Autophagy and thyroid carcinogenesis: genetic and epigenetic links

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Abstract

Thyroid cancer is the most common cancer of the endocrine system and is responsible for the majority of deaths from endocrine malignancies. Although a large proportion of thyroid cancers belong to well differentiated histologic subtypes, which in general show a good prognosis after surgery and radioiodine ablation, the treatment of radio-resistant papillary-type, of undifferentiated anaplastic, and of medullary-type thyroid cancers remains unsatisfactory. Autophagy is a vesicular process for the lysosomal degradation of protein aggregates and of damaged or redundant organelles. Autophagy plays an important role in cell homeostasis, and there is evidence that this process is dysregulated in cancer cells. Recent in vitro preclinical studies have indicated that autophagy is involved in the cytotoxic response to chemotherapeutics in thyroid cancer cells. Indeed, several oncogenes and oncosuppressor genes implicated in thyroid carcinogenesis also play a role in the regulation of autophagy. In addition, some epigenetic modulators involved in thyroid carcinogenesis also influence autophagy. In this review, we highlight the genetic and epigenetic factors that mechanistically link thyroid carcinogenesis and autophagy, thus substantiating the rationale for an autophagy-targeted therapy of aggressive and radio-chemo-resistant thyroid cancers.

Key Words

autophagy, thyroid cancer, oncogenes, epigenetics, microRNA

Introduction

Thyroid cancer accounts for almost 90% of all endocrine-related cancers, and is responsible for the majority of deaths from endocrine malignancies (Siegel et al. 2013). Thyroid cancers may arise from either the follicular (thyroid hormone-producing) or the parafollicular (calcitonin-producing) cells (Fig. 1). The large majority of follicular cell-derived thyroid cancers are well differentiated and are classified as papillary (about 80% of all thyroid cancers) or follicular thyroid cancer (PTC and FTC, respectively), and a minor portion show a poorly differentiated or undifferentiated (anaplastic) phenotype (named as poorly differentiated thyroid cancer (PDTC) and anaplastic thyroid cancer (ATC), respectively). Thyroid cancers arising from parafollicular cells, named medullary thyroid cancers (MTC), account for 3–5% of all thyroid cancers. PTC is generally associated with favorable outcomes after surgery and radioactive iodine therapy, although 5% of these tumors show radio- and chemoresistance (Fassnacht et al. 2009, Grodski & Delbridge 2009). On the other hand, ATC is extremely aggressive and soon leads the patient to death (Ain 1998, Smallridge 2012, Smallridge et al. 2012). MTC also have a generally
good prognosis, with an overall survival rate at 10 years of \( \sim 95\% \) if the tumor is confined to the thyroid gland, which drops to \( \sim 40\% \) in the presence of metastases (Roman et al. 2006). Patients with an unresectable tumor or with distant metastases can be treated with chemotherapeutics (e.g., doxorubicin, 5-fluorouracil, cisplatin), yet the response rate is very low. Molecular therapy with inhibitors of mitogenic kinases has been disappointing, because it has not substantially improved the survival of patients with aggressive thyroid cancers, while showing an adverse side-effect profile (Gild et al. 2011). For instance, the multikinase inhibitor vandetanib, which has been approved for the treatment of inoperable or metastatic MTC (Thornton et al. 2012), has shown a modest efficacy toward MTC progression, but an extremely toxic profile that includes gastrointestinal, cardiovascular, and neurological disorders (Chau & Haddad 2013). Similarly, the results of a phase II clinical trials on the efficacy of the mammalian target of rapamycin (mTOR) inhibitor everolimus for the treatment of locally advanced or metastatic thyroid cancer have been disappointing (Lim et al. 2013). Thus, the lack of efficacious and safe treatment options provokes the search for novel molecular targeted drugs for the cure of such highly malignant thyroid cancers.

Recently, autophagy has emerged as a potential target for the therapy of hematologic and epithelial malignancies (Chen & Karantza 2011, Gundara et al. 2012, Wu et al. 2012). In vitro pre-clinical studies support the possibility of harnessing autophagy for the therapy of thyroid cancers (Lin et al. 2009, 2010, 2012a,b, Lu et al. 2012, Jin et al. 2013). Autophagy (literally, ‘self-eating’) is the process through which damaged or redundant cytoplasmic constituents are degraded within lysosomes. Several oncogenes and oncosuppressor genes regulate the induction of autophagy. Autophagy is also epigenetically regulated through the methylation of autophagy regulatory genes, the activity of histone deacetylases (HDAC), and the expression of microRNAs (miRNAs). Here, we examine the genetic and epigenetic links between autophagy and thyroid carcinogenesis. A better understanding of such mechanistic connections could help to identify new targets for a more accurate diagnostic, prognostic, and therapeutic management of thyroid cancers.

**The autophagy machinery**

Macroautophagy is a vesicular-driven process through which protein macroaggregates, large portions of membranes, and entire organelles can be delivered to lysosomes for complete degradation. This process is distinct from chaperon-mediated autophagy and microautophagy in which, respectively, only a single protein at a time or a small amount of cytoplasmic material is internalized in the lysosome. Readers may refer to the many excellent reviews in which the morphological and biochemical features of these processes are described in detail (Orenstein & Cuervo 2010, Yang & Klionsky 2010, Mizushima & Komatsu 2011, Sahu et al. 2011). Here, we will focus on macroautophagy (from now on simply named autophagy), as this is the major pathway contributing to the macromolecular turnover and cell homeostasis. In the following paragraphs, we briefly detail the key morphological and regulatory steps of autophagy.

**Morphological features and physiological significance**

Autophagy comprises the following principal steps: i) the formation of a vacuole, named the autophagosome, that entraps the cargo to be degraded; ii) the fusion of the autophagosome with endosomes and lysosomes that leads to the formation of an autophagolysosome; and iii) the degradation of the autophagy cargo (Fig. 2). The autophagosome is a double-layered vesicle that forms in the proximity of the trans-Golgi network. The progenitor membrane donor of the autophagosome is the smooth
endoplasmic reticulum, though membranes from other sources, including the plasma membrane and the outer mitochondrial membrane, are subsequently recruited and contribute to the expansion of this vesicle (Ravikumar et al. 2010, Tooze & Yoshimori 2010, Rubinsztein et al. 2012, Hamasaki et al. 2013). During this process, the lipidated form of light chain 3 (LC3, also known as ATG8) is post-translationally inserted into the expanding autophagosomal membrane through the intervention of several autophagy-related (ATG) proteins (Mizushima et al. 2011; box in Fig. 2). The synthesis and membrane translocation of LC3II is considered a hallmark of autophagosome biogenesis (Klionsky et al. 2012). Autophagy substrates are specifically sequestered in the lumen of the nascent autophagosome through the intervention of proteins that bridge the substrate to LC3 in the internal membrane (Noda et al. 2010; box in Fig. 2). The autophagy process proceeds with the fusion of the autophagosome with several endosomes and lysosomes (at the end an autophagolysosomal vacuole is formed) and the subsequent full

Figure 2
Morphological features of the (macro)autophagy process. The process can be dissected in three main steps. The key events and the relative protagonists of each step are indicated. (A) Formation of the autophagosomes (APH). Vesicle nucleation and membrane expansion start from the endoplasmic reticulum (ER). The autophagosome is marked by the presence on its internal and external membranes of LC3-PE, arising from MAP-LC3 (MAP-LC3, microtubule associate protein light chain 3; PE, phosphatydylethanolamine). The autophagy cargo includes portions of cytoplasm, protein aggregates, and mitochondrion, which are targeted by specific proteins such as p62, neighbor of BRCA1 (NBR1), and Bcl2/adeno-virus E1B 19-kDa interacting protein (BNIP3). (B) Fusion of the autophagosome with late endosomes (LE, identified by RAB7) to form an amphisome, and with lysosomes (LYS, identified by LAMP1) to form an autophagolysosome. This step requires HDAC6-mediated deacetylation of tubulin and the activity of dynein. Tethering of autophagosomes and lysosomes relies on soluble N-ethylmaleimide-sensitive factor-attachment protein (SNARE) proteins. (C) Degradation of autophagy cargo and recycling of substrates. In the autophagolysosome, the inner membrane of the autophagosome along with its cargo is degraded by lysosomal acid enzymes (essentially the cathepsins). This process is marked by the consumption of LC3 present in the inner membrane of the autophagosome. Substrates are then exported in the cytoplasm and recycled in the biosynthetic pathway. Full colour version of this figure available via http://dx.doi.org/10.1530/ERC-13-0271.
degradation of the autophagy substrates is conducted by lysosomal acid hydrolases (Eskelinen 2005). Finally, fully degraded substrates are exported to the cytoplasm and reutilized in biosynthetic pathways. It is to be stressed that autophagy has to proceed to completion to exert its prosurvival effects. The production of autophagosomes that do not completely fuse with lysosomes is of no benefit to the cell, because the autophagy substrates are not fully degraded and recycled, and may eventually become toxic. Therefore, to understand the pathophysiological outcome of autophagy, it is important to clearly determine the formation of autophagosome vs the autophagy flux (see section Detection of autophagy in thyroid cancer cells).

**Biochemical regulation of autophagy at a glance**

The induction and progression of autophagy are controlled by a complex network of signaling pathways that involve a number of protein- and lipid-kinases, protein- and lipid-phosphatases, and monomeric and trimeric GTPases (Mehpour et al. 2010, Chen & Klionsky 2011). The pathways illustrated in Fig. 3 represent an obvious, though efficacious, oversimplification. The master signal that triggers autophagy comes from the Unc51-like kinase 1 (ULK1, homolog of yeast Atg1) complex (Wong et al. 2013). Two upstream kinases, namely the mTOR-raptor complex 1 (mTORC1) and AMPk, control the activation of ULK1, the former acting as a repressor (Ganley et al. 2009, Jung et al. 2009) and the latter acting as an activator (Egan et al. 2011). mTORC1 integrates the signals from: i) the phosphatidylinositol-3-kinase (PI3k) class I/AKT pathway, which senses the presence of growth factors; ii) the AMPK pathway, which senses the lack of energy; and iii) the Rag A/B (a Ras-related GTPase) complex, which senses the availability of amino acids. In the presence of growth factors, the PI3k/ Akt pathway negatively regulates autophagy through a tonic activation of mTORC1 via the tuberous sclerosis complex (TSC) and Rheb (Ras homolog enriched in the brain) (Petiot et al. 2000, Arico et al. 2001, Inoki et al. 2002). The lipid phosphatase activity of phosphatase and tensin homolog (PTEN) shuts down this pathway, thus abolishing the mTOR-mediated repression of ULK1. When amino acids are abundant, the RagA/B complex activates mTORC1 (Sancak et al. 2010), while the lack of amino acids is sensed by the RAS–BRAF–ERK1/2 pathway that triggers autophagy through the stimulation of heterotrimeric GTP proteins (Ogier-Denis et al. 1995, 2000). Glucose depletion and other metabolic stresses that reduce the production of ATP or provoke the production of reactive oxygen species (ROS) activates the AMPK pathway, that in turn represses mTORC1 and activates ULK1 (Alers et al. 2012), thus initiating autophagy (Alexander et al. 2010, Castino et al. 2011, Janda et al. 2012, Wong et al. 2013). Downstream to ULK1, class III PI3k (also known as Vps34) produces phosphatidylinositol-3-phosphate (PI3P), the starting platform for the biogenesis of the autophagosome (Noda et al. 2010). Vps34 is activated through its interaction with Beclin1 (also known as ATG6 or Vps30) and p150 (homolog of Vps15), besides other regulating proteins (He & Levine 2010). This pathway is impaired when Beclin1 is sequestered through the binding with BCL2 (Pattinigre et al. 2005).

**Role of autophagy in cancer development and progression**

In quiescent and appropriately fed cells, autophagy runs at a constant basal level that ensures the homeostatic macromolecular turnover (Ravikumar et al. 2010), and it is
autophagy is upregulated allowing cancer cells to survive despite the prohibitive metabolic conditions (Degenhardt et al. 2006), possibly in a dormant state (Lu et al. 2008). These cells resist to chemo- and radio-therapeutic treatments, and eventually give rise to cancer relapse. Further, a transient upregulation of autophagy is observed during the epithelial–mesenchymal transition (EMT; Akalay et al. 2013), and this function prevents the cell death by anoikis of cancer cells which have detached from the basement membrane to invade the extracellular matrix (Fung et al. 2008). Thus, autophagy is differently regulated during the carcinogenic process and its actual level in the cell could vary in subclones, depending on the acquisition of new oncogenic assets. The situation is far more complicated considering that autophagy is influenced by epigenetic factors (see below) and by extracellular factors such as oxygen, glucose, nutrients, growth factors, hormones, and cytokines.

From the above considerations it appears clear that autophagy has a great impact on the progression of tumors and on the response to therapeutic treatments, and therefore influences the prognosis. Consistently, certain autophagy-related proteins have been shown to be of prognostic value. For instance, the hyperexpression of BECLIN1 and of LC3 in general associates with a better prognosis in patients with glioblastoma (Pirtoli et al. 2009), colorectal cancer (Li et al. 2009, Koukourakis et al. 2010), lymphomas (Nicotra et al. 2010, Huang et al. 2011), or duodenal adenocarcinoma (Wu et al. 2013). Conversely, low expression of BECLIN1 or of LC3 associates with poor prognosis in patients with hepatocarcinoma (Ding et al. 2008), glioblastoma (Huang et al. 2010), colorectal cancer (Koukourakis et al. 2010), lymphoma (Nicotra et al. 2010), or lung carcinoma (Won et al. 2012).

**Autophagy and thyroid cancer**

A systematic study addressing the prognostic value of autophagy in thyroid cancers has not yet been performed. Still, some in vitro studies have proven the involvement of autophagy in the cytotoxic response of thyroid cancer cells to anti-tumor drugs (Table 1). In this section, we provide some technical tips for assessing the presence of autophagy in thyroid cancer biopsies and discuss the mechanistic links between autophagy and thyroid carcinogenesis.

**Detection of autophagy in thyroid cancer cells**

The expression of autophagy protein markers can be demonstrated in ex-vivo thyroid tumor tissue and in
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3-MA, 3-methyladenine.
cultured thyroid cancer cells. Paraffin-embedded and cryostatic tissue sections can be processed for immunohistochemistry and immunofluorescent detection of autophagy markers, while western blotting analysis is better performed in freshly isolated or frozen biopsy tissues. Both these techniques are complementary and should be employed.

As an example, we report our preliminary observations on the detection of autophagy markers in tissue biopsies and in cultured cells of thyroid cancer origin. Western blotting of LC3 reveals the presence of the autophagosome-bound LC3II isoform, which arises from LC3I (Fig. 5A and C). One important caveat is that infiltrating fibroblasts, macrophages, and mastocytes might also express autophagy markers. This should be taken into consideration when performing a western blot with the whole homogenate of a biopsy, unless cancer cells are isolated by laser microdissection. In immunofluorescence, nontumor cells can be discriminated by using appropriate markers for stromal cells. A faintly detectable diffuse cytoplasmic signal of LC3 is considered as negative background, while a pattern of many LC3-positive puncta (in general, more than 10 per cell) is indicative of ongoing autophagy (Fig. 5B and D).

Immunocostaining with multiple markers (e.g., LC3, p62, BECLIN1, lysosome-associated membrane protein (LAMP1)) is recommended for a better assessment of the autophagy flux and of the signaling molecules involved. The true level of ongoing autophagy is much easier assayed in cultured cells through the pharmacologic or genetic manipulation of the autophagy flux. For instance, in the presence of drugs that alkalinize the lysosome pH (e.g. ammonium chloride) all the autophagosomes produced during the incubation time accumulate in the cell as they do not fuse with lysosomes (Kawai et al. 2007, Klionsky et al. 2012), and this reflects in the accumulation of LC3II protein (Fig. 5C and D).

The genetic connection: oncogenes and oncosuppressor genes

Numerous oncogenes and tumor suppressor genes regulate autophagy (Maiuri et al. 2009). In general, oncogenic proteins exert a negative activity and oncosuppressor proteins exert a positive activity on autophagy induction and progression. Several oncogenes and oncosuppressors implicated in thyroid carcinogenesis also play a role in the regulation of autophagy.

The main signaling pathways that link thyroid carcinogenesis with autophagy deregulation are the
RAS–RAF–ERK and the class I PI3k–AKT–mTOR pathways. The RAS/RAF/MEK/ERK pathway controls the mTOR-dependent pathway by sensing the absence of amino acids (Ogier-Denis et al. 2000). Aberrant signaling through the RAS/RAF/MEK/ERK cascade has been implicated in thyroid tumor initiation and development. For instance, the RET/PTC rearrangement, which leads to the RET/PTC fusion oncoprotein, activates the RAS–RAF–MAPK cascade (Knauf et al. 2003, Santoro et al. 2004). However, the most frequent aberration of this signaling pathway in thyroid cancer is associated with the oncogenic activation of BRAF. The BRAF V600E mutation, which leads to constitutive activation of BRAF kinase, is frequently found in PTC (Xing 2007) and, though less frequently, also in ATC (Nikiforova et al. 2003, Takano et al. 2007) and PDTC (Begum et al. 2004). In melanomas, oncogenic BRAF has been associated with inhibition of mTOR and upregulation of basal autophagy (Maddodi et al. 2010). However, another study showed that in metastatic melanomas oncogenic BRAF opposed the induction of autophagy by chemotherapeutics or rapamycin (Armstrong et al. 2011). Another oncogene of this same pathway which is mutated in a large percentage of thyroid cancers is the RAS oncogene (Motoi et al. 2000, Nikiforova & Nikiforov 2009). Activating mutations of RAS are associated with aggressive phenotypes of thyroid cancer and poor prognosis (Garcia-Rostan et al. 2003). Remarkably, the oncogenic mutants Ha-RAS and K-RAS have been shown to confer a metabolic advantage to cancer cells through the upregulation of basal autophagy (Guo et al. 2011, Kim et al. 2011). The above findings on the effects of active BRAF and Ha-RAS on autophagy seem to contradict the general rule that oncogenes signal to downregulate autophagy. Besides the fact that basal and stress-induced autophagy should be distinguished, it is likely that the true effect of oncogenic BRAF and RAS on autophagy regulation is cell context dependent and also reliant on the extracellular trigger. In addition, it should be considered that oncogenic RAS can signal through either the RAF–MEK–ERK1/2 pathway or the PI3K/AKT pathway, with a different impact on the regulation of autophagy (see below). Therefore, the final outcome on autophagy regulation by oncogenic RAS will depend on which downstream pathway will predominate.

The class I PI3K-(PTEN)–AKT–mTOR pathway is the other oncogenic pathway aberrantly hyperactive in thyroid cancer cells and is also known to regulate autophagy (see Fig. 3). Growth factors activate class I PI3k, which then phosphorylates phosphatidylinositol-3,4-diphosphate into phosphatidylinositol-3,4,5-triphosphate (PIP3), the phosphate donor needed for the phosphorylation of AKT. Active AKT then phosphorylates a number of downstream targets that ultimately regulate various cellular functions, including cell survival, proliferation, autophagy, protein synthesis, angiogenesis, and migration. Genetic alterations in the PI3k/AKT signaling pathway have been linked to thyroid cancers (Garcia-Rostan et al. 2005, Shinohara et al. 2007, Wang et al. 2007). The PIK3CA gene (encoding the catalytic subunit of p110α of class I PI3k) has been found amplified or mutated in thyroid carcinomas (Wu et al. 2005, Wang et al. 2007). Increased AKT activity has been associated with the aggressive behavior of FTCs and PTCs (Ringel et al. 2001, Shinohara et al. 2007). AKT negatively regulates autophagy through the mTOR pathway (Arico et al. 2001, Castino et al. 2008) and, directly, through phosphorylation of BELCIN1 (Wang et al. 2012). The class I PI3k/AKT pathway may be abnormally upregulated as a consequence of PTEN loss-of-function. The lipid phosphatase activity of PTEN removes the phosphate in position 3 from PIP3, thus limiting the availability of PIP3 needed for the activation of AKT. By shutting down the activation of AKT, PTEN relieves the AKT–mTOR block on autophagy (Arico et al. 2001). It is worth noting that mutations or deletions of the tumor suppressor gene PTEN have been recognized as an important step in the development of thyroid gland carcinomas (Dahia et al. 1997, Eng 2002).

Another oncogene that might link autophagy deregulation with thyroid carcinogenesis is c-MET. This proto-oncogene encodes a membrane tyrosine kinase receptor for the hepatocyte growth factor (HGF), which is a potent mitogen for epithelial cells and promotes cell motility and invasion in carcinoma cells (Stella et al. 2010). A large cohort study revealed that about 50% of PTCs are characterized by MET overexpression (Di Renzo et al. 1992), and this represents a sign of more aggressive disease (Ramirez et al. 2000, Mineo et al. 2004). Very recently, it has been shown that c-MET overexpression or its activation by HGF negatively regulates autophagy in A549 carcinoma cells (Liu et al. 2012). In the context of thyroid cancer, it has been reported that induction of autophagy by RAD001-mediated inhibition of mTOR sensitized PTC cells to chemo- and radio-therapy through the inhibition of c-MET (Lin et al. 2010).

What about other tumor suppressors, besides PTEN, that are deleted or mutated in thyroid cancers and might play a role in the regulation of autophagy?

The haplo-insufficient tumor suppressor gene BECLIN1 was the first oncosuppressor gene that proved the link between autophagy and cancer susceptibility.
The epigenetic liaisons: the role of DNA methylation, histone deacetylases, and miRNAs

Epigenetics refers to heritable (i.e., transmitted via meiosis or mitosis) changes in the expression of a gene or a set of genes not dependent on variations in the primary DNA sequence. Given that all cells in the same organism bear the same genome, epigenetics explains the different cellular phenotypes in the body as a result of the silencing of different subsets of genes. It is now clear that epigenetics plays a role in cancer, as cancer cells have their own epigenome. During cell proliferation, the epigenome is transmitted to daughter cells, although novel epigenetic signatures may emerge in the progeny as a consequence of (micro)environmental interference, thus explaining the appearance of clones with different behavior in the context of the tumor (Timp & Feinberg 2013). There are four epigenetic mechanisms known to regulate gene expression: DNA methylation in correspondence to the promoter region, histone conformation changes (essentially dictated by acetylation and deacetylation of certain lysine residues), chromatin remodeling (both histone conformation changes and chromatin remodelling affect DNA accessibility), and miRNAs (short, noncoding mRNAs that impair RNA translation by hybridizing to specific domains of the UTR of target mRNAs).

In recent years, a large body of evidence has accumulated showing the pivotal role of epigenetic changes in thyroid tumorigenesis driven by DNA methyl transferases (DNMTs), HDAC, and miRNAs (reviewed in Pallante et al. (2010), Braun & Hüttelmaier (2011), Russo et al. (2011) and Catalano et al. (2012a)). In this section, we provide a brief overview of the proteins and of the mechanisms involved in the epigenetic regulation in thyroid cancer that also have an impact on the regulation of autophagy.

For instance, the hypermethylation of the PTEN promoter region sporadic thyroid cancers has been reported (Alvarez-Nuñez et al. 2006). The lack of PTEN expression maintains active AKT in thyroid cancer cells, and consequently autophagy in these cells will be repressed.

The promoter of death-associated protein kinase (DAPk) has also been found to be hypermethylated in a large proportion of thyroid cancers (Hoque et al. 2005). This kinase induces autophagy by disrupting the BECLIN1–BCL2 complex (Zalckvar et al. 2009), and its epigenetic silencing in thyroid cancer cells might impair the induction of autophagy under stress conditions.

An intriguing epigenetic liaison between autophagy and thyroid carcinogenesis could involve the tumor suppressor ARHI, a Ras homolog that was recently shown to induce autophagy and autophagy-mediated dormancy in ovarian cancer cells (Lu et al. 2008). ARHI is generally monoallelically expressed (from the paternal allele), as the maternal allele is inherited in the hypermethylated (and therefore silenced) state. ARHI maps to 1p31, a region that is frequently deleted in thyroid cancers, particularly in FTCs (Weber et al. 2005). It has been hypothesized that silencing of ARHI expression, as a result of combined hypermethylation of the maternal allele and deletion of the paternal allele, is pivotal to thyroid carcinogenesis (Weber et al. 2005).

Histone deacetylation promoted by HDACs negatively affects gene transcription. There is evidence that certain HDACs (namely SIRT1, HDAC1, HDAC2, HDAC6) can
regulate the autophagy process at the level of gene transcription and of protein function (Moresi et al. 2012, True & Matthias 2012, Füllgrabe et al. 2013). As histone deacetylation decreases DNA accessibility, the inhibitors of HDACs promote gene transcription. Indeed, the treatment with the HDAC inhibitor suberoylanilide hydroxamic acid was shown to induce autophagy in several cell types (Shao et al. 2004, Gammoh et al. 2012). There is promising evidence that HDAC inhibitors can be used in combination with other chemotherapeutics to improve their effectiveness in the treatment of thyroid cancers. HDAC inhibition was shown to increase the expression of E-cadherin, thus promoting cell–cell adhesion and reducing the migration of in vitro cultured thyroid cancer cells (Catalano et al. 2012b). E-cadherin is downregulated during the EMT process that precedes the metastasization of cancer cells, and, it is worth noting, the actual level of autophagy in cancer cells increases at this step in concomitance with E-cadherin silencing (Akalay et al. 2013). Whether the reexpression of E-cadherin following HDAC inhibition also associates with repression of autophagy in thyroid cancer cells has yet to be proven. Besides histones, some HDACs also deacetylate target cytoplasmic proteins, among which are also some proteins involved in apoptosis. For instance, SIRT1 deacetylates ATG5, ATG7, and ATG8 (Lee et al. 2008), which are essential for the formation of autophagosomes, while HDAC6 deacetylates the cytoskeletal protein tubulin, thus favoring the fusion of autophagosome with lysosomes (Lee et al. 2010).

The third epigenetic mechanism that potentially links autophagy and thyroid cancer are the miRNAs, a class of noncoding RNAs of 20–24 nucleotides that control gene expression at the post-transcriptional level (Ghildiyal & Zamore 2009). The link between miRNAs and epigenetics is bidirectional, as on one hand the expression of miRNAs is dictated by the methylation and acetylation status of DNA, and on the other hand miRNAs themselves regulate the expression of DNMTs and HDACs (Iorio & Croce 2009). For simplicity, we will only refer to those miRNAs that interfere with the expression of proteins involved in the regulation of autophagy and that are abnormally expressed in thyroid cancers.

Several miRNA profiling studies have identified changes in miRNA patterns occurring during thyroid cancer development and progression, opening a new field for the understanding of this disease and providing improved diagnostic, prognostic, and therapeutic approaches (reviewed in Pallante et al. 2010, Braun & Hüettelmaier (2011), De la Chapelle & Jazdzewski (2011) and Gundara et al. (2012)). Autophagy in itself, as a metabolic process regulated by an intricate network of proteins, is regulated by miRNAs at various levels (Gundara et al. 2011, Frankel & Lund 2012, Zhai et al. 2013). In principle, any miRNA targeting a signaling pathway involved in the control of autophagy would exert its regulatory activity on this pathway. For instance, miR221/222 and miR21, which target PTEN and consequently sustain the hyperactivation of AKT (Garofalo et al. 2009, Chun-Zhi & Taron 2009). The link between miRNAs and epigenetics is bidirectional, as on one hand the expression of miRNAs is dictated by the methylation and acetylation status of DNA, and on the other hand miRNAs themselves regulate the expression of DNMTs and HDACs (Iorio & Croce 2009). For simplicity, we will only refer to those miRNAs that interfere with the expression of proteins involved in the regulation of autophagy and that are abnormally expressed in thyroid cancers.

More recently, miRNAs specifically targeting the mRNA of autophagy proteins are being identified. Here, we will mention only those miRNAs involved in both the regulation of autophagy and the progression of thyroid cancers. The first miRNA described in this field is miR30a, which downregulates the expression of Beclin1 (Zhu et al. 2009). In the same family, miR30d was shown to target the mRNA of various autophagy proteins including BECLIN1, Bcl2/adenovirus E1B 19-kDa interacting protein (BNIP3L, which plays a role in mitophagy), ATG2, ATG5, and ATG12 (Yang et al. 2013). miR30a and miR30d were found to be expressed at a low-level in PTCs (Tetzlaff et al. 2007) and at a very low-level in ATCs (Schwertheim et al. 2007), respectively. It is intriguing to note that the miR30 family also antagonizes TGFβ-induced EMT and in vitro invasiveness of ATC-derived cells (Braun et al. 2010). miR130a, one of the most significantly downregulated miRNAs in thyroid cancer cells with BRAF mutation (Cahill et al. 2007),
Autophagy targeted therapy is nowadays considered a valuable strategy to combat radio- and chemo-resistant cancers (Chen & Karantza 2011, Yang et al. 2011, Gundara et al. 2012). Accumulating experimental data suggest that the efficacy of such therapies is strictly dependent on the actual level of ongoing autophagy in tumor cells, which is dictated by both genetic mutations and epigenetic phenomena, besides the dynamic influence of the tumor microenvironment.

The first report suggesting the involvement of autophagy in the response to therapeutic treatments of thyroid cancer dates back only a few years. Lin et al. (2009) found that both doxorubicin and radiation induced autophagy and cell death in cultured PTC cells. As the inhibition of Vps34-mediated autophagy by 3-methyl adenine increased the resistance toward these treatments, these authors concluded that autophagy was instrumental to cell toxicity in both treatments.

With regard to the therapy of thyroid cancer, besides radiation, new molecular therapies are emerging which employ kinase inhibitors, proteasome inhibitors, and epigenetic modulators (Catalano et al. 2010), and some of these drugs have been shown to also affect the autophagy process. For instance, sorafenib and sunitinib, two small molecules that inhibit the activity of RET kinase and that are commonly used for the treatment of MTCs, were shown to induce autophagosome accumulation in MTC cultured cells (Lin et al. 2012a,b). Apoptosis of MTC cells induced by these two drugs was abrogated when the essential autophagy protein ATG5 was silenced, and conversely it was enhanced when autophagy was concomitantly upregulated by co-treating with the mTOR inhibitor, everolimus (Lin et al. 2012a,b).

Everolimus and other mTOR inhibitors are being tested for their potential efficacy against thyroid cancers (Gild et al. 2013, Lim et al. 2013). Everolimus is a rapamycin analog and it was introduced to the clinical management of epithelial cancers because of its ability to halt the biosynthetic and proliferative pathways downstream of the AKT–mTOR axis, but it is now recognized that rapamycin analogs may also elicit their beneficial effects via induction of autophagy. Consistently, sensitization of PTC cells to doxorubicin and radiotherapy by everolimus (known also as RAD001) was shown to strictly depend on autophagy (Lin et al. 2010).

Statins, when used for the treatment of thyroid cancers, may also act through the induction of autophagy. In a study, a xenograft of ATC in mice was successfully treated by combining paclitaxel, a cytoskeleton disrupting agent, with combretastatin A4 phosphate, a vascular-inhibiting drug, and it was found that the latter drug induced autophagy in cancer cells, besides inducing apoptosis of endothelial cells (Yeung et al. 2007). In addition, rosuvastatin, a statin with antiproliferative activity, was shown to induce autophagy and to promote the switch from pro-survival to pro-death autophagy in PTC cells (Zeybek et al. 2011).

Further, reversine, a synthetic purine analog with promising therapeutic potential, has recently been shown to induce growth arrest and apoptosis in FTC cells through the induction of autophagy (Lu et al. 2012).

Figure 6
Genetic and epigenetic links between thyroid carcinogenesis and autophagy regulators. The scheme summarizes the potential links between autophagy and thyroid cancer progression at both genetic and epigenetic levels. Oncogenes are represented by rhombus and oncosuppressor genes by rectangles. Epigenetic regulations by DNMTs and miRNAs are indicated. GF, growth factor. Full colour version of this figure available via http://dx.doi.org/10.1530/ERC-13-0271

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is known to downregulate the expression of ATG2B (Kovaleva et al. 2012), while miR181a, which is expressed at a very low level in the presence of RET/PTC1 rearrangement (Cahill et al. 2006), is known to downregulate ATG5 (Huang et al. 2012, Tekirdag et al. 2013). Finally, miR183 was recently shown to negatively regulate the expression of LC3 in MTC cells (Abraham et al. 2011).

The scheme in Fig. 6 summarizes the potential links between autophagy and thyroid cancer progression at both genetic and epigenetic levels.
More recently, autophagy was shown to mediate the resistance to apoptosis induced by tumor necrosis factor-related apoptosis inducing ligand (TRAIL) in PTC and ATC cells (Jin et al. 2013).

As for epigenetic modulators, the use of HDAC inhibitors for autophagy therapy in cancer has been proposed (Yang et al. 2011). The HDAC inhibitor valproic acid (VPA) has been successfully employed in a combination therapy in ATC (Noguchi et al. 2009). VPA sensitized ATC cells to paclitaxel (Catalano et al. 2007) and to doxorubicin (Catalano et al. 2006). The small molecule lithium chloride was shown to synergize with VPA to inhibit the growth of cultured MTC cells (Adler et al. 2010). It is interesting to note, in this context, that lithium chloride is an inducer of mTOR-independent autophagy (Fornai et al. 2008), and that VPA, by inhibiting HDAC6, negatively interferes with the formation of the autophagolysosome (Lee et al. 2010).

Demethylating agents could also work in this manner. For instance, decitabine (2′-deoxy-5-azacytidine) has been shown to favor apoptosis by conventional chemotherapeutics in leukemic cells through the hyperinduction of autophagy (Schnekenburger et al. 2011).

Finally, in the near future we might be able to exploit miRNA-targeting autophagy for the cure of thyroid cancers (Gundara et al. 2012).

Concluding remarks

The paradoxical role of autophagy in cancer development and progression has important clinical implications in therapy, because it suggests that autophagy-inducer drugs may have benefits in preventing the development and growth of cancer cells while autophagy-inhibitor drugs should improve the efficacy of anti-cancer therapies in developed and metastatic cancers. Indeed, both pro- and anti-autophagy therapeutic drugs have shown their efficacy in in vitro and in vivo models of cancer, as well as in clinical trials (Chen & Karantza 2011, Gundara et al. 2012, Wu et al. 2012). These contradictory results could be explained by considering that the actual level of autophagy in cancer cells was likely to be different in the different experimental models because of differences in the genetic and epigenetic background, and also because of the influence of stromal factors (e.g., vascularization, presence of cytokines, interactions with fibroblasts and macrophages).

Whether autophagy can represent a valuable target for the therapy of thyroid cancers remains speculative. A deeper knowledge of the mechanistic links between autophagy and thyroid carcinogenesis is expected to clarify the diagnostic and prognostic potential of autophagic-related biomarkers and could greatly contribute to a more rational use of novel therapeutic approaches based on the modulation of autophagy to cure thyroid cancers.

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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