

## Review Article

# New insights into autophagy in hepatocellular carcinoma: mechanisms and therapeutic strategies

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**Abstract:** Autophagy is a mechanism by which cellular substances are transported to lysosomes for degradation, allowing the basic transformation of cellular components, and providing energy and macromolecular precursors. In cancer, the contradictory role of autophagy in tumor suppression and promotion has been widely acknowledged. Activation and suppression of autophagy have been proposed as cancer therapies, resulting in targeted treatment of cancer by autophagy being considered ambiguous. The dynamic effect of autophagy can also be applied to hepatocellular carcinoma (HCC), a malignant tumor with high incidence and a low survival rate. In this review, we introduce characteristics of different types of autophagy and summarize which genes, non-coding RNAs, and related signaling pathways are involved in autophagy and the regulation of the formation and progress of HCC. More importantly, we discuss the role of autophagy in the treatment of HCC, such as in traditional chemotherapy, molecular targeted drugs, and natural products.

**Keywords:** Autophagy, hepatocellular carcinoma, signaling pathways, noncoding RNAs, therapy

## Introduction

Autophagy is an intracellular catabolic pathway. By removing misfolded proteins, damaged organelles, and lipid droplets, autophagy plays a crucial role in energy balance and cytoplasmic quality control, and promotes liver homeostasis [1, 2]. Autophagy is active at a basic level in cells. It may be further upregulated in response to several types of stress that interfere with cell homeostasis, such as low ATP levels, nutrient and growth factor deficiency, hypoxic conditions, endoplasmic reticulum (ER) stress, pathogen entry, or anticancer drugs [3]. The role of autophagy in cancer is important. It is believed that autophagy can prevent the development of cancer. However, once cancer has formed, increased autophagic flux tends to enable cancer cells to survive and grow [4, 5]. Accordingly, a major challenge in cancer treatment is should we try to enhance or inactivate autophagy?

Hepatocellular carcinoma (HCC) is ranked as the sixth most common cancer and the third

leading cause of cancer death [6]. HCC is one of the leading causes of cancer-related death worldwide and is refractory to nearly all currently available anti-cancer therapies [7, 8]. Despite new breakthroughs in treatment and surgery, the 5-year survival rate remains unsatisfactory [9]. In addition, the use of anticancer drugs to treat HCC is limited by the occurrence of primary and acquired drug resistance [10, 11]. Increasing numbers of studies have shown that autophagy greatly affects HCC. Autophagy is associated with risk factors for HCC, such as oxidative stress, persistent inflammation, viral infection, metabolic dysfunction, liver alcohol disorders, and fatty liver disease [5, 12-14]. Therefore, a comprehensive understanding of the role of autophagy in HCC may be beneficial to develop new diagnostic and therapeutic techniques. From a therapeutic point of view, understanding whether, when, and how autophagy can be used to cure HCC remains a challenge.

In this review, we summarize the characteristics of autophagy and focus on some new research

hotspots, such as non-traditional autophagy, secretory autophagy, and selective autophagy. We then summarize which genes, non-coding RNAs, and related signaling pathways are involved in autophagy, and the regulation of the formation and progress of HCC. Finally, we discuss the role of autophagy in the treatment of HCC.

### Autophagy

#### *The characteristics of autophagy*

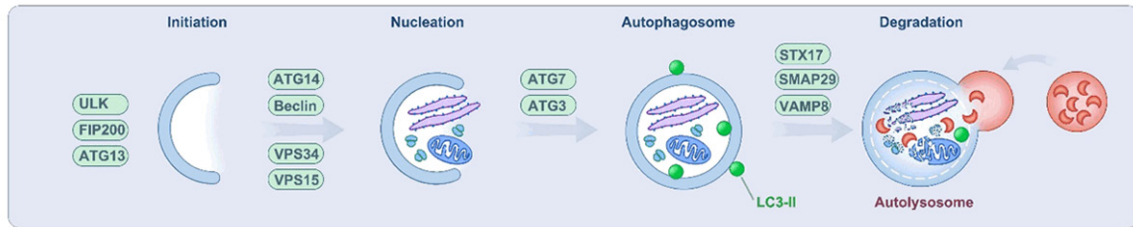
Autophagy mainly has three forms: Microautophagy, macroautophagy (referred to hereafter as autophagy), and chaperone-mediated autophagy. Macroautophagy is an evolutionarily conserved metabolic process, including the formation of double membrane vesicles called autophagosomes [15]. In the formation of autophagosomes, a portion of the cytoplasm, which may include organelles, protein aggregates, and lipid droplets, is sequestered in large quantities or selectively [16]. Then, the outer membrane of the autophagosome fuses with a lysosome (forming an autolysosome), which leads to degradation of the enclosed materials along with the inner membrane of the autophagosome. The amino acids and other small molecules produced by autophagic degradation are transported back to the cytoplasm for recycling or energy production. Autophagy is controlled by a series of highly regulated signaling events that occur at a basic level in all cells, and may be induced by different signals and cellular stresses [17]. Macroautophagy is mediated by a group of evolutionarily conserved genes, termed autophagy-related genes (ATGs), which were first found via yeast gene screening [18]. To date, more than 40 ATGs have been identified and their functions have been extensively evaluated. ATGs are involved in the formation, nucleation, expansion, and elongation of autophagic membranes, the binding and fusion with lysosomes, and the degradation of intracapsular products. With a few exceptions, all ATG genes are required for efficient fusion of autophagosomes and lysosomes [19]. The process of autophagy mainly comprises the following processes: (a) The activation of the ULK1 (Unc-51 like autophagy activating kinase 1, also known as ATG1) complex [20]; (b) the activation of the class III PI3K (phosphatidylinositol-4,5-bisphosphate 3-kinase) complex, ATG-

14, Beclin 1, p63, and AMBRA1 (autophagy and beclin 1 regulator 1) [21]; (c) the ATG5ATG12 complex then conjugates with ATG16 to expand the autophagosome membrane and members of the LC3 (microtubule associated protein 1 light chain 3 alpha) and GABARAP (GABA type A receptor-associated protein) families of proteins are conjugated to the lipid phosphatidylethanolamine (PE) and recruited to the membrane [22, 23]; (d) ATG4B, in conjunction with ATG7, conjugates LC3-I and PE to form LC3-II [24]; and finally (e) autophagic degradation. Microautophagy involves inward invagination of the lysosomal membrane, which delivers a small portion of the cytoplasm into the lysosomal lumen [25]. Chaperone-mediated autophagy (CMA) is a pathway for protein degradation in intracellular lysosomes. Chaperone-mediated autophagy involves the direct translocation of cytosolic proteins across the lysosomal membrane, which requires protein unfolding via chaperone proteins [26]. In addition to classical autophagy, there are several non-traditional types of autophagy that have received research attention (**Figure 1**).

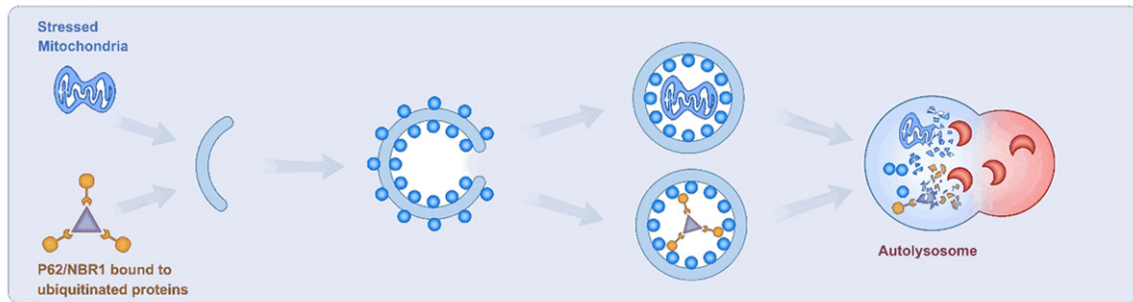
#### *Other kinds of autophagy*

Non-canonical autophagy is a process that does not require the entire set of ATG proteins, in particular Beclin 1, to form an autophagosome. Scarlatti et al. found that overexpression of BCL2 (BCL2 apoptosis regulator) was unable to reverse the non-canonical autophagy triggered by the polyphenol resveratrol in the breast cancer cell line MCF-7 [27]. Besides, Beclin 1-independent autophagy mediated by the neurotoxin 1-methyl-4-phenylpyridinium is associated with neuronal cell death [28]. Smith et al. found that arsenic trioxide induces a Beclin 1-independent autophagic pathway in ovarian carcinoma cells and implicates SnoN (SKI like proto-oncogene) in promoting arsenic trioxide-mediated autophagic cell survival [29]. These studies suggested that it is feasible to treat cancer by inducing non-canonical autophagy with pro-apoptotic compounds when the function of typical autophagic proteins is impaired. Some ATG genes are involved in the digestion of unwanted extracellular (rather than intracellular) material. One such alternative function of autophagy proteins is LC3-associated phagocytosis (LAP), which is a macroautophagy-like process [30]. During LAP, the

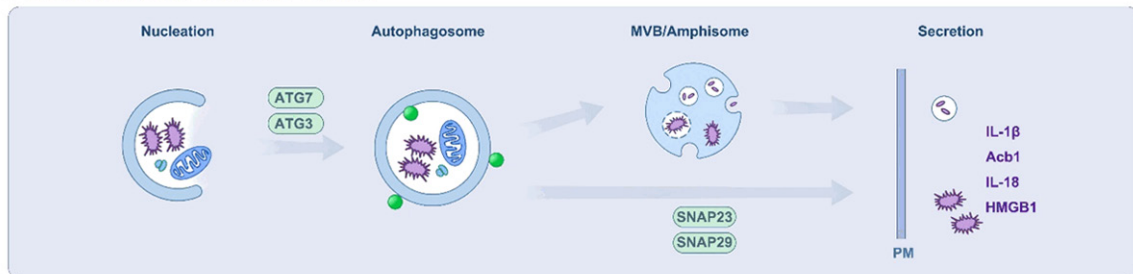
**A CLASSICAL AUTOPHAGY**



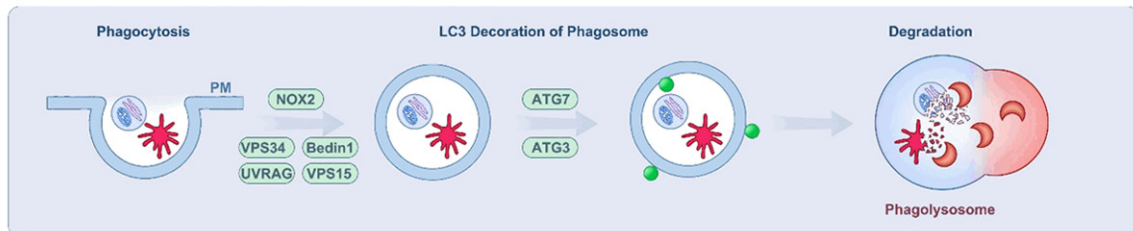
**B SELECTIVE AUTOPHAGY**



**C SECRETORY AUTOPHAGY**



**D LC3-ASSOCIATED PHAGOCYTOSIS**



**Figure 1.** Molecular Mechanisms of different types of autophagy. A. Classic autophagy: Different stimuli cause aggregation and activation of multiple ATGs and other regulatory proteins to construct double membrane autophagosomes. Lipidation of LC3 (LC3-II) is essential for capturing autophagy cargo and stabilizing the autophagosome inner membrane. Then, autophagosomes fuse to lysosomes in a STX17-dependent manner, resulting in lysosomal enzymes degrading the vesicle contents. B. Selective autophagy: Selective autophagy contributes to intracellular homeostasis by modulating the degradation of cytoplasmic substances, such as aggregated proteins, damaged or excessive organelles, and invading pathogens. Its mechanism must ensure efficient identification and isolation of cargo in autophagy. C. Secretory autophagy: ATGs mediate unconventional secretion of multiple proteins lacking the N-terminal signal sequence. First, ATGs promote the formation of LC3+ autophagosome-like intermediates, and the contents encapsulated in the autophagy inner membrane are released extracellularly rather than degraded in lysosomes. Second, the target of secretory autophagy is transferred to the intramembranous space of the LC3+ double-membrane vesicle, which is directly fused to the plasma membrane or fused to the secreted MVB intermediate. Finally, secretory autophagy may involve extracellular release of MVB/Amphisome intermediates. D. LC3-associated phagocytosis: The phagocytosis of pathogens recruits UVRAG and Rubicon (RUBCN), thereby activating the Beclin-1-VPS34 complex. With the participation of ATG3 and ATG7, lysosome fusion and pathogen degradation are accelerated. It is noteworthy that the phagocytic vesicles formed by LAP are single membraned.

phagosomes phagocytose extracellular contents, such as microorganisms or dying cells,

which are then transported to lysosomes. Cunha et al. revealed that the anti-tumor

effects of LAP impairment require tumor-infiltrating T cells, and are dependent upon STING (stimulator of interferon genes) and the type I interferon response [31]. Muniz-Feliciano et al. found that retinal pigment epithelial cells promote LAP through the expression of RUBCN/Rubicon (RUN domain and cysteine-rich domain containing Beclin 1-interacting protein) and suppress autophagy through the activation of EGFR (epidermal growth factor receptor) [32]. As a pathway related to autophagy, the physiological importance of LAP and its value in tumor research deserve further exploration.

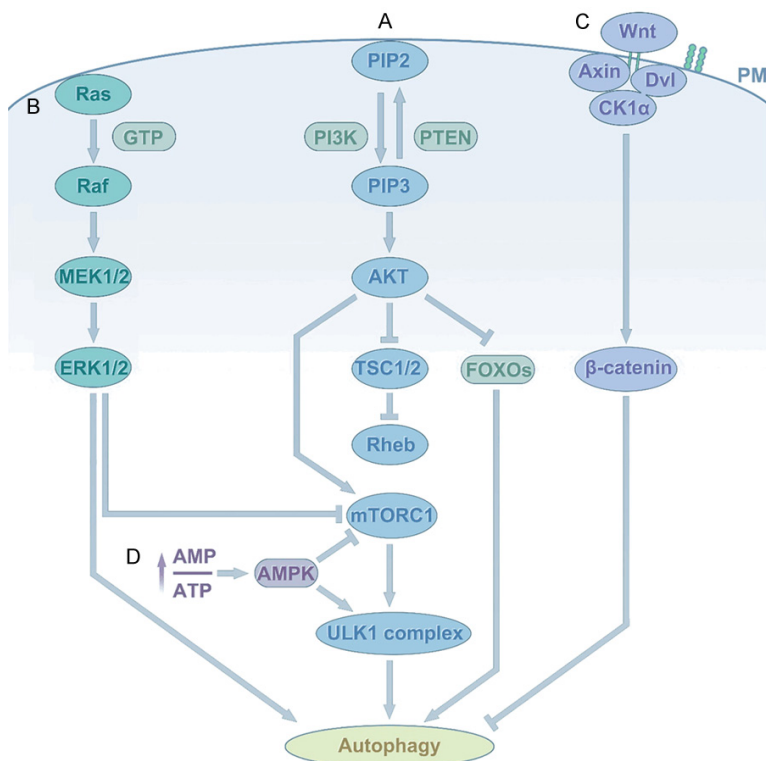
Recent findings indicated that ATGs lack N-terminal signal sequences and are involved in unconventional protein secretion. ATGs may be involved in a process that is significantly different from classical autophagy. In addition to its role in lysosomal degradation, autophagy also controls extracellular secretion. ATGs' involvement in this process was first discovered in yeast secretion of Acb1 (acyl-CoA-binding protein) [33]. The role of the selective secretion pathway of ATGs regulates the genetic requirements of GRASP55 (Golgi reassembly stacking protein 55) and GRASP65 for Golgi accumulation. This discovery enriched the function of autophagy and demonstrated its involvement in secretion [34, 35]. Kimura et al. found that the prototypical cytosolic secretory autophagy cargo, interleukin 1 beta (IL-1 $\beta$ ) is recognized by specialized secretory autophagy cargo receptor TRIM16 (tripartite motif containing 16) and that this receptor interacts with the R-SNARE Sec22b to recruit cargo to the LC3-II<sup>+</sup> sequestration membranes [36]. Moreover, Adam utilized the autophagy-based involvement in cellular secretion to identify shed proteins associated with autophagy levels in melanoma [37]. Jacob hypothesized that autophagy-dependent secretion of tumor-promoting factors by HNSCC (head and neck squamous cell carcinoma)-associated CAFs (cancer-associated fibroblasts) may explain their role in malignant development [38]. Interestingly, autophagy is also associated with the recent research hotspot, exosomes. Autophagy probably contributes to the decreased exosome release induced by ISGylation (conjugation of proteins to Interferon stimulated gene 15) [39]. Dias demonstrated that PRNP (prion protein) supports CAV1 (Caveolin 1)-suppressed autophagy to protect multivesicular bodies (MVBs)

from sequestration into phagophores, thus facilitating exosome secretion. These results indicated that secretory autophagy could affect the microenvironment of the tumor; therefore, further analysis of the cellular mechanisms by which autophagy promotes these different secretory processes remains an important topic for future research.

For a long time, researchers thought that autophagy lacked cargo specificity. However, we now understand that the control of the choice of cargoes is extremely specific. This process is called 'selective autophagy', which plays an important role in preventing most mammalian diseases. Liang et al. proposed a spatiotemporal model wherein recruitment of AMPK (AMP-activated protein kinase) in association with components of the VPS34 (phosphatidylinositol 3-kinase catalytic subunit type 3) and ATG16 complex to damaged mitochondria regulates selective mitophagy to maintain cancer cell viability [40]. The selectivity of autophagy is achieved by target recognition: Kimura demonstrated that a subset of tripartite motif (TRIM) proteins mediate selective autophagy of key regulators of inflammatory signaling [41]. By removing dangerous cytoplasmic components, selective autophagy protects cells from oxidative and genotoxic stress, which may constitute a tumor suppressor mechanism. In addition, all mechanisms for earmarking cargo must be tightly coordinated with the formation of autophagosomes to ensure final cargo disposal. The mechanisms involved in the recognition of selective autophagy substrates may play an active role in the initiation of autophagy [42, 43]. Selective autophagy involves a variety of mechanisms; the ultimate goal is to ensure proper movement of cargo. Substrate phosphorylation is also a common mechanism for targeting selective autophagy, possibly by activating specific kinases that enhance selective autophagy [44]. A more plausible explanation for the tumor-suppressing effect of autophagy may be its role as a selective degradation pathway [45]. Selective autophagy might ensure tumor survival by degrading misfolded proteins and damaged organelles accumulated in genetically unstable tumor cells. Therefore, targeting nonspecific autophagy and its selective forms may prove beneficial in the fight against malignant tumors.



## Autophagy and hepatocellular carcinoma



**Figure 2.** Autophagy signaling in HCC. A. PI3K/AKT/mTOR: Classic autophagy: Binding of growth factors to receptors triggers PI3K, and then activation of PI3K catalyzes the production of PIP3, phosphorylation of PIP3, and activation of Akt serine/threonine kinase. Subsequently, phosphorylation of AKT activates mTORC1, thereby inhibiting autophagy. In addition, activated AKT leads to activation of Rheb. Rheb then activates mTORC1. In addition to direct or indirect activation of mTORC1, active AKT can also directly regulate transcription leading to inhibition of autophagy. B. The RAS/RAF/MEK/ERK pathway: RAS switches from inactive (GDP-bound) to the active (GTP-bound) form. Activated RAS binds and recruits RAF kinase to the cell membrane for RAF dimerization and activation. Subsequently, activated RAF phosphorylates and activates MEK; MEK in turn phosphorylates and activates ERK/MAPK. Finally, phosphorylated ERK directly activates autophagy, or phosphorylates a variety of substrates that trigger autophagy by inhibiting mTORC1. C. The Wnt/ $\beta$ -catenin signaling pathway: This pathway can negatively regulate autophagy.  $\beta$ -catenin is a special target for degradation by autophagy in starvation stress. D. The AMPK signaling pathway: AMPK is an  $\alpha\beta$  heterotrimer that is activated by decreasing ATP concentrations and increasing AMP concentrations. It induces autophagy via the activation of ULK1 or the inactivation of mTOR.

### Roles of autophagy in HCC

Autophagy plays a contradictory role in HCC, protecting cells from carcinogenesis at the early stage and promoting tumor progression at the advanced stage [46-49]. This dual role illustrates the complexity of targeting autophagy to treat HCC. Autophagy-related genes, non-coding RNAs, and related signaling pathways (Figure 2) are involved in autophagy and the regulation of the formation and progress of

HCC. The exact function of autophagy in HCC has not been fully determined and is controversial. Further in-depth research is required to understand the role of autophagy in the development of HCC.

### Autophagy-related genes

ATG-mediated autophagy has a significant impact on HCC. Deletion of the genes encoding Beclin-1, ATG5, or ATG7 in mice damaged autophagy and promoted the occurrence of spontaneous liver tumors in aged mice [46, 50, 51]. At the same time, the expression level of Beclin-1 correlated negatively with HCC grading, suggesting that to some extent, Beclin-1 correlates positively with HCC, and the low expression of Beclin-1 in HCC tissues was associated with the recurrence and survival rates [52, 53]. In addition, Takamura reported that mice with systemic mosaic deletion of *Atg5* and liver-specific *Atg7*<sup>-/-</sup> mice develop benign liver adenomas [54]. This result revealed that autophagy has an anti-tumor effect on specific liver cancers and may have a preventative effect on the occurrence and development of HCC. Tian et al. utilized an ATG5 knockdown model to verify that impairing autophagy in hepatocytes would induce oxidative stress

and DNA damage, followed by the initiation of hepatocarcinogenesis [55]. Another study showed that p62 is necessary for HCC induction in mice and that its high expression level in non-tumor human liver predicts rapid HCC recurrence after curative ablation [56]. P62 is an ubiquitin-binding autophagy receptor and signaling protein that accumulates in premalignant liver diseases and most HCCs. Ji et al. reported that HuR (human antigen R) functions as a pivotal regulator of autophagosome forma-

tion by enhancing the translation of *ATG5*, *ATG12*, and *ATG16* mRNAs. Augmented expression of HuR and ATGs may participate in the malfunction of autophagy in HCC cells [57]. In addition, UVRAG (UV radiation resistance associated) interacts with BECN1 and PIK3C3, and is a significant regulator of mammalian autophagy. Feng et al. provided *in vitro* and *in vivo* evidence that UVRAG ubiquitination at lysine residues 517 and 559 promotes autophagosome maturation and enhances the lysosomal degradation of EGFR, which significantly inhibits HCC cell growth [58]. These reports indicated that ATGs are involved in the progress of HCC and offer insights into autophagy regulation and therapeutic combinations in HCC.

### Noncoding RNAs

Noncoding RNAs (ncRNAs), including microRNAs (miRNAs) and long noncoding RNAs (lncRNAs), are attracting more attention as potential new drug targets for human diseases. In recent years, the interaction between ncRNAs and autophagy has become a hotspot in the study of HCC. MiRNAs are a class of endogenously expressed, short noncoding RNAs, which regulate gene expression post-transcriptionally [59]. MiRNAs can affect many biological processes, such as cell development, infection, immunity, and carcinogenesis [60]. MiRNAs are involved in various stages of autophagy, including phagophore induction, nucleation and expansion; the maturation of autolysosomes and autophagosomes; and have a regulatory role [61]. MiRNAs are increasingly recognized to play an important role in physiological and pathological processes, including the development and progression of tumors. Many microRNAs are involved in autophagy regulation of HCC [59]. For example, Glycine decarboxylase overexpression inhibited migration and invasion via an increase in cellular autophagy. This effect was reduced by miR-30d-5p transfection [62]. Furthermore, miRNAs regulate autophagy by targeting autophagy-related genes in HCC. Xiu-Tao Fu et al. noted downregulated miR-30a in metastatic HCC, which mediates Beclin 1 and Atg5-dependent autophagy and confers anoikis resistance in HCC cells [63]. In addition, the first reported miRNA, miR-375, with proapoptotic functions, can inhibit autophagy and reduce cell viability in HCC cells by binding directly to ATG7 under

hypoxic conditions [64]. In another study, miR-26 family members (miR-26a, miR-26b, and miR-26a/b) could act as potential autophagy inhibitors, making HCC cells sensitive to doxorubicin (Dox) and promoting apoptosis by directly inhibiting the expression of serine/threonine protein kinase ULK1, which is a key promoter of autophagy [65]. Interestingly, Lan et al. were the first to reveal that autophagy selectively regulates miR224 expression through an autophagosome-mediated degradation system. They also found that the off-label use of amiodarone, an antiarrhythmic agent, effectively suppressed HCC tumorigenesis through autophagy-mediated miR224 degradation, both *in vitro* and *in vivo* [66]. In general, autophagy and miRNAs are important regulators of HCC development.

Emerging evidence indicates that lncRNAs act as competitive platforms for both miRNAs and mRNAs [67]. lncRNAs are non-coding RNAs longer than 200 nucleotides [68, 69]. lncRNAs have a crucial role in various fundamental pathophysiological processes, such as carcinogenesis, that play a regulatory role in the progression of cancer [70, 71]. The discovery of lncRNAs provides a new way to regulate genes in almost all essential biological processes, including autophagy. A series of studies have shown that many lncRNAs are abnormally expressed in HCC tissues and participate in their biological behaviors, such as proliferation, apoptosis, metabolism, migration, and invasion [72, 73]. In hepatocellular carcinoma, PTEN (phosphatase and tensin homolog) and PLLP (Plasmalipin) interact with miRNA17, miRNA19B and miRNA20A, inhibiting the PI3K-AKT (AKT kinase)-mTOR (mammalian target of rapamycin) signaling pathway to inhibit cell proliferation, migration/invasion as well as induced autophagy and apoptosis [74]. Thereafter, lncRNA *HULC* was observed to accelerate the development of HCC by inhibiting PTEN through co-operation with the autophagy of miRNA15A, and *HULC* enhanced the interplay between LC3 and ATG3 [75]. Our research group confirmed that lncRNA *HOTAIR* activates autophagy by upregulating ATG3 and ATG7 in HCC [76]. We also showed that *PVT1* (plasmacytoma variant translocation 1) could promote autophagy as a competing endogenous RNA (ceRNA) by targeting miR-365 in HCC [77]. As more and more lncRNAs are identified that reg-

ulate autophagy, it will be interesting to see if autophagy also affects the expression of lncRNAs. Given the limitations of the studies conducted to date, we have limited understanding of the underlying mechanisms of regulation between identified lncRNAs and autophagy. Of course, lncRNAs have more complex functions in autophagy regulation, which requires further clarification. Studies also suggest that we may need to classify lncRNAs according to their role in different types of autophagy, to explore the functions of lncRNAs more specifically. Both, lncRNAs and miRNAs are often deregulated in liver cancer, underlining the importance of ncRNAs in hepatocarcinogenic processes [78, 79]. Therefore, a joint intervention targeting ncRNAs and autophagy may be a promising therapeutic strategy in HCC.

### *Signaling pathways of autophagy in HCC*

**PI3K/AKT/mTOR:** The PI3K/Akt/mTOR pathway plays an important role in promoting autophagy and regulates cell growth, survival, metabolism, and apoptosis under physiological conditions, which has great significance for the occurrence and survival of various solid tumors, including HCC [80-83]. As a typical survival pathway, the PI3K/Akt/mTOR pathway plays an increasingly important role in the occurrence of HCC. The PI3Ks, which are divided into three classes (class I (A and B), class II, and class III), are important kinases regulating cell survival, proliferation, and differentiation [84, 85]. AKT is a key factor in signaling pathways that regulate autophagy in a variety of ways [86-88]. AKT induces the activation (phosphorylation) of mTORC1, a serine/threonine kinase, using the phosphatase PTEN, which can decrease the level of PI3K and initiate the formation of autophagosomes. Evidence indicates that abnormal activation of the PI3K/Akt/mTOR signaling pathway frequently occurs in HCC [89, 90]. Activating or inhibiting this pathway can inhibit or activate autophagy, which has different effects on HCC. Wang et al. demonstrated that overexpressed AFP (alpha-fetoprotein) interacts with PTEN in HCC cells, resulting in activation of PI3K/Akt/mTOR and a reduction in autophagy [91]. Wang applied H<sub>2</sub>S (hydrogen sulfide) to induce cell autophagy by inhibiting the PI3K/AKT/mTOR signaling pathway in HCC [92]. Moreover, Li et al. verified that IL-37 (anti-inflammatory cytokine interleukin-37) regulates

autophagy in HCC via inhibition of the PI3K/AKT/mTOR signaling pathway. In addition, using  $\beta$ -Thujaplicin combined with an autophagy blocker or agonist treatment in HepG2 cells, Zhang found that  $\beta$ -Thujaplicin induced autophagic cell death (ACD), mediated by reactive oxygen species (ROS), which caused inhibition of the Akt-mTOR signaling pathway [93]. In summary, targeting this pathway might result in autophagic cancer cell death, and could be used to treat HCC.

**The RAS/RAF/MEK/ERK pathway:** This pathway is involved in the induction of apoptosis and autophagic cell death in many cancer cell lines [94-96]. The RAS/RAF (Raf-1 proto-oncogene, serine/threonine kinase)/MEK (MAPK/ERK kinase 1)/ERK (extracellular signal-regulated kinase) pathway plays multiple roles in cell cycle regulation, apoptosis, and differentiation [97]. The mechanism of its involvement in autophagy regulation is extremely complex and sometimes seems to be contradictory. In particular, how it fine regulates autophagy in a specific environment has not yet been clarified. Studies have shown that activation of RAF/MEK/ERK can alter the expression levels of autophagy markers LC3 and SQSTM1 (Sequestosome 1) [98]. At the same time, there is evidence that ERK triggers autophagy by inhibiting mTORC1, which can also affect autophagy by regulating Beclin-1 [99, 100]. By contrast, ERK can cause the downregulation of LAMP1 (lysosomal-associated membrane protein 1) and LAMP2, and prevent the binding of autophagosomes to lysosomes, thereby inhibiting the degradation of autophagosomes [101]. Frequent mutations in RAS/RAF/MEK/ERK pathway members are thought to contribute to the development, tumor progression, and metastasis of many solid tumors, including HCC. RAS was the first human oncogene to be identified [102]. To overcome the effects of RAS mutations, only EGFR inhibitors and RAF-MEK-ERK pathway therapies have any effect [103]. RASSF1A (Ras association domain family 1 isoform A) can inhibit HCC by activating autophagy, thus improving the survival rate [104]. Wang et al. reported a novel 2-phenylloxypyrimidine derivative, E5, which induced autophagy via activation of the MAPK (mitogen activated protein kinase)/ERK pathway in HCC cells [105]. Additionally, cytoplasmic sequestration of ERK by binding to PEA-15 (prolifera-

tion and apoptosis adaptor protein 15) promotes autophagy [106]. These results indicated that the RAS/RAF/MEK/ERK pathway mediates autophagy and plays a crucial role in HCC.

*Wnt/ $\beta$ -catenin signaling pathway:* The Wnt signaling pathway is a key signaling pathway that directly determines cell proliferation, cell polarity, and cell fate during embryonic development and in the regulation of tissue homeostasis [107, 108]. Mutations in any molecule in the Wnt pathway may cause birth defects, cancer, and a range of other diseases [109]. The Wnt/ $\beta$ -catenin pathway regulates various cell processes, such as initiation, growth, survival, migration, differentiation, and apoptosis in HCC [110-112]. Poor prognosis and disease progression in liver cancer usually involve upregulation of wnt/ $\beta$ -catenin signaling [113]. In addition, this pathway can negatively regulate autophagy. Inhibition of the Wnt/ $\beta$ -catenin pathway leads to the accumulation of autophagy proteins such as LC3-II, ATG7, and Beclin-1 [114, 115]. Petherick demonstrated that  $\beta$ -catenin inhibits autophagy and the expression of the autophagy adapter p62, whereas under conditions of nutrient deficiency,  $\beta$ -catenin undergoes proteasome-independent degradation through its interaction with autophagy protein LC3 [116]. However, in terms of autophagy, the relationship between the Wnt pathway and HCC is rarely reported. Lilia's study revealed that the Wnt/ $\beta$ -catenin pathway inhibitor fh535 and its derivatives (fh535-N) exert anti-tumor effects on hepatoma cells by regulating autophagy activity [117]. Unexpectedly, Wang et al. used Wnt secretion inhibition in HCC to show that autophagy was not successfully induced [118]. Zhang et al. reported the tetrandrine suppresses HCC cell migration via suppression of Wnt/ $\beta$ -catenin signaling, which is regulated by tetrandrine-induced autophagy [119]. Our previous study verified that autophagy could act as an upstream regulatory factor to activate Wnt/ $\beta$ -catenin signaling [120]. These results indicated that the Wnt/ $\beta$ -catenin pathway has a complex relationship with the dynamic effects of autophagy and the development of HCC, indicating that it could represent a new target for liver cancer research.

*Other pathways:* PERK (pancreatic EIF2-alpha kinase) is a common upstream signaling pathway between autophagy and apoptosis that is

induced by endoplasmic reticulum (ER) stress. Under ER stress, PERK is activated and phosphorylates and inactivates EIF2 $\alpha$  (eukaryotic translation initiation factor 2 subunit alpha). This results in the selective induction of ATF4 (activating transcription factor 4), which induces autophagy and apoptosis [121]. Autophagy lies downstream of the PERK signaling axis and ultimately leads to tumor cell survival [122]. In addition, hepatocyte growth factor (HGF) and its receptor tyrosine kinase, MET were first discovered in the 1980s because they are highly active in many liver cancers [123, 124]. Activated hepatic stellate cells promote the progression of HCC cells after sublethal heat treatment from autophagic survival to proliferation via HGF/c-Met signaling [125]. HGF/c-MET signaling inhibits autophagy by interacting with the PI3K/AKT pathway, while high expression of c-MET is observed in HCC samples [126]. When treated with HGF-MET kinase activity-targeted drugs, tyrosine 1234/1235-dephosphorylated MET activated autophagy in HCC [127]. There are also many pathways involved in the interaction between autophagy and HCC, such as the Hippo pathway [128], EGFR crosstalk [129], and the AMPK pathway [130]; however, all these pathways require further exploration.

### Autophagy and HCC therapy

Currently, liver cancer is the second leading cause of cancer-related death worldwide [131, 132]. Poor prognosis has led to a 5-year survival rate of patients with HCC of less than 5% [133]. To date, the most effective treatment for HCC is surgical resection, interventional radiotherapy, or liver transplantation [134]. Therefore, in this section, we will summarize clinical and basic studies that focused on autophagy in the context of HCC treatment (**Table 1**).

#### *Conventional chemotherapeutics*

In recent years, more and more chemotherapy drugs have been used to treat advanced HCC, often involving combined treatment with a variety of chemotherapy drugs. For example, cisplatin combined with doxorubicin, 5-fluorouracil, and interferon (INF) can significantly improve the survival rate of advanced HCC; however, is prone to chemotherapy resistance [135, 136]. Therefore, it is essential to study how HCC resists chemotherapy and develop new drug strategies to overcome chemotherapeutic



## Autophagy and hepatocellular carcinoma

**Table 1.** Autophagy and treatment of hepatocellular carcinoma

Classification	Treatment	Autophagy status	HCC lines	Reference
Conventional chemotherapeutics	Oxaliplatin	↑	Huh-7 SMMC-7721 HepG2	[139, 140]
	Epirubicin	↑	HepG2 Huh7	[142]
	Cisplatin	↑	SMMC-7721 HuH-7 HepG2	[144]
	5-FU	↑	SMMC-7721 Hep3B HepG2	[143]
	Doxorubicin	↑	HepG2 Hep3B	[145, 184]
	Sorafenib	↑	SMMC-7721 HepG2 Huh7 Hep3B	[157, 185]
	Panobinostat	↓	Huh7 Hep3B HepG2	[186]
Molecular Targeting Drugs	Egorafenib	↑	HepG2 Hep3B	[159]
	Bevacizumab	↑	SMMC-7721 Hep3B	[163]
	Salinomycin	↓	HepG2 Huh7	[166]
	β-Thujaplicin	↑	HepG2 SMMC-7721 HCCLM3	[93]
Natural Product	<i>P. bistorta</i> aqueous extract	↑	Hep3B HepG2	[170]
	Arenobufagin	↑	HepG2 Hep3B Bel-7402	[171]
	Baicalin	↑	SMMC-7721	[172]
	Oroxilin A	↑	HepG2	[173]

Note: ↑, means that increase of autophagosomes in HCC; ↓, means that decrease of autophagosomes in HCC.

resistance. Autophagy is a double-edged sword for MDR (multidrug resistance), which occurs after long-term chemotherapy, leading to refractory cancer and recurrence of tumors [137]. Autophagy participates in the development of MDR and protects cancer cells from chemotherapy; however, it also kills MDR cancer cells in which apoptosis pathways are inactive. Oxaliplatin-based chemotherapy has

recently been shown to be effective to treat advanced HCC [138]. Studies have shown that Oxaliplatin can activate autophagy in HCC [139, 140]. Ren et al. identified EVA1A (transmembrane protein 166, an autophagy-related protein) as a target of miR-125b, and showed that it was upregulated in HCC tissues from Oxaliplatin-resistant patients, suggesting that EVA1A plays a role in resistance to chemother-

apy [141]. In general, the response of cancer cells to chemotherapy is usually to increase autophagy. Meanwhile, restraining autophagy makes cancer cells sensitive to anticancer drugs. For example, HSF1 (heat shock transcription factor 1) could upregulate ATG4B expression and enhance epirubicin-induced protective autophagy in HCC [142]. In another study, the inhibition of autophagy using 3-methyladenine or siRNA targeting Beclin-1 increased chemotherapy (cisplatin or 5FU)-induced apoptosis and increased damage to the mitochondrial membrane potential in HCC cells [143]. In addition, Wu et al. demonstrated that autophagy could cause HCC resistance to cisplatin [144]. Moreover, miR-101 inhibited autophagy and synergized with either doxorubicin or fluorouracil to induce apoptosis in HCC [145]. In summary, targeting autophagy is a promising therapeutic strategy to enhance the effects of chemotherapy and improve clinical outcomes in patients with HCC.

### *Molecular targeting drugs*

Sorafenib, a multitargeted kinase inhibitor, has greatly revolutionized the treatment of HCC [146]. Currently, representative phase III trials have shown that Sorafenib significantly improves overall survival in patients with advanced HCC [147]. The role of Sorafenib includes blocking the RAF-MEK-ERK signaling pathway to inhibit the proliferation of cancer cells, and targeting the vascular endothelial growth factor receptor (VEGFR) and platelet-derived growth factor receptor (PDGFR) to prevent angiogenesis [148]. Although it is now recognized that Sorafenib can activate autophagy and apoptosis, it can also induce autophagy through the ERK/MAPK pathway independently, thus promoting the survival of HCC cells *in vivo* or *in vitro* [149-151]. Unfortunately, the long-term value of Sorafenib is limited because of primary and acquired resistance, in which autophagy activation is a factor [152-154]. For example, Lu et al. found that CD24 (a glycoprotein expressed on the surface of most B lymphocytes) could regulate Sorafenib resistance via activating autophagy in HCC [155]. Wu et al. verified that ADRB2 ( $\beta$ -2 adrenergic receptor) signaling promotes HCC progression and Sorafenib resistance by inhibiting autophagic degradation of HIF1 $\alpha$  [156]. In another experiment, targeting ATG5/ATG16L1 inhibited

autophagy and increased the sensitivity of HCC cells to Sorafenib [157]. In addition, Adriamycin, a traditional chemotherapeutic drug, can be inhibited by Sorafenib, leading to cell progression, increased survival, and reduced autophagy of HCC [158]. In short, Sorafenib can induce autophagy formation and enhance autophagy activity, allowing HCC cells to survive. At the same time, inhibition of autophagy may be an attractive strategy to release the anti-tumor potential of Sorafenib in HCC.

Other targeted drugs also have autophagy activation effects. For instance, Regorafenib may act as an adjunctive therapy for patients with liver cancer. Regorafenib delays the proliferation of HCC by inducing autophagy [159]. Tong found ANXA3 (Annexin A3) inhibition sensitized HCC cells to Regorafenib treatment via suppressing autophagy and activating apoptosis [160]. Concomitantly, autophagy can be induced by EGFR inhibitors [161]. In one study, P57-mediated autophagy promoted the efficacy of Erlotinib/Cetuximab (EGFR inhibitors) in HCC [162]. In addition, Bevacizumab, which targets VEGF, induces autophagy and combined inhibition of autophagy with Bevacizumab can significantly inhibit tumor growth in HCC [163]. Another inhibitor of VEGF, Linifanib, also induces autophagy in HCC cells. After ATG5 and ATG7 were inhibited by pharmacological inhibitors or short interfering RNAs (siRNAs), cell death induced by Linifanib increased significantly [164]. In addition, Wu et al. found that the calcium phosphate nanoparticle system could be further developed for co-delivery of FTY720 (Fingolimod) and a Beclin 1 siRNA to treat HCC, which enhanced the anticancer efficacy of FTY720 [165]. In another study, Klose et al. reported that Salinomycin suppresses the late stages of HCC autophagy [166]. In conclusion, the relationships among small molecule targeted drugs, autophagy and HCC need further research to provide new strategies to treat HCC.

### *Natural products*

Many natural products have been shown to have autophagic effects on the growth and survival of HCC cells. For example,  $\beta$ -Thujaplicin, a natural tropolone derivative, exhibits a variety of biological properties, including antibacterial, antifungal, antiviral, anti-inflammatory, and

anticancer potential [167-169]. A study found that  $\beta$ -Thujaplicin might inhibit the growth of HCC cells by inducing autophagy [93]. In another study, *P. bistorta* (*Bistorta officinalis* (synonym *Persicaria bistorta*) aqueous extract (PB) induced autophagy, subsequently triggering caspase-dependent apoptosis in HCC. *P. bistorta* is used in traditional Chinese medicine owing to its anticancer activities [170]. In addition, Arenobufagin, a natural bufadienolide from toad venom, induces apoptosis and autophagy in human HCC cells through inhibition of the PI3K/AKT/mTOR pathway [171]. Meanwhile, Baicalin has been demonstrated to exert anticancer effects mainly through the induction of tumor cell apoptosis and cell cycle arrest. Baicalin induces autophagic cell death in HCC cells [172]. In addition, Zou et al. reported that Oroxylin A, which is a natural mono-flavonoid extracted from *Scutellariae radix*, exhibits autophagy-mediated antitumor activity in a dose and time-dependent manner in human HCC cells [173]. Similarly, Berberine, Allicin, Matrine, and Glycyrrhetic acid are plant-derived molecules that show anti-tumor effects by inducing apoptosis and/or autophagy of HCC cells [174-176]. Natural products have been recognized as a new source of anti-cancer drugs and new adjuvant therapy to improve the efficacy of chemotherapy and to reduce the side effects associated with cancer chemotherapy [177].

### Other approaches

Increasing evidence suggests that both autophagy inhibitors and inducers contribute to the response of HCC therapies. Autophagy inhibitors, such as 3-Methyladenine, chloroquine, or knockdown of different ATG genes have been reported to enhance the efficacy of Oxaliplatin, Cisplatin, 5-Fu and Sorafenib in the treatment of HCC [140, 143, 178]. These studies show that inhibition of autophagy rendered HCC cells susceptible to chemotherapy-induced apoptosis and cell growth inhibition, identifying autophagy as a sensitizer that can improve the efficacy of conventional chemotherapeutic drugs for HCC. Additionally, Rapamycin, an inhibitor of mTOR, activates autophagy both *in vitro* and *in vivo* [179]. Rapamycin showed an anti-tumor effects in therapy for HCC [180]. Another study showed that mTOR inhibition significantly reduced HCC growth and improved

survival primarily via antiangiogenic effects [181]. These results indicated that autophagy can be both a promoter and inhibitor of HCC. Currently, this mechanism underlying this paradox is unknown. In addition, the previously mentioned ATGs and non-coding RNAs can also participate in autophagy and the treatment of HCC. For example, Thomas et al. reported that altered expression of autophagy genes was associated with poor prognosis [182]. MiR-375 inhibits autophagy by reducing the expression of ATG7 and impairs the viability of HCC cells under hypoxic conditions [64]. MiRNAs that inhibit autophagy of HCC cells may be developed as therapeutics. Some inhibitors of autophagy-related pathways might also have anti-HCC effects. Recent studies have shown that at an early time point, Sorafenib increases ER stress, which induces the autophagic survival process in HCC cell lines by regulating the JNK/AMPK signaling pathway [183]. Although targeting autophagy in the treatment of HCC is complex, many basic and clinical studies have shown that autophagy can be a potential therapeutic target that could enhance the anticancer potency of both native tumor suppressor mechanisms and chemotherapy.

### Conclusion

In general, autophagy plays a double role in HCC. Most studies support the view that autophagy inhibits tumors. Autophagy plays an anti-tumor role in normal hepatocytes by maintaining cell homeostasis. However, once tumors are formed, it will promote the survival of HCC cells in the tumor microenvironment. Autophagy-related genes, non-coding RNAs, and related signaling pathways are involved in autophagy and the regulation of the formation and progress of HCC. In addition, the effects of autophagy on traditional chemotherapy, molecular targeted drugs, and natural products can also be associated with the treatment of HCC. Although it remains a challenge to understand the specific molecular mechanisms of autophagy in different stages of HCC, this understanding will help to develop therapeutic targets and overcome resistance to current therapies.

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### Disclosure of conflict of interest

None.

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