

Differential regulatory functions of three classes of phosphatidylinositol and phosphoinositide 3-kinases in autophagy

Xinlei Yu,¹ Yun Chau Long,^{1,*} and Han-Ming Shen^{2,*}

¹Department of Biochemistry; Yong Loo Lin School of Medicine; National University of Singapore; Singapore; ²Department of Physiology; Yong Loo Lin School of Medicine; National University of Singapore; Singapore

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Abbreviations: 3-MA, 3-methyladenine; AMBRA1, autophagy/Beclin 1 regulator 1; ATG, autophagy related; ATM, ATM serine/threonine kinase; ATR, ATR serine/threonine kinase; BH3, Bcl-2 homology 3; CCD, coiled-coil domain; CDK, cyclin-dependent kinase; CISD2, CDGSH iron sulfur domain 2; class I/II PI3K, class I/II phosphoinositide 3-kinase; class III PtdIns3K, class III phosphatidylinositol 3-kinase; DAPK1, death-associated protein kinase 1; DDR, DNA damage response; EIF4EBP1, eukaryotic translation initiation factor 4E binding protein 1; ER, endoplasmic reticulum; FOXO, forkhead box O; FYCO1, FYVE and coiled-coil domain containing 1; GAP, GTPase-activating protein; HMGB1, high mobility group box 1; HSPA1A, heat shock 70kDa protein 1A; IR, ionizing radiation; MAPK8, mitogen-activated protein kinase 8; MEFs, mouse embryonic fibroblasts; MTMR, myotubularin-related protein; MTOR, mechanistic target of rapamycin (serine/threonine kinase); MTORC1, mechanistic target of rapamycin complex 1; MVBs, spherical multivesicular bodies; NRBF2, nuclear receptor binding factor 2; PAS, phagophore assembly site; PDPK1, 3-phosphoinositide dependent protein kinase 1; PE, phosphatidylethanolamine; PIKFYVE, phosphoinositide kinase, FYVE finger containing; PINK1, PTEN-induced putative kinase 1; PtdIns3K-C1, class III phosphatidylinositol 3-kinase complex I; PtdIns3K-C2, class III phosphatidylinositol 3-kinase complex II; PKB, protein kinase B; PRKA, protein kinase, AMP-activated; PRKD1, protein kinase D1; PRKDC, protein kinase, DNA-activated, catalytic polypeptide; PtdIns5P, phosphatidylinositol 5-phosphate; PtdIns4P, phosphatidylinositol 4-phosphate; PtdIns(4,5)P₂, phosphatidylinositol 4,5-bisphosphate; PtdIns3P, phosphatidylinositol 3-phosphate; PtdIns(3,5)P₂, phosphatidylinositol 3,5-bisphosphate; PtdIns(3,4,5)P₃, phosphatidylinositol 3,4,5-trisphosphate; RHEB, Ras homolog enriched in brain; RPS6KB1, ribosomal protein S6 kinase, 70kDa, polypeptide 1; SQSTM1, sequestosome 1; TECPR1, tectonin β-propeller repeat containing 1; TFEB, transcription factor EB; TRIM28, tripartite motif containing 28; TSC, tuberous sclerosis; UV, ultraviolet; UVRAG, UV radiation resistance associated; WDFY3, WD repeat and FYVE domain containing 3; WIPI, WD repeat domain, phosphoinositide interacting; ZFYVE1, zinc finger, FYVE domain containing 1.

Autophagy is an evolutionarily conserved and exquisitely regulated self-eating cellular process with important biological functions. Phosphatidylinositol 3-kinases (PtdIns3Ks) and phosphoinositide 3-kinases (PI3Ks) are involved in the autophagic process. Here we aim to recapitulate how 3 classes of these lipid kinases differentially regulate autophagy. Generally, activation of the class I PI3K suppresses autophagy, via the well-established PI3K-AKT-MTOR (mechanistic target of rapamycin) complex 1 (MTORC1) pathway. In contrast, the class III PtdIns3K catalytic subunit PIK3C3/Vps34 forms a protein complex with BECN1 and PIK3R4 and produces phosphatidylinositol 3-phosphate (PtdIns3P), which is required for the initiation and progression of autophagy. The class II enzyme emerged only recently as an alternative source of PtdIns3P and autophagic initiator. However, the orthodox paradigm is challenged by findings that the PIK3CB catalytic subunit of class I PI3K acts as a

positive regulator of autophagy, and PIK3C3 was thought to be an amino acid sensor for MTOR, which curbs autophagy. At present, a number of PtdIns3K and PI3K inhibitors, including specific PIK3C3 inhibitors, have been developed for suppression of autophagy and for clinical applications in autophagy-related human diseases.

Introduction

Macroautophagy (hereafter referred as autophagy) is a cellular degradation process conserved in eukaryotic cells in which intracellular organelles and proteins are engulfed by double-membrane compartments termed phagophores that mature into autophagosomes, which subsequently fuse with lysosomes for degradation. Basal autophagy constitutively occurs as a house-keeping mechanism to clear “cytotoxic” components such as misfolded proteins and damaged organelles.¹ This process is enhanced under nutrient-limiting conditions to provide the needed nutrients for cell survival.^{2–4} Given that intracellular components are broken down during this process, essential elements must be spared and the initiation and progression of autophagy

*Correspondence to: Yun Chau Long, Email: bchlongy@nus.edu.sg, Han-Ming Shen, Email: phsshm@nus.edu.sg
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must be tightly controlled, which is ensured by intricate regulatory mechanisms via numerous kinases and signaling pathways. One of the most pivotal groups of kinases controlling autophagy are the phosphatidylinositol 3-kinases (PtdIns3Ks) and the phosphoinositide 3-kinases (PI3Ks). In this review, we will discuss the multilateral and multipronged regulation of autophagy by 3 classes of PtdIns3K and PI3K enzymes (Fig. 1).

The Process of Autophagy and its Machinery

The entire process of autophagy can be viewed as being comprised of the following stages: initiation, nucleation, expansion, maturation, and degradation. Numerous autophagy-related (*ATG*) genes have been identified and the corresponding ATG proteins are sequentially activated to regulate different stages of autophagy. These proteins can be grouped into various complexes based on their functions: the ULK1 kinase complex, the ATG9-ATG2-WIPI1/Atg18 complex, PIK3C3/Vps34-BECN1-PIK3R4/p150/Vps15 complex, and 2 ubiquitin-like conjugation systems, which include the ATG12-ATG5 and LC3/GABARAP proteins.⁵⁻⁷ In mammalian cells, under autophagy-stimulating conditions, the ULK1 complex (mainly composed of ULK1,

ATG13, ATG101 and RB1CC1/FIP200) undergoes a series of phosphorylation/dephosphorylation events, which lead to the activation of this complex and the initiation of autophagy.⁸ After the initiation step, a cup-shaped, primary double-membrane structure, the phagophore, is gradually formed.^{8,9} The nucleation of the phagophore membrane takes place at a site termed the phagophore assembly site (PAS) in yeast,¹⁰ whereas an additional site, the omegasome, may play a similar role in mammalian cells.⁹ The recruitment of the ULK1 and PIK3C3 complexes to the nucleation site is the initial step for autophagy,¹¹⁻¹⁵ and ULK1 relocalization is a prerequisite for ATG14-PIK3C3 complex targeting.^{11,14,15} The PIK3C3 complex generates phosphatidylinositol 3-phosphate (PtdIns3P) at the nucleation site,¹⁶ which creates a PtdIns3P-enriched milieu, reinforcing the localization of the ULK1 complex and other ATG proteins at the growing membrane^{9,12} and triggering the assembly of PtdIns3P-binding effector proteins, which is critical for the subsequent elongation of the phagophore and maturation of the autophagosome.^{7,17} The ATG12 ubiquitin-like conjugation system mediates the conjugation of ATG12 to ATG5, which then binds to ATG16L1.^{9,14} The latter, which resides at the elongating membrane, facilitates the subsequent modification of LC3 into a phosphatidylethanolamine (PE)-linked form.^{5,9,14,15} The lipidated

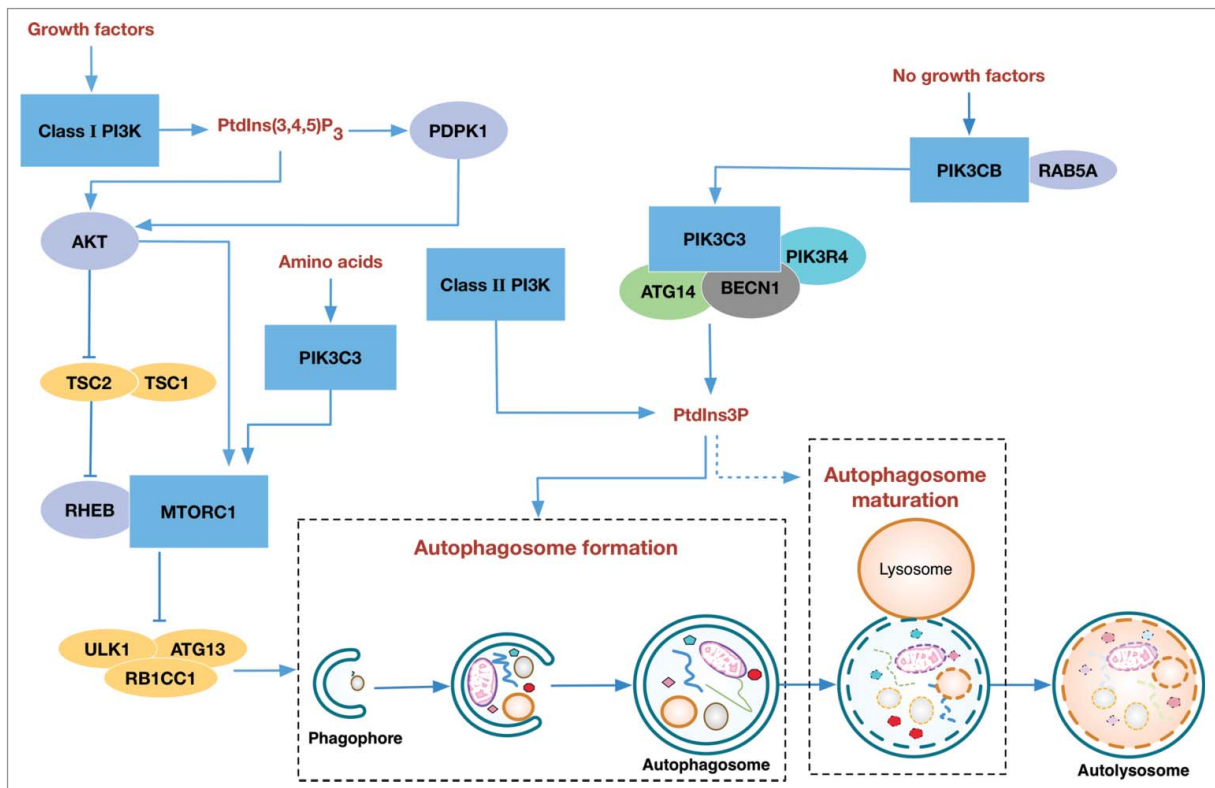


Figure 1. Regulation of autophagy by 3 classes of PtdIns3K and PI3Ks. The main regulatory pathways are illustrated: class I PI3K responds to growth factor signaling and produces PtdIns(3,4,5)P₃ which negatively regulates autophagy via the AKT-MTORC1-ULK1 complex, whereas the class III PtdIns3K, mainly the ATG14-containing PtdIns3K-C1, as well as class II PI3K, contributes to the initiation and progression of autophagy through the production of PtdIns3P. PtdIns3P positively regulates the formation of autophagosome. However, the function of PtdIns3P in the maturation step is controversial (depicted in dotted line): its presence is required for the recruitment of effector proteins for the maturation of autophagosome, but its turnover is also essential for the fusion of the autophagosome with the lysosome. Moreover, the PIK3CB subunit of class I PI3K activates PtdIns3K-C1 through RAB5A when growth factor is unavailable, thus promoting autophagy. In addition, PIK3C3 may also act as a sensor of amino acid and an activator of MTORC1.

LC3 then accumulates on phagophore and autophagosomal membranes, which presumably plays a role in membrane bending, curvature, and closure,^{9,18} tethering of unidentified precursor structures of autophagosomes,⁸ and selective targeting of autophagy substrates.^{9,19} During phagophore expansion, the ATG9-ATG2-WIPI1 complex is likely involved in recruiting lipids to the growing phagophore.²⁰⁻²² In the final step, the trafficking and fusion of autophagosomes with lysosomes is facilitated by PtdIns3P-binding proteins, PIK3C3 complexes, and interacting partners, as well as RAB proteins.^{7,16,23} The dynamics of the autophagic process, from the growth and closure of membrane structures to the acquisition of membrane-bound proteins, can be viewed as a membrane trafficking process, reminiscent of the endosomal trafficking pathway. It is not surprising that cells utilize an overlapping set of phospholipids, lipid kinases, and membrane-bound proteins in both the autophagy and endosomal pathways.

Three Classes of PtdIns3K and PI3K enzymes

In mammalian cells, PtdIns3Ks and PI3Ks are grouped into 3 classes based on their structural features and substrate specificities, as summarized in **Table 1**. Class I PI3Ks are heterodimeric kinases composed of a catalytic subunit (PIK3CA, PIK3CB, PIK3CD, or PIK3CG) and a regulatory subunit, and they are further subdivided to class IA (with PIK3CA, PIK3CB, or PIK3CD as the catalytic subunit) and class IB (with PIK3CG as the catalytic subunit).^{24,25} Class I PI3Ks can phosphorylate PtdIns, PtdIns4P and PtdIns(4,5)P₂ in vitro, but they may preferentially use PtdIns(4,5)P₂ to produce PtdIns(3,4,5)P₃ in vivo.²⁴ Class II PI3Ks are monomeric kinases which have 3 isoforms (PIK3C2A, PIK3C2B and PIK3C2G), and they prefer PtdIns and PtdIns4P as substrates to produce PtdIns3P and PtdIns(4,5)P₂.²⁶ Both class I PI3K and class II PI3K are downstream effectors of receptor tyrosine kinases and G-protein-coupled receptors.²⁴ Note that both class I and II enzymes can function as either phosphatidylinositol 3-kinases (phosphorylating the 3' hydroxyl of phosphatidylinositol) or phosphoinositide 3-kinases (i.e., adding an additional phosphate to a

phosphoinositide) in vitro, but are referred to as PI3Ks for simplicity. Class III PtdIns3K forms large multi-subunit complexes with PIK3C3 as the catalytic subunit and PIK3R4 as the regulatory subunit, and their composition diversifies in different biological context. Class III PtdIns3K generates PtdIns3P, and functions as the most pivotal positive regulator of autophagy.^{24,27}

MTOR (mechanistic target of rapamycin), ATM serine/threonine kinase (ATM), ATR serine/threonine kinase (ATR), and PRKDC (protein kinase, DNA-activated, catalytic polypeptide) constitute the PI3K-related kinase family, sometimes referred to as class IV PI3K, based on their sequence homology with other PI3Ks.^{28,29} The mechanistic role of MTOR in autophagy regulation will be reviewed in details below. ATM, ATR, and PRKDC are key signaling transducers in the DNA damage response (DDR) network.^{30,31} They are activated by ultraviolet (UV) light, ionizing radiation (IR), and DNA damaging chemicals, relay the DNA damage signal to DNA repair proteins, TP53/p53 and other transcription effectors, checkpoint kinases, and other cell cycle regulators to facilitate DNA damage repair and to make cell fate decisions.³⁰⁻³² Accumulating evidence has unveiled the complex crosstalk between DDR pathways and autophagy. Activation of ATM³³⁻³⁶ by various insults induces autophagy, and TP53³⁷⁻³⁹ and MTOR^{35,36,39-41} are 2 representative downstream signaling nodes connecting the DDR pathways to autophagy. The descriptions of autophagy regulation by ATR are rather scarce, but there is strong evidence showing that ATR is a potential upstream regulator of autophagy.⁴² With regard to PRKDC, its connection to the autophagy pathway is less clear, albeit there is evidence suggesting the presence of such a link.^{38,43,44} The mobilization of autophagy via these DDR transducers can be pro-survival^{38,39,45-48} or anti-survival,^{38,39,48,49} and the dual roles that autophagy plays in cell fate determination under DNA damage stress conditions add to the complexity of its involvement in DDR, and may influence the outcome of anticancer chemotherapy. The interplay between DDR and autophagy is a burgeoning area of research in the autophagy field, linking autophagy with genomic integrity. In light of the fact that class IV PI3Ks are an unconventional class of PI3Ks, we do not cover their regulatory functions in autophagy in this review.

Table 1. Composition and substrate preference of 3 classes of PI3Ks in mammalian cells

Class	Subunits		Lipid substrates	Products	Function in autophagy	
	Catalytic subunit	Regulatory subunit				
Class I PI3K	Class IA	PIK3CA	PIK3R1	PtdIns	PtdIns3P	Anti-autophagy
		PIK3CB	PIK3R2	PtdIns4P	PtdIns(4,5)P ₂	
PIK3CD		PIK3R3	PtdIns(4,5)P ₂	PtdIns(3,4,5)P ₃		
	Class IB	PIK3CG	PIK3R5 PIK3R6			
Class II PI3K		PIK3C2A PIK3C2B PIK3C2G	—	PtdIns PtdIns4P	PtdIns3P PtdIns(3,4)P ₂	Pro-autophagy
Class III PtdIns3K		PIK3C3	PIK3R4	PtdIns	PtdIns3P	Pro-autophagy

Dash (—) indicates that it does not exist in mammalian cells.

Differential Regulation of Autophagy by PtdIns3K and PI3Ks

In mammalian cells, 3 classes of PI3K enzymes localize at distinct subcellular compartments and specialize in controlling disparate stages of autophagy in response to diverse stimuli. The first observation of differential regulation of autophagy by class I PI3K and class III PtdIns3K was reported by Petiot et al.⁵⁰ in human colon cancer cells. This distinct regulatory mechanism is now recognized as the canonical paradigm: whereas class I PI3Ks act as the negative regulator of autophagy at the plasma membrane, class III PtdIns3K is the indispensable kinase producing PtdIns3P at the precursor membrane which drives autophagy progression (Fig. 1). However, the real regulatory network of autophagy by PtdIns3K and PI3Ks is far more complicated than what this simplified picture represents, and the role of class II PI3K in autophagy is just beginning to emerge.

Regulation of autophagy by class I PI3Ks

The signaling cascade through which class I PI3K-AKT-MTORC1 regulates autophagy has been well characterized (Fig. 1). Upon ligand-receptor binding (e.g., growth factors binding to respective receptors), class I PI3Ks translocate onto the inner leaflet of the plasma membrane, where they phosphorylate PtdIns(4,5)P₂ to generate PtdIns(3,4,5)P₃.⁵¹ PtdIns(3,4,5)P₃ recruits proteins bearing PH domains. Among these proteins, the serine/threonine protein kinase AKT/PKB has a pivotal role in class I PI3K signaling networks. AKT binds to the PtdIns(3,4,5)P₃-rich region on the plasma membrane along with another PH domain-containing kinase, PDK1/PDK1 (3-phosphoinositide dependent protein kinase 1). AKT then undergoes phosphorylation mediated by PDK1 and MTORC2, rendering AKT fully active.⁵¹ Activated AKT in turn regulates various downstream targets to promote nutrient uptake, metabolism, cell growth, and proliferation.^{51,52}

One of the most important signaling pathways downstream of class I PI3K and AKT in regulation of autophagy is MTOR complex 1 (MTORC1).^{52,53} MTORC1 is composed of MTOR, RPTOR, MLST8, AKT1S1/PRAS40, and DEPTOR, and it integrates a variety of signals, including growth factors, amino acids, and glucose via distinct signaling pathways.⁵⁴ Amino acids regulate MTORC1 via their control of the nucleotide status of RAG proteins and lysosomal localization of MTORC1.⁵⁵⁻⁵⁷ Glucose availability modulates MTORC1 through PRKA/AMPK (protein kinase, AMP-activated), which is activated by an increase in the cytosolic AMP/ATP ratio.^{56,58,59} The input of growth factor signals from the plasma membrane is transmitted by class I PI3K-AKT to the tuberous sclerosis (TSC) complex, resulting in the phosphorylation of TSC2 by AKT and thereby the inactivation of TSC1-TSC2. TSC1-TSC2 inactivation abolishes its GTPase-activating protein (GAP) activity toward RHEB (Ras homolog enriched in brain), and preserves RHEB in its GTP-bound state, which is required for MTORC1 activation.^{56,59,60} In addition to the TSC1-TSC2-RHEB-MTORC1 arm, AKT can directly regulate MTORC1 by phosphorylating and displacing AKT1S1, a negative regulator of MTORC1.^{54,59}

Active MTORC1 docks at lysosomes, promoting protein synthesis, and cell growth through EIF4EBP1/4E-BP1 (eukaryotic translation initiation factor 4E binding protein 1) and RPS6KB1/S6K1 (ribosomal protein S6 kinase, 70kDa, polypeptide 1), and inhibits autophagy via phosphorylation of ULK1 and ATG13.^{53,54} Phosphorylation of the latter proteins by MTORC1 destabilizes the ULK1-ATG13-ATG101-RB1CC1 complex and inhibits ULK1 kinase activity, leading to inhibition of autophagy initiation.⁵³ When MTORC1 is inhibited, ULK1 and ATG13 become dephosphorylated and the ULK1 complex is engaged as an autophagy initiator and recruiter for other effectors such as ATG14.²⁷ Moreover, ULK1 is subject to ubiquitination mediated by AMBRA1 (autophagy/beclin-1 regulator 1) under proautophagic conditions, stabilizing this kinase and increasing its activity, whereas AMBRA1 is under the regulation of MTORC1.⁶¹ In addition, MTORC1 negatively regulates lysosomal biogenesis and function via impeding the nuclear translocation of TFE3 (transcription factor EB);^{23,62-64} therefore, MTORC1 influences the degradative capacity of lysosomes, which provides another link between class I PI3K and autophagy.

The second pathway underlying the regulatory function of class I PI3K and AKT in autophagy is related to the fact that AKT promotes glucose uptake and glycolysis, which can contribute to ATP production.^{27,52} As mentioned above, when the cytosolic AMP/ATP ratio is elevated, PRKA is activated and suppresses MTORC1, either by TSC2 activation or RPTOR inhibition through phosphorylation.⁵⁸ Conversely, the preservation of ATP level by enhanced glucose utilization prevents the induction of autophagy. In addition to the effect through MTORC1, PRKA is also able to activate autophagy via phosphorylation of ULK1, when cellular energy becomes scarce.⁶⁵ Therefore, promotion of glucose metabolism by AKT prevents the activation of PRKA and autophagy induction.

The third possible mechanism associated with the regulatory effect of class I PI3K and AKT is via the FOXO (forkhead box O) nuclear transcription factors. It has been well established that AKT phosphorylates FOXOs, resulting in their cytoplasmic retention and inactivation.⁶⁶ FOXOs are a family of transcription factors in charge of the transcription of a series of autophagy-related genes, such as *ATG12*, *BCEN1* and *GABARAPL1*.⁶⁷ Thus, class I PI3K controls not only the initiation of autophagy, but also the replenishment of autophagic machinery during autophagy.

Fourth, it is intriguing that the activity of MTORC1 is negatively associated with that of class III PtdIns3K, and this relationship is specific to the ATG14-containing class III PtdIns3K complex,⁶⁸ indicating that class I PI3K signaling is coordinated with class III PtdIns3K activity.

However, there is an exception to this paradigm: the PIK3CB/p110 β catalytic subunit of class I PI3K. In contrast to the role of class I PI3K, which generally suppresses autophagy, PIK3CB acts as a positive regulator of autophagy. *Pik3cb*-deficient mouse embryonic fibroblasts (MEFs), liver and heart display impaired autophagic function, whereas overexpression of PIK3CB activates autophagy.⁶⁹ Subsequently, it was found that upon growth factor withdrawal, PIK3CB dissociates from the growth receptor

complex and interacts with RAB5A/RAB5, keeping this small GTPase in the GTP-bound state.⁷⁰ GTP-loaded RAB5A plays a role in the activation of PIK3C3.⁷¹ Through association with RAB5A, PIK3CB enhances PIK3C3 activity and promotes autophagy.⁷⁰ In contrast to the class I PI3K holokinases, which carry the signals from growth factors and indirectly curb autophagy, the PIK3CB subunit acts as a sensor of growth factor availability and stimulates autophagy under circumstances of growth factor limitation.

Regulation of autophagy by class III PtdIns3K

The primary clue for the dependence of autophagy on PtdIns3K activity was yielded by the study showing that wortmannin and LY294002 inhibit autophagy in isolated rat hepatocytes, although it was unclear which class of PI3K accounted for autophagy regulation.⁷² The first revelation of the relevance of PIK3C3/Vps34 to autophagy was provided by a study in the yeast *Hansenula polymorpha*, showing that its PIK3C3 homolog participates in pexophagy, a selective form of autophagy.⁷³ After the dissection of the specific functions of 2 Vps34 complexes in autophagy and vacuolar protein sorting,⁷⁴ the involvement of mammalian class III PtdIns3K in autophagy was subsequently

uncovered in a study which described the opposing functions of class I and III PI3K and PtdIns3K enzymes.⁵⁰ Class III PtdIns3K forms different protein complexes, which are organized in a divergent and multilayered fashion (Fig. 2). The stratification can be viewed based on their interaction and stability: PIK3C3-PIK3R4-BECN1, the most stable and prevalent complex, constitutes the core; while ATG14 and UVRAG (UV radiation resistance associated) are combined with the core in PtdIns3K complex I (PtdIns3K-C1; ATG14-containing PtdIns3K complex) and PtdIns3K complex II (PtdIns3K-C2; UVRAG-containing PtdIns3K complex), respectively;⁷⁵⁻⁷⁸ KIAA0226/Rubicon is a regulatory subunit that is thought to stably bind to UVRAG-containing complexes;^{77,78} AMBRA1, NRBF2 (nuclear receptor binding factor 2) and other accessory factors transiently or unstably interact with either BECN1 (e.g., AMBRA1)^{79,80} or ATG14 (e.g., NRBF2),⁸¹⁻⁸³ thus comprising the peripheral components.^{84,85} UVRAG also exists in a separate complex excluding ATG14, which holds an important role in the regulation of autophagy at the maturation step.^{84,86} Atg14/ATG14 and Vps38/UVRAG are present exclusively in 2 Vps34/PIK3C3 complexes (PtdIns3K complex I and II in yeast, and class III PtdIns3K-C1 and PtdIns3K-C2 in mammalian cells, respectively), which are organized in similar V-shape conformations with Vps15/PIK3R4 at the base.⁸⁷ In yeast, PtdIns3K complex I and II play a role in autophagy and the vacuolar protein sorting pathway, respectively.⁷⁴ In mammalian cells, PtdIns3K-C1 and PtdIns3K-C2 mainly function in autophagy and endosomal trafficking, respectively,^{75,88,89} however, both are implicated in autophagy.^{75,76,86} In the PIK3C3 complexes, PIK3R4 is required for the kinase activity of PIK3C3,⁸⁹⁻⁹² and it serves as a bridge linking PIK3C3 with ATG14-BECN1, or with UVRAG-BECN1.⁸⁷ For clarity, the compositions of Vps34/PIK3C3 complexes in yeast and mammals and their functional specificity are summarized in Table 2. In the following sections, we will discuss in more detail how each of the components in class III PtdIns3K complexes functions as a point in the autophagy-regulatory network under different circumstances and the composition of the corresponding complexes (Fig. 2).

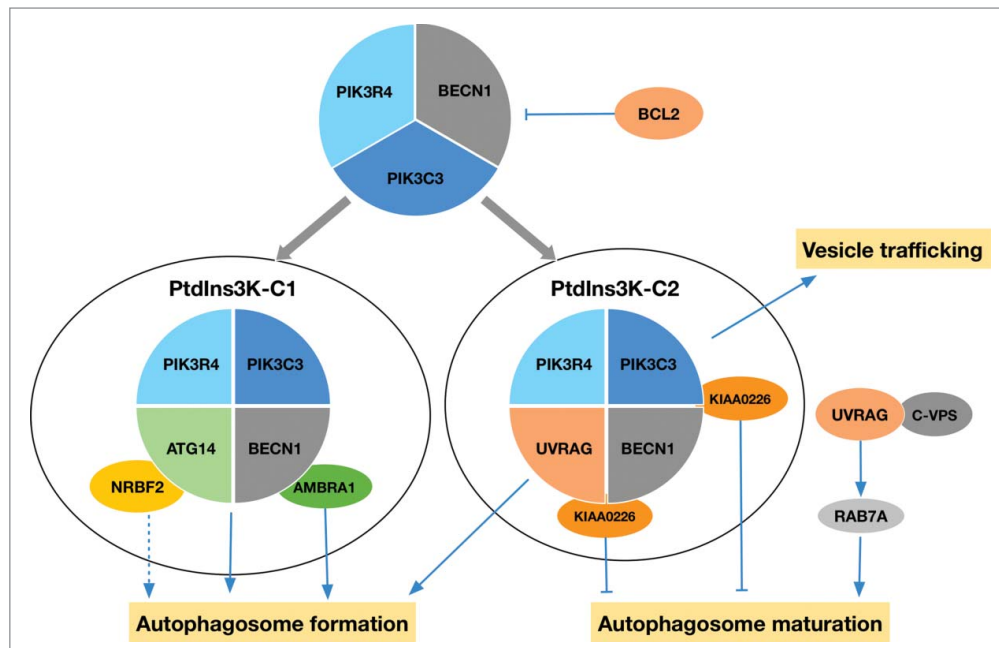


Figure 2. Diversified composition of class III PtdIns3K complexes and their roles in autophagy. PIK3C3-PIK3R4-BECN1 is the core complex; a proportion of the core complex is combined with ATG14 or UVRAG in a mutually exclusive manner, constituting PtdIns3K-C1 and PtdIns3K-C2, respectively. Both PtdIns3K-C1 and PtdIns3K-C2 contribute to autophagosome formation, and UVRAG can regulate autophagosome maturation independent of BECN1 through interacting with the class C VPS complex (C-VPS) and activating RAB7A. BCL2, by binding to BECN1, inhibits the formation of class III PtdIns3K complexes. KIAA0226 is considered as a negative regulator of autophagosome maturation, which interacts with PtdIns3K-C2 through directly binding to PIK3C3, BECN1, and UVRAG. As peripheral proteins, AMBRA1 and NRBF2 both interact with PtdIns3K-C1. AMBRA1 activates autophagy at an early step, while NRBF2 plays regulatory roles in autophagosome formation (dotted line denotes that there is controversy about the effect of NRBF2 on autophagy). Additional peripheral components of class III PtdIns3K complexes have also been reported, which are not included in the diagram.

Table 2. Composition and functional specificity of Vps34/PIK3C3 complexes in yeast and mammals

Complex	Yeast		Mammals	
	PtdIns3K complex I	PtdIns3K complex II	PtdIns3K-C1	PtdIns3K-C2
Core kinase	Vps34	Vps34	PIK3C3	PIK3C3
Regulatory subunits	Vps30	Vps30	BECN1	BECN1
	Vps15	Vps15	PIK3R4	PIK3R4
	Atg38		NRBF2	
Defining component	Atg14	Vps38	ATG14	UVRAG
Biological function	Autophagy	Vacuole protein sorting	Autophagy	Endosomal trafficking and autophagy*

*The role of PtdIns3K-C2 in autophagy is still controversial.

PtdIns3P is a key phospholipid required for the progression of autophagy

PtdIns3P acts as a signaling molecule and platform for the assembly and coordination of various effector proteins during the autophagic process. Under basal conditions, PtdIns3P is detected using a 2 × FYVE probe on early endosomes, spherical multivesicular bodies (MVBs), and the nucleus in mammalian cells, reflecting its role in vesicle trafficking.⁹³ Upon autophagy induction, this phospholipid migrates and becomes punctate, periodically forming an omega-shaped structure, which presumably corresponds to the omegasome.¹⁶ The dynamic evolution of the PtdIns3P-positive compartment was monitored by ZFYVE1/DFCP1 (zinc finger, FYVE domain containing 1) using live cell imaging.¹⁶ This structure expands following amino acid withdrawal, and at a certain time point LC3 accumulates and co-localizes with ZFYVE1. The membrane structure positive for both ZFYVE1 and LC3 dilates with time until LC3 exits from the PtdIns3P-enriched membrane, after which the ring-shape becomes increasingly invisible. Although the origin of the phagophore remains a question of extensive debate (with the endoplasmic reticulum [ER], mitochondria, Golgi apparatus, and plasma membrane all being candidates as a membrane source for autophagy¹⁷), this study demonstrated that the PtdIns3P-containing punctate structures are in close association with the ER.¹⁶ The spatial and temporal dynamic involvement of PtdIns3P-positive structure suggests a critical role of PtdIns3P for autophagosome biogenesis.¹⁶ Indeed, production of PtdIns3P serves as the most primary signal for autophagosome formation through recruiting a number of effectors. As the very early event of autophagy initiation, most of the ULK1 complexes form punctate structures spatially overlapping with omegasomes; however, only when PtdIns3Ps are generated and enriched at the loci is the punctation of ULK1 stabilized and enhanced.¹² The other PtdIns3P effectors at the early stages include ZFYVE1, WIPI (WD repeat domain, phosphoinositide interacting) proteins, and WDFY3/ALFY (WD repeat and FYVE domain containing 3).^{7,27} The role of ZFYVE1 in autophagy remains elusive, but the punctation of ZFYVE1 is one of the early observable events during nucleation.¹⁶ WIPI proteins (WIPI1 to WIPI4), mammalian homologs of yeast Atg18, may have the ability to sense and regulate PtdIns3P levels and participate in the initiation and maturation of the omegasome.^{7,27,94,95} WDFY3 is implicated in cargo

selection and delivery in selective autophagy.^{17,27,96} It is further conjectured that the PtdIns3P synthesized in situ, together with its effector proteins, signals the de novo synthesis of other phospholipids (e.g., phosphatidylcholine, phosphatidylethanolamine, and phosphatidylserine), which constitute the autophagosomal membrane.⁹⁷ At the late stage of autophagy, additional PtdIns3P effectors interact with PtdIns3P. TECPR1 (tectonin β-propeller repeat containing 1), associating with both PtdIns3P and the ATG12–ATG5 complex, mediates the fusion of autophagosomes with lysosomes,⁹⁸ whereas FYCO1 (FYVE and coiled-coil domain containing 1) is also involved in the maturation and trafficking of autophagosomes.^{17,99} The stringent requirement of phospholipids in the progression of autophagy points to the indispensable role of their producers, PtdIns3Ks and PI3Ks, in the autophagic pathway.

However, it should be mentioned that PtdIns3P is not persistently and equally concentrated in both leaflets of autophagosomal membrane during the course of autophagy.^{16,100,101} The completion of autophagy requires the clearance of PtdIns3P from the autophagosome, enabling the disassembly of its effectors and the fusion of the autophagosome with the lysosome. The dephosphorylation of PtdIns3P is carried out by phosphoinositide 3-phosphatases in the myotubularin protein family.¹⁰² Among these phosphatases, the involvement of MTMR14/Jumpy (myotubularin-related protein 14),^{103,104} MTMR3,¹⁰⁵ MTMR6 and MTMR7¹⁰³ in autophagy has been documented. The yeast PtdIns3P phosphatase Ymr1 is essential for the late stage of autophagy, and the absence of this protein results in the accumulation of autophagosomes in the cytoplasm; the failure in the turnover of PtdIns3P and dissociation of Atg proteins from the autophagosomal membrane presumably accounts for the defect in autophagosome-vacuole fusion in the *ymr1*^{C397S} phosphatase-inactive strain.¹⁰¹ Therefore, it is clear that the balance of PtdIns3P, which is tightly controlled by both kinases and phosphatases, may determine the timing and extent of autophagic flux. In addition to the dose, the asymmetric distribution of PtdIns3P on the 2 faces of the double autophagosomal membrane is also critical, which may be related to the recruitment of effectors to specialized sites as well as the remodeling of the associated membrane. For the latter notion, the study by Cheng et al.¹⁰⁰ may provide supporting evidence. An intensive delineation of PtdIns3P distribution on autophagosomal membranes indicated that in yeast, PtdIns3P is located in both leaflets of the

autophagosome, with more abundance in the luminal leaflet than the cytoplasmic leaflet. Conversely, mammalian PtdIns3P is exclusively distributed in the cytoplasmic leaflet during autophagy. It was further shown that Ymr1 partially accounts for the PtdIns3P asymmetry, and, interestingly, abrogation of this asymmetry results in the aberrant structure of autophagosomal vesicles.¹⁰⁰ The regulatory role of phosphatases in autophagy is equally important to that of PtdIns3Ks and PI3Ks; however, the scope of this review precludes in-depth discussion on the functions of the former in autophagy.

The list of autophagy-relevant phosphoinositides does not end with PtdIns3P. PtdIns4P, PtdIns(4,5)P₂, PtdIns5P, and PtdIns(3,5)P₂ have also been described to participate in autophagy (e.g., selective autophagy, and/or a certain stage/stages of macroautophagy; for a detailed review, see ref. 17).^{17,106} Intriguingly, PtdIns5P, produced by the type III PtdInsP 5-kinase PIKFYVE (phosphoinositide kinase, FYVE finger containing) or the phosphatase MTMR3 plays a predominant role in glucose starvation-induced autophagy, in which the role of PtdIns3P is dispensable.¹⁰⁶ In the case of autophagy induced in HBSS starvation medium, PtdIns5P also has a compensatory effect to sustain autophagy if PtdIns3P is depleted.¹⁰⁶ In particular, the noncanonical autophagy pathways stimulated by nonstarvation conditions are likely to be mediated by PtdIns3P-independent mechanisms.¹⁰⁷⁻¹⁰⁹ This emerging body of evidence points to the need to revisit the requirement of PtdIns3P for autophagy; in spite of the discrepancy, PtdIns3P is still widely accepted as a key phospholipid for the autophagic process, which remains one of the main focuses in this review.

Regulation of autophagy by PIK3C3 via formation of protein complexes and direct post-translational modifications

PIK3C3 is so far recognized as the predominant source of PtdIns3P, and it holds a fundamental role in both endosomal trafficking and autophagy.⁹⁰ *Pik3c3* knockout mice are embryonic lethal,¹¹⁰ whereas tissue specific ablation of *Pik3c3* blocks autophagic degradation and protein turnover, and severely debilitates liver and heart function.¹¹¹

As the core catalytic subunit in the class III PtdIns3K complex, PIK3C3 per se is a point of regulatory convergence by diverse autophagy-modulating mechanisms. A study by Kim et al.¹¹² demonstrated the presence of 2 different regulatory mechanisms controlling the role of PIK3C3 in autophagy via: (i) formation of different protein complexes and (ii) direct phosphorylation of PIK3C3. In their study, PIK3C3 is present in 2 types of class III PtdIns3K complexes, nonautophagic and proautophagic; and glucose starvation selectively elevates the kinase activity of ATG14- or UVRAG-containing class III PtdIns3K complexes (proautophagic), but suppresses that of PIK3C3 in complexes lacking these 2 proteins (nonautophagic). This dichotomous regulation is enabled by the preferential phosphorylation of free PIK3C3 (T163/S165) or BECN1 (S91/S94) in proautophagic class III PtdIns3K complexes by PRKA.¹¹² In addition to this selected modification under starvation, it is interesting that PIK3C3 activity is probably modulated in sync with cell cycle

progression, supported by the evidence that CDK1 (cyclin-dependent kinase 1) and CDK5 phosphorylate PIK3C3 at distinct sites, which represses its activity.¹¹³ Additionally, PRKD1/PKD (protein kinase D1) phosphorylates PIK3C3 under conditions of oxidative stress,¹¹⁴ and is dependent on acetylated HSPA1A (heat shock 70kDa protein 1A), whereas TRIM28/KAP1 (tripartite motif containing 28) is able to mediate PIK3C3 SUMOylation in response to autophagy-inducing stress,¹¹⁵ both of which activate autophagy.

PIK3C3 is widely accepted as a positive regulator of autophagy; however, the function of PIK3C3 in amino acid sensing adds another layer of complexity to its regulatory role in autophagy. The amino acid sensing model through Ca²⁺-CALM/calmodulin-PIK3C3 has been reported previously.¹¹⁶ In this model, PIK3C3 is part of the MTOR complex; amino acids stimulate an elevation in the intracellular Ca²⁺ level and Ca²⁺-CALM/calmodulin binding, which increases PIK3C3 activity; consequently, PtdIns3Ps produced by PIK3C3 activate MTOR by replacing FKBP8/FKBP38 with RHEB.¹¹⁶ This model is consistent with earlier studies showing that PIK3C3 is required for MTOR-RPS6KB1 signaling activity,^{117,118} and is supported by the evidence that amino acid restimulation of MTOR activity is impaired in *Pik3c3* KO MEFs¹¹¹ and MTOR activity is remarkably ablated in *Pik3c3* KO embryos.¹¹⁰ However, several issues are still under dispute concerning the amino acid-Ca²⁺-CALM-PIK3C3-MTOR signaling model. For instance, the increase in intracellular Ca²⁺ by amino acid stimulation as shown in the study¹¹⁶ was contradicted by the result of another investigation demonstrating that amino acid withdrawal, rather than addition, resulted in cytosolic Ca²⁺ increase.¹¹⁹ Second, the dependence of PIK3C3 activity on Ca²⁺-CALM¹¹⁶ is refuted by the evidence that neither Ca²⁺ chelator nor CALM inhibitor blocks PIK3C3 activity.⁹¹ More importantly, the effect of amino acid withdrawal on different PIK3C3 complexes remains unsettled: contradictory observations were reported showing the activation of general PIK3C3^{116,118,120} but suppression of ATG14-interacting PIK3C3^{68,120} after amino acid deprivation. It should be noted that the study by Russel et al.¹²⁰ may offer a potential explanation: the opposing effects of amino acid withdrawal on class III PtdIns3K activity in PIK3C3-BECN1 and PIK3C3-ATG14 immunoprecipitates were demonstrated, and the presence of ATG14 is likely to determine the specific activation of the ATG14-containing PIK3C3 complex mediated by ULK1 phosphorylation of BECN1. Together with the evidence of differential regulation of PIK3C3 complexes by energy deprivation,¹¹² a hypothesis that may reconcile the contradictory roles of PIK3C3 in MTOR signaling and autophagy could be proposed: certain PIK3C3-interacting components, for instance ATG14, may specify the differential regulation of distinct PIK3C3 complexes by nutrients, or determine the spatial distribution of PIK3C3 that confers divergent biological functions. Alternatively, the requirement of PIK3C3 for MTORC1 activity may be ascribed to the release of amino acids by autophagic degradation. Our group¹²¹ and others¹²² have demonstrated that the generation of amino acids by autophagy is essential for MTORC1 activity; thus, the impairment of autophagy by *Pik3c3* knockdown or

inhibition may influence this feedback circuit. Additionally, since a proportion of PIK3C3 complexes are involved in the endosomal system and are plausibly important for proper lysosomal function,^{75,76,111,123} *Pik3c3* ablation may affect the activation of MTORC1 by amino acids at the lysosome, which is dependent on the function of several lysosomal proteins⁵⁵⁻⁵⁷ and normal lysosomal degradation.^{122,124} In contrast, yeast Vps34 is the sole PtdIns3K and it functions only in vacuolar trafficking/autophagy but not in the TORC1 regulatory network;¹²⁵ whether and why mammalian PIK3C3 has evolved to harbor bifurcate functions in MTOR modulation and autophagy is a mystifying question. This perplexing issue notwithstanding, the paradoxical roles of PIK3C3 in MTOR stimulation in response to amino acid and autophagy induction highlight PIK3C3 as a key node in the cell signaling network, worthy of intensive study.

Regulation of autophagy by PIK3C3 via BECN1

BECN1 (the mammalian homolog of yeast Vps30/Atg6) is among the first mammalian homologs of yeast Atg proteins discovered. It binds to BCL2 family-antiapoptotic proteins through its BCL2 homology 3 (BH3) domain, interacts with PIK3C3 via its coiled-coil domain (CCD) and evolutionarily conserved domain, and associates with UVRAG or ATG14 through the CCD.^{126,127} Similar to *Pik3c3* deletion, knockout of *Becn1* results in embryonic mortality.¹²⁸ BECN1 is required for PIK3C3 activity and autophagy, and deficiency in BECN1 results in impaired autophagic function.^{128,129} Binding of BCL2 to BECN1 blocks autophagy, as BCL2 shields BECN1 from class III PtdIns3K complexes and prevents autophagy.^{126,127} Nutrient-rich conditions promote BCL2-BECN1 binding and inhibit autophagy,¹³⁰ whereas various stresses disrupt this interaction and unfetter BECN1 as an autophagy initiator.^{131,132} The phosphorylation of BCL2 by MAPK8/JNK1 (mitogen-activated protein kinase 8) under starvation conditions,¹³¹ and CDKN2A/p19Arf/ARF at the mitochondria,¹³² reduce BCL2 and BECN1 interaction, resulting in the activation of autophagy. Modification of BECN1 itself is another way to modulate autophagy. BECN1 phosphorylation by ULK1 at Ser14 is one of the key initiating events required for autophagy induction upon starvation or MTOR inhibition, leading to activation of the ATG14-containing class III PtdIns3K complexes.¹²⁰ The aforementioned PRKA phosphorylation of BECN1 under glucose starvation also enhances the activity of ATG14- or UVRAG-containing class III PtdIns3K complexes.¹¹² Of note, BECN1 is an important downstream target of AKT, which inhibits autophagy, and aberrant BECN1 phosphorylation by AKT is implicated in tumorigenesis.¹³³ In this scenario, AKT-mediated phosphorylation of BECN1 increases the binding of BECN1 with YWHA/14-3-3 proteins, which tethers BECN1 to the intermediate filament protein VIM/vimentin, leading to the suppression of autophagy.¹³³ Thus, AKT modulates the indirect interaction of BECN1 with intermediate filaments, mirroring the AMBRA1-regulated subcellular localization of BECN1-PIK3C3 to another kind of cytoskeleton, microtubules (to be discussed below).⁸⁰ In addition, DAPK1 (death-associated protein kinase 1) phosphorylates

BECN1 at its BH3 domain and releases BECN1 from BCL2, which promotes autophagy.¹³⁴ EGFR can also phosphorylate BECN1, but is inhibitory for PIK3C3 activity and autophagy.¹³⁵ There are also different circumstances that result in the linkage of BECN1 to diverse types of ubiquitin chains, which exert distinct effects on BECN1 and autophagic activity.^{136,137} For instance, ubiquitination of BECN1 through Lys-11-linked¹³⁸ or Lys-48-linked¹³⁹ ubiquitin chains promotes the degradation of BECN1, which possibly decreases autophagy, whereas Lys-63-linked ubiquitination enhances autophagy through dissociating BECN1 from BCL2.¹⁴⁰ More importantly, BECN1 serves as a platform to coordinate various regulators of autophagy, which has been termed the "BECN1 interactome."^{85,141} These secondary interacting proteins of class III PtdIns3K complexes, some of which are viewed as the peripheral components of class III PtdIns3K complexes, include AMBRA1, HMGB1 (high mobility group box 1), BIRC5/survivin, PINK1 (PTEN induced putative kinase 1), CISD2/NAF-1 (CDGSH iron sulfur domain 2), and the abovementioned regulators including BCL2; these proteins can either promote (e.g., AMBRA1, HMGB1, BIRC5, PINK1) or inhibit (e.g., CISD2, BCL2) autophagy.⁸⁵

Regulation of autophagy by PIK3C3 via ATG14

As shown in **Figure 2**, ATG14 is an integral component of the class III PtdIns3K complex, and its activity is a prerequisite for the proper function of autophagy. The coiled-coil region of ATG14 binds to the CCD region of BECN1 as well as the N-terminal C2 domain of PIK3C3.^{75,77} Interaction between ATG14 and PIK3C3 can elevate the activity of the latter when BECN1 is present.⁷⁷ Deletion of *ATG14/Atg14* impairs autophagosome formation,^{75,77,78,142} characterized by accumulation of LC3-II and ubiquitinated protein inclusions.^{75,77} During autophagosome formation, ATG14 translocates to phagophore and/or omegasome membranes,¹⁴³ and it is likely to target a proportion of PIK3C3 to the ER, which is crucial for PtdIns3P production and autophagy induction.^{142,144} Indeed, the Barkor/Atg14(L) autophagosome targeting sequence/BATS domain of ATG14 has been confirmed to be required for targeting the PIK3C3 complex to the phagophore and/or omegasome membrane and for the initiation of autophagosome formation.¹⁴⁵ Exogenously expressed ATG14 colocalizes with LC3, ATG12 and ATG5, indicating that ATG14 may engage in the recruitment of LC3, ATG12, and ATG5 at an early step of autophagy.^{75,77,78} More interestingly, ATG14 likely mediates the differential regulation of PIK3C3 in different class III PtdIns3K complexes. ATG14 may be the determining factor dictating the selective inhibition of the ATG14-containing class III PtdIns3K complex by MTORC1 under nutrient-rich conditions,⁶⁸ and the activation of PtdIns3K-C1 by ULK1¹²⁰ and proautophagic class III PtdIns3K complexes by PRKA upon nutrient starvation.¹¹²

Regulation of autophagy by PIK3C3 via UVRAG

Human *UVRAG* cDNA was first isolated and discovered to be able to confer partial UV-resistance on a xeroderma pigmentosum cell line.¹⁴⁶ Mutation of *UVRAG* is frequently observed in

various human cancers and may be responsible for the etiology of these cancers.¹⁴⁷⁻¹⁵⁰ UVRAG is critical for DNA repair and chromosomal stability, especially in response to radiation.¹⁵¹⁻¹⁵³ Using GST affinity isolation, UVRAG was identified as a binding partner of BECN1-PIK3C3, which directly interacts with BECN1 via its CCD.⁷⁶ UVRAG also binds to the N-terminal C2 domain of PIK3C3.⁷⁵ UVRAG overexpression enhances the activity of autophagy, the presence of UVRAG can enhance class III PtdIns3K kinase activity, and UVRAG is required for autophagosome formation.⁷⁶ The essential role of UVRAG in autophagy was further confirmed in *Uvr*ag-deficient mice, in which autophagic flux is abated.¹⁵⁴ Additionally, UVRAG was reported to be a target of AKT1, which inhibits autophagy through reduction of UVRAG.¹⁵⁵ Interestingly, UVRAG, as a PtdIns3P-binding effector per se, shuttles between ER and autophagic membranes, coordinating different membrane trafficking events, and maintaining organelle homeostasis under various conditions.¹⁵⁶ In a PtdIns3P-dependent manner, UVRAG is bound to the ER tethering protein complex RINT1-ZW10-NBAS, involved in Golgi-to-ER transport; however, when autophagy is induced, UVRAG is dissociated from the ER and is bound to the SH3GLB1/Bif-1-BECN1-PIK3C3 complex.¹⁵⁶

UVRAG is necessary for vesicle tethering and fusion in the endocytic system.⁸⁶ The role of UVRAG in vesicle trafficking extends to autophagic membrane trafficking; however, the function of UVRAG in autophagosome-lysosome fusion seems not to require BECN1.⁸⁶ In a BECN1-independent manner, UVRAG reinforces the association of the class C VPS complex with the autophagosome and activates RAB7A/RAB7, thereby facilitating autophagosome maturation and degradation of autophagic cargo by lysosomes.⁸⁶ It should be noted that the UVRAG-containing class III PtdIns3K complex is more abundant than the ATG14-containing complex,^{77,78} probably due to its constitutive function under normal conditions. Finally, there are studies arguing against the requirement of UVRAG for autophagy, which show that UVRAG does not colocalize with LC3 under starvation conditions, and its knockdown does not lead to a defect in autophagy.^{75,157,158} Although controversy remains regarding the mechanistic role of UVRAG in the regulation of autophagy, its implication in the autophagic process cannot be overlooked, and how it functions in different stages of autophagy awaits further elucidation (Fig. 2)

Regulation of autophagy by PIK3C3 via other interacting partners

In addition to BECN1, ATG14, and UVRAG as discussed above, there are several other important proteins in the class III PtdIns3K complexes that are implicated in the autophagic process; due to limited space, herein we only cover a few of them briefly.

KIAA0226/Rubicon is an important negative regulator in the maturation step of autophagy as well as endocytic trafficking. KIAA0226 was identified as a stable partner interacting with a proportion of BECN1-PIK3C3-UVRAG complexes,^{77,78} but whether it co-exists with ATG14 remains controversial.⁷⁷

Overexpression of KIAA0226 retards LC3-II and SQSTM1/p62 (sequestosome 1) degradation and autophagosome/lysosome maturation, whereas knockdown of this protein results in a decline of LC3-II and SQSTM1 as well as an increase in the number of autolysosomes.^{77,78}

AMBRA1 plays a positive role in autophagy presumably by regulating the BECN1-PIK3C3 interaction.^{79,80} AMBRA1 also acts as a tether controlling BECN1-PIK3C3 subcellular localization. Under normal conditions, AMBRA1 anchors the BECN1-PIK3C3 core complex to microtubules by interacting with dynein light chains 1/2; upon induction of autophagy, ULK1 phosphorylates AMBRA1 and releases the core complex, enabling the latter to translocate to the ER and initiate autophagosome formation.⁸⁰ In addition, as mentioned above, AMBRA1 is negatively regulated by MTOR; together with the E3-ligase TRAF6, AMBRA1 engages in ULK1 ubiquitination, which promotes ULK1 activity under autophagy-inducing conditions.⁶¹

NRBF2 was identified as a protein involved in autophagy, which is present only in the ATG14-containing class III PtdIns3K complex in mammalian cells.^{81-83,159} The yeast ortholog of NRBF2 is presumed to be Atg38, although there are sequence diversities.^{82,160} Likewise, Atg38 is recognized as a component of the Atg14-containing Vps34 complex I in yeast, which is required for the autophagy pathway.¹⁶⁰ Intriguingly, in yeast Atg38 is responsible for the stability of Vps34 complex I, which connects Vps34-Vps15 with Atg14-Vps30,¹⁶⁰ reminiscent of the function of NRBF2 in mediating ATG14, PIK3C3-PIK3R4, and BECN1 interaction in mammalian cells.⁸² However, it is a question under debate whether NRBF2 positively^{81,83} or negatively⁸² regulates autophagy in higher eukaryotes.

The emerging role of class II PI3Ks in autophagy

Since PtdIns3P is the major phosphorylated lipid that drives the progression of autophagy, it is plausible that multiple sources of PtdIns3P exist in eukaryotic cells. Notably, in vitro studies demonstrated that PtdIns is the preferred target of class II PI3K, although this kinase also displays activity toward PtdIns4P.¹⁶¹ It is therefore plausible that class II PI3K is a contributor to the PtdIns3P pool in addition to class III PtdIns3K. In support of this hypothesis, there is emerging evidence that class II PI3K is a significant producer of PtdIns3P, and class II PI3K holds a wide spectrum of functions ranging from cell signaling, to cell migration and vesicle trafficking.¹⁶¹⁻¹⁶⁶ One hint implying a role of class II PI3K in autophagy was provided by the studies on cell corpse clearance by phagocytosis in *C. elegans*.^{167,168} In this process, autophagy is required for phagosome maturation and clearance of apoptotic cells; most importantly, class II PI3K was identified as a complementary kinase producing PtdIns3P on phagosomes, indispensable for the degradation of cell corpses in *C. elegans*.^{167,168} However, studies from several *Pik3c3* knockout animal models suggest that PtdIns3P generation and autophagic function rely predominantly on PIK3C3 activity.^{111,169,170} The question of whether class III PtdIns3K is the exclusive kinase responsible for PtdIns3P generation during autophagy remained unsolved until a recent study by Devereaux et al. revealed an alternative source

of PtdIns3P in *Pik3c3* knockout MEFs.¹⁷¹ In *Pik3c3* KO MEFs, it is surprising that PtdIns3P is still detectable using a higher affinity PtdIns3P probe and the PtdIns3P-binding protein WIPI1, and autophagosomes are still observed under starvation conditions; class II PI3K was confirmed as another contributor to the PtdIns3P pool during autophagy, and depletion of class II PI3K further decreases autophagic flux, which is inhibited by *Pik3c3* deletion.¹⁷¹ Thus, cells may ensure the adequate and timely production of autophagic PtdIns3P by involving more than one producer (Fig. 1).

PtdIns3K and PI3K Inhibitors and their Application in Autophagy and Diseases

Development of potent PtdIns3K and PI3K inhibitors has been a focus of research for years, and great progress has been made in the development of tools to constrain the activity of PI3Ks. The fact that aberrant signaling activity of PtdIns3Ks and PI3Ks is correlated with various pathological conditions and mutations in these enzymes is frequently observed in cancer makes these lipid kinases one of the most sought-after drug

Table 3. Examples of PtdIns3K and PI3K inhibitors, their status in clinical development and effects on autophagy

Selectivity	Name of the inhibitor	Molecular targets	Effects on on autophagy	Status in clinical trials	References
Pan-class	Wortmannin	PtdIns3K and PI3K enzymes, as well as PI3K-related kinases	Inhibition	Failed to enter clinical trial	26,72,175,177,178,181,190-192
	LY294002	PtdIns3K and PI3K enzymes, as well as PI3K-related kinases	Dual effect: activation and inhibition	Failed to enter clinical trial	26,72,175,177
	SF1126	PtdIns3K and PI3K enzymes, as well as PI3K-related kinases	Unknown	Phase I	177,194-201
Class I-specific	PX-866	PIK3CA, PIK3CB, PIK3CD, PIK3CG	Activation	Phase I/II	National Cancer Institute (USA) http://www.cancer.gov/clinicaltrials/24,202-211
	XL147	PIK3CA, PIK3CB, PIK3CD, PIK3CG	Activation	Phase I/II	24,212-219
	BKM120	PIK3CA, PIK3CB, PIK3CD, PIK3CG	Activation	Phase I/ II/III	National Cancer Institute (USA) http://www.cancer.gov/clinicaltrials/24,26,220-224
Dual PI3K and MTOR	BAY80-6946	PIK3CA, PIK3CB	Unknown	Phase I/ II	National Cancer Institute (USA) http://www.cancer.gov/clinicaltrials/24,26,225
	NVP-BGT226	PIK3CA, PIK3CB, PIK3CD, PIK3CG, MTOR	Activation	Phase I/ II	24,173,182,226,227
	BEZ235	PIK3CA, PIK3CB, PIK3CD, PIK3CG, MTOR	Activation	Phase I/ II	National Cancer Institute (USA) http://www.cancer.gov/clinicaltrials/24,228-233
Class I-Isoform specific	XL765	PIK3CA, PIK3CB, PIK3CD, PIK3CG, MTOR	Activation	Phase I/ II	National Cancer Institute (USA) http://www.cancer.gov/clinicaltrials/24,234-238
	BYL719	PIK3CA	Unknown	Phase I/ II	National Cancer Institute (USA) http://www.cancer.gov/clinicaltrials/
	INK1117	PIK3CA	Unknown	Phase I	National Cancer Institute (USA) http://www.cancer.gov/clinicaltrials/
Class I-Isoform specific	GSK2636771	PIK3CB	Unknown	Phase I/II	National Cancer Institute (USA) http://www.cancer.gov/clinicaltrials/
	SAR260301	PIK3CB	Unknown	Phase I	173
	IPI-145	PIK3CG, PIK3CD	Unknown	Phase I/ II/ III	National Cancer Institute (USA) http://www.cancer.gov/clinicaltrials/239
	GDC-0941	PIK3CA, PIK3CD	Activation	Phase I/ II	National Cancer Institute (USA) http://www.cancer.gov/clinicaltrials/175,219,240-244
	GS-1101	PIK3CD	Unknown	Phase I/ II/ III	National Cancer Institute (USA) http://www.cancer.gov/clinicaltrials/245-251
Class III-specific	Compound 31 ((2S)-8-[(3R)-3-Methylmorpholin-4-yl]-1-(3-methyl-2-oxobutyl)-2-(trifluoromethyl)-3,4-dihydro-2H-pyrimido[1,2- α]pyrimidin-6-one)	PIK3C3	Unknown	NA	186
	PIK-III	PIK3C3	Inhibition	NA	185
	SAR405	PIK3C3	Inhibition	NA	183
	VPS34-IN1	PIK3C3	Unknown	NA	184

NA: Not available.

targets.^{24,172} Based on their target selectivity, the available PtdIns3K and PI3K inhibitors can be classified as pan-PI3K inhibitors, dual PI3K-MTOR inhibitors and class or isoform-selective inhibitors, as summarized in **Table 3**.^{24,26,173-175}

Pan-PI3K inhibitors have potent inhibitory effect on all class I PI3Ks, but their off-target effects on other PI3K-related kinases such as MTOR confound their application and therefore display unfavorable side effects in clinical trials.^{175,176} Wortmannin and LY294002 are among the early-discovered pan-PI3K inhibitors; however, they are not ideal for clinical applications because of nonselectivity and poor pharmacological properties.^{24,26,175,177} In light of these limitations, novel pan-PI3K inhibitors (e.g., BKM120, BAY80–6946) have been developed and demonstrate improved pharmaceutical potential and decreased toxicity in clinical trials.^{24,26,177} Additionally, since wortmannin and LY294002 impose inhibitory effects on class III PtdIns3K, they are also used to block autophagy.^{72,178} 3-methyladenine (3-MA), first discovered as an autophagy inhibitor,¹⁷⁹ shows functional similarity with LY294002, which may exert dual effects on class I and class III PtdIns3Ks.^{178,180} In comparison to 3-MA, which has been shown to have a dual effect on autophagy due to its transient inhibitory effect on class III PtdIns3K, wortmannin is a preferred autophagy inhibitor based on its persistent inhibition of class III PtdIns3K.¹⁸¹ Nevertheless, caution must be taken when these autophagy inhibitors are used, with nutrient conditions and biological contexts taken into account. Dual PI3K inhibitors are designed to inhibit both catalytic subunit of all class I PI3Ks and MTOR (e.g., NVP-BGT226, XL765).^{173,175,182} They are more effective in dampening PI3K-MTOR signaling, because they act on 2 nodes of this pathway and prevent the feedback activation of IRS1-PI3K by MTOR in the case of inhibiting MTOR alone. Isoform-specific PI3K inhibitors only target a specific isoform of PI3Ks, for instance, the PIK3CA inhibitor INK1117, the PIK3CB inhibitor GSK2636771, and the PIK3CD inhibitor GS-1101, which display fewer side effects and increased selectivity compared to the other classes of inhibitors in clinical trials.^{26,175}

Inspiring progress has been made recently in the development of effective and specific inhibitors targeting PIK3C3.¹⁸³⁻¹⁸⁶ An early study resolved the molecular structure of PIK3C3, and revealed that PIK3C3 has a smaller and more rigid ATP binding pocket than that of PIK3CG, which restricts the binding of classical PI3K inhibitors.¹⁸⁷ This molecular dissection of PIK3C3 paved the way for the subsequent development of novel inhibitors that fit well within the PIK3C3 ATP cavity. A number of recent studies reported new PIK3C3 inhibitors, including VPS34-IN1,¹⁸⁴ Compound 31 (a tetrahydropyrimidopyrimidinone derivative),¹⁸⁶ PIK-III,¹⁸⁵ and SAR405,¹⁸³ among them, Compound 31 and SAR405 exhibit the highest potency (IC₅₀ PIK3C3 equals 2 nM and 1.2 nM, respectively) and favorable selectivity toward PIK3C3.^{183,186} Notably, PIK-III and SAR405, both of which bind the ATP binding pocket of PIK3C3, exert efficient inhibition on autophagy as well as LC3 lipidation.^{183,185} The application of PIK-III led to the identification of a novel substrate of selective autophagy, NCOA4, which mediates the degradation of ferritin and turnover of iron.¹⁸⁵ Moreover,

SAR405 displays a potential anticancer therapeutic property, as it shows synergistic antiproliferative activity in combination with the MTOR inhibitor everolimus.¹⁸³ These PIK3C3 inhibitors will prove to be valuable tools in delineating the function of class III PtdIns3K in each stage of autophagy as well as other cellular processes; also, they are promising pharmaceutical candidates for augmenting the activity of current anticancer drugs as well as having a potential application to other diseases.

Development of selective inhibitors targeting class II PI3Ks are significantly lagging, which impedes the elucidation of this cryptic class of PI3Ks. In response to pan-PI3K inhibitors, PIK3C2B and PIK3C2G exhibit similar sensitivity to wortmannin as class I PI3Ks and class III PtdIns3Ks, but PIK3C2A only responds to higher doses of wortmannin and LY294002.^{161,166} Several inhibitors that demonstrate increased effectivity and selectivity toward specific isoforms of class II PI3Ks have been described recently,^{188,189} offering hope for developing more selective inhibitors of class II PI3Ks. Since this class of PI3Ks is equally important in malignant transformation and carcinogenesis,^{161,175} finding specific and effective class II PI3K inhibitors are among the important research goals for cell signaling studies and cancer treatment.

Concluding Remarks and Perspective

Autophagy has been an intensive research area in the last decade and the mechanisms of how autophagy is regulated have been intensively studied. Meanwhile, possible strategies have been proposed for manipulating this crucial pathway for the purpose of curing diseases and promoting health. PtdIns3Ks and PI3Ks are the cardinal type of kinases imperative for the proper functioning of autophagy. Generally, class I PI3Ks keep autophagy at bay in response to upstream stimulation; class III PtdIns3Ks, as well as class II PI3Ks, are required for the initiation and progression of autophagy. However, there are still gaps and discrepancies in our knowledge on the regulation of autophagy by these enzymes. For instance, how PIK3C3 reconciles its amino acid sensing function with its kinase activity under different conditions, and whether class II PI3Ks play a more pronounced role in autophagy and how they are regulated by certain autophagy-inducing stresses remain to be settled. Additionally, the contribution of phospholipids other than PtdIns3P to the biogenesis of the autophagosome as well as the later stages of autophagy also requires more attention from researchers. The progress in studying the involvement of lipid kinases in autophagy not only greatly facilitates our understanding of the molecular mechanisms controlling the autophagic process, but also promotes the discovery of pharmaceutical and therapeutic strategies targeting autophagy to cure related human diseases. Among them, development of class-specific PtdIns3K and PI3K inhibitors remains an important research objective in the realm of autophagy research.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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