residual or recurrent disease, including the use of Tg levels for PTC and FTC, and calcitonin for medullary thyroid cancer (MTC).

CLASSIFICATION

Thyroid neoplasms can arise in each of the cell types that populate the gland, including thyroid follicular cells, calcitonin-producing C cells, lymphocytes, and stromal and vascular elements, as well as metastases from other sites (Table 405-10). The American Joint Committee on Cancer (AJCC) has designated a staging system using the tumor, node, metastasis (TNM) classification (Table 405-12). Several other classification and staging systems are also widely used, some of which place greater emphasis on histologic features or risk factors such as age or gender.

PATHOGENESIS AND GENETIC BASIS

Radiation Early studies of the pathogenesis of thyroid cancer focused on the role of external radiation, which predisposes to chromosomal breaks, leading to genetic rearrangements and loss of tumor-suppressor genes. External radiation of the mediastinum, face, head, and neck region was administered in the past to treat an array of conditions, including acne and enlargement of the thymus, tonsils, and adenoids. Radiation exposure increases the risk of benign and malignant thyroid nodules, is associated with multicentric cancers, and shifts the incidence of thyroid cancer to an earlier age group. Radiation from nuclear fallout also increases the risk of thyroid cancer. Children seem more predisposed to the effects of radiation than adults. Of note, radiation derived from ^{131}I therapy appears to contribute minimal increased risk of thyroid cancer.

TSH and Growth Factors Many differentiated thyroid cancers express TSH receptors and, therefore, remain responsive to TSH. Higher serum TSH levels, even within normal range, are associated with increased thyroid cancer risk in patients with thyroid nodules. These observations provide the rationale for T_4 suppression of TSH in patients with thyroid cancer. Residual expression of TSH receptors also allows TSH-stimulated uptake of ^{131}I therapy (see below).

TABLE 405-12 THYROID CANCER CLASSIFICATION[a]

Papillary or Follicular Thyroid Cancers		
	<45 years	>45 years
Stage I	Any T, any N, M0	T1, N0, M0
Stage II	Any T, any N, M1	T2, N0, M0
Stage III	—	T3, N0, M0
		T1–T3, N1a, M0
Stage IVA	—	T4a, any N, M0
		T1–T3, N1b, M0
Stage IVB		T4b, any N, M0
Stage IVC		Any T, any N, M1
Anaplastic Thyroid Cancer		
Stage IV	All cases are stage IV	
Medullary Thyroid Cancer		
Stage I	T1, N0, M0	
Stage II	T2 or T3, N0, M0	
Stage III	T1–T3, N1a, M0	
Stage IVA	T4a, any N, M0	
	T1–T3, N1b, M0	
Stage IVB	T4b, any N, M0	
Stage IVC	Any T, any N, M1	

[a]Criteria include: T, the size and extent of the primary tumor (T1a ≤1 cm; T1b >1 cm but ≤2 cm; T2 >2 cm but ≤4 cm; T3 >4 cm or any tumor with extension into perithyroidal soft tissue or sternothyroid muscle; T4a invasion into subcutaneous soft tissues, larynx, trachea, esophagus, or recurrent laryngeal nerve; T4b invasion into prevertebral fascia or encasement of carotid artery or mediastinal vessels); N, the absence (N0) or presence (N1a level IV central compartment; N1b levels II–V lateral compartment, upper mediastinal or retro/parapharyngeal) of regional node involvement; M, the absence (M0) or presence (M1) of distant metastases.

Source: American Joint Committee on Cancer staging system for thyroid cancers using the TNM classification, 7th edition.

Oncogenes and Tumor-Suppressor Genes Thyroid cancers are monoclonal in origin, consistent with the idea that they originate as a consequence of mutations that confer a growth advantage to a single cell. In addition to increased rates of proliferation, some thyroid cancers exhibit impaired apoptosis and features that enhance invasion, angiogenesis, and metastasis. Thyroid neoplasms have been analyzed for a variety of genetic alterations, but without clear evidence of an ordered acquisition of somatic mutations as they progress from the benign to the malignant state. On the other hand, certain mutations are relatively specific for thyroid neoplasia, some of which correlate with histologic classification (Table 405-13).

As described above, activating mutations of the TSH-R and the $G_{s\alpha}$ subunit are associated with autonomously functioning nodules. Although these mutations induce thyroid cell growth, this type of nodule is almost always benign.

Activation of the RET-RAS-BRAF signaling pathway is seen in up to 70% of PTCs, although the types of mutations are heterogeneous. A variety of rearrangements involving the *RET* gene on chromosome 10 bring this receptor tyrosine kinase under the control of other promoters, leading to receptor overexpression. *RET* rearrangements occur in 20–40% of PTCs in different series and were observed with increased frequency in tumors developing after the Chernobyl radiation accident. Rearrangements in PTC have also been observed for another tyrosine kinase gene, *TRK1*, which is located on chromosome 1. To date, the identification of PTC with *RET* or *TRK1* rearrangements has not proven useful for predicting prognosis or treatment responses. *BRAF V600E* mutations appear to be the most common genetic alteration in PTC. These mutations activate the kinase, which stimulates the mitogen-activated protein MAP kinase (MAPK) cascade. *RAS* mutations, which also stimulate the MAPK cascade, are found in about 20–30% of thyroid neoplasms (*NRAS* > *HRAS* > *KRAS*), including both PTC and FTC. Of note, simultaneous *RET*, *BRAF*, and *RAS* mutations rarely occur in the same tumor, suggesting that activation of the MAPK cascade is critical for tumor development, independent of the step that initiates the cascade.

RAS mutations also occur in FTCs. In addition, a rearrangement of the thyroid developmental transcription factor PAX8 with the nuclear receptor PPARγ is identified in a significant fraction of FTCs. Overall, about 70% of follicular cancers have mutations or genetic rearrangements. Loss of heterozygosity of 3p or 11q, consistent with deletions of tumor-suppressor genes, is also common in FTCs.

Most of the mutations seen in differentiated thyroid cancers have also been detected in ATCs. *BRAF* mutations are seen in up to 50% of ATCs. Mutations in *CTNNB1,* which encodes β-catenin, occur in about two-thirds of ATCs, but not in PTC or FTC. Mutations of the tumor-suppressor *P53* also play an important role in the development of ATC. Because *P53* plays a role in cell cycle surveillance, DNA repair, and apoptosis, its loss may contribute to the rapid acquisition of genetic instability as well as poor treatment responses (Chap. 102e) (Table 405-13).

The role of molecular diagnostics in the clinical management of thyroid cancer is under investigation. In principle, analyses of specific mutations might aid in classification, prognosis, or choice of treatment. Although *BRAF V600E* mutations are associated with loss of iodine uptake by tumor cells, there is no clear evidence to date that this information alters clinical decision making. Higher recurrence rates have been variably reported in patients with *BRAF*-positive PTC, but the impact on survival rates is unclear. Sequencing of thyroid cancers as part of the Cancer Genome Atlas (TCGA) is likely to lead to new classification schemes based on molecular abnormalities in tumors.

MTC, when associated with multiple endocrine neoplasia (MEN) type 2, harbors an inherited mutation of the *RET* gene. Unlike the rearrangements of *RET* seen in PTC, the mutations in MEN 2 are