ENDOCRINE TUMOURS

Genetic predictors of thyroid cancer outcome

Catarina Tavares¹,²,³*, Miguel Melo¹,²,⁴,⁵*, José Manuel Cameselle-Teijeiro⁶,
Paula Soares¹,²,³,⁷ and Manuel Sobrinho-Simões¹,²,³,⁷,⁸

¹Instituto de Investigação e Inovação em Saúde, Universidade do Porto, 4200-135 Porto, Portugal, ²Cancer Biology, Institute of Molecular Pathology and Immunology of the University of Porto (IPATIMUP), Rua Dr Roberto Frias, s/n, 4200-465 Porto, Portugal, ³Medical Faculty, University of Porto, Al. Prof. Hernâni Monteiro, P-4200 Porto, Portugal, ⁴Endocrinology, Diabetes and Metabolism Department, Centro Hospitalar e Universitário de Coimbra, Praca Mota Pinto, 3000-075 Coimbra, Portugal, ⁵Medical Faculty, University of Coimbra, Azinhaga de Santa Comba, 3000-548 Coimbra, Portugal, ⁶Department of Pathology, Medical Faculty, Servicio Gallego de Salud–SERGAS, Clinical University Hospital, University of Santiago de Compostela, 15705 Santiago de Compostela, Spain, ⁷Department of Pathology and Oncology, Medical Faculty of Porto University, Porto, Portugal and ⁸Department of Pathology, Hospital de S. João, Al. Prof. Hernâni Monteiro, P-4200 Porto, Portugal

*(C Tavares and M Melo contributed equally to this work)

Abstract

Genetic predictors of outcome are reviewed in the context of a disease – cancer – that can be (too) simplistically described as a ‘successful, invasive clone of our own tissues’. Context has many faces that determine a thyroid cancer patient’s outcome beyond the influence of genetic markers. There is also plenty of evidence on the prognostic meaning of the interplay between genetics and context/microenvironment factors (encapsulation, degree of invasion, staging, etc.). This review addresses only genetic alterations detected by molecular methods in surgically resected specimens, thus ruling out immunohistochemistry and (F)ISH, despite their crucial relevance as topographically oriented methods. For the sake of the discussion, well-differentiated carcinomas were divided into two main morphologic types: papillary carcinoma (classic and most variants) displaying BRAFV600E mutations and RET/papillary thyroid carcinoma rearrangements and the group of follicular patterned carcinomas that encompasses follicular carcinoma and the encapsulated form of follicular variant of papillary carcinoma, displaying RAS mutations and PAX8/PPARγ rearrangement. TERT promoter mutations have been recently described (and associated with distant metastases and reduced survival) in papillary and follicular carcinomas, as well as in poorly differentiated and undifferentiated carcinoma. TP53 mutations, previously thought to be restricted to less differentiated carcinomas, were also detected in papillary and follicular carcinoma and found to carry a guarded prognosis. Besides their putative importance for targeted therapies, the prognostic meaning of such mutations is discussed per se and in the setting of concurrent BRAF mutation.

Invited Author’s profile

M Sobrinho-Simões, MD, PhD is Professor and Director of the Department of Pathology and Oncology of Porto Medical Faculty, Chief of Service of Pathology at S. João Hospital and Director of the Institute of Molecular Pathology and Immunology of the University of Porto (IPATIMUP), which he co-launched in 1989. His main interests are oncobiology and thyroid cancer in the frame of translational research. He has been particularly involved in the integration of ultrastructural, immunocytochemical and molecular data in pathology and oncology of endocrine organs. His research group has published seminal papers on GRIM-19 and Hürthle cell tumours, BRAF mutations in PTC and TERT promoter mutations in thyroid cancer.
Introduction

Assuming that cancer can be defined, in an oversimplified way, as a ‘highly regulated, successful invasive clone of our own tissues’ or, in a less simplified but still too simplistic way, as a ‘highly regulated, successful, invasive clone of our own tissues’, involving a multistep accumulation of mutations in genes regulating major signalling pathways that are frequently heterogeneous genetically, epigenetically and phenotypically, as well as the cross talk of such mutations with cellular and extracellular alterations at the surrounding tissues’, it does not make sense to discuss genetic predictors of thyroid cancer (or any other cancer type) outside host and surgical pathology context.

The aforementioned context has many faces that determine patients’ outcomes beyond the influence of genetic markers. This applies to the age and/or gender of the patients, and the site, size and macroscopic characteristics of the cancer – namely, its pushing or infiltrative borders. The degree of invasiveness, both locally and at a distance, is measured by the TNM staging, which is the most powerful predictor of outcome of almost all cancer patients. The histological characteristics of the cancer are also a major factor of prognosis: morphological subtype, degree of differentiation, extension of necrosis, mitotic index and signs of invasion (parenchymatous, lymphovascular and to adjacent organs). The histological context can be, and frequently is, enriched by immunohistochemical data that allow to evaluate more precisely cell proliferation, overexpression (or misplacement) of oncogene products and underexpression (or, again, misplacement) of tumour-suppressor gene products and the number and the type of cells involved in the immunomodulation of cancer development.

The sort of molecular approach that immunohistochemistry provides is also achieved, and frequently reinforced, by in situ demonstration of gene rearrangement and gene amplification (FISH is frequently the best method to detect such genetic alterations). Both immunohistochemistry and in situ methods provide, furthermore, topographic information that complements the molecular data and are often crucial for understanding carcinogenesis. This has been demonstrated, for instance, by Eloy et al. (1) who showed that the interaction between transforming growth factor beta/Smad pathway activation and BRAF mutation plays different roles in circumscribed and infiltrative papillary thyroid carcinoma (PTC); in the latter, the interaction is associated with epithelial-to-mesenchymal transition and local invasion, as well as to nodal metastization of infiltrative PTCs (1).

Thyroid carcinomas are classified according to the cell type they derive from, their degree of differentiation and their cytoarchitecture. Follicular cell-derived tumours comprise well-differentiated thyroid carcinoma (WDTC), poorly differentiated thyroid carcinoma (PDTC) and undifferentiated thyroid carcinoma (UTC). The well-differentiated group encompasses, according to cytoarchitecture and nuclear features of the neoplastic cells, follicular thyroid carcinoma (FTC) and PTC, with the latter having two main variants: classic PTC (cPTC) and follicular variant PTC (FVPTC). The minority of carcinomas that derive from parafollicular C cells are named medullary thyroid carcinoma (2).

In this review, we will just focus on genetic alterations detected by molecular methods in surgically resected specimens, thus skipping their usefulness in cytopathology. To keep the paper within an adequate size, we will only address the importance of the genetic predictors of outcome of patients with follicular cell-derived carcinomas displaying good or moderate differentiation, thus avoiding medullary carcinoma and UTC. PDTC will be discussed together with the respective better differentiated counterparts PTC and its variants, namely, FVPTC and FTC.

Clinico-pathological factors vs genetic predictors of outcome

In a recent article on the usefulness of molecular biomarkers in thyroid cancer, we concluded that, for the moment, clinical and histopathological prognostic factors remain much more important than genetic factors for diagnostic and prognostic purposes (3). This conclusion is, however, challenged almost every day by the publication of new molecular data in the different types of thyroid cancer. The most important of such publications was the ‘Integrated genomic characterization of papillary thyroid carcinoma’ that provided a detailed description of the genomic landscape of 496 cases of PTC under the auspices of The Cancer Genome Atlas (TCGA) Research Network Initiative (4).

Besides a huge amount of genetic and epigenetic information that will take time to fully understand, it is interesting to realize that the aforementioned study (4) confirmed the existence of two main genetic types of differentiated thyroid carcinoma (DTC) that correspond to cPTC (and some variants of PTC such as the tall cell and Warthin-like variant) and to the group of follicular...
patterned carcinomas that encompass FVPTC, as our group and others have suggested years ago (5, 6, 7). The absence of solid prospective studies on thyroid cancer and the close relationship between clinical, pathological, immunohistochemical and genetic factors turn very difficult to discuss out of the global context the prognostic role played by the latter (8).

Of the numerous genetic alterations detected in WDTC and PDTC, we included in the present review those that are more prevalent and/or seem to play a more important prognostic role. It is the case of BRAF, RAS, TERT promoter and TP53 mutations and of RET/PTC and PAX8/PPARγ rearrangements.

**RET/PTC and PAX8/PPARγ rearrangements**

**RET/PTC** rearrangements are quite frequent in PTC, whereas PAX8/PPARγ rearrangement is often detected in follicular patterned lesions (FVPTC and FTC) (3, 5, 6, 7, 9); the overall evidence indicates that tumours with either of these rearrangements rarely evolve to less differentiated forms (i.e. their prevalence is very low in PDTC and UTC). RET/PTC is a chimeric gene generated by the fusion of the RET tyrosine kinase (TK) domain with the 5′ terminal region of genes that are constitutively expressed in thyroid follicular cells (10) allowing dimerization of the RET TK domain and its constitutive activation. The most frequent forms of this oncogene in PTC are RET/PTC1 and RET/PTC3, both arising from chromosome 10 inversions (11). RET/PTC1 rearrangement appears to be associated with small, classic type PTC displaying low proliferation and occurring in young patients (12, 13, 14, 15). At variance with this, RET/PTC3 rearrangement is prevalent in the solid variant of PTC that is frequent in children and was often found in PTCs occurring in the setting of the Chernobyl accident (16), being more prone to a more aggressive behaviour (13, 14, 15, 17). Despite being associated with signs of clinical aggressiveness (namely nodal and lung metastases), cases of solid variant of PTC arising in young patients, with or without RET/PTC3 rearrangement, respond well to radioactive iodine (RAI) treatment and are not significantly associated with a worse survival of the patients.

Taking the data on record in the literature as well as our own experience into account, it may be concluded that the prognostic value of RET/PTC rearrangement in thyroid cancer has not been fully clarified yet.

**PAX8/PPARγ** rearrangement has been associated with some adverse prognostic features (e.g. multifocality and vascular invasion) in some series, but the gathered evidence is not strong enough to identify this rearrangement as a genetic predictor of outcome in thyroid cancer (9, 18). Furthermore, **PAX8/PPARγ** rearrangements have been also detected in 14% of the cases of follicular thyroid adenoma (FTA) (19).

**RAS mutations and prognosis**

RAS are small GTPase-proteins that act as a molecular switch propagating signals from TK and non-TK receptors and activating the MAPK and other signalling pathways. RAS mutations are more prevalent and seem to be more relevant as a prognostic indicator in follicular patterned lesions (FVPTC, FTC and, namely, PDTC) than in cPTC (18). All of the three RAS genes (H, K and N-RAS) were shown to be mutated in both benign and malignant thyroid tumours but the frequency of the mutations is higher in FTC (36%), PDTC (55%) and UTC (52%) and more frequently affects the N-RAS gene (20).

RAS mutations are less prevalent in benign and malignant Hürthle cell tumours (5 and 11% respectively) than in their non-Hürthle cell counterparts and less prevalent in PTC (10%) than in PDTC (25–30%) (7, 20). Within PTC, RAS mutations are rare in its classic form, whereas in FVPTC, its prevalence falls within the range of other follicular patterned tumours (~25%) (6).

The controversy on the prognostic value of RAS mutations in thyroid cancer results partially, at least, from the fact that RAS mutations are present along all of the whole spectrum of thyroid lesions, from FTA to the deadly UTC. García Rostan et al. (21) have shown that patients with RAS mutated carcinomas, namely PDTC, harbour distant metastases more frequently and have higher mortality, being RAS mutations an independent predictor of poor survival (21). Other studies disclosed a similar association between (N) RAS mutation and distant metastases and/or lower survival in FTC (22, 23).

The assumption that RAS mutations can predispose to differentiation loss in thyroid cancer derives from their presence in DTC with areas of dedifferentiation and from their greater prevalence in PDTC and UTC than in DTC (24).

It has been difficult to demonstrate the prognostic value of RAS mutations due to the relatively small size of the majority of the series (in particular concerning FTC, PDTC and UTC that are less frequent than PTC) and the too short follow-up in most situations. Large, multicentric studies will be necessary to establish definitely the prognostic value of RAS mutations.
BRAF and NIS expression

BRAF gene encodes a serine/threonine kinase that belongs to the RAS–RAF–MEK–ERK–MAP kinase pathway, whose biological role is to mediate cellular responses to growth factors. There are several BRAF mutations, the BRAFT1796A (in exon 15) is largely the more prevalent, leading to a substitution of a valine by a glutamic acid at position 600. Such a mutation causes increased BRAF kinase activity and the subsequent phosphorylation of MEK1/2 and ERK1/2, turning the activation of the MAP kinase pathway independent from upstream factors activation (25).

BRAFV600E mutation is the most prevalent point mutation in PTC, being present in 36–83% of cases. It rarely co-exists with other prevalent genetic events such as RET/PTC rearrangement or RAS mutation (18). BRAFV600E mutation exhibits a strong genotype–phenotype association; it is (almost) exclusively detected in PTC exhibiting a papillary or mixed follicular/papillary growth pattern, regardless of being a cPTC or any of the PTC variants (other than the encapsulated FVPTC) (5).

Besides the frequent BRAFV600E mutation, other alterations were detected in the BRAF gene in UTCs: the BRAFK601E mutation, which occurs mainly in FVPTC (<10% of the cases) (5), and the in-frame deletion VK600-1E that has been detected in rare cases of solid variant of PTC. BRAF rearrangements, namely the AKAP9–BRAF fusion, were also described as rare events preferentially found in radiation-induced PTC (18). At present, there is not enough evidence to evaluate the putative prognostic role of the aforementioned rare BRAF alterations.

Although functional studies, using thyroid-targeted BRAFV600E transgenic mice (26) and BRAFV600E transfected thyroid cell lines (27), indicate that BRAF mutations lead to a more ‘aggressive type’ of PTC, several other studies, addressing the correlation between BRAFV600E and the clinical features of PTC, provided discrepant results (see below).

Some studies reported significant associations between BRAF mutation and poor prognostic indicators like older age (28, 29), male gender (30, 31), extrathyroid extension (28, 32), regional metastases (29, 32), distant metastases (33), higher tumour staging (28, 32, 33), tumour size (31, 34, 35) and tumour recurrence (32, 36). Other studies have not observed the aforementioned associations (37, 38, 39). Furthermore, Elisei et al. (40) have demonstrated that the search for BRAFV600E mutation may prove useful to modulate the treatment among low-risk PTC patients, those who require less or more aggressive treatment. Recently, a multicenter retrospective study showed that BRAFV600E was significantly associated with increased cancer-related mortality among patients with PTC, but the association was not independent of several clinico-pathological features of aggressiveness (41).

We observed that BRAFV600E PTCs tended to occur in older patients and did not exhibit a significant association with signs of clinico-pathological aggressiveness – namely larger size, extrathyroidal extension, vascular invasion and lymph node metastases (5, 8) – or poor circumscription (8). This does not mean, however, that BRAF mutation cannot contribute for progression of PTC toward less differentiated carcinomas in the appropriate context, because our group and others (28, 33, 42) detected BRAFV600E mutation in 10–35% of UTC.

Despite the BRAF mutation controversial association with guarded prognostic features, its association with a decrease in expression of several ‘thyroid specific genes’ or ‘iodine handling genes’ (36, 43, 44) is widely acknowledged. The association of BRAF mutation with the loss of RAI avidity in recurrent PTC has been confirmed in vitro and in vivo (36, 45). It was recently shown that MEK inhibition may restore RAI incorporation, turning BRAF and/or MEK inhibitors into promising targets to treat RAI-refractory thyroid cancers (45, 46).

TERT promoter mutations

About two-thirds of thyroid carcinomas display telomerase activation that is more frequent in UTC than in DTC (42). Capezzone et al. (47) observed telomerase activity in most sporadic and familial malignant thyroid tumours, as well as in some adenomas. Recently, mutations in the promoter region of the telomerase (TERT) gene were reported in follicular cell-derived thyroid carcinomas (FCDTC) (48, 49, 50). These mutations occur in two hotspot positions, located at −124 and −146 bp upstream from the ATG start site (−124G>A and −146G>A, C>T on opposite strand) and confer enhanced TERT promoter activity, putatively by generating a consensus-binding site (GGAA) for ETS transcription factors within the TERT promoter region (51).

In a large series of 469 carcinomas, we found TERT promoter mutations in 7.5% of PTC, 17.1% of FTC, 29.0% of PDTC and 33.0% of UTC (52). This stepwise increase in the frequency of TERT promoter mutations from well to poorly differentiated and undifferentiated carcinomas was also reported in other studies (49, 50). No TERT promoter mutations were found in normal tissues, benign lesions or
medullary thyroid carcinomas. Like RAS mutations, the frequency of TERT promoter mutations seems to be lower in tumours with oncocytic features than in their non-oncocytic counterparts; these observations reinforce the assumption that oncocytic tumours have a different set of molecular alterations and probably also alternative mechanisms for cell survival (53, 54, 55). The majority (about 80%) of mutated cases present the −124G>A mutation. In PTC, TERT promoter mutations were significantly more frequent in BRAF mutated tumours (50, 52). TERT promoter mutations were associated with increased mRNA expression, and this increase was more pronounced in tumours harbouring both BRAF and TERT promoter mutations (48).

Several studies analysed the relationship between TERT promoter mutations and clinico-pathological features (49, 50, 52, 56, 57), and four studies also analysed the implications of the presence of these mutations on patients’ clinical outcomes (52, 56, 58, 59). TERT promoter mutations were associated with older age of the patients at diagnosis, larger tumour size, distant metastases and a higher stage in several studies (50, 52, 57). The association with distant metastases seems to be particularly consistent and has been reported in most of the studies, strongly suggesting that there is a link between TERT promoter mutations and the metastatic potential of FCDTC. From the clinical standpoint, this association is extremely relevant because distant metastases are major determinants of prognosis, especially in older patients (60).

In our study (52), patients with DTC harbouring TERT promoter mutations were less prone to be disease free at the end of follow-up, and similar results were found in three other studies (56, 58, 59). Our study also showed that patients with TERT-mutated tumours were submitted to more treatments with radioiodine with higher cumulative doses, as well as to other treatment modalities like surgery for recurrent disease, external beam irradiation or treatment with TK inhibitors (52). Furthermore, patients with tumours harbouring TERT promoter mutations had increased disease-specific mortality, and this finding was independent of age and gender (52).

As previously mentioned, TERT-mutated PTC harbours more frequently BRAF mutations than TERTwt tumours. Horn et al. (51) advanced that the mutation creates newly consensus binding sites for TCF subfamily transcription factors (Elk1 and Elk4) that can be activated by BRAF. Our results in TERT mRNA expression corroborated this assumption, showing an increased TERT expression in tumours harbouring BRAF and TERT mutation (48). Because BRAF has also been associated with worse prognosis in some studies, several authors hypothesized that both mutations could cooperate toward a worse prognosis (50, 61). One still ignores the mechanism behind the putative cooperation between BRAF and TERT promoter mutation. It is nevertheless tempting to speculate, considering the pro-senescent effect of BRAF mutation alone (62), that TERT promoter mutations may contribute to abrogate such effect through their role leading to evasion from senescence (63, 64, 65). Taking into account that the prognostic value of BRAF is currently under debate and that TERT promoter mutations were independently associated with aggressive clinico-pathological features and worse outcome in all of the large series published to date (66), we think that, at present, the most important question is to clarify, whether or not, after controlling the clinical importance of TERT mutations, BRAF goes on adding a significant prognostic value (66). Multicentric studies with large series of patients will be necessary to clarify if the ‘addition’ of BRAF mutational status to a TERT-mutated tumour has indeed value for prognostic stratification (66).

**TP53 mutations**

Most TP53 mutations lead to the expression of a mutant protein or, less commonly, to its absence (67, 68). In thyroid carcinomas, TP53 mutations are not different from those of cancers at other sites and have been described in exons 5–9, with 273 being the codon most often altered (42, 67, 69, 70, 71, 72, 73). No p53 expression or mutation has been found in normal thyroid or in benign lesions, including follicular adenoma, adenomatous goitre and chronic thyroiditis (72, 73, 74, 75, 76). For years it was repeated that more than 98% of DTC (PTC and FTC) had a normal TP53 gene (18, 69, 70, 71, 72, 73, 75, 77), even when cases secondary to radiation exposure were included (78). This scenario may be changing due to the utilization of next-generation sequencing; using this methodology, Nikiforova et al. (79) reported the presence of TP53 mutations in 3.5% of PTC (2/57) and in four of 36 FTC (11.1%); the four FTC cases were oncocytic carcinomas and three were widely invasive (75). In the recent TCGA study (4), TP53 mutations were detected in 0.7% of PTC thus confirming their scarcity in PTC, but no clinicohistopathological data were provided on the mutated cases. The results of the study by Nikiforova et al. (75) study regarding the high clinical aggressiveness of TP53 mutated DTC fit with previously reported results. A small proportion of aggressive PTC are associated with TP53 mutations and/or p53 expression; the tall cell variant of
PTC is associated with a significantly higher rate of p53 than common PTC (80). Positivity for p53 protein has been detected in rare aggressive thyroid tumours such as a mixed columnar and tall cell variant of PTC (81) and a squamous cell carcinoma associated with the tall cell variant of PTC (82). Positivity for p53 protein has also been reported in some aggressive cases of the cribriform–morular variant of PTC (83, 84). Immunohistochemical evaluation of the columnar cell variant of PTC showed a predominantly weak nuclear p53 staining in both indolent and aggressive tumours (81).

Loss of cellular polarity/cohesiveness, hobnail features and micropapillary structures, either alone or in combination, are independent predictive factors for lymph node metastasis both in common PTC and in papillary microcarcinoma (82, 83, 84, 85). All of these peculiar morphological features are characteristic of the so-called micropapillary/hobnail variant of PTC (85, 86, 87, 88, 89), an aggressive type of PTC carrying poor outcome, which is consistently positive for p53 (85, 86, 87, 89) at the immunohistochemical level. Hobnail features were most commonly observed in association with PDTC and UTC (90). These features have also been associated with other histologic variants that are known to be more clinically aggressive, such as increased mitotic activity and/or necrosis and lymph node metastases at presentation. It has therefore been suggested that hobnail features may be a manifestation of 'higher-grade transformation' (90). The recent observation by our group (91) of two fatal cases of the micropapillary/hobnail variant of PTC positive for p53 by immunohistochemistry (Fig. 1) and TP53 mutated at the molecular level with progression to UTC supports the involvement of p53 in such transformation (90, 92).

miRNA and IncRNA in thyroid cancer outcome

Of the numerous molecules and mechanisms described in recent years in the oncology field, miRNA and IncRNA arise as major players due to their action on the modulation of known cancer genes and/or their products (oncogenes, tumour suppressor genes and apoptotic proteins).

It has been hypothesized that some of the miRNA and/or IncRNA (or a set of) can help in the differential diagnosis of benign and malignant tumours, however scarce information is available regarding their putative role on prognosis. Nevertheless, some miRNA have been repeatedly found dysregulated in thyroid cancer, in particular in PTC (miR-146b, miR-181b, miR-187, miR-221 and miR-222) and the same set of molecules has been associated with tumour aggressiveness in some studies (92). Unfortunately, the relevant set of miRNAs varies from one report to the other, turning difficult or even impossible to draw, at present, any meaningful conclusions.
The same holds true concerning the available data on IncRNAs. The complexity of the available evidence is huge because these long (longer than 200 nt) RNAs can play a role at both the transcriptional and the post-transcriptional gene regulation level. IncRNAs NAMA, AK023948 and PTSC3AA (PTC susceptibility candidate 3) are among the (yet) reduced number of IncRNAs that have been associated with PTC (93, 94). Until now it has not been possible to ascertain any role to IncRNA in the prognosis of thyroid cancer patients.

**Final remarks**

The importance of genetic markers for predicting thyroid cancer outcome is limited by the pre-eminence of clinical, histopathological, immunological and other context-driven features. Despite this, there is enough evidence to claim that TERT promoter mutations and TP53 mutations are major molecular biomarkers of prognosis and to suggest that BRAF and RAS mutations may also play a prognostic role in some conditions. Besides prognosis, the aforementioned mutations and the respective molecular pathways, as well as other genetic and epigenetic alterations recently identified by the Cancer Genome Atlas (4), will probably serve as targets for the so-called personalized therapy.

**Declaration of interest**

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

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