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Read, Martin; Seed, Robert; Fong, Jim; Modasia, Bhavika; Ryan, Gavin; Spruce, Rachel; Gagliano, Teresa; Smith, Vicki; Stratford, Anna L.; Kwan, Perkin; Sharma, Neil; Dixon, Olivia M; Watkinson, John; Boelaert, Kristien; Franklyn, Jayne; Turnell, Andrew; McCabe, Christopher

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The PTTG1-Binding Factor (PBF/PTTG1IP) Regulates p53 Activity in Thyroid Cells


School of Clinical and Experimental Medicine (M.L.R., R.I.S., J.C.W.F., B.M., G.A.R., R.I.W., V.E.S., P.K.K., N.S., O.M.D., K.B., J.A.F., C.J.M.) and School of Cancer Sciences (A.S.T.), University of Birmingham, Birmingham, United Kingdom; Department of Medical Sciences (J.G.), University of Ferrara, Ferrara, Italy; Department of Pediatrics (A.L.S.), University of British Columbia, Vancouver, British Columbia, Canada; and University Hospitals Birmingham National Health Service Foundation Trust (J.C.W.), Birmingham, United Kingdom

The PTTG1-binding factor (PBF/PTTG1IP) has an emerging repertoire of roles, especially in thyroid biology, and functions as a protooncogene. High PBF expression is independently associated with poor prognosis and lower disease-specific survival in human thyroid cancer. However, the precise role of PBF in thyroid tumorigenesis is unclear. Here, we present extensive evidence demonstrating that PBF is a novel regulator of p53, a tumor suppressor protein with a key role in maintaining genetic stability, which is infrequently mutated in differentiated thyroid cancer. By coimmunoprecipitation and proximity-ligation assays, we show that PBF binds specifically to p53 in thyroid cells and significantly represses transactivation of responsive promoters. Further, we identify that PBF decreases p53 stability by enhancing ubiquitination, which appears dependent on the E3 ligase activity of Mdm2. Impaired p53 function was evident in a transgenic mouse model with thyroid-specific PBF overexpression (transgenic PBF mice), which had significantly increased genetic instability as indicated by fluorescent inter simple sequence repeat-PCR analysis. Consistent with this, approximately 40% of all DNA repair genes examined were repressed in transgenic PBF primary cultures, including genes with critical roles in maintaining genomic integrity such as Mgmt, Rad51, and Xrcc3. Our data also revealed that PBF induction resulted in up-regulation of the E2 enzyme Rad6 in murine thyrocytes and was associated with Rad6 expression in human thyroid tumors. Overall, this work provides novel insights into the role of the protooncogene PBF as a negative regulator of p53 function in thyroid tumorigenesis, in which PBF is generally overexpressed and p53 mutations are rare compared with other tumor types. (Endocrinology 155: 1222–1234, 2014)

Thyroid cancer is the fastest increasing cancer in both men and women, with incidence rates rising by 6.6% per year from 1997 to 2009 (1). Genetic alterations that govern cancer initiation and progression have been identified in approximately 75% of cases, which typically involve effectors of the MAPK and phosphatidylinositol 3-kinase pathways (2). Despite effective first-line treatments to ablate abnormal thyroid tissue, recurrence occurs in approximately 8–30% of patients (3, 4), and those genetic alterations driving tumor recurrence remain obscure. Recent progress has been made in associating the BRAF V600E mutation with increased cancer-related mortality among patients with papillary thyroid cancer (5). However, the key molecular mechanisms underlying thyroid
carcinogenesis still need to be better defined to enable development of more effective and targeted therapies.

Also known as PTTG1IP, the pituitary tumor transforming gene 1 binding factor (PBF) is a ubiquitously expressed protooncogene that was first identified through its ability to bind the human securin PTTG1 (6). Previously, we showed that sc expression of PBF induced tumors in athymic nude mice, and that PBF expression was higher in differentiated thyroid carcinomas than in normal thyroid (7). Separate studies have now identified a role for PBF in regulating the sodium iodide symporter and the monocarboxylate transporter 8 in thyroid cells (8–10). We also recently demonstrated that thyroid-targeted expression of PBF resulted in the repression of sodium iodide symporter function in vivo and induced hyperplastic growth and macrofollicular thyroid lesions. In contrast to our previous sc study, however, thyroid tumor induction was absent in the transgenic mouse model (11). Collectively, these observations indicate that PBF has an emerging repertoire of roles, especially in thyroid biology, and likely functions as a protooncogene. Recently the significance of PBF as a prognostic biomarker was also demonstrated in a study of 153 patients with papillary thyroid cancer (12). High PBF expression was significantly correlated with locoregional recurrence, distant metastasis at diagnosis, and disease-specific mortality in patients. The precise role of PBF in thyroid tumorigenesis, however, has not been established.

A critical event in the pathogenesis of most, if not all, human cancers is the disruption of p53 function, a key regulator in maintaining genetic stability (13) and mediating crucial responses to a range of cellular stresses including irradiation-induced DNA damage. For many cancers, inactivation of the TP53 gene by somatic mutation typically occurs late in tumor progression and is often correlated with cancer aggressiveness and poor survival (14, 15). For instance, p53 mutations have been identified in 55% of anaplastic thyroid carcinomas, which have a very poor prognosis due to their aggressive behavior and resistance to cancer treatments (16). This is in stark contrast to well-differentiated thyroid malignancies in which the prevalence of p53 mutations is much lower at approximately 11% (13, 17). There is increasing evidence, however, that p53 inactivation is also caused by physical interactions of p53 with inhibitory proteins that are commonly overexpressed in cancer (18, 19). For instance, the E3 ubiquitin ligase Mdm2/Hdm2 (20, 21) and high mobility group factor A (17, 22) have both been implicated in the pathogenesis of papillary thyroid carcinomas due to their ability to bind and inhibit p53 function (23). It is unclear whether disruption of p53 function by such proteins also contributes toward the increased sensitivity of thyroid glands to radiation-induced oncogenesis (24).

Despite the significant progress made in characterizing proteins that interact with p53, regulation of p53 is highly complex and involves a myriad of different pathways (25, 26). For instance, PTTG1 has been shown to block binding of p53 to DNA, thereby inhibiting its ability to induce apoptosis (27) and to cause p53 stimulation and apoptosis following overexpression in MCF-7 cells (28). A more detailed understanding is thus required of the molecular events that occur following inhibition of p53 function that help tumor cells escape the tight regulation of key processes governing survival and proliferation.

Here, we provide extensive evidence that PBF is a novel regulator of p53 function in thyroid cells and propose that PBF’s mechanism of action in thyroid tumorigenesis is via dysregulation of p53 activity. We have further characterized target DNA repair genes downstream of p53 that are affected by PBF overexpression and have critical roles in maintaining genomic integrity. This study therefore provides a novel insight into understanding the role of PBF in the pathogenesis of thyroid cancer.

Materials and Methods

Cell culture

Primary murine thyrocyte cultures were performed as described elsewhere (11). Human thyroid papillary carcinoma TPC1 and anaplastic thyroid carcinoma SW1736 cells were kindly provided by Dr Rebecca Schweppe (Division of Endocrinology, University of Colorado, Denver, CO), and thyroid papillary carcinoma K1 cells were obtained from the Health Protection Agency Culture Collections. The human non-small-cell lung cancer H1299 cells were purchased from American Type Culture Collection (ATCC). All cell lines were kept at low passage number and cultured in RPMI 1640 (Invitrogen) supplemented with 10% fetal calf serum. Both TPC1 and K1 papillary carcinoma cells express wild-type (WT) p53 (29, 30), whereas H1299 and SW1736 cells are both p53 null due to either a homozygous partial deletion of the TP53 gene or marked down-regulation of p53 mRNA (31). All cell lines used were confirmed as genuine by short tandem repeat analysis (DNA Diagnostics Centre) following comparison with reported profiles [Supplemental Figure 1 published on The Endocrine Society’s Journals Online web site at http://endo.endojournals.org; (32)]. Primary thyrocytes were cultured in modified Ham’s F12 media supplemented with 300 mU/L TSH (Sigma), 100 μg/L insulin (Sigma), and 5% fetal calf serum. Serum was omitted after 72 hours of culture and experiments were performed between 7 and 11 days of culture.

Animals

WT FVB/N and transgenic PBF-Tg mice (11) were bred at the University of Birmingham, and all experiments were performed in accordance with UK Home Office regulations. Thyroids were dissected from 6-week-old male PBF-Tg and WT mice for all
genetic instability, focused RT²Profiler PCR array, and real-time PCR validation experiments. Expression of thyroidal PBF and Rad6 was examined by immunohistochemistry in aged male and female PBF-Tg mice with a mean age of 15 months (461 ± 44 days; n = 9). Similar trends in protein expression were observed for male and female PBF-Tg mice compared with age- and sex-matched WT controls.

**Human thyroid samples**

Matched tumor and normal tissue specimens were obtained from 11 patients undergoing surgery for thyroid cancer at the University Hospital Birmingham National Health Service Trust, UK. Normal specimens were taken from the contralateral lobe at the time of surgery and were shown to be noncancerous upon histologic examination. All specimens harvested at the time of resection were collected with appropriate local ethical committee approval and informed patient consent.

**Transfections**

Plasmid DNA and small interfering RNA (siRNA) transfections were performed with Fugene6 (Roche) and Lipofectamine-2000 (Invitrogen) according to manufacturer’s instructions. Cells were transfected using pooled PBF-specific siRNA (catalog nos. 4399 and 147350), pooled Rad6-specific siRNA (catalog nos. 4390824 and 4390825), or negative control siRNA (AM4635) at a final concentration of 100 nM (Ambion). For plasmid DNA experiments, cells were transected with pcDNA3 containing full-length WT PBF cDNA with a hemagglutinin (HA)-tag, the Rad6 expression vector pCMV6-Ube2a (Cambridge Biosciences), or empty pcDNA3 (Invitrogen) as vector only (VO) unless otherwise stated, using conditions previously described (9).

**Western blot**

Western blot analyses were performed as described previously (9, 33). Blots were probed with specific antibodies against PBF (9, 33), 1:200; hemagglutinin (HA; Covance Research Products), 1:2000; p53 (D0–1) (Santa Cruz Biotechnology), 1:1000, and Rad6 (Abcam, catalog no. ab31917), 1:1000. Antigen-antibody complexes were detected using the ECL Plus chemiluminescence detection system (Amersham Biosciences). Actin expression was determined using mouse monoclonal anti-β-actin antibody clone AC-15 (Sigma-Aldrich) at 1:10 000. Protein quantification was performed on cell lysates using the Bradford assay. To quantify detected bands by densitometry, blots were scanned into Photoshop (Adobe Systems) keeping all scanning parameters the same and analyzed using ImageJ software (34).

**Binding assays**

WT p53 and deletion mutants were cloned into pGEX4T-1 for bacterial expression. L-α-[35S]methionine-labeled PBF was expressed in vitro using a TNT T7 Coupled Reticulocyte Lysate System according to the manufacturer’s guidelines (Promega Corp.). In vitro glutathione-S-transferase (GST) pull-down assays using [35S]PBF and GST-p53 proteins were performed using established protocols (35). GST pull-down and communoprecipitation (co-IP) assays were performed as described previously (9). The Duolink in situ proximity ligation assay (PLA) was performed according to manufacturer’s instructions (Olink Bioscience). In our experiments thyroid cells were seeded onto cover slips and transfected with expression vectors for p53 (pcDNA3-p53) and HA-tagged PBF (pcDNA3-PBF) 24 hours later prior to the PLA assay.

**p53 stability assays**

In p53 half-life experiments, cells were incubated in 100 μM anisomycin for 2 hours prior to cell lysate extraction using standard protocols. Nutlin-3 (Sigma-Aldrich) was added to cells at 50 μM concentration for 6 hours prior to assessment of p53 stability. In p53 ubiquitination experiments, cells were incubated in 20 μM MG132 for 2 hours prior to cell lysate extraction.

**Quantitative RT-PCR and sequencing**

Total RNA was extracted using the RNeasy Micro Kit (Qiagen) and reverse transcribed using the Reverse Transcription System (Promega). Expression of specific mRNAs was determined using 7500 Real-time PCR system (Applied Biosystems). Gene expression of total RNA extracted from primary thyrocytes was analyzed using the DNA damage signaling pathway-focused RT² Profiler PCR Array (SA Biosciences) according to manufacturer’s instructions. cDNA was sequenced to determine p53 mutational status of human thyroid tumors essentially as described elsewhere (36). Primer sequences are listed in Supplemental Figure 8.

**Irradiation and genetic instability (GI) assays**

DNA damage was induced by Cs137 irradiation using an irradiator BLM 437C type H unit (CIS Bio international). Fluorescent inter simple sequence repeat (FISSR)-PCR amplifications were performed essentially as described previously (37) using a 5’-6-carboxyfluorescein-labeled primer (CA)4RG with 5 ng of genomic DNA. PCR products were electrophoresed on an ABI3730 capillary sequencer (Applied Biosystems), and data were analyzed using Peak Scanner v1.0 software. Five replicate experiments were performed to verify the reproducibility of the assay. The degree of genetic instability was determined according to Basik et al (38) to generate the GI index, which represents the standard measure of GI with ISSR-PCR analysis.

**Reporter gene assays**

The p53 reporter plasmids phdm2-Luc and p21-Luc have been described previously (39) and contain fragments of either the hdm2 or p21 promoter linked to the firefly reporter gene. H1299 cells were transfected with 400 ng pClneo-PBF (PBF), 5 ng pcDNA3-p53 (p53), and 150 ng of the indicated p53 reporter plasmid. The empty plasmid pClneo without the PBF cDNA was used VO as indicated. The Renilla luciferase control plasmid pRL (Promega) was used (20 ng per transfection) as an internal control to normalize firefly luciferase expression. Cells were harvested in Passive Lysis Buffer, and the Dual Luciferase Reporter Assay System (Promega) was used to measure luciferase activity. Data were normalized to Renilla activity.

**Immunohistochemistry and analysis of thyroid morphology**

Thyroid glands were removed from mice using a dissecting microscope. Tissue was fixed in 10% formal saline for at least 24 hours prior to being paraffin embedded and cut into 5-μm sections according to standard protocols. Formalin-fixed paraffin-
Apoptosis Kit (Promega), and assays were performed according to the manufacturer’s instructions.

**Statistical analysis**

Data are displayed as mean ± SE. Normally distributed data were analyzed using a two-tailed Student’s *t* test, unless otherwise indicated. *P* < .05 was considered to be statistically significant.

**Results**

**PBF binds to p53**

To investigate a role for PBF in thyroid tumorigenesis, we examined whether PBF interacts with p53, a protein critical in suppressing human cancers. Initial GST pull-down assays demonstrated that l-cysteine-labeled PBF binds to the p53 protein (Figure 1A). Successive deletion mutants of GST-p53 altered the stringency of PBF binding. For instance, PBF did not bind efficiently to the N terminus region of p53 located between amino acids 1–100. Instead, the strongest binding sites for PBF appeared to be located between amino acids 1–100 and 318–393 of p53 (Figure 1A). Endogenous co-IP assays in papillary thyroid cancer TPC1 and K1 cells confirmed that p53 specifically associates with PBF (Figure 1B).

p53 is maintained at low cellular levels but stabilized by irradiation-induced DNA damage. We therefore determined the radiation dose and timing required to yield an optimal p53 response in both TPC1 and K1 cells (Figure 1C and Supplemental Figure 2) and examined the subsequent interaction between p53 and PBF. Irradiation treatment using these optimal conditions (ie, 15 Gy, 8 hours) led to an increased quantity of coimmunoprecipitated p53 with PBF in both TPC1 and K1 cells (Supplemental Figure 3C).

Cell survival and apoptosis assays

The cellular viability of TPC1 and SW1736 cultures was determined using the CellTiter 96 AQueous One Solution Cell Proliferation assay (Promega) according to the manufacturer’s instructions. Absorbance readings were determined using a Victor3 plate reader (PerkinElmer) after incubation for 1 hour at 37°C in a humidified chamber containing 5% CO₂.

Relative levels of apoptosis were determined by measuring caspase 3 and 7 enzyme activity using the Caspase Glo 3/7 Assay Kit (Promega), and assays were performed according to the manufacturer’s instructions.

**Results**

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PBF increases turnover and ubiquitination of p53

p53 is an intrinsically unstable protein that is subject to rapid degradation and is rarely mutated in differentiated thyroid cancers.
thyroid cancer. To further investigate the relationship between PBF and p53 in thyroid cells, we examined whether interaction with PBF resulted in altered p53 stability. Half-life studies using anisomycin to block de novo protein synthesis showed that overexpression of PBF significantly increased turnover of p53 protein in TPC1 (\(P = 0.01\); Figure 2A and B) and K1 (\(P = 0.05\); Figure 2C) cells compared with VO controls after 120 minutes. Importantly, control experiments showed that p53 mRNA levels did not change significantly in TPC1 cells following overexpression of PBF compared with VO (Figure 2D). To determine whether the reverse relationship held true, we depleted PBF (Figure 2E) and observed greater p53 stability, with more than 4-fold higher p53 levels (\(P < 0.05\)) in K1 cells compared with negative controls after 120 minutes, and no significant turnover over the time course (Figure 2, F and G). Increased p53 stability was also evident in PBF-depleted TPC1 cells compared with controls at 120 minutes after anisomycin treatment (data not shown).

Given that modulation of PBF expression was associated with altered p53 stability, we examined p53 ubiquitination in cells treated with the proteasome inhibitor MG132. A significant increase in the level of high molecular weight p53 conjugates was present in PBF-transfected TPC1 cells treated with MG132 (Figure 3A), which is consistent with the accumulation of ubiquitinated p53. Mdm2 has been identified as the major E3 ubiquitin ligase of p53, binding and targeting it for proteasome-mediated degradation. We therefore investigated whether the increased turnover of p53 by PBF in thyroid cells was dependent on the E3 ligase activity of Mdm2. The addition of the inhibitor nutlin-3 to block binding of Mdm2 to p53 led to a significant increase in p53 stability in VO- (Figure 3B).
PBF inhibits p53 activity and alters sensitivity of thyroid cells to irradiation

Following our observations that PBF binds and regulates p53 stability, we next analyzed whether PBF altered the transactivation activity of p53 in transient reporter assays in H1299 cells, which are p53 null. When coexpressed, PBF significantly repressed hdm2-mediated hdm2 promoter activity by approximately 60% (P < .001; Figure 4A), as well as p21 promoter activity (~25%; P < .01; Figure 4B). We next depleted PBF (Figure 4, C and D) and observed a significant increase in the mRNA expression of p21, a well-characterized p53-responsive gene, in both TPC1 (2.4-fold; P < .05) and K1 (3.7-fold; P < .001) papillary thyroid cells (Figure 4E). Examination of apoptotic markers also indicated a corresponding increase in caspase-3/7 activity in PBF-depleted TPC1 (2.4-fold; P < .05; Figure 4F) and K1 cells (1.45-fold; P < .05; Supplemental Figure 4A).

To further investigate the physiological relevance of our finding that PBF alters p53 stability and activity, we next examined the influence of manipulating PBF expression on apoptosis and cell survival in response to irradiation. Interestingly, depletion of PBF in TPC1 cells appeared to enhance their sensitivity to irradiation with a greater fold-change in caspase-3/7 activity (4.35-fold; P < .01; Figure 4F) and a significant decrease in cell viability (P < .05; Supplemental Figure 4B). Furthermore, in the absence of PBF, TPC1 cell survival was reduced by approximately 20% in response to irradiation (Figure 4G), whereas cells transfected with PBF demonstrated no decrease in cell survival (P > .001). Importantly, there was no difference in the cell viability of irradiated p53-null SW1736 thyroid cells transfected with either VO or PBF (P = NS; Supplemental Figure 4C), suggesting that the effects of PBF on cell survival may be p53 dependent. Together these results support the notion that the functional consequences of PBF dysregulation are via regulation of p53 activity.

PBF dysregulates DNA repair genes and promotes genetic instability

We next examined whether PBF depletion in thyroid cell lines also caused dysregulation of other p53-responsive genes. Figure 5A shows that significant mRNA changes were indeed observed in PBF-depleted TPC1 and K1 cells for a number of other genes including DNA repair genes such as Rad50, Rad51, Brca1, and Brca2. To understand the effect of PBF dysregulation in a more physiologically relevant thyroid-disease model, we next examined the transcriptional profile of a panel of 83 p53-regulated genes in murine primary PBF-Tg thyrocytes compared with WT thyrocytes (Figure 5B). A total of 27

Figure 3. Effect of PBF on p53 ubiquitination. A, Detection of high molecular weight (mwt) p53 conjugates by Western blot analysis in TPC1 cells transfected with either VO or PBF and then treated with 10 μM MG132. B and C, Western blot analysis of p53 in TPC1 cells transfected with either VO or PBF and then incubated with 50 μM nutlin-3 prior to 100 μM anisomycin treatment. Dimethylsulfoxide (DMSO) was used as vehicle. D, Mean p53 protein levels relative to β-actin quantified from 3 independent experiments are shown. Data presented as mean ± SE. *, P < .05; NS, not significant (P > .05).
genes showed significant expression changes \((P < .05)\), suggesting wide-ranging dysregulation in response to raised PBF. Of these, 12 genes showed altered mRNA expression more than 1.5-fold (Figure 5C), including several genes known to maintain genomic integrity, such as \(Xrcc3\) \((0.42 \pm 0.09; P = .003)\), \(Fancg\) \((0.58 \pm 0.1; P = .02)\), and \(Rad51c\) \((0.65 \pm 0.09; P = .02)\).

Primary thyrocyte cultures from PBF-Tg mice were next irradiated in order to identify additional p53-responsive candidate genes that might be disrupted by elevated endogenous PBF in nontransformed cells. A total of 10 genes, including \(Rad51\), \(Chek1\), and \(Rad6\), showed significant changes \((>1.5\text{-fold}; P < .05)\) in their mRNA levels following irradiation of PBF-Tg thyrocytes compared with WT (Supplemental Figure 5). Normalization of data to adjust for PBF effects on gene expression identified 8 genes most significantly dysregulated by elevated PBF following irradiation (Figure 5D). For example, irradiation-induced expression of the p53-responsive genes \(Mgmt\) \((2.0 \pm 0.03\text{-fold})\) and \(Polk\) \((1.7 \pm 0.08\text{-fold})\) was significantly suppressed in PBF-Tg thyrocytes compared with WT \((P = .0007\) and \(P = .05\) respectively; Figure 5D). In contrast, the degree of irradiation-induced inhibition for several genes, including \(Ung\) \((P = .02)\), \(Fancg\) \((P = .05)\), and \(Mbd4\) \((P = .04)\), was abrogated in PBF-Tg thyrocytes following irradiation. Validation experiments using individual qPCR assays also confirmed significant differences in expression of \(Mgmt\) \((P = .009)\), \(Rad51\) \((P = .0002)\), and
Chek1 (P = .002) in PBF-Tg thyrocytes after irradiation (Supplemental Figure 6). Furthermore, irradiation did not cause any transcriptional changes in either TP53 (Figure 5D) or PBF (Figure 5E).

To investigate whether the ability of PBF to abrogate p53 activity and downstream DNA repair genes might also influence genetic stability in vivo, we next used fluorescent inter simple sequence repeat (FISSR) PCR (37) to analyze genetic instability in thyroid glands dissected from PBF-Tg and WT mice. In comparison with age- and sex-matched WT mice (arbitrarily assigned a GI of 0%), the thyroids of 6-week old PBF-Tg mice demonstrated signif-
significantly disrupted genomes, with a mean GI index of 19.8 ± 1.8% (P < .001; Figure 5F). Altogether, these results identify a panel of p53-responsive DNA repair genes that are dysregulated by elevated PBF levels in primary thyrocytes and are associated with genetic changes underlying the increased GI index observed in PBF-Tg thyroids. Among these, the expression of Rad6, also known as the ubiquitin-conjugating enzyme E2A (Ube2a), was the sole gene up-regulated more than 1.5-fold (P = .008) in PBF-Tg thyrocytes.

**Functional interaction between p53 and Rad6 in thyroid cells**

Recently, Rad6 has been shown to form a ternary complex with Mdm2 and p53 that contributes to p53 degradation in HeLa cells (41). We therefore examined whether Rad6 also binds to p53 in thyroid cells. Exogenous co-IP assays confirmed that Rad6 specifically binds to p53 in TPC1 cells (Figure 6A). Importantly, overexpression of Rad6 in both TPC1 (Figure 6A) and K1 (Figure 6B) thyroid cells led to a significant decrease in p53 protein levels. In addition, depletion of Rad6 in K1 cells increased p53 protein levels (Figure 6B).

Having established that a functional interaction exists between Rad6 and p53 in thyroid cells, we next examined the relationship between PBF and Rad6 in thyroid disease models in vivo. For these experiments we used thyroid glands dissected from PBF-Tg mice, which have an enlarged and hyperplastic phenotype [Figure 6C; (11)]. Immunostaining revealed elevated Rad6 expression in thyroids from 15-month-old PBF-Tg mice compared with

![Figure 6](https://example.com/figure6.png)

**Figure 6.** Association of Rad6 and PBF in vivo. A, Western blot analysis (upper) of co-IP of Rad6 with p53 in TPC1 cells transfected for 24 hours with either VO (−) or pCMV6-Ube2a (+). ISO, isotype control antibody. Nab, no antibody control. Western blot analysis of Rad6 (middle) and p53 (lower) in cell lysates from transfected TPC1 cells are also shown. B, Western blot analysis of Rad6 and p53 following either overexpression (upper) or depletion (lower) of Rad6 in K1 cells. Control lanes are indicated. C, Representative enlarged thyroids dissected from aged PBF-Tg mice compared with WT. Thyroids were typically approximately 3- to 4-fold heavier in PBF-Tg mice. D and E, Representative images of Rad6 staining in normal regions (D) and hyperplastic lesions (E) in WT (n = 6) and PBF-Tg (n = 9) thyroids are shown. Arrows highlight elevated nuclear expression of Rad6 (E). F, Correlation of PBF and Rad6 mRNA expression in human thyroid tumors (n = 11). Statistics analyzed using Spearman rank correlation. G, Graph shows quantification of Rad6 mRNA expression in thyroid tumors relative to normal thyroid. Scale bars, 100 μm. Data presented as mean ± SE. **, P < .01.
age-matched WT thyroids (Figure 6D and Supplemental Figure 7A). Previous studies have indicated weak cytoplasmic Rad6 staining in normal cells compared with intense nuclear reactivity in invasive tumor cells (42). Here, Rad6 expression was most prominent in nuclear compartments of follicular epithelial cells in PBF-Tg thyroids, whereas WT cells displayed mostly diffuse cytoplasmic staining (Figure 6D). Importantly, the greatest abundance of Rad6 nuclear immunoreactivity was detected in distinct hyperplastic lesions (Figure 6E), which also colocalized with highest expression of the HA-tagged PBF transgene (Supplemental Figure 7B). In further studies, evaluation of matched normal and tumor human thyroid specimens also revealed a significant positive correlation between PBF and Rad6 mRNA expression (Figure 6F; $P < .001$; $r_s = 0.9$), with a significant $1.6 \pm 0.2$-fold induction ($P = .008$) in Rad6 mRNA levels in thyroid tumors compared with normal tissue (Figure 6G). cDNA sequence analysis showed all human thyroid tumors had WT p53 (Supplemental Figure 8). Taken together, these results suggest a significant association between elevated PBF and Rad6 expression in thyroid disease with WT p53 status. The low mutation rate of the p53 gene in differentiated thyroid cancer may therefore belie functional inactivation of the protein by PBF, which is up-regulated in differentiated thyroid cancer, increases p53 turnover, and induces the expression of Rad6, a known regulator of p53 activity.

**Discussion**

The functional disruption of p53 activity has a critical role in promoting tumorigenesis in many different types of cancer (15). However, the mechanisms governing p53 inactivation remain to be fully defined, especially in tumors such as in differentiated thyroid cancer that have a lower incidence of p53 mutations (16, 17). Our current findings now indicate that the role of the relatively uncharacterized gene PBF in cell transformation most likely reflects its interaction with p53, thus providing a novel insight into the ability of PBF to promote endocrine tumorigenesis.

There has been relatively little reported concerning a possible role for PBF in tumorigenesis, despite identification of the PBF gene in 1998 (43). We previously described PBF overexpression in thyroid (7), pituitary (44), and breast cancers (33). Subsequent functional studies highlighted that PBF was a transforming gene in vitro and induced high-grade malignant tumor formation in athymic nude mice (7). However, the underlying role for PBF in tumorigenic growth in vivo remains unclear, especially because transgenic mice with thyroid-specific PBF expression did not develop thyroid cancer (11).

To therefore gain further insight into the role of PBF in tumorigenesis we investigated the ability of PBF to bind p53 by GST pull-down, co-IP and PLAs. Our data showed that PBF bound specifically to p53 in vitro and the relative level of p53-PBF communoprecipitates in thyroid cells was enhanced by γ-irradiation. These results most likely reflect the greater abundance of stabilized p53 protein following irradiation because p53 protein levels were, as expected, increased in irradiated TPC1 and K1 cells, in contrast to minimal changes in PBF protein (data not shown).

It is well documented that proteins such as Mdm2 and USP10 (45) can bind p53 and target it for degradation or promote its intracellular stability. This led us to investigate whether the ability of PBF to interact with p53 might also alter its turnover. Our results indicated that PBF has a role in diminishing p53 stability because PBF overexpression significantly increased p53 turnover in thyroid cancer cells. Further evidence was provided by depleting PBF protein, which increased p53 stability, as well as the enhanced ubiquitination of p53 in PBF-overexpressing cells as evidenced by the accumulation of high molecular weight p53 conjugates. These findings might infer a direct role for PBF in ubiquitinating p53, but the amino acid sequence for PBF does not contain a typical ubiquitin-conjugating (UBC) or E3 ligase domain (47). Additionally, p53 degradation was blocked by the inhibitor nutlin-3 with no synergistic or additive effects in the presence of elevated PBF, thereby indicating that the effects of PBF on p53 ubiquitination may involve Mdm2.

GST pull-down assays using deletion mutants of p53 highlighted 2 possible regions that might be involved in binding PBF. One of these, located between residues 318 and 393, contains the key lysines ubiquitinated by Mdm2 (48), which binds the N-terminal domain of Mdm2 (49). We therefore envisage that PBF may modulate the association of p53/Mdm2 with interacting proteins such as histone deacetylases (50), P300/CREB-associated factor (51), p300/CREB-binding protein (51), and Tip60 (52) that are known to alter p53 acetylation and ubiquitination status. The regulation of Mdm2 is, however, a focal point of numerous regulatory pathways for p53, including both transcription and nontranscriptional targets of p53 (26). For example, the transcription factor YY1 enhances p53 degradation by increasing the binding of Mdm2 to p53 (53). Future investigations will thus need to focus on the precise functional relationship between PBF and p53/Mdm2-interacting partners, as well as the interaction between Mdm2 and p53 itself.

Previous studies have identified that PBF can interact with the protooncogene PTTG1 to facilitate its translocation into the nucleus (6). Hence, it is possible that an al-
ternative mechanism exists such that PBF might augment PTTG1’s nuclear function as the human securin, inhibiting mitosis and generating intrachromosomal breaks, as well as increasing the interaction between PTTG1 and p53 (27, 28, 54). Indeed, we have also reported that PTTG1 induces genetic instability in colorectal cells, and that PTTG1 expression correlates with genetic instability in vivo (37). Against this, our current data reveal the novel finding that PBF and p53 bind specifically, particularly in the presence of DNA damage, and that p53 stability was significantly altered by PBF. Furthermore, preliminary co-IP experiments showed that the PBF-p53 interaction was not significantly altered in PTTG1-depleted TPC1 cells (data not shown). These results therefore imply an independence of action for PBF.

Disruption of p53 by interaction with other proteins typically results in loss of activity of p53-responsive genes. Our data of reduced transactivation of Hdm2 and p21 promoters in p53-null H1299 cells transfected with PBF and p53 are therefore in keeping with those in the literature. Indeed, the magnitude of this inhibition was broadly equivalent to proteins such as Polo-like kinase 1 (Plk1) that also physically interact with p53 (55). Importantly, we showed that depletion of PBF in thyroid cells also increased expression of the p53-responsive gene p21, further emphasizing the role of PBF as a negative regulator of p53 activity. Our group recently reported the generation of a PBF-Tg mouse with targeted human PBF overexpression in the thyroid gland (11). In this study, we were able to show dysregulated expression of approximately 40% of all DNA repair genes examined (32 of 83) in PBF-Tg primary thyrocytes. It will be important to determine the relative contribution of p53-independent pathways, if any, to the ability of PBF to disrupt expression of these genes. However, expression of many of the genes identified, such as Mgmt, are known to be modulated by ionizing radiation in a classical WT p53 gene-dependent manner (56); thus, the ability of PBF to abrogate these genes provides an invaluable starting point for defining a role for PBF in regulating p53 pathways.

Higher levels of mRNA encoding the E2 enzyme Rad6 in PBF-Tg thyrocytes highlighted a potential route via which PBF might disrupt p53 stability. Subsequent examination of PBF-Tg thyroid glands revealed an increased abundance of nuclear Rad6 protein, a feature of invasive tumor cells (42), which colocalized with high PBF expression, especially at hyperplastic lesions. Recently it was shown that Rad6 plays a critical role in regulating p53 protein levels by forming a ternary complex with Mdm2 and p53 that contributes to p53 degradation in HeLa cells (41). Our results therefore indicate that PBF might also up-regulate Rad6 expression in order to decrease p53 stability. The precise mechanism by which PBF induces Rad6 is the subject of further work, although p53 response elements are located in the Rad6 promoter (57). However, we were able to confirm for the first time in thyroid cells that Rad6 coimmunoprecipitates with p53 and overexpression of Rad6 decreases p53 protein levels. In addition, a significant correlation was evident between PBF and Rad6 mRNA expression in human thyroid cancer specimens, further emphasizing the interaction between these 2 genes in thyroid disease.

Genomic instability is an evolving hallmark of cancer but the molecular basis is poorly defined (58). In our study elevated genetic instability was present in PBF-Tg mouse thyroids and associated with extensive repression of DNA repair genes. Of particular importance, the disruption of several genes highlighted in this study, including the Rad51 family (ie, Rad51, Xrcc3, Xrcc2, and Rad51c), have been associated with an increased risk of thyroid cancer (59). Furthermore, inactivation of Mgmt has been suggested to cause somatic mutations in RAS (60), a gene commonly mutated in thyroid neoplasms. Our results in this study would therefore suggest a novel mechanism for tumorogenesis such that PBF overexpression may disrupt DNA repair enzymes with critical roles in the pathogenesis of cancer, as well as contributing to the overall genetic instability typically associated with tumor progression (61).

We previously showed that thyroid cancers displaying recurrence demonstrate particularly high PBF levels (7). Similarly, a recent study showed that high PBF expression was significantly correlated with locoregional recurrence and distant metastases at diagnosis in patients with papillary thyroid cancer (12). These findings support a large-scale clinical evaluation to determine whether PBF expression in thyroid cancer correlates with genetic instability and somatic mutations typically associated with aggressive disease and increased mortality such as BRAF V600E (5).

In summary, we describe PBF as a novel interacting partner of p53, which alters p53 stability and transactivation capabilities. In defining a role for PBF, we demonstrate that it interferes with DNA repair pathways and induces genetic instability in thyroid cells in vivo. This work therefore provides an important insight into the role of the protooncogene PBF as a negative regulator of p53 in thyroid tumorigenesis, where PBF is generally overexpressed and p53 mutations relatively rare. It will also be important to determine whether high thyroidal PBF is a risk factor for irradiation-associated tumors, especially in individuals with multinodular goiters in which elevated PBF expression has been described (11). Together these...
findings further emphasize that PBF has an increasingly important role in the etiology of thyroid disease.

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Address all correspondence and requests for reprints to: Professor Christopher J. McCabe, Professor of Molecular Endocrinology, School of Clinical and Experimental Medicine, Institute of Biomedical Research, University of Birmingham, Birmingham, B15 2TH, UK. E-mail: mccabcjz@bham.ac.uk.

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