCND1 locus. Cyclin D1 immunohistochemistry was negative in normal thyroid tissue (Table 3). In the PTC cohort, we detected nuclear immunoexpression of cyclin D1 (Fig. 4C and D), and in addition, cytoplasmic staining was also noted in some cases, which was not included in the scorings. The mean proportion of positive PTC cells was 27% ranging from 0 to 90%. Sixty-eight cases showed expression with $<10\%$ positive cells in 25 cases, 10–49% positive cells in 25 cases, and $\geq50\%$ positive cells in the remaining 18 cases according to the previously applied cutoff levels for subgroups (34). No association was detected between the expression level and clinical characteristics. FISH analysis in normal thyroid tissue showed two signals for the CCND1 probe. Moreover, FISH analyses revealed two bright green and two bright orange signals in all representative PTC cells for all cases. This observation suggests that the observed cyclin D1 expression was not a consequence of CCND1 regional amplification.

**Expression of BCL2**

Immunohistochemical expression of BCL2 was identified in the majority of PTC cases and observed in normal thyroid tissue and goiter (Table 3 and Fig. 4E and F). Among the 70 PTC cases, the mean level of expression was 48% ranging from 0 to 100% positively stained cells. Altogether, 53 cases exhibited BCL2 expression, in 1–25% of the cells for 13 cases, in 26–50% of cells for eight cases, and in $>50\%$ of cells in 32 cases. The remaining 17 cases were negative without immunoreactive PTC cells. Normal thyroid tissue and goiter were strongly positive with $>75\%$ positively stained cells in 4/5 samples (Table 3). No association with clinical parameters was identified.
Comparison between genetic and immunohistochemical phenotypes

Possible relationships between the genetic findings and immunohistochemical parameters assessed in the study were determined by Spearman’s rank order correlation test. Several statistically significant observations were made. MIB-1 index showed a positive correlation with expression levels of both cyclin A \( (r = 0.38, P < 0.05) \) and cyclin D1 \( (r = 0.34, P < 0.05) \). Cyclin D1 expression levels showed a positive correlation with cyclin A expression \( (r = 0.39, P < 0.05) \) and a negative correlation with the presence of RET/PTC1 \( (r = -0.26, P < 0.05) \). Finally, a positive correlation was found between BRAF mutation and BCL2 expression \( (r = 0.24, P < 0.05) \). However, for all identified correlations, Cohen’s effect size was < 0.5, suggesting that the detected correlations are relatively weak.

Discussion

In this study, we present a comparably large cohort of patients operated on for PTC, who were exposed to radioactive fallout in their childhood or as teenagers after the Chornobyl nuclear plant accident in 1986. The clinical features do not appear to be significantly different compared with other cohorts of PTC patients who were not exposed to radioactivity. Whether this cohort has a significantly different clinical course awaits follow-up; however, the time allowing for prognostic evaluation is presently too short. One weakness of the study is the lack of a control group in the experiments, in order to shed light over the specificity of the findings. A control group, however, would require recruitment from a totally different age group, or from another, noncontaminated geographic area with a different demographic profile. Therefore, we decided not to include a control group in the experiments but to compare all the findings with existing data on similar cohorts found in the literature.

To further characterize the cohort, we have applied some established markers often used in the work-up of PTC patients. Some of these markers are summarized in Table 4, containing details of observations from published studies of postradiation PTCs and nonradiation-associated PTCs. The frequency of BRAF mutation in the entire cohort was 37%, which is similar to many series of nonradiation PTC \( (35, 36) \). By contrast, BRAF mutation has been less frequently observed in postradiation PTC, i.e. 4–24% (Table 4). It is worth noticing that BRAF mutation was significantly underrepresented among the patients with PTC/CLT compared with PTC only, which is in accordance with the previous studies \( (37, 38) \). The finding may also reflect the facts that BRAF mutation has been associated with more aggressive PTC \( (39, 40) \) while the presence of CLT in PTC seems to lead to a better prognosis \( (41, 42) \). Thus, the fewer occurrences of BRAF mutation in PTC/CLT patients may also be connected to good prognosis.

In this study, we determined the proportion of BRAF mutant alleles to be below 50% (mean 28%), which could be related to contamination of nontumor cells in the samples studied as well as intratumoral heterogeneity of the BRAF mutation. The latter situation was recently shown by Guerra et al. \( (43) \). In our study, histopathological examination of all samples indicated a high PTC representativity with minor proportions of non-PTC cells. This was also true for the PTC/CLT cases in which large areas of lymphocytic infiltrations were not observed. Taken together with the sensitivity of the

![Figure 4](https://www.eje-online.org/content/images/1055.png)

**Figure 4** Immunohistochemical analysis of cyclin A, cyclin D1, and BCL2 expression shown in small (objective ×16, left) or large magnification (objective ×40, right). (A and B) Cyclin A expression of 2.8% in a large-sized PTC > 2 cm; (C and D) cyclin D1 expression of 70% in a sample of PTC only; and (E and F) BCL2 expression of 90% in a PTC-only sample.
Table 4 Comparison between published series of PTC.

<table>
<thead>
<tr>
<th>PTC case no.</th>
<th>Area of exposure</th>
<th>Age at exposure mean years (range)</th>
<th>Age at surgery mean years (range)</th>
<th>RET/PTC1 mutation no. (%)</th>
<th>RET/PTC1 no. (%)</th>
<th>RET/PTC3 no. (%)</th>
<th>Total no. (%)</th>
<th>MIB-1 index mean, % nuclei (range)</th>
<th>Reference</th>
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<tr>
<td>70</td>
<td>Ukraine</td>
<td>10 (&lt;1–18)</td>
<td>30 (19–39)</td>
<td>26 (37)</td>
<td>20 (29)</td>
<td>4 (6)</td>
<td>24 (34)</td>
<td>0.8 (0.05–4.5)</td>
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<td>38 (20–61)</td>
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<td>1 (8)</td>
<td>2 (17)</td>
<td>3 (29)</td>
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<td>(15)</td>
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<td>26 (87)</td>
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<td>27</td>
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<td>&lt; 16</td>
<td>14 (8–16)</td>
<td>1 (4)</td>
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<td>–</td>
<td>12 (45)</td>
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<tr>
<td>55</td>
<td>Belarus, Ukraine</td>
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<td>2 (4)</td>
<td>6 (11)</td>
<td>26 (47)</td>
<td>32 (58)</td>
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<td>12 (36)</td>
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<td>5 (33)</td>
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<td>(45)</td>
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<td>PTC cases without previous radiation</td>
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<td>61</td>
<td>–</td>
<td>–</td>
<td>54</td>
<td>–</td>
<td>1 (1.6)</td>
<td>2 (3)</td>
<td>3 (5)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>10</td>
<td>–</td>
<td>–</td>
<td>43 (25–97)</td>
<td>5 (50)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td></td>
<td></td>
</tr>
<tr>
<td>54</td>
<td>–</td>
<td>–</td>
<td>– (≤45–&gt;45)</td>
<td>42 (78)</td>
<td>1 (1.8)</td>
<td>4 (7)</td>
<td>5 (9)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>169</td>
<td>–</td>
<td>–</td>
<td>– (≤45–&gt;45)</td>
<td>–</td>
<td>40 (23.7)</td>
<td>5 (3)</td>
<td>45 (27)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>18</td>
<td>–</td>
<td>–</td>
<td>49 (36–63)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>1.7 (0.1–3.8)</td>
<td>(28)</td>
</tr>
<tr>
<td>30</td>
<td>–</td>
<td>–</td>
<td>62 (27–80)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>1.9 (0.3–11.8)</td>
<td>(19)</td>
</tr>
<tr>
<td>185</td>
<td>–</td>
<td>–</td>
<td>48 (12–94)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>2.9 (0–40)</td>
<td>(20)</td>
</tr>
<tr>
<td>108</td>
<td>–</td>
<td>–</td>
<td>– (&lt;35–&gt;55)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>(&gt;1–&lt;10)</td>
<td>(18)</td>
</tr>
<tr>
<td>371</td>
<td>–</td>
<td>–</td>
<td>49 (17–83)</td>
<td></td>
<td></td>
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</table>

'–', not analyzed, not available or not applicable.

Current study.

In this study, three cases showed both RET/PTC1 and three rearrangements.
pyrosequencing (by which \(BRAF\) 1799T\(\rightarrow\)A was observed in gDNA of a PTC after dilution), our observations would support intratumoral heterogeneity for \(BRAF\) 1799T\(\rightarrow\)A. 

\(RET/PTC\) rearrangements in the form of \(RET/PTC1\) and \(RET/PTC3\) were demonstrated in 29 and 6% respectively. While previous studies on \(RET/PTC\) have reported highly varying frequencies from 5 to 87% (Table 4), postradiation cases have generally shown the highest frequencies. In comparison with these reports, our finding of 34% \(RET/PTC\) positivity falls within the lower range of postradiation PTC and is comparable to the highest frequencies among non-radiation PTCs (15, 37, 44). However, with regard to the specific fusion type involved, we found \(RET/PTC1\) to be five times more common than \(RET/PTC3\), which is in contrast to other reported postradiation PTCs but in agreement with nonradiation PTCs (45). Overall, the presence of \(RET/PTC\) is usually considered to be a sign of poor prognosis in PTC. Moreover, \(RET/PTC\) accompanied by a \(BRAF\) 1799T\(\rightarrow\)A mutation is associated with a high risk of disease recurrence and metastases. 

In the current study, co-occurrence of \(RET/PTC\) and \(BRAF\) mutation was detected in four PTCs. Although the clinical features at surgery were not indicative of poor prognosis, these cases should be considered for close follow-up for early recognition of signs for PTC recurrence as reported in the literature (13, 39). 

Moreover, different frequencies of \(RET/PTC1\) and \(RET/PTC3\) were reported in childhood post-Chernobyl PTC. However, these studies showed significant variation of these genetic aberrations depending on the histopathological type of PTC. Thus, \(RET/PTC1\) was associated with the classical and diffuse sclerosing variants of PTC, whereas \(RET/PTC3\) was associated with the solid follicular type (46, 47). On the other hand, the solid follicular type of PTC is more common in pediatric patients, while the classical PTC is more common in adults (47). The patient’s age is also an important factor for the \(BRAF\) 1799T\(\rightarrow\)A mutation, which is commonly found in adult patients, but is rare in childhood PTC, which is consistent with our finding (9, 10).

\(MIB-1\) index is increasingly used in the immunohistochemical work-up of several cancer types. The \(MIB-1\) MAB is directed toward the nuclear antigen Ki-67 and is used for identification of proliferative cells and areas of tumors with a high degree of proliferation. This index has been suggested to predict the prognosis in many cancer varieties, including PTC (19, 20, 21). PTC exhibits varying proportions of infiltrating lymphocytes, which was pronounced in the PTC/CLT entity and was less abundant in several PTC-only cases. As \(MIB-1\) immunostaining targets proliferating cells, both proliferating lymphocytes and tumor cells will be stained, with associated risks of misclassification and false-positive or negative scoring as a consequence. To achieve optimal scoring conditions, we used double staining with \(MIB-1\) and LCA in addition to regular \(MIB-1\) staining of all cases. Typical examples of the result are illustrated in Fig. 3. Overall, lower \(MIB-1\) proliferation index was revealed using the \(MIB-1/LCA\)-based analysis compared with \(MIB-1\) only (mean 0.8 vs 1.5%; Table 2). If substantiated in follow-up studies, the observations suggest that double staining of \(MIB-1\) and LCA should be considered for use in clinical routine work-up of PTC instead of regular \(MIB-1\)-only analysis. 

Associations between \(MIB-1\) proliferative index and clinical features were not observed. In the five cases with \(MIB-1\) index above the \(\geq\) 1.85% border applied in our previous studies (19, 20), signs of aggressive clinical features were not observed concerning histopathological and clinical features present at the time of surgery. However, in some previous publications, increased \(MIB-1\) index in PTC has been associated with adverse outcome during follow-up (19, 20, 22). Possible prognostic implications of \(MIB-1\) index in this cohort cannot be presently assessed given the lack of follow-up. 

Expression of the antiapoptotic protein \(BCL2\) was observed in the majority of PTCs. All normal thyroid tissue samples and 53/70 PTCs expressed \(BCL2\), suggesting that \(BCL2\) could have a protective role to prevent apoptosis in normal thyroid, which is partly lost in malignancy. In contrast to a previous study, no correlation was observed between \(BCL2\) expression and \(MIB-1\) index in PTC/CLT cases (48). However, a positive correlation was observed between \(BCL2\) expression and \(BRAF\) mutation. Although this correlation was not strong, it is consistent with the study by Preto et al. (49), showing inhibition of \(BCL2\) in PTC cell lines treated with the \(BRAF\) and kinase inhibitor sorafenib. Moreover, the lack of association between clinical features and \(BCL2\) expression in our cohort is consistent with the observations by Siironen et al. (18). Given that phosphorylation is needed for the antiapoptotic effect of \(BCL2\) (50), further determination of phosphorylated \(BCL2\) expression levels would add more information about the antiapoptotic status of PTC. 

We observed significantly elevated expression of cyclin A in PTCs larger than 2 cm. Previous studies of this protein have reported overexpression in poorly differentiated and undifferentiated thyroid cancers, indicating a role in thyroid carcinoma de-differentiation (25). Our finding of an association between cyclin A expression and tumor size implies that cyclin A could have prognostic value in irradiation-associated PTC; however, much longer follow-up is required to prove or disprove this. Although the possible utility of cyclin A for routine clinical practice is presently unclear, the observed association warrants further investigation of cyclin A in relation to follow-up. 

Cyclin D1 expression was detected in the majority of PTCs. This was not accompanied by regional amplification of the \(CCND1\) locus, suggesting that cyclin D1 is deregulated at the transcriptional, translational, or posttranslational level. In our scorings,
we have included nuclear expression of cyclin D1 as suggested elsewhere (34). However, we have also observed cytoplasmic staining, which could be explained by cytoplasmic sequestration of cyclin D1 due to inhibition of its transportation to the nucleus (51, 52). Elevated expression of cyclin D1 was found to be correlated with elevated MIB-1 index, an association that was also demonstrated by Alama et al. (53) in meningioma. No other associations to clinical or pathological features were observed, which is in agreement with the previous studies (34, 54). However, others have reported that cyclin D1 overexpression may be a prognostic marker for PTC (55, 56).

In summary, we report a cohort of adult PTC patients exposed to the radioactive fallout from the Chernobyl accident during their childhood or as teenagers. Our results from genetic and molecular characterization suggest that this cohort is characterized by frequent BRAF 1799T>A mutation and RET/PTC1 rearrangement as well as low proliferation, which are partly overlapping and partly distinguishing from other reported cohorts of postradiation- and nonradiation-related PTC. Moreover, BRAF mutation was significantly underrepresented in the PTC/CLT group, and cyclin A expression was associated with tumor size in this entity. Long-term follow-up in this cohort will eventually identify possible effects on patient outcome in this patient group.

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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