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Genomic and transcriptomic hallmarks of poorly differentiated and anaplastic thyroid cancers

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CONCLUSIONS. These data support a model of tumorigenesis whereby PDTCs and ATCs arise from well-differentiated tumors through the accumulation of key additional genetic abnormalities, many of which have prognostic and possible therapeutic relevance. The widespread genomic disruptions in ATC compared with PDTC underscore their greater virulence and higher mortality.

FUNDING. This work was supported in part by NIH grants CA50706, CA72597, P50-CA72012, P30-CA008748, and 5T32-CA160001; the Lefkovsky Family Foundation; the Society of Memorial Sloan Kettering; the Byrne fund; and Cycle for Survival.

Introduction

A comprehensive investigation of the genomic landscape of papillary thyroid carcinomas (PTC), the most common thyroid malignancy, was recently reported by The Cancer Genome Atlas Network (TCGA Network) (1). These well-differentiated tumors were found to have a low frequency of somatic alterations (2), with the majority harboring mutually exclusive activating mutations in BRAF (60%) and RAS-family genes (13%), as well as fusion oncoproteins, primarily involving receptor tyrosine kinases (RTKs) such as RET, NTRK1 or -3, and ALK. Distinct signaling and transcriptomic consequences were observed between BRAFV600E-like tumors, which showed higher MAPK transcriptional output and lower expression of genes involved in iodine metabolism, and RAS-like tumors, which had lower MAPK signaling and comparatively preserved expression of iodine-related genes.

The TCGA study excluded poorly differentiated thyroid cancers (PDTCs) and anaplastic thyroid cancers (ATCs) from their analysis in order to focus on a homogeneous histological cohort that would provide sufficient power to identify low-frequency genomic events. Although PDTCs and ATCs account for approximately 5%-10% of thyroid cancers, they represent a major clinical challenge. Patients with PDTC and ATC have a mean survival after diagnosis of 3.2 and 0.5 years, respectively, and account for approximately a third of deaths caused by this disease (3). Virtually all cases are refractory to radioiodine therapy, and traditional chemotherapy and radiotherapy are of marginal benefit (4, 5). Molecularily targeted approaches are being tested in preclinical...
as expression profiling in the largest series of PDTC and ATC ever investigated, and we identified a wide spectrum of somatic mutations, genetic fusions, and copy number alterations (CNAs) that clearly delineate profound genomic differences between the two advanced forms of the disease. Moreover, when analyzed in the context of the PTC TCGA study (1), this study provides insights into tumor microevolution, suggesting that PDTCs and ATCs evolve from their well-differentiated counterparts.

**Results**

**Samples, clinical data, and overall approach**

One-hundred and seventeen advanced thyroid tumors, including 84 PDTCs and 33 ATCs, met the sequencing quality standards and are reported in this study. Clinicopathological features are summarized in Table 1 and Supplemental Table 1 (supplemental material available online with this article; doi:10.1172/JCI85271DS1). Median age was 58 and 66 years for PDTC and ATC, respectively. Female/male ratios were 1.5:1 (PDTC) and 1.2:1 (ATC), which are similar to those in the TCGA series (1). Median tumor purity was 72% and 42% for PDTCs and ATCs, respectively, consistent with the known heavy macrophage infiltration in ATCs and highlighting the need for deeper sequence coverage in these tumors (Figure 1B). Average depth of coverage was 584× for tumors and 236× for paired normal tissues. Average coverage was 500× for FFPE and frozen tumors, respectively. Coverage for ATCs was 739×.

**Somatic mutations**

ATCs harbored a higher number of mutations than PDTCs (median ± interquartile range [IQR]: 6 ± 5 and 2 ± 3, respectively, \( P < 1 \times 10^{-4} \)) (Figure 1A). The mutation burden in PDTCs was increased compared with the PTCs from the TCGA study (considering mutations in the 341 gene set only): 2 ± 3 and 1 ± 1, respectively (\( P < 1 \times 10^{-4} \)). These differences remained highly significant after removing tumors with defects in mismatch excision repair (MMR) genes, which showed a disproportionately higher number of mutations. Mutation burden in PDTCs (expressed as number of mutations below, equal, or above the median) was greater in older patients (47 vs. 58 vs. 64 years, \( P < 1 \times 10^{-3} \)) and associated with tumor size (36% vs. 43% vs. 71% > 4 cm, \( P = 0.04 \)), presence of distant metastasis (8% vs. 29% vs. 57% > 4 cm, \( P = 0.04 \)), and associated with tumor size (36% vs. 43% vs. 71% > 4 cm, \( P = 0.04 \)).

Drivers and frequently altered genes. \( B R A F^{V600E} \) mutations were present in 33% of PDTCs and 45% of ATCs, whereas mutations in \( N R A S, H R A S, \) or \( K R A S \) occurred in 28% and 24% of PDTCs and ATCs, respectively, and were mutually exclusive with \( B R A F \) and gene fusions (Figure 1, C and D, and Supplemental Tables 3 and 4). There was a dichotomy in the distribution of \( R A S \) and \( B R A F \) mutations of PDTCs according to their histological features. Ninety-
two percent of RAS mutations were found in PDTCs fulfilling the Turin definition of the disease (PDTC-Turin; see Methods, ref. 26). By contrast, 81% of BRAF mutations were found in PDTCs defined based only on MSKCC criteria (PDTC-MSK): high mitotic rate and necrosis irrespective of growth pattern (ref. 27 and Figure 1, B and C). BRAF-mutant PDTCs were smaller and had higher frequency of nodal metastases, whereas their RAS-mutant counterparts were larger and had a higher rate of distant metastasis (Supplemental Table 5). BRAF-mutant PDTCs were significantly overrepresented among female patients (P = 0.005).

Neurofibromin 1 gene (NFI) mutations were identified in 3 BRAF/RAS WT ATCs. There were also low-frequency mutations in TSHR and STK11 in both PDTCs and ATCs (Figure 1C). Mutations in PIK3CA and PTEN, which encode key effectors of the PI3K/AKT pathway, were particularly prevalent in ATCs (18% and 15%, respectively, Supplemental Table 3) and were overrepresented with respect to PDTCs (P = 4 × 10⁻⁴ and 6 × 10⁻³, respectively). PIK3CA and PTEN showed distinct patterns of co-occurrence in ATCs. All 3 ATCs harboring NFI mutations also had truncating alterations in PTEN (P = 2 × 10⁻³), whereas PIK3CA and BRAF mutations tended to co-occur. All 5 PIK3CA helical domain mutations (ES42K or ES45K) occurred in ATCs, whereas the single kinase domain mutation (H1047R) was found in a PDTC (Figure 1C).

The EIFIAX-RAS association. Mutations in the eukaryotic translation initiation factor EIFIAX were initially discovered in uveal melanomas (28) and were also reported in 1% of PTCs (6/402), largely occurring in a mutually exclusive manner with BRAF and RAS (1). By contrast, 11% of PDTCs and 9% of ATCs harbored EIFIAX mutations (Figure 1C and Figure 2A), which were strongly associated with RAS (4/15, P < 1 × 10⁻⁴, Figure 2B and Table 2). EIFIAX mutations clustered in two regions: the N-terminal domain, as also observed in uveal melanomas (28) and other tumors (Figure 2A), or at a unique splice acceptor site between exons 5 and 6 (p.A113splice), which was the most prevalent abnormality and which has not been reported in other tumor types. The C-terminal p.A113 splice prediction (not shown). EIFIAX mutations were associated with larger tumors and predicted for shorter survival in PDTCs (Figure 2C and Supplemental Table 6).

TERT in advanced thyroid cancer. There was a high prevalence of telomerase reverse transcriptase (TERT) promoter mutations in these advanced thyroid tumors, and their presence was associated with aggressive and metastatic phenotypes (Figure 1E). Together, 40% of PDTCs and 73% of ATCs harbored TERT promoter mutations (49/117 C228T [c.-124G>A]; 8/117 C250T [c.-146G>A]) as compared with 9% of PTCs from TCGA (Figure 3, A and B, and Table 3). Whereas TERT promoter mutations were subclonal in the small subset of PTC that harbored them, they were clonal in PDTC and ATCs (Figure 3C). TERT mutations co-occurred with BRAF/RAS mutations in PDTCs and ATCs combined (P = 4 × 10⁻⁴; Figure 3B and Table 3), consistent with the proposed mechanism whereby the TERT mutations generate de novo binding elements for ETS-family transcription factors activated by MAPK signaling, such as GABPA (29). Survival of ATC patients harboring TERT promoter mutations was markedly diminished (732 vs. 147 days, P = 0.03, Supplemental Table 7), particularly in cancers with coexisting mutations of BRAF or RAS (Figure 3D). TERT-mutated PDTCs developed more distant metastases (56% vs. 20%, P = 0.01) and had a trend toward greater mortality (Supplemental Table 7). RAS-mutant ATCs with TERT (5/8) and EIFIAX mutations (3/8) did not overlap (odds ratio = 0.01; P = 0.02), consistent with alternate pathways toward progression to ATC.

TP53 and other tumor-suppressor genes. Inactivation of p53 has been considered as a hallmark of advanced thyroid tumors (14, 30). We found that TP53 mutations, although highly prevalent in ATCs, were relatively rare in PDTCs (73% vs. 8%, P < 1 × 10⁻⁴, Figure 1F), which contrasts with previous reports (refs. 11, 31, and Supplemental Table 8) and constitutes a key distinguishing event in the biology of these tumors. ATM, a cell-cycle checkpoint and DNA damage response gene, was mutated in 7% of PDTCs and 9% of ATCs. ATM-mutated tumors had a higher mutation burden: median was 5 and 2 in ATM-mutant versus WT PDTCs (P = 0.04), and 19 and 5.5 in ATC, respectively (P = 7 × 10⁻⁴). A higher mutation burden is consistent with the loss of the canonical function of this checkpoint kinase, which is activated in response to DNA double strand breaks and is required for appropriate DNA repair (32). Infrquent truncating mutations were also found in R1, NF2, and MEN1.

Novel genes and pathways altered in advanced thyroid tumors. Mutations of genes encoding members of the PI3K/AKT/mTOR pathway were seen more frequently in ATCs than PDTCs (39% vs. 11%, P = 1 × 10⁻¹). Besides PIK3CA and PTEN, mutations of PIK3C2G, PIK3CG, PIK3C3, PIK3R1, PIK3R2, AKT3, TSC1, TSC2, and MTOR were also present (Figure 1G, Figure 4, A and E, and Supplemental Figure 1).

Genes encoding components of the SWI/SNF chromatin remodeling complex were mutated in 36% of ATCs and 6% of PDTCs (P = 1 × 10⁻⁹). This is the first report of mutations in ARID1A, ARID1B, ARID5B, SMARCBI, PBKMI, and ATRX in advanced thyroid tumors. Consistent with evidence that disruption of one protein in this complex is typically sufficient to impair function (33), we observed a pattern of mutual exclusivity of mutations in this category of genes (Figure 4B). The single exception was for an ATC with concurrent missense mutations in ARID1A (minor allele fre-
Other genes and functional categories were mutated in a small proportion of PDTCs and ATCs (Supplemental Figure 1 and Supplemental Table 4), i.e., RTKs such as EPHA3 (3 mutations, exclusively in ATCs), EGFR, FLT1 (VEGFR1), FLT4 (VEGFR3), and KDR (VEGFR2), as well as in all four members of the NOTCH family (NOTCH1–4). Finally, there were infrequent mutations of the histone methyltransferases (HMTs) KMT2A, KMT2C, KMT2D, and SETD2 were found in 24% of ATCs and 7% of PDTCs (P = 0.02) (Figure 4C). Additional mutations in chromatin remodeling and epigenetic regulators other than SWI/SNF and HMTs were also seen, including frequent alterations affecting the histone acetyltransferase CREBBP and sporadic inactivating mutations in other epigenetic players such as EP300, BCOR, and BCL6 (Supplemental Figure 1). Mutations in a few epigenetic regulators (ARID1B, KMT2A, and KMT2C) were also identified in 1%–2% of PTCs from the TCGA, but these events are clearly enriched in advanced thyroid tumors.

Alterations in members of the DNA MMR pathway, including MSH2, MSH6, and MLH1, were found in 12% of ATCs and 2% of PDTCs (Figure 4D). MMR mutant tumors showed a “hypermutator phenotype” (as described in ATCs; ref. 21): median mutation number in MMR-mutant vs. WT ATCs was 16.5 and 5 (P = 1 × 10–3) and, in PDTCs, 7.5 and 2 (P = 9 × 10–3), respectively.

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Table 2. Contingency analysis of EIF1AX-RAS mutations in advanced thyroid cancers (PDTCs and ATCs)

<table>
<thead>
<tr>
<th></th>
<th>RAS WT</th>
<th>RAS mutant</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>EIF1AX WT</td>
<td>100 (80.6)</td>
<td>24 (19.4)</td>
<td>124 (100.0)</td>
</tr>
<tr>
<td>EIF1AX mutant</td>
<td>1 (6.7)</td>
<td>14 (93.3)</td>
<td>15 (100.0)</td>
</tr>
</tbody>
</table>

Number of samples and percentage (in parentheses) of RAS mutations in EIF1AX WT and mutant samples. The ATC series combines 33 samples from this study and 22 from Kuntsman et al. (21). Statistical analysis show a highly significant co-occurrence of EIF1AX and RAS mutations (odds ratio = 58.3; 2-tailed Fisher’s exact test associated P < 0.001).
mutations (mutated in at least 2 ATCs or 3 PDTCs) in DIS3, FAT1, POLE, RBM10, RAD54L, RECQL4, and SF3B1.

Mutations of genes encoding members of the WNT signaling pathway—i.e., CTNNB1 (β-catenin), AXIN1, and APC—have previously been reported as genetic hallmarks of ATCs (12, 13), with mutation frequencies >60% for CTNNB1 (reviewed in Supplemental Table 8). The deep-sequencing results in our cohort do not replicate these findings. We found a single tumor carrying a missense mutation (p.L347P) in CTNNB1, which is distinct from the CTNNB1-exon 3 gain-of-function hotspot previously reported in this disease. Variants in AXIN1 were found in 2/117 tumors, both without paired normals available and both of which may have represented low-frequency germline polymorphisms. A single truncating mutation in APC (p.Q1529X) was found in an ATC with an unusually high mutation burden.

In addition, our results do not support a relevant role for mutations in genes in the apoptosis, Hedgehog, homologous recombination, immune response, insulin-like, JAK-STAT, tricarboxylic acid, nucleotide excision repair, polycomb, ubiquitination, or TGFβ pathways in PDTC and ATC tumorigenesis. With respect to mutations reported in single cases in a recent exome sequencing study of ATCs (21), we replicated these findings in the cyclin-dependent kinase inhibitors CDKN1B and CDKN2C (and found an additional truncating mutation in CDKN2A), as well as in other genes such as ERBB2, PTCH1, and DAXX (Supplemental Figure 1), but not in TRAF7 and NCOR1.

Gene fusions

Chromosomal rearrangements involving genes known to be translocated in thyroid tumors were frequent events in PDTCs (14%) but were absent in ATCs and did not overlap with BRAF, RAS, TSHR, or STK11 mutations (Figure 1D). RET/PTC rearrangements were detected in 5 PDTCs and involved the most common RET partners CCDC6 and NCOA4. Translocations leading to PAX8-PPARG fusions were observed in 3 PDTCs, whereas fusions involving ALK gene were detected in another 3 tumors. The kinase domain of ALK was recombined with three different upstream partners, including the known STRN and EML4, as well as CCDC149, a novel ALK fusion partner, which is a coiled-coil family gene located on chromosome 4 (fusion included CCDC149 exons 1–10 and ALK exons 20–29). The 11 PDTCs harboring gene fusions occurred in younger patients (49 vs. 58 years, P = 0.04; Supplemental Table 5).

A single ATC without known driver mutations carried a t(15;19)(q13;p13.1) translocation involving the NUT gene (NUTMI, NUT midline carcinoma, family member 1) and BRD4 (bromo-
domain containing 4), resulting in an in-frame NUT-BRD4 fusion (NUT exons 1–2 and BRD4 exons 14–20). It was detected in an ATC with areas of PDTC in a 34-year-old woman who underwent total thyroidectomy and laryngopharyngectomy, plus radiotherapy, and who is alive 10 years after diagnosis. It clearly represents an outlier from the clinical behavior standpoint, which matches with her unique genetic alteration, involved in large-scale chromatin remodeling (34).

**Somatic CNAs**
Tumor purity of PDTCs was similar to PTCs (median tumor content 74% and 72%, respectively) whereas it was much lower in ATCs (42%) (Supplemental Figure 2). By correcting for tumor purity, we greatly enhanced our sensitivity for detecting CNAs even in most of the heavily infiltrated ATCs, as well as in some PDTCs. The ability of IMPACT to call arm-level CNAs was explored in 37 tumors that were simultaneously profiled by array-CGH. As seen in Supplemental Figure 3, CNA calls were efficiently replicated in both platforms. In addition, IMPACT identified CNAs that were not detected by array-CGH, particularly in heavily infiltrated tumors.

Whereas the genome of PTCs is largely diploid, CNAs in advanced thyroid tumors were common and widespread (Supplemental Figure 4). Interestingly, CNAs were more frequent in the ATCs and PDTCs that lacked driver mutations (Figure 5A). A similar subset of PTCs from the TCGA analysis also possessed a high prevalence of CNAs in the absence of driver mutations (1). Overall, 8 arm-level recurrent CNAs were represented in our array (Supplemental Figure 5). All 13 BRAF V600E-mutated PDTCs and ATCs were BRAF-mutant PDTC that was heavily infiltrated with macrophages (tumor purity = 46%, high M2-macrophage signature score, see also Figure 7A).

**Gene expression profiling: signaling and differentiation**
We used a subset of fresh-frozen specimens of 17 PDTCs and 20 ATCs to derive insights into the gene expression profiles of advanced thyroid cancers. The 37-tumor dataset was representative of the main driver genetic alterations described and included 13 BRAF, 12 RAS, 5 with alterations in other drivers (NF1, NCOA4, RET, CCDC149-ALK, NUT-BRD4, and STK11), and 7 without known driver mutations (Supplemental Table 9).

A principal component analysis efficiently separated both entities based on their global gene expression (Figure 6A). Only 2 tumors clustered out of their tumor type group: an ATC from a metastatic specimen (the single one in this subset of 20 ATCs) and a BRAF-mutant PDTC that was heavily infiltrated with macrophages (tumor purity = 46%, high M2-macrophage signature score, see also Figure 7A).

**MAPK signaling: the BRAF-RAS score.** As a consequence of their genomic simplicity, the key oncogenic drivers of PTCs are associated with distinct biological, signaling, and gene expression properties. Pertaining to this study, the recently published TCGA analysis of 390 PTCs showed clear gene expression differences between BRAF and RAS tumors, which were used to construct a BRAF-RAS score (BRS) (1). We aimed to evaluate whether these driver-dependent gene expression characteristics persist in advanced cancers, which harbor a more complex cancer genome. Sixty-seven out of the 71 genes in the BRS were present in the mRNA array and were assessed in our PDTCs and ATCs with known driver mutation status. We found a high correlation between BRS values and BRAF/RAS mutation status (Figure 6B and C). All 13 BRAF V600E-mutated PDTCs and ATCs were BRAF-like. However, although RAS-mutant PDTCs were strongly RAS-like, RAS-mutant ATCs were BRAF-like ($P = 3 \times 10^{-3}$), suggesting that a high MAPK transcriptional output is a characteristic property of ATCs, regardless of the driver mutation (Figure 6C and Supplemental Figure 5).

**Macrophage infiltration.** ATCs are known to be extensively infiltrated with macrophages (22, 23). Although it is assumed that these are M2 macrophages, which promote tumorigenesis, this has not been proven. We applied a previously characterized signature (35) of 78 genes overexpressed in M2 macrophages (68 of which were represented in our array) to the 37 tumors (Figure 7A and Supplemental Figure 6) and found that it was sufficient to discriminate ATCs from the great majority of PDTCs, which are less prone to macrophage infiltration. The only 3 PDTCs that clustered with ATCs had a lower median estimated tumor purity than the

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**Table 3. Contingency analysis of TERT-BRAF/RAS mutations in thyroid cancers**

<table>
<thead>
<tr>
<th></th>
<th>TERT WT</th>
<th>TERT mutant</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>BRAF/RAS WT</strong></td>
<td>103</td>
<td>4</td>
<td>107</td>
</tr>
<tr>
<td><strong>BRAF/RAS mutant</strong></td>
<td>243</td>
<td>31</td>
<td>274</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>346</td>
<td>35</td>
<td>381</td>
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</table>

<table>
<thead>
<tr>
<th></th>
<th>TERT WT</th>
<th>TERT mutant</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>PDTC + ATC</strong></td>
<td>29</td>
<td>13</td>
<td>42</td>
</tr>
<tr>
<td><strong>BRAF/RAS WT</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>BRAF/RAS mutant</strong></td>
<td>30</td>
<td>45</td>
<td>75</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>59</td>
<td>58</td>
<td>117</td>
</tr>
</tbody>
</table>

*Papillary thyroid cancers from the TCGA study (1), n = 381. *PDTC and ATC from the current study (n = 84 + 33). TERT and BRAF/RAS mutations significantly co-occur both in PTCs (contingency test: OR = 3.3; $P = 0.03$) and in PDTCs and ATCs combined (contingency test: OR = 3.4; $P = 0.004$). Odds ratios and $P$ values are derived from 2-tailed Fisher’s exact tests.

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rest of the PDTCs, suggestive of significant stromal contamination (46% vs. 84%, respectively; median purity in ATCs was 36%). Consistent with this, the prevalence of likely clonal mutations in ATCs, such as BRAF and TERT, is higher in this study than that described in prior reports (refs. 10, 17–20, 36–38, and Supplemental Table 8), probably due to IMPACT’s deeper coverage.

**Thyroid differentiation score.** Loss of expression of thyroid differentiation markers is one of the hallmarks of advanced thyroid cancers and has profound consequences for the clinical management of these patients, who are usually refractory to radioiodine therapy due to loss of expression of NIS (sodium iodide symporter, SLC5A5) and other genes required for iodine incorporation. The TCGA analysis of PTCs used a thyroid differentiation score (TDS) consisting of 16 genes involved in iodine metabolism and thyroid specification to investigate driver-dependent effects on these parameters. We compared the TDS in PDTCs and ATCs with 8 PTCs profiled with the same platform (39). Overall, PDTCs and PTCs did not differ greatly, whereas ATCs had profoundly suppressed mRNA levels for TG, TSHR, TPO, PAX8, SLC26A4, DIO1, and DUOX2 genes (Figure 7B and Supplemental Table 9). None of the tumor types expressed THRB, DUOX1, SLC5A5, or SLC5A8. Unsupervised clustering based on the TDS discriminated ATCs from PDTCs (Supplemental Figure 7), with the exception of 3 PDTCs. These clustered with ATCs and corresponded to patients who died of the disease, two of whom were the only BRAFV600E-mutated PDTCs in this subset.

**Discussion**

Most PDTCs and ATCs are thought to arise from preexisting PTCs based on their frequent co-occurrence in the same tumor specimen, where they consistently share a driver mutation (36, 40).
PDTCs, and 73% in ATCs) (1, 17–20). Interestingly, TERT mutations are subclonal in the few PTCs that harbor them, whereas they are clonal in PDTCs and ATCs, pointing to selection during tumor evolution, possibly by inducing cell immortalization. TERT promoter mutations also track with virulence of advanced disease. They are significantly associated with BRAF or RAS mutations.

Our results, analyzed in the context of the PTC TCGA study, provide insights into tumor microevolution and lend support to this model of tumorigenesis. Particularly compelling in this regard is the fact that mutations in the TERT promoter, which are known to activate its transcription, display a stepwise increase in frequency along the spectrum of disease progression (9% in PTCs, 40% in PDTCs, and 73% in ATCs) (1, 17–20). Interestingly, TERT mutations are subclonal in the few PTCs that harbor them, whereas they are clonal in PDTCs and ATCs, pointing to selection during tumor evolution, possibly by inducing cell immortalization. TERT promoter mutations also track with virulence of advanced disease. They are significantly associated with BRAF or RAS mutations,
consistent with the proposed mechanism by which mutations in the promoter, by generating novel consensus motifs for the ETS family of transcription factors, promote TERT overexpression in cells with constitutive activation of MAPK signaling.

By using a platform with a depth of sequencing optimized to identify mutations in tumors known to be associated with abundant stromal contamination, primarily by tumor associated macrophages (TAMs) (22, 23), we identified key genetic lesions that...
NF1 mutations were only found in ATCs in our series. The TCGA study of PTCs showed that BRAF- and RAS-mutant tumors exhibited profound differences in their clinical and histological characteristics and in their gene expression profile. The BRS is a 71-gene panel that distinguishes BRAFV600E from RAS-mutant PTCs. It was highly correlated to the transcriptional output of the MAPK pathway, which was highest in BRAF-mutant cancers. This is explainable because ERK activation in RAS-mutant cells induces a negative feedback that disrupts RAF dimerization, thus attenuating pathway output. By contrast, BRAFV600E signals as a main driver alteration, BRAF mutations were less prevalent in advanced tumors compared with PTCs, whereas RAS mutations were more frequent. Rearrangements commonly seen in radiation-induced and, to a lesser extent, in sporadic PTCs (RET/PTC, PAX8-PPARG and ALK fusions) were present in a subset of PDTCs but absent in the ATCs we sampled.

distinguish PDTCs from ATCs (i.e., TPS3, TERT, and genes encoding effectors in the PI3K pathway). This includes genetic defects that implicate functional programs not previously associated with thyroid cancer, such as the SWI/SNF complex, HMTs, and others.

With respect to the main driver alterations, BRAF mutations were less prevalent in advanced tumors compared with PTCs, whereas RAS mutations were more frequent. Rearrangements commonly seen in radiation-induced and, to a lesser extent, in sporadic PTCs (RET/PTC, PAX8-PPARG and ALK fusions) were present in a subset of PDTCs but absent in the ATCs we sampled (9, 41, 42). NF1 mutations were only found in ATCs in our series. The TCGA study of PTCs showed that BRAF- and RAS-mutant tumors exhibited profound differences in their clinical and histological characteristics and in their gene expression profile. The BRS is a 71-gene panel that distinguishes BRAFV600E from RAS-mutant PTCs. It was highly correlated to the transcriptional output of the MAPK pathway, which was highest in BRAF-mutant cancers. This is explainable because ERK activation in RAS-mutant cells induces a negative feedback that disrupts RAF dimerization, thus attenuating pathway output. By contrast, BRAFV600E signals as...
a monomer and is unresponsive to this constraint, resulting in a greater flux through the pathway (1, 43). We found that these sharp demarcations between BRAF- and RAS-mutant disease persisted in PDTC but were largely lost in ATC. PDTCs that met the standard histological definition of that entity (Turin proposal, ref. 26) were strongly associated with RAS mutations. By contrast, those defined based on the presence of high mitotic rate and necrosis irrespective of other characteristics (27) were markedly enriched for BRAF. They also had distinct clinical behaviors: BRAF-mutant PDTCs primarily developed locoregional nodal metastases, whereas RAS-mutant PDTCs presented with distant metastases. The BRS tracked with the underlying driver mutation in PDTCs but not in ATCs. This was also true for a score derived from a gene set consisting of mRNAs encoding proteins required for the differentiated function of thyrocytes (the TDS). The greater genomic complexity of ATCs may account for blurring the association of gene expression with the nature of the underlying driver mutation, in particular because of the higher frequency of mutations of genes encoding chromatin modifiers or genes that activate parallel pathways. Interestingly, even ATCs with RAS or other mutations tend to be BRAF-like, as defined by the BRS. In addition, ATCs are extensively infiltrated by TAMs. Accordingly, nonhierarchical analysis of a gene set that defines M2 macrophages clearly separated ATCs from PDTCs. It may be that the greater cellular heterogeneity of ATCs may account in part for the attenuation of the oncogenic driver effects on gene expression.

EIF1AX, which encodes for a key component of the translation preinitiation complex (PIC), is mutated in only 1% of PTCs but in approximately 10% of PDTCs and ATCs. The concordance of EIF1AX with RAS mutations is extremely strong, which is distinct from PTC, where these are largely mutually exclusive. The biological consequences of this association are currently unknown. The mutations of EIF1AX cluster in specific N- and C-terminal residues. The C-terminal p.A113 splice mutation is specific to thyroid cancer and predicts for alternative usage of a cryptic splice acceptor within exon 6, resulting in a 12-amino acid in-frame deletion. Our analysis of RNASeq data from two cases with this mutation in the PTC TCGA confirms this prediction (not shown). EIF1A plays a key role in regulating the conformation of the PIC and in scanning for the AUG initiation codon, which is disrupted in distinct ways by N-terminal and C-terminal mutations in yeast (44). Interestingly, EIF1AX mutations are mutually exclusive with alterations in any of the PI3K/AKT/mTOR pathway members, suggesting that they may confer overlapping functional gains. In addition, EIF1AX mutations are predictive of worse survival in PDTCs, providing a potentially useful marker for risk stratification in a heterogeneous disease in need of better prognostic indicators (45, 46).

Both entities differed in overall mutation burden, which was significantly higher in ATCs. Within PDTCs, a higher number of mutations was associated with larger tumors, presence of metastasis, and shorter survival. TP53 mutations, in particular, distinguished ATCs from PDTCs (73% vs. 8%, respectively). CNAs, some of which had been previously reported at very low frequencies (47–51), proved to be distinctive of each tumor type. PDTCs have a greater frequency of 1p losses, whereas 8p and 17p losses, as well as 20q gains, were more common in ATCs. Interestingly, 22q losses were strongly associated with RAS-mutant PDTCs. Loss of the 22q tumor suppressor gene NF2, which encodes for merlin, has been recently implicated in this association. Consistent with this, the combined activation of oncogenic Ras with NF2 loss leads to development of PDTC in mice. This is because inactivation of the Hippo pathway through Merlin loss leads to a YAP-TEAD–dependent transcriptional activation of oncogenic and WT Ras, thus enhancing MAPK transcriptional output and promoting transformation (1, 52).

We compared the results of our targeted cancer gene NGS (IMPACT) approach with a recently reported whole exome sequencing (WES) study of 22 ATCs (21). The greater depth of sequencing achieved by IMPACT (739× vs. 264× in the WES study) may explain the differences observed between both platforms in the frequency of TP53 (73% by IMPACT vs. 27% by WES), BRAF (45% vs. 27%), PIK3CA (18% vs. 9%), and PTEN (15% vs. 0%) and may improve detection of subclonal events. This is particularly relevant in ATCs because of their low tumor purity, which calls into question the suitability of WES as the platform of choice. Moreover, the WES approach failed to detect mutations in members of the SWI/SNF and HMT functional groups that we report here and that likely play a fundamental role in the biology of these tumors. We acknowledge, however, the drawbacks of sequencing a limited set of cancer genes. For instance, RASALI, USH2A, HECTD1, MLH3, and MSH5, which were rarely mutated in ATCs by WES, were not included in IMPACT. Two of these, MLH3 and MSH5, are MMR genes, a functional group that we find to be disrupted in at least 12% of ATCs.

The biological consequences of the novel drivers (e.g., EIF1AX and RAS) and functional groups (SWI/SNF) in the context of thyroid tumorigenesis remain to be explored. Others recapitulate phenotypes observed in genetically engineered mouse models of advanced thyroid cancers, such as PTEN and TP53 (53), BRAF and TP53 (54), RAS and TP53 (55), RAS and NF2 (52), and BRAF and PIK3CA (56).

The findings reported here provide tools that can be leveraged to improve the molecular diagnosis of these clinical entities, many of which likely have prognostic implications. Particularly relevant is the strong association of PDTC-Turin tumors with RAS mutations, whereas PDTC-MSK tumors were strongly associated with BRAF. In addition, RAS- and BRAF-mutant PDTCs have distinct tropism for metastases, with the former tending to home at a distance, whereas the latter metastasize to locoregional lymph nodes. Moreover, the discovery in well-differentiated tumors of subclonal mutations of genes that we show to be enriched in advanced disease should raise particular concerns. This also opens a path to explore the biology of novel genetic associations that may point to tumor dependencies that can be exploited therapeutically.

**Methods**

**Patient tissue samples.** PDTC and ATC samples were randomly selected from the pathology department files of the institution from 1986–2015. ATCs were classified according to the last WHO classification of endocrine tumors, whereas PDTCs were defined as follows: (i) according to the Turin proposal, by architectural and high-grade features (mitosis and necrosis), the presence of a solid/nested/insular growth, the absence of nuclear features of PTC, and either convoluted nuclei, mitotic activity ≥ 3 × 10 high power fields (HPF), or tumor necrosis (26); and (ii) as a carcinoma display-
ing high mitotic activity (≥ 5 mitosis/10 HPF, ×400) and/or tumor necrosis, and showing follicular cell differentiation at the morphological or immunohistochemical level (27). MSK-IMPACT targeted sequencing was performed in all 117 tumors (84 PDTCs and 33 ATCs); 80 from formalin-fixed paraffin-embedded tissues (FFPE) and 37 from fresh-frozen material. The 37 frozen tumors, 17 PDTCs and 20 ATCs, were also expression profiled with Affymetrix U133 plus 2.0 array and with the Agilent SurePrint G3 CGH 1x1M array-CGH platform to validate copy number calls.

Single nucleotide variant and indel calling and filtering. Single nucleotide variants (SNVs) and short indels (<30 bp in length) were automatically annotated by the MSK-IMPACT pipeline, as previously described (24). Tumor samples without paired normals (11/117; 5 ATCs and 6 PDTCs) were compared against pooled normals. All variants were annotated based on the information available in catalog of somatic mutations in cancer (COSMIC; http://cancer.sanger.ac.uk/cosmic), NCBI-dbSNP (http://www.ncbi.nlm.nih.gov/snp), and the 1,000 Genomes Project (http://www.1000genomes.org/). Variants highlighted in this study were subsequently manually reviewed. For the 106 tumors with paired normals, all variants confirmed as somatic were reported, regardless of location and clonality. For tumors compared against pooled normals, MSK-IMPACT automatically called SNVs with reported frequencies <1%. We manually reviewed the 11 tumors fulfilling these criteria as follows: (i) keeping variants reported in COSMIC; (ii) removing variants reported as polymorphic (with an reference sequence code in dbSNP); and (iii) removing variants with allele frequencies that were >10% of the allelic fraction of the driver mutation in the same tumor.

MSK-IMPACT sequencing data is publicly available at the cBioPortal for Cancer Genomics (http://www.cbioportal.org/). Mutation plots were generated using the OncoPrinter (v1.0.1) and Mutation-Mapper (v1.0.1) tools, which are available at the cBioPortal (57, 58).

Chromosomal rearrangements were called for genes whose introns were covered by MSK-IMPACT, which included most of the previously reported fusions in thyroid tumors (with the notable exceptions of NTRK1 and NTRK3).

CNAs and estimation of tumor purity. DNA CNAs were primarily called from IMPACT by comparing sequence reads of targeted regions in tumors relative to a standard diploid normal sample, as described (24). Although IMPACT targets a discrete number of exons in each chromosome arm, it efficiently identified arm-level chromosomal genetic gains and losses, as confirmed by a genome-wide Agilent SurePrint G3 CGH 1x1M array-CGH platform in a subset of 37 advanced thyroid tumors (Supplemental Figure 3), which showed excellent agreement in the copy number calls between the two methodologies.

As the macrophage infiltration of advanced thyroid tumors (particularly ATCs) can impact the sensitivity of CNA detection, we corrected CNA values for each tumor based on tumor purity. Tumor purity was calculated based on the mutant allele frequencies of clonal heterozygous somatic mutations in regions lacking overt CNAs (see also Supplemental Figure 2). For tumors with a BRAF or RAS mutation (heterozygous mutations considered clonal events) (59), purity was calculated by doubling the frequency of the alternate allele (e.g., in a tumor with a BRAF

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log plots. Kaplan-Meier survival curves were built, and the log-rank test was used to assess for significance of the surviving function. A $P$ value less than 0.05 was considered significant.

**Study approval.** The study was approved by the Institutional Review Board of MSKCC.

**Author contributions**

IL, IG, and JAF designed the study; IL, TI, RS, JCRF, and GPK conducted experiments; TI, LB, RHS, NS, MFB, and RG acquired data; IL, LB, RS, JAK, RHS, MFB, CS, BST, IG, and JAF analyzed data; SD, BX, and RG provided samples or reagents; IL and JAF wrote the manuscript.

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