

Virus, Exosome, and MicroRNA: New Insights into Autophagy

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Abstract

Autophagy is known as a conserved selfeating mechanism that contributes to cells to degrade different intracellular components (i.e., macromolecular complexes, aggregated proteins, soluble proteins, organelles, and foreign bodies). Autophagy needs formation of a double-membrane structure, which is composed of the sequestered cytoplasmic contents, called autophagosome. There are a variety of internal and external factors involved in initiation and progression of

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autophagy process. Viruses as external factors are one of the particles that could be associated with different stages of this process. Viruses exert their functions via activation and/or inhibition of a wide range of cellular and molecular targets, which are involved in autophagy process. Besides viruses, a variety of cellular and molecular pathways that are activated and inhibited by several factors (e.g., genetics, epigenetics, and environment factors) are related to beginning and developing of autophagy mechanism. Exosomes and microRNAs have been emerged as novel and effective players anticipated in various stages of autophagy. More knowledge in these pathways and identification of accurate roles of them could help to provide better therapeutic approaches in several diseases such as cancer. We highlighted the roles of viruses, exosomes, and microRNAs in the autophagy processes.

Keywords

Autophagy · Cancer · Chemoresistance · Exosome · MicroRNA · Viral infection

1 Autophagy

Although autophagy was recognized around 50 years ago in mammalian cells, its molecular function was revealed vastly in the past decade. Autophagy usually occurs as an evolutionary conserved mechanism in all eukaryotic cells for sustaining cell homeostasis. Recent studies have revealed that autophagy is one of the vital biological mechanisms, which is related to health, longevity, differentiation, starvation, homeostasis, cell survival, adaptation, elimination of microorganisms, and cell death (Shafabakhsh et al. [2021\)](#page-58-0). This process begins with the formation of double-membrane

vesicles (DMVs), which is generally termed autophagosome, as well as by various processes, such as fusing with lysosomes. This event leads to degradation/recycling of components which exist in cytoplasmic lysosomes (Cuervo [2004](#page-49-0)). Critical roles of autophagy process in longevity, homeostasis, and cell death have been recently demonstrated (Mizushima [2007\)](#page-56-0). In eukaryotic cells, autophagy includes microautophagy, macroautophagy, and chaperone-mediated autophagy (CMA), three key intracellular pathways. Core molecular machinery of autophagy referred to subset of autophagy-related (ATG) proteins is essential for autophagosome formation (Fig. [1\)](#page-2-0) (Mizushima [2007](#page-56-0)). P53 and Bcl-2 protein\families with dual regulatory properties play significant roles in autophagy induction (Yoon et al. [2012](#page-63-0); Singletary and Milner [2008\)](#page-59-0). Autophagy is involved in various pathologies, such as neurodegenerative and age-related disorders, infections, and inflammatory/immunity diseases, and especially in invasion and cancer progression (Yang and Klionsky [2010\)](#page-63-0). Increasing evidences show the importance of autophagy in cancer and support the concept when it gets disturbed, it can lead to an accelerated tumorigenesis. Also, comparative evidences have shown that degradation of autophagy or proteolysis in tumors is less than normal cells (Yang et al. [2011\)](#page-63-1). Anticancer role of autophagy is due to elimination of damaged cell component and inhibition of tumor growth. However, autophagy can cause tumor cells withstand stress in undesirable conditions leading to survival. Stress-induced autophagy may result in resistance to treatment and result in the progression of tumor cells (Yang et al. [2011](#page-63-1); Kondo et al. [2005\)](#page-53-0). Additionally, the efficacy of autophagy inhibitors, along with chemotherapy, in preventing tumor growth and inducing cell death is far better than the chemotherapy alone. Recent investigations have shown that autophagy may play an important role in drug resistance. It means that autophagy may contribute to increase tumor cells resistance to chemotherapeutic

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Fig. 1 A schema various stages of autophagy. Viruses, through the production of different proteins, can affect different stages of autophagy, such as the early stages of autophagy (phagophore and elongation), and the ending stages (Autophagosome and autolysosome), in order to survive in the host cell longer. Some of the viruses that can affect the autophagy process are hepatitis C and B viruses and HIV. For example, the hepatitis C virus by producing NS5B protein influences the ATG5 autophagy regulatory protein, which proceeds autophagy in the elongation phase, or, by producing the NS4B protein, affects the Rhab5 factor and drives autophagy from the elongation phase to autophagosome formation. Hepatitis B virus targets and impedes mToR protein kinase through the production of HBX protein, increases the efficiency of the ULK protein, and leads to the initial phase of autophagy, the formation of phagophore. It has also

and anticancer agents. Therefore, autophagy regulation can be considered as an appropriate therapeutic target in the therapy of cancer. Thus, various autophagy-modulating approaches may be assumed to circumvent chemoresistance (Huang et al. [2016;](#page-52-0) YiRen et al. [2017](#page-63-2)). Mounting evidences have revealed that autophagy along with chemotherapy and its association with chemoresistance can be a new therapeutic goal to succeed in cancer treatment.

2 MicroRNA and Autophagy

2.1 Regulation of Autophagy by **MicroRNAs**

MicroRNAs (miRNAs) are a group of noncoding small RNA molecules $(\sim)19-22$ nucleotides long)

been observed that some of the proteins of the virus (HBe and HBc) inhibit the early stage of autophagy by increasing the efficiency of the mToR protein kinase. HIV produces nef and thus affects one of the major proteins in autophagy called BECN1, which causes the autophagy to progress from the elongation stage to the formation of autophagosome, or by producing TAT stops a factor necessary for the formation of autophagosome (LC3-II-PE complex), losing the autophagosome form. There are other viruses that can apply their effects on the autophagy process. For example, coronaviruses prevent lysosomal incorporation with the PLP2TM protein and impede the formation of autolysosomes. Enterovirus 71 affects and disables autolysosomes. Influenza virus via M2 protein destroys autophagosome. HSV prevents the formation of phagophore by producing Icp34.5 and inhibiting BECN1

which regulate protein-coding genes (Mollazadeh et al. [2019](#page-56-1); Neshati et al. [2018;](#page-57-0) Letafati et al. [2022;](#page-53-1) Mousavi et al. [2022;](#page-57-1) Balandeh et al. [2021;](#page-47-0) Razavi et al. [2021;](#page-58-1) Mirzaei and Hamblin [2020\)](#page-56-2). The main miRNA mechanisms are translational repression and mRNA degradation. In the nucleus, RNA polymerase II (RNAPII) produces long primary transcripts (pri-miRNAs), which acts as a substrate for RNase III enzymes and Drosha-DGCR8 complex (a microprocessor that is essential for miRNA maturation) to produce precursor miRNAs (pre-miRNAs). Then, pre-miRNA is exported from the nucleus into the cytoplasm by exportin-5 and Ran-GTP. In the cytoplasm, pre-miRNA is cleaved by another RNase III enzyme, Dicer, into miRNA duplexes approximately 19–22 nucleotides long. Mature miRNA is incorporated into RNA-induced silencing complex (RISC) where it remains stable and binds to its complementary target mRNA. miRNAs are involved in many major biological functions such as intracellular signaling, cellular metabolism, differentiation, pathological processes, and regulation of gene expression (Su et al. [2015\)](#page-59-1). Some miRNAs are only expressed in specific cell types. Expression patterns of miRNAs are unique to individual tissues and differ between cancer and normal tissues (Jafari et al. [2018](#page-52-1)). Aberrant expression of miRNAs is associated with multiple human diseases, such as metabolic disease, neurological disorders (Tavakolizadeh et al. [2018\)](#page-60-0), cardiovascular complications, viral diseases (Keshavarz et al. [2018\)](#page-53-2), immune-related diseases, and especially malignancies (Bartels and Tsongalis [2010\)](#page-47-1).

Autophagy-related protein 7 (ATG7) was recently considered as a potential target of miR-96-5p. The aberrant expression of this miRNA reduces autophagy activity (Yu et al. [2018a\)](#page-63-3). Based on the current data, miR-20a-5p inhibits cell proliferation and autophagy and promotes apoptosis through negative regulation of ATG7 (Yu et al. [2018b\)](#page-63-4). Moreover, the overexpression of miR-140-5p/miR-149 inhibits apoptosis and promotes autophagy by downregulating fucosyltransferase1 (FUT1) (Wang et al. [2018a](#page-61-0)). According to the investigation conducted by Liu et al. $(2017a)$ $(2017a)$ $(2017a)$ miR-20a negatively relates to autophagy/lysosome pathway. They reported that miR-20a inhibited autophagy and lysosomal proteolytic activity through targeting several key regulators of autophagy, including BECN1, ATG16L1, and sequestosome 1 (SQSTM1) (Liu et al. [2017a\)](#page-55-0). Various molecular components involve in autophagy cascade, including Atg1/unc-51-like kinase (ULK) complex, Beclin-1/class III phosphatidylinositol 3-kinase (PI3K) complex, Atg9 and vacuole membrane protein 1(VMP1), two ubiquitin-like protein (Atg12 and Atg8/LC3) conjugation systems, and proteins which mediate fusion between autophagosomes and lysosomes (Kroemer et al. [2010\)](#page-53-3). Some of these core components of autophagy pathway are direct targets of miRNAs (such as miR-30a, miR-23a, and miR-129-5p) and have key roles in the inhibition/ induction of autophagy process (Fig. [2\)](#page-4-0) (Xiao et al.

[2015](#page-62-0); Guo et al. [2017a](#page-51-0); Zhu et al. [2009](#page-65-0); Sadri Nahand et al. [2021](#page-58-2); Pourhanifeh et al. [2020a,](#page-57-2) [b;](#page-58-3) Rezaei et al. [2020;](#page-58-4) Jamali et al. [2020\)](#page-52-2). In the following, the role of miRNAs in the regulation of autophagy and their potential molecular mechanisms has been reported in some disorders.

Meng and colleagues revealed the clinical significance of miR-138 in patients with malignant melanoma, which inhibits cell proliferation and induces apoptosis. Overexpression of miR-138 increases cell autophagy by LC3 protein induction as well as the suppression of PI3K/AKT/ mTOR and PDK1 (Meng et al. [2017\)](#page-56-3). It was exhibited that the upregulation of miR-18a-5p in melanoma cell lines and tissues had promising role in melanoma pathogenesis mediated by EPHA7 silence leading to tumor development as well as apoptosis and autophagy blockage (Guo et al. [2021](#page-51-1)).

Long et al. reviewed the association between miRNAs and autophagy in colorectal cancer (CRC) and concluded that miRNA-regulated autophagy could be up- or downregulated in various CRC conditions associated with the tumor microenvironment. In this context, it can referrer to the roles of miR-140-5p and miR-502 in inhibition of autophagy in chemotherapy of CRC stem cells; miR-214, miR-183-5p, and miR-31 in inhibition of autophagy in radiotherapy of CRC; and miR-124, miR-18a, and miR-210 in promotion of autophagy in metabolism and hypoxia of CRC. Also, blockage of autophagy in inflammatory bowel disease could be mediated via miR-142-3p, miR-143, miR-130a, etc. (Long et al. [2020](#page-55-1)).

In hepatocellular carcinoma (HCC), autophagy could be reduced via miR-490-3p/ ATG7 (Ou et al. [2018](#page-57-3)) or microRNA-181a/Atg5 axis, suggestive of the profounding value of autophagy deficiency in HCC (Yang et al. [2018\)](#page-63-5). Jin et al. showed that miR-513b-5p attenuated tumorigenesis of liver cancer cells in HCC via inactivation of PIK3R3-mediated autophagy (Jin et al. [2021](#page-52-3)). Zhang et al. demonstrated that downregulation of miR-638 in human liver cancer led to a noticeable reduction in malignancy of liver cancer cell accompanied by increase of autophagosomes and

Fig. 2 Various factors involved in the formation of the autophagy mechanism, each of which is affected by different microRNAs that somehow regulate the autophagy steps. The PTEN protein by inhibiting the PIK3-akt pathway paves the way for autophagy to start, increasing the expression of mir-21 that inhibits this protein, thus activating the pik3-akt pathway, and preventing the onset of autophagy (1). Autophagy starts/miR-193b-3p declines, and this protein is most produced and autophagy occurs more (2). Reb has an incremental effect on the mTOR protein that activates this pathway and prevents the formation of the initial autophagy phase. The expression of miR-199a-5p decreases, the inhibitory effect on Reb is inactivated, and autophagy is inhibited (3). Foxo3 disables Akt and causes the MPT pathway to be deactivated/miR-27a decreases its expression, and the foxo3 protein is further produced and autophagy continues to function (4). mTOR, one of the important pathways involved in the autophagy mechanism, has an inhibitory effect on this process and does not allow autophagy to begin and applies its effect on the ULK1/2 factor/miR-7 declines, and its inhibitory effect on this pathway is removed, and the autophagy does not start (5). ULK1/2 is one of the important factors for the onset of autophagy and phagophore formation, declining miR-26b and its inhibitory effect on ULK2, and autophagy begins its pathway, but the expression of miR-290-295 cluster is increased, and the ULK1 protein level is reduced, and the phagophore is not formed, so autophagy does not occur (6). Beclin-1 is somehow one of the important proteins in the development of phagophore and the onset of autophagy. The expression of mir-20a increases, and its inhibitory effect on the gene does not allow the formation of proteins and, accordingly, autophagy does not begin, but miR-30a expression reduces, the Beclin-1 gene is more expressed, and autophagy starts (7). ATG14 has an increased effect on Beclin-1 and makes phagophore more likely to form miR-135a expression increases, thereby inhibiting ATG14 gene and autophagy formation (8). HMGB1

stimulates the Beclin-1 gene and causes the autophagy to start its first phase/miR-34a expression decreases, and its inhibitory effect on the HMGB1 gene is removed, and Beclin-1expression increases (9). UVRAG interferes somehow behind the initial pathway of autophagy and reaches the formation of autophagosome/the miR-183 which disrupts the process by targeting and inhibiting the gene (10). FIP200, present in ULK complex and is effective in the formation of phagophore/miR-224-3p expression, is increased, and an inhibitory effect on this gene is increased, and the initial phase of autophagy does not occur, but miR-20b, which declines, causes an increase in the expression level of FIP200, and phagophore is formed (11). AMK with inhibitory effect on MTOR pathway and TSC1/TSC2 stimulation inhibits autophagy. The expression of miR-185 is reduced, AMK is more expressed, and autophagy is more active (12). ATG7 is a factor accelerating the conversion of lc3-I to Lc3-II, which is an important process for the onset of autophagosome formation. miR-490-3p expression declines and further stimulates its target and ATG7, and autophagy continues (13). ATG5 is a protein that causes autophagy to evolve from the phagophore formation phase to the next formation of the process. miR-181a is increased, and most of the ATG5 gene is inhibited, and this functional trend is disrupted (14). ATG16L is a factor that accelerates the formation of autophagosomes. The expression of miR-130a is increased, the level of the ATG16L protein decreases, and the autophagy is inhibited/expression of the miR-410 decreases, and this process continues (15). The activity of ATG12 is similar to that of ATG16L. The expression of MIR-23a is reduced, its inhibitory effect on this gene is reduced, and autophagy continues its process. miR-378 inhibits the autophagy process by inhibiting the gene (16). ATG10 is a protein that stimulates the activity of ATG5, ATG16L, and ATG12 proteins and accelerates the process of autophagosome formation. miR-20 has an inhibitory effect on this protein, which can disrupt this activity (17). ATG3 is a factor to stimulate the formation autolysosomes, suggestive of tumor-suppressive role of miR-638 via silence of EZH2 (Zhang et al. [2021a](#page-64-0)).

In osteosarcoma (OS), miR-210-5p induced epithelial-mesenchymal transition (EMT) and oncogenic autophagy via PIK3R5/AKT/mTOR axis (Liu et al. [2020a\)](#page-55-2). Also, upregulation of miR-22 in OS suppressed autophagy and induced apoptosis resulted in increased sensitivity to cisplatin (Meng et al. [2020](#page-56-4)). In prostate cancer (PC) cells, overexpression of miR-381 increased cellular autophagy and apoptosis, while decreased cell proliferation mediated by reelin (RELN) suppression (Liao and Zhang [2020\)](#page-55-3). Deng et al. recognized that miR-493 respectively activated cytotoxic autophagy and reduced invasion of PC cells via up-modulation of BECN1 and ATG7 (Deng et al. [2020](#page-49-1)).

In cervical cancer cells, miR-211 overexpression targeted autophagy and apoptosis through Bcl-2 regulation (Liu et al. [2020b\)](#page-55-4). Besides, aberrant expression of miR-106a in cervical squamous cell carcinoma (CSCC) was related to malignancy parameters of CSCC tissues. Based, overexpression of miR-106a elevated CSCC growth and suppressed autophagy via binding to 3UTR of LKB1 in human papilloma virus (HPV) 16-positive CSCC (Cui et al. [2020\)](#page-49-2). Consistently, miR-378 has a potential impact on cervical cancer progression via binding to ATG12-regulated autophagy (Tan et al. [2018\)](#page-60-1). In the ovarian cancer (OC), increased expression of miR-34 activates apoptosis and autophagy followed by significant reduction in the proliferation of cancerous cells (OVACAR-3 cells) via silencing Notch 1 (Jia et al. [2019\)](#page-52-4). Shao et al. identified that miR-1251-5p upregulation had oncogenic effects on human ovarian cancer via preventing TBCs (negative modulator of autophagy) (Shao et al. [2019](#page-58-5)).

In bladder cancer, reduced expression of miR-221 facilitated autophagy through increasing TP53INP1 levels, indicative of the valuable importance of miR-221 as therapeutic targets in this malignancy (Liu et al. [2020c\)](#page-55-5). Dai et al. represented the tumorigenic capacity of miR-130 in bladder cancer cells as it was proved by autophagy induction through blocking CYLD (Dai et al. [2020\)](#page-49-3). Also, Zhang et al. displayed that upregulation of miR-21 in bladder tumor cells (T24 cells) promoted T24 cells progression alongside with apoptosis and autophagy obstruction via downregulation of, Beclin-1, PTEN, caspase-3, LC3-II, and E-cadherin (Zhang et al. [2020a](#page-64-1)). Similarly, Rezaei et al. focused on the impacts of up-/downregulation of miRNAs in the different lung diseases including lung cancer either in in vitro and in vivo conditions or human. In this regard, up- and downregulation of respectively miR-210 and miR-181 inactivated autophagy, while down- and upregulation of respectively miR-3127-5p and miR-21 activated autophagy (Rezaei et al. [2020](#page-58-4)).

In esophageal squamous cell carcinoma (ESCC), autophagy is triggered by miR-503 via PKA/mTOR pathway followed by inhibition of ESCC invasiveness (Wu et al. [2018](#page-62-1)). In another study, Li et al. focused on the effect of miR-126 on apoptosis and autophagy of ESCC cells and found that miR-126 expression was increased in ESCC followed by enhancement of apoptosis and autophagy; however, miR-126 inhibition reversed current trend via suppression of STAT3 (Li et al. $2020a$). Phatak et al. (2021) (2021) clarified that miR-141-3p could act as an oncogene in esophageal cancer cells via binding to TSC1 mRNA which led to tumor progression as well as autophagy reduction (Phatak et al. [2021](#page-57-4)).

In gastric cancer (GC) cells, miR-let-7a/Rictor/ Akt-mTOR axis modulates autophagy activity

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Fig. 2 (continued) of LC3-PE, which causes the LC3 protein binding to phosphatidylethanolamine and the formation of autophagosome and maintains its stability. The expression of miR-1 is reduced, this factor is further developed, and autophagosome is formed (18). ATG2 protein is effective in the formation of autolysosome. The expression of miR-143 is increased, the ats2 gene is suppressed, and this process is disrupted (19). ATG9 is an

agent for stimulating the formation of autolysosome and accelerating the process of lysosome fusion with autophagosome/miR-29a expression which is decreased and the level of atg9 increased, and this trend continues (20). Akt is a stimulant factor for the mTOR pathway and prevents the formation of autophagy/miR-185 which targets this gene and inhibits autophagy (21)

(Fan et al. [2018\)](#page-50-0). Among another regulators of autophagy in GC, it can mention miR-183 which its downregulation blocks apoptosis and autophagy via interacting with MALAT1 and SIRT1 through PI3K/AKT/mTOR pathway (Li et al. [2019a](#page-54-1)). Li et al. evidenced that miR-133a-3p could strengthen autophagy and proliferation of GC cells via downregulation of FOXP3 (Li et al. [2020b\)](#page-54-2). In breast cancer cells, transfection of MCF-7 with miR-26b mimic reduced autophagy dependent to irradiation through silence of DRAM1 (Meng et al. [2018\)](#page-56-5). Ai et al. ([2019\)](#page-47-2) clarified that overexpression of miR-107 in breast cancer cell lines (MDA-MB-231 and MDA-MB-453 cells) causes significant reduction in cellular autophagy, proliferation, and metastasis via silencing HMGB1. ULK1 and lysosomal protein transmembrane 4 beta (LAPTM4B), autophagy-related mediators, have also been identified as direct targets of miR-489 which is downregulated in the most of breast cancer cells and several drug resistant breast cancer cell lines (Soni et al. [2018a\)](#page-59-2).

In the metabolic diseases such as osteoporosis, the condition can be exacerbated via miR-15 overexpression which modulates osteoblast genesis and autophagy alongside with downregulation of USP7 (Lu et al. [2021](#page-56-6)). Wang et al. provided evidences that in osteoarthritis (OA), joint disease, miR-140-5p/miR-149 could affect autophagy, apoptosis, and proliferation of chondrocytes via their potential target, FUT1 (Wang et al. [2018a](#page-61-0)). Also, miR-20 has a pivotal impact on OA evidenced by inhibition of autophagy and chondrocytes proliferation through ATG10/PI3K/AKT/mTOR axis (Vojtechova and Tachezy [2018\)](#page-60-2). Besides, He et al. ([2018\)](#page-51-2) assigned that the inhibition of miR-20 promoted proliferation and autophagy machinery in articular chondrocytes by targeting ATG10 via PI3K/AKT/mTOR signaling pathway (He and Cheng [2018](#page-51-2)). Furthermore, pathogenesis of intervertebral disc degeneration (IDD) can be influenced by miRNA-regulated autophagy including decreased autophagy facilitated by upregulation of miR-210 and miR-202-5p via targeting ATG7 (Lan et al. [2020\)](#page-53-4). Yun et al.

[\(2020](#page-64-2)) highlighted the promising role of miR-185 in preventing IDD via improving cell survival and suppressing apoptosis and autophagy of nucleus pulposus cell via blockage of galectin-3/Wnt/β-catenin pathway (Yun et al. [2020\)](#page-64-2). Similar results have been achieved by miR-142-3 overexpression in controlling and inhibiting IDD (Xue et al. [2021](#page-63-6)).

Moreover, evidences are in a favor of miR-145-3p in exerting autophagic flux in multiple myeloma (MM) via HDAC4 inhibition (Wu et al. [2020](#page-62-2)). In the neurodegenerative disorders such as Parkinson's disease (PD) defined by dopaminergic neurons apoptosis, Wen et al. ([2018a](#page-61-1)) confirmed that AMPK/mTORregulated autophagy and apoptosis could be a potential therapeutic platform as this axis can be inhibited by miR-185 overexpression leading to prevention of dopaminergic cells death in PD model (Wen et al. [2018a](#page-61-1)). Similarly, Li et al. [\(2018a\)](#page-54-3) observed that autophagy in PD could be triggered by miR-181b/PTEN/Akt/mTOR axis in a way that overexpression of miR-181b is associated with increased cell viability. Also, Lu et al. [\(2020](#page-55-6)) conducted similar research on PD model and reached to the findings that upregulation of miR-133a in a PD cell model increased cell proliferation and inhibited autophagy and apoptosis by binding to 3 UTR of RAC1 (Lu et al. [2020\)](#page-55-6). Wen and colleagues demonstrated that overexpression of miR-185 inhibited autophagy and apoptosis through regulating the AMPK/mTOR signaling pathway in PD (Wen et al. [2018b\)](#page-61-2). In Alzheimer's disease (AD), the amounts of miRNA-101a was significantly decreased in patients as well as in vivo model and resulted in autophagy regulation through the MAPK pathway (see Table [1](#page-7-0)) (Li et al. [2019b\)](#page-54-4). Another novel therapeutic option in AD could be proposed by upregulation of miR-16-5p or downregulation of BTG2, which inhibit neuronal damage and autophagy (Dong et al. [2021](#page-49-0)). Yang et al. [\(2020](#page-63-7)) pinpointed that melatonin could reduce neuronal death and autophagy in cerebral ischemia-reperfusion injury (CIRI) mechanistically through regulation of miR-26a-5p/NRSF as well as JAK2-STAT3

| | | | Inhibition/ | | | |
|---------------|------------|--------------------------|-------------|---|---|---------------------------|
| miRNA | Expression | Target | induction | Disease | Note | Ref |
| m iR-26 b | Down | ULK2 | Induction | Prostate cancer | Downregulation of mTOR | Clotaire et al. (2016) |
| $miR-21$ | Up | Rab11 | Inhibition | Renal ischemia- reperfusion | Reduction of Beclin-1andLC3-II expression and upregulation of p62 | Liu et al. (2015a) |
| $miR-185$ | Down | mTOR AMPK | Induction | Parkinson | Increase of neuronal apoptosis through elevating AMPK/ mTOR signaling pathway activity, upregulation of Beclin-1, LC3-I/ $LC-II$ | Wen et al. (2018a) |
| $miR-96-5p$ | Up | FOXO1 | Inhibition | Breast cancer | Increase of migration, invasiveness, and proliferation by decreasing apoptosis | Doan et al. (2017) |
| $miR-502$ | Down | Rab1B DHODH | Induction | Colon cancer | Increase of cell proliferation and metastasis | Zhai et al. (2013) |
| $miR-100$ | Down | mTOR $IGF-1R$ | Inhibition | HCC | Decrease of LC3B- II and Akt proteins enhance tumor growth | Ge et al. (2014) |
| miR-30a | Down | Beclin-1 | Induction | Breast cancer Lung cancer Glioma | $\overline{}$ | Zhu et al. (2009) |
| m iR-143 | Down | ATG2B HK ₂ | Induction | Non-small-cell lung cancer (NSCLC) | Promotion of cell proliferation, metastasis and Warburg effect | Wei et al. (2015) |
| $miR-23a$ | Down | ATG12 | Induction | Melanoma | Increase of the expression of RUNX2 reduces m iR-23a Increase of metastasis and invasion via blocking AMPK- RhoA pathway | Guo et al. (2017a) |
| miR-130a | Up | ATG16L | Inhibition | COPD | Enhancement of apoptosis and increase of the development of COPD | Li et al. (2016a) |
| miR-193b-3p | Down | TSC ₁ | Induction | Amyotrophic lateral sclerosis (ALS) | Increase of cell survival by increase of TSC1 expression, and decrease of mTORC1 activity, apoptosis | Dhital et al. (2017) |

Table 1 microRNAs and autophagy

| | | | Inhibition/ | | | |
|------------------------------|--------------------------|-------------------------------|-------------|---|---|------------------------|
| miRNA | Expression | Target | induction | Disease | Note | Ref |
| m i R -185 | Down | AKT1 RICTOR RHEB | Inhibition | HCC | Increase of cell proliferation by overexpression of mTOR Decrease of apoptosis via Bcl-2, upregulation of cyclin D1 | Zhou et al. (2017) |
| $miR-96-5p$ | Up | ATG7 | Inhibition | Liver fibrosis | $TGF-\beta1 promotes$ m iR-96-5p expression, inverse cell proliferation, inhibition of mRNA, and protein levels of α -SMA and $Col1\alpha1$ | Yu et al. (2018b) |
| miR-101 | Down | EZH ₂ | Induction | HCC | Increase of chemoresistance and decline of apoptosis | Xu et al. (2014) |
| m i $R-101$ | $\overline{}$ | $\overline{}$ | Inhibition | Liver ischemia/ reperfusion injury (LIRI) | miR-101 can inhibit autophagy and reduce LIRI by activating the mTOR pathway | Song et al. (2019) |
| miR-101a | Down | $\qquad \qquad -$ | Inhibition | Alzheimer's disease (plasma) | miRNA-101a could regulate autophagy by targeting the MAPK pathway | Li et al. (2019b) |
| miR-129-5p | Up | Beclin-1 | Inhibition | Prostate cancer | Increase of resistance to the Norcantharidin (NCTD) | Xiao et al. (2016) |
| miR-140-5p/ m i $R-149$ | Down | FUT1 | Inhibition | Osteoarthritis | Decrease of chondrocyte proliferation, overexpression of IL-1 β , and promotion of apoptosis | Wang et al. (2018a) |
| $mR-124$ | Down | Bim | Inhibition | Parkinson | Increase of apoptosis and inhibition of autophagosome accumulation and lysosomal depletion | Wang et al. (2016) |
| $miR-124$ | $\overline{}$ | p62/p38 | Induction | Parkinson | miR-124 can suppress neuroinflammation during the Parkinson's disease development via targeting autophagy, p62, and p38 | Yao et al. (2019) |

Table 1 (continued)

| | | | Inhibition/ | | | |
|--------------------|------------|-----------------|-------------|------------------------------------|---|---------------------------|
| m _{RNA} | Expression | Target | induction | Disease | Note | Ref |
| m iR-224-3p | Up | FIP200 | Inhibition | Cervical cancer | Promotion of cell proliferation | Fang et al. (2016) |
| m i R -143 | Down | GABARAPL1 | Induction | Gastric cancer | Increase of resistance to the quercetin | Du et al. (2015) |
| $miR-22$ | Up | PTEN | Inhibition | Diabetic nephropathy | Increase of renal tubulointerstitial fibrosis, increase of glucose inducing $miR-22$ and promoting AKT/mTOR pathway | Zhang et al. (2018a) |
| miR-130a | Down | ATG2B DICER1 | Induction | Chronic lymphocytic leukemia | Promotion of cell proliferation | Kovaleva et al. (2012) |
| miR-181a | Up | MTMR3 | Inhibition | Gastric cancer | Promotion of cell proliferation, metastasis and inhibition of apoptosis | Lin et al. (2017) |
| $miR-21$ | Up | PTEN | Inhibition | HCC | Increase of resistance to sorafenib, promotion of AKT pathway | He et al. (2015a) |
| miR-409-3p | Down | Beclin-1 | Induction | Colon cancer | Increase of resistance to oxaliplatin | Tan et al. (2016) |
| $miR-30a$ | Down | Beclin-1 | Induction | Renal carcinoma | Increase of resistance to sorafenib, upregulation of ATG5 and decrease of apoptosis | Zheng et al. (2015) |
| $miR-503$ | Up | PRKACA | Inhibition | Esophageal carcinoma | Promotion of cell proliferation, metastasis, increase of PKA/mTOR signaling pathway activity | Wu et al. (2018) |
| m i R -143 | Up | ATG2B | Inhibition | Crohn's disease | Blockage of autophagy in intestinal epithelial cells, decline of autophagosome and autolysosome formation. downregulation of Iκ $B\alpha$ Promotion of pro-inflammatory cytokine expression: IFN-γ, TNF- α , and IL-8 | Lin et al. (2018) |

Table 1 (continued)

pathway (Yang et al. [2020\)](#page-63-7). It was suggested that neuronal deficit and autophagy in ischemic stroke could be abolished by miR-378 trough targeting GRB2, while lncRNA MEG3 could sponge the miR-378 and activate the expression of GRB2 (Luo et al. [2020](#page-56-10)).

Shi et al. clarified that miR-126 loss of function could activate myocardial autophagy induced by Beclin-1 and contributed in acute myocardial infarction (AMI) development (Shi et al. [2020\)](#page-59-8). In contrast, miR-18a downregulation had protective effects against AMI via activation of BDNF expression and inhibition of Akt/mTOR axis (Lin et al. [2019](#page-55-13)). In the Su et al. study (Su et al. [2020\)](#page-59-0), it was manifested that downregulation of miR-30e-3p lessened autophagy and activated apoptosis and injury in cardiomyocytes under ischemia/hypoxia conditions potentially through Egr-1 regulation (Su et al. [2020](#page-59-0)). MiRNAregulated abnormal apoptosis and autophagy of cardiomyocyte have a great of importance in heart failure (HF). Alongside with reduced expression of miR-29b-3p in HF patients, the level of this miRNA was decreased in an in vitro HF model under hypoxia condition followed by elevated apoptosis and autophagy via inactivation of SPARC and regulation of TGF-β1/Smad3 cascade (see Table [1\)](#page-7-0) (Zhou et al. [2019\)](#page-65-3).

In the liver complications such as liver fibrosis characterized by hepatic stellate cell (HSC) activation, the regulation of HSC autophagy has attracted research interests. There is line of evidence shown that introduction of miR-96-5p into HSCs (LX-2 cells) is accompanied by repressing autophagy in the cells via ATG7 regulation (Yu et al. [2018c\)](#page-63-16).

In the renal problems including renal tubulointerstitial fibrosis (TIF) as a main result of diabetic nephropathy (DN), accumulating data implicated the major role of miRNAs in the autophagy regulation. Zhang et al. findings represented that miR-22 partially targets PTEN-blocked autophagy followed by TIF development (Liu et al. [2018a](#page-55-14)). Furthermore, p53/miR-214/ULK1 axis affects autophagy dysregulation in diabetic kidney disease (DKD) (Ma et al. [2020](#page-56-11)). Moreover, Liu et al. disclosed that the expression of miR-25-3p was increased in polycystic kidney

disease (PKD) model via interacting with ATG14-activated autophagy as well as promoting proliferation of renal cell (Liu et al. [2020d\)](#page-55-15). Table [1](#page-7-0) lists some miRNAs regulating autophagy in some human cancer cells.

2.2 MiRNAs Interactions in Chemo-Induced Autophagy

Increasing data have reported that autophagy, along with chemotherapy and its association with chemoresistance can be a new therapeutic platform to succeed in cancer treatment. To find the correlation between miRNAs and chemotherapy-induced autophagy, experimental investigations were reviewed. More importantly, the cross talk between miRNAs (modulators of multiple pathways) and autophagy holds promise to overcome chemoresistance in malignancies (Soni et al. [2018b](#page-59-9)).

Chen and colleagues found that miR-519a not only plays a role in glioma by regulating STAT3 mediated autophagy pathway but also affects autophagy in glioblastoma multiforme (GBM) cells and also temozolomide (TMZ) chemosensitivity. The results showed that miR-519a enhanced the sensitivity of GBM cells to TMZ. Also, a significant association was found between miR-519a effects and autophagy. Overall, miR-519a promoted autophagy in glioblastoma through targeting STAT3/Bcl-2 signaling pathway (Li et al. [2018b\)](#page-54-9). Besides, overexpression of miR-29b in GBM cells inhibited cell survival, activated apoptosis and autophagy, and sensitized tested cells to TMZ (Xu et al. [2021](#page-63-17)). Because of TMZ importance in the treatment of glioblastomas and its ability to induce autophagy, Xu and colleagues assessed the regulatory role of miR-30a in glioblastoma cells treated with TMZ. They revealed that miR-30a increases U251 glioblastoma cells' chemosensitivity to TMZ through direct target of Beclin-1 and inhibition of autophagy (see Table [2\)](#page-21-0) (Xu et al. [2018a](#page-62-8)). In an in vivo study, Chakrabarti and colleagues proved that antitumor activities of luteolin and silibinin, chemotherapeutic agents, were augmented due to the overexpression of miR-7-1-3p leading to

inhibition of autophagy and induction of apoptosis in glioblastoma cells (Chakrabarti and Ray [2016\)](#page-48-8). In addition, miR-224-3p weakened resistance to TMZ in glioblastoma cells (LN229 cells) via abolishing autophagy under hypoxia via ATG5 downregulation (Liu et al. [2020e](#page-55-16)).

Xiao et al. [\(2016](#page-62-4)) investigated the role of miR-199a-5p in reducing chemoresistance to cisplatin or diamminedichloridoplatinum (II) (DDP) in OS. They showed that treatment of OS cells with DDP attenuated the expression level of miR-199a-5p; increased the level of various proteins, such as Beclin-1 and LC3; and induced autophagy machinery, which highlights the relationship between treatment cytotoxicity, autophagy inhibition, and their effects on chemoresistance (see Table [2](#page-21-0)) (Li et al. [2016d](#page-54-10)). Chen and colleagues observed that overexpression of miR-155 during chemotherapy induced autophagy leading to mediate chemoresistance in OS (Chen et al. [2014a](#page-48-7)). Wang et al. noted that upregulation of miR-22 in OS cells (MG-63) increased sensitivity to cisplatin mediated via negative regulation of autophagy by down-expression of MTDH (Wang et al. [2019c](#page-61-9)). Alongside, miR-193b/FEN1 axis ameliorated the epirubicin sensitivity of OS cells through autophagy induction (Dong et al. [2019\)](#page-49-8). miR-375 could be another target to sensitize OS to cisplatin as its overexpression in cisplatin-resistant OS models delayed tumor progression and autophagy via targeting ATG2B (Gao et al. [2020a](#page-50-6)). Qased et al. investigated the role of miR-18a in autophagy process in HCT116 (human CRC cells). To do so, HCT116 cells were irradiated, and the expression levels of miR-18a were subsequently measured in the cells. The results showed that the radiation led to increased expression level of miR-18a and enhanced autophagy induction (Qased et al. [2013\)](#page-58-7). Li et al. showed that the expression levels of miR-22 are enhanced during chemotherapy and target HMGB1, which results in inhibition of HMGB1-induced autophagy (see Table [2](#page-21-0)) (Li et al. [2014a](#page-54-11)).

He et al. reported that miR-152 plays an important role in autophagy regulation and drug resistance in ovarian cancer (OC) (He et al. [2015b\)](#page-51-8). They showed that miR-152 was

significantly downregulated in cisplatin-resistant cells. It has been reported that overexpression miR-152 leads to induction of apoptosis in cisplatin-resistant cancer cells as well as a decrease of cisplatin-induced autophagy. In this in vitro study, it was documented that ATG14 downregulation by EGR1-miR-152 sensitizes ovarian cancer cells to cisplatin-induced apoptosis through inhibiting cyto-protective autophagy (He et al. [2015b](#page-51-8)). Vescarelli et al. verified that miR-200c considerably sensitized chemoresistant OC cells to olaparib via regulating NRP1 (Vescarelli et al. [2020](#page-60-6)). In addition, miR-29c-3p overexpression inhibited autophagy which in turn reversed cisplatin resistance of OC by downregulation of FOXP1/ATG14 pathway (Hu et al. [2020](#page-52-12)). Esfandyari et al. [\(2021](#page-50-7)) demonstrated that miR-143 overexpression in cervical cancer cells (CaSki cells) could increase cisplatin sensitivity of treated cells via induction of apoptosis and autophagy (Esfandyari et al. [2021\)](#page-50-7). Tamoxifen (TAM) and fulvestrant (FUL) are considered as effective drugs for patients with ER-positive breast cancer, but the rate of response to these therapies is limited because of various barriers, such as endocrine resistance. In this regard, Yu and colleagues found that miR-214 enhanced breast cancer cells sensitivity to TAM and FUL through autophagy inhibition (Yu et al. [2015a](#page-63-18)). In a comparable study on breast cancer, Soni et al. identified that miR-489 enhanced sensitivity to doxorubicin (Dox) as a result of autophagy inhibition dependent to LAPTM4B downregulation (Soni et al. [2018b](#page-59-9)).

Xu et al. reported that miR-199a-5p downregulation induced by cisplatin enhances drug resistance through activating autophagy in HCC (Xu et al. [2012\)](#page-62-9). Soni et al. evaluated the role of miR-155-5p on Adriamycin (ADR) resistant liver carcinoma cells (HepG2/ADR), and their findings indicated the effects of miR-155-5p as sensitizer of ADR, activator of apoptosis, and inhibitor of autophagy via attaching to ATG5 3UTR (Soni et al. [2018b\)](#page-59-9). Also, higher expression of miR-541 inhibited the autophagy in HCC cells by targeting ATG2A and RAB1B leading to promising response to sorafenib (Xu et al. [2020a\)](#page-63-19). In another

study, it was revealed that upregulated miR-142- 3p increased sensitivity of HCC cells to sorafenib by targeting ATG5 and ATG16L1 as negative modulators of autophagy (Zhang et al. [2018b\)](#page-64-14). Similar findings have been reported for miR-101/ RAB5A/STMN1/ATG4D axis in the HCC cells (HepG2) which improved the response to cisplatin due to inhibition of autophagy mechanism (Xu et al. [2013\)](#page-62-10). Consistently, Ren et al. demonstrated that miR-125b/EVA1A axismediated autophagy reversed resistance of HCC cells to oxaliplatin (Wei-Wei et al. [2018\)](#page-61-12).

Chemoresistance of nasopharyngeal carcinoma (NPC) has been investigated by Zhao et al. ([2020](#page-65-4)) study in which they verified that miR-1278 expression was decreased in NPC tissues associated with worse chemotherapy response. Nonetheless, upregulation of miR-1278 dramatically raised anticancer effects of cisplatin in NPC cells together with reduced autophagy via inhibiting ATG2B (Zhao et al. [2020](#page-65-4)).

Yang et al. ([2021](#page-63-20)) showed that miR-136-5p upregulation not only had negative effects on malignant progression of laryngeal squamous cell carcinoma (LSCC) and hypopharyngeal squamous cell carcinoma (HPSCC) cells but also reversed cisplatin resistance in the tested cells via inactivation of ROCK1 Akt/mTOR axis (Yang et al. [2021](#page-63-20)).

Recently, Xi et al. explored the lncRNA MALAT1/miR-30b/ATG5 axis in cisplatin resistance of GC cells (AGS/CDDP and HGC-27/ CDDP) and documented that miR-30b attenuated cisplatin resistance by reduced expression of not only MALAT1-activated autophagy but also ATG5 (see Table [2\)](#page-21-0) (Xi et al. [2019](#page-62-12)). In another study, Chen et al. [\(2020a\)](#page-49-9) identified that miR-30a could sensitize gastrointestinal stromal tumors (GISTs) cells to imatinib (IM) via silence of Beclin-1-regulated autophagy (Chen et al. [2020a](#page-49-9)). Also, He et al. ([2020a\)](#page-51-1) discovered that miR-153-5p upregulation in oxaliplatin (L-OHP) resistant CRC cells could overcome L-OHP resistance via silencing Bcl-2-induced autophagy (He et al. [2020a](#page-51-1)). Furthermore, Liu et al. [\(2020f](#page-55-17)) indicated that lncRNA NEAT1 upregulation sponged miR-34a in CRC. Additionally, NEAT1 inhibition significantly slowed down CRC tumorigenesis and elevated sensitivity of cells to 5-fluorouracil (5-FU). miR-34a overexpression also showed comparable trends with NEAT1 inhibition via binding to autophagy components (HMGB1, ATG4B, and ATG9A) (Liu et al. [2020f](#page-55-17)). The role of miRNA in chemoresistance of pancreatic cancer (PC) cells was evaluated by miR-137 overexpression in PANC-1 cell lines. The results indicated that miR-137 chemo-sensitized the cells to Dox via ATG5-triggered autophagy (Wang et al. [2019d\)](#page-61-1).

The main hurdle for the proper treatment of multiple myeloma (MM) is still chemoresistance. Of note, the cross talk between miRNA dysregulation and autophagy illustrated that miR-221/222 could suppress dexamethasone (Dex) sensitivity in MM cells via inhibition of autophagy associated with ATG12/p27-mTOR axis (Xu et al. [2019b](#page-62-14)). In various studies, drug resistance in non-small-cell lung cancer (NSCLC) has been investigated. In a research conducted by Hua et al., overexpression of miR-1 reversed cisplatin resistance in NSCLC by suppression of ATG3-regulated autophagy (Hua et al. [2018\)](#page-52-8). Therefore, miRNAs have regulatory roles in chemoresistance due to their effects on autophagy induction. These mediators should be further investigated in numerous in vivo and in vitro studies to find the molecular mechanisms related to resistance. Table [2](#page-21-0) lists the effects of autophagy-related miRNAs on some human cancer chemotherapy.

3 Exosome and Autophagy

Exosomes, membrane-coated vesicles with 30–120 nm size, are released by several cells, such as lymphocytes, platelets, epithelial cells, mast cells, dendritic cells, neurons, and endothelial cells (Théry et al. [2002;](#page-60-7) Hashemipour et al. [2021\)](#page-51-9). Exosome has main roles in biological events, including inflammation, tumorigenesis, metastasis, and response to therapy (Kharaziha et al. [2012](#page-53-9)). Various researches have demonstrated that exosomes can also be considered as diagnostic means and targeted drug delivery system. It has been identified that almost all biological body fluids, including blood, serum, saliva, milk, amniotic fluid, semen, breast milk, and urine contain exosomes (Keller et al. [2011;](#page-53-10) Lässer [2015](#page-53-9)).

Exosomes carry diverse unique molecular cargos, including lipids, proteins, and nucleic acid fragment. Some of the proteins are involved in assembly, movement, and organization of exosomes (e.g., annexins, actins, tumor susceptibility gene 101, vesicle-associated membrane protein 8, and fibronectin) and observed in the structures of exosome. Furthermore, a cluster of proteins known as exosome surface markers, such as CD9, CD63, CD81, and CD82, are useful for the detection of exosomes (Zhao et al. [2015b;](#page-64-15) Barclay et al. [2017\)](#page-47-3). Mounting evidence has established that exosomes have a wide range of roles in human pathological and physiological processes. Since exosomes deliver their constituents into recipient cells, they are able to play a prominent role in cell signaling and local/ distant cell-to-cell communication (Lakkaraju and Rodriguez-Boulan [2008](#page-53-2); Van Niel et al. [2006\)](#page-60-8). These data demonstrated that exosomal molecular constituents can represent disease conditions (Feng et al. [2013](#page-50-8)). The idea of the RNAs presence in exosomes has attracted great attention in the research of exosomal RNAs, especially miRNAs as potential diagnostic biomarkers (Taylor and Gercel-Taylor [2008\)](#page-60-9). Recent experiments have demonstrated that exosomal miRNAs are resistant to RNase degradation and thus remain stable in circulating plasma and serum. On the other hand, they are easily evaluated, are minimally invasive, and have high sensitivity and specificity. This evidence indicates that exosomal miRNAs are ideal biomarkers for early clinical diagnostic applications (Lin et al. [2015](#page-55-18); Li et al. [2014b\)](#page-54-2).

As cited above, the autophagic process contains five key stages including initiation, nucleation, elongation and maturation, fusion, and degradation (Li et al. [2020c\)](#page-54-13). mTOR acts as the regulator of the initiation stage, and its activation is associated with prohibition of autophagy, whereas its inactivation is able to induce autophagy. It has been revealed that mTOR and the ULK complex (consist of ULK1, FIP200, and autophagy-related protein 13 [Atg13]) is inactivated and activated, respectively, in stress situations. Beclin-1, an essential component for autophagosome formation, in combination with Vps34 and Atg14L produces a complex, which is necessary for induction autophagy nucleation (Liang et al. [1999](#page-54-14); Levine et al. [2015;](#page-53-3) He and Klionsky [2009;](#page-51-10) Kihara et al. [2001](#page-53-11)). In the elongation along with maturation stage, two ubiquitin-like conjugation systems are warranted to facilitate autophagosome membrane expansion. The first system involves the microtubuleassociated protein light chain 3 (LC3) phosphatidylethanolamine (PE) complex. LC3 is cleaved by Atg4 at its C terminal to produce intracellular LC3-I, which is conjugated with PE in the ubiquitin-like reactions of Atg7 and Atg3. The lipid form of LC3 (LC3-II) is attached to the autophagosome membrane (Yu et al. [2015b](#page-63-21)). The second system involves the Atg12-Atg5-Atg16 complex, in which Atg12 is conjugated with Atg5 via ubiquitin-like reactions of Atg7 and Atg10. The Atg12-Atg5 conjugate interacts noncovalently with Atg16 to form a large complex. While lysosomes bind to autophagosomes to form autolysosomes in the fusion stage, cargo within autolysosomes will be degraded in the degradation stage. Autophagy is tightly modulated to keep homeostasis. Following autophagy initiation, lots of Atg proteins collaborate to manage the next stages of autophagy. It is yet not clear that autophagy conveys protective or detrimental effects in diseases (Saha et al. [2018;](#page-58-10) Xiong [2015](#page-62-15)). For example, lack of autophagy is associated with excess amount of tau and synuclein proteins, which induces neurodegenerative disorders. Evidences are in support of the fact that autophagy has a dual effects on cancer cells and initially acts as a tumor inhibitor; however, later it defends tumor cells against the immune system's attacks (Sharma et al. [2021;](#page-59-12) Hassanpour et al. [2020\)](#page-51-11). Likely, it has been demonstrated that autophagy regulates cardiac and hepatic disorders positively and negatively, respectively. Thus, the control of autophagy via exosomes can have various positive and negative effects on a variety of diseases (Xing et al. [2021\)](#page-62-16).

The role of exosomes in cellular stresses has been evidenced. However, some researches indicate that the interaction between exosomes and autophagy machinery may preserve intracellular protein and homeostasis (Baixauli et al. [2014\)](#page-47-4). In addition, autophagy induction due to nutrient deprivation leads to inhibited exosome secretion (Fader and Colombo [2009](#page-50-9)). There are some exosomal proteins markers related to autophagy mechanism. Dias et al. showed that PRNP (prion protein gene) is essential to promote the release of exosomes regulating CAV1/ caveolin-1-suppressed autophagy (Dias et al. [2016\)](#page-49-10). Moreover, significant levels of autophagy proteins, including WIPI2, LC3, NBR1, and p62, are present in exosomal fractions secreted by apilimod-treated cells (Hessvik et al. [2016\)](#page-51-12). Importantly, different exosomal and autophagic proteins can be applied as potential biomarkers regarding the type of cancer (Salimi et al. [2020\)](#page-58-11).

Also, the role of exosomal miRNAs in autophagy regulation has been demonstrated by various investigations. Yang et al. reported that high serum levels of exosomal miR-30a were observed in AMI patients. Also, they observed that inhibition of miR-30a increased the expression level of Beclin-1, Atg12, and LC3-II/LC3-I known as the regulators of core autophagy machinery and contributed to preserve the hypoxia-induced autophagy (Yang et al. [2016b](#page-63-22)). Liu and colleagues conducted a study on AMI rat model and in vitro model of hypoxic H9c2 cells to investigate the cardioprotective role of miR-93-5pencapsulating exosomes released from adiposederived stromal cells (ADSCs) in ischemiainduced cardiac damage. They found overexpression of inflammatory cytokines as well as miR-93-5p in both patients and rat models with AMI. In addition, the comparison of the protective effects of exosomes on infarction-induced cardiac damage revealed that exosomal treatment containing miR-93-5p derived from ADSCs caused more protection than simple exosomes (Liu et al. [2018b\)](#page-55-19). Also, Li et al. highlighted the impact of bone marrow-derived mesenchymal stem cells (BMMSCs)-derived exosomes enriched in miR-29c on negative regulation of autophagy in cardiac ischemia/reperfusion (I/R) injury through PTEN/Akt/mTOR pathway (Li et al. [2020d\)](#page-54-15). Similarly, human umbilical cord mesenchymal stem

cells-exosome (hucMSC-ex) abolished coxsackievirus B3 (CVB3)-activated myocarditis due to upregulation of autophagy function mediated by AMPK/mTOR axis and reduction of cardiomyocyte death (Gu et al. [2020](#page-50-10)). Santoso et al. ([2020](#page-58-1)) demonstrated that induced pluripotent stem cells and their differentiated cardiomyocytedelivered exosome (iCM-Ex) treatment had cardioprotective effects against post-MI via improvement of autophagy machinery in vivo and in vitro (Santoso et al. [2020\)](#page-58-1). Besides, Li and colleagues isolated exosomes released by human aortic smooth muscle cells and identified that isolated exosomes contained miR-221/222. They found that miR-221/222 could target 3'UTR of PTEN. Also, overexpression of miR-221/222 downregulated the expression of ATG5, LC3-II and Beclin-1, suggestive of the inhibitor role of exosomal miR-221/222 in autophagy process (Li et al. [2016e](#page-54-16)).

Yuwen et al. [\(2017](#page-64-16)) reported that the expression level of exosomal miR-146a-5p in NSCLC is correlated with chemosensitivity and chemotherapy response to cisplatin. Low levels of miR-146a-5p in serum exosomes were detected in advanced NSCLC patients. In both NSCLC cells and exosomes, the expression level of miR-146a-5p was gradually decreased due to chemoresistance to cisplatin. In addition, miR-146a-5p also inhibited the autophagy through targeting Atg12 (Yuwen et al. [2017\)](#page-64-16). Wang et al. investigated the role of tumor environment such as acute shear stress (ASS) in NSCLC invasion. Their data indicated that ASS activated cell death by exerting the secretion of autophagy and exosome components via SIRT2/ TFEB axis (Wang et al. [2020a](#page-61-13)). In the severe lung injury and respiratory deficit, Wei et al. illustrated that huMSC-ex-delivered miR-377-3p could improve acute lung injury (ALI) induced by lipopolysaccharide through targeting RPTOR followed by autophagy activation (Wei et al. [2020\)](#page-61-7).

Exosomal miR-1910-3p derived from breast cancer cell attenuated metastasis, growth, and autophagy via MTMR3 suppression and NF-κB and wnt/β-catenin signaling induction (Wang et al. [2020b\)](#page-61-14). Since exosomes loaded with

miR-1910-3p increased autophagy and breast cancer development via silencing MTMR3 and inducing NF-κB and wnt/β-catenin pathway, it could be considered as a diagnostic biomarker for breast cancer (Wang et al. [2020b\)](#page-61-14). Moreover, hucMSCs-ex transferring miR-224-5p could hamper cellular apoptosis and mount proliferation and autophagy in breast cancer via silence of HOXA5 (Wang et al. [2021a](#page-61-15)). In another interesting study, Han et al. [\(2020](#page-51-13)), showed that exosome-shuttled miR-567 repressed autophagy and chemo-sensitized breast cancer cells to trastuzumab via interacting with ATG5 (Han et al. [2020](#page-51-13)). Additionally, the anticancer effects of gemcitabine in breast cancer (luminal-b type) could be improved using exosome-overexpressed small interfering RNA (siRNA) MTA1, which suppressed autophagy and EMT/HIF- α pathway (Li et al. [2020e](#page-54-17)).

In the field of thyroid research, papillary thyroid cancer (PTC) cell exosome-delivered SNHG9 lncRNA could prevent autophagy flux and upregulate apoptosis of human normal thyroid epithelial cell line (Nthy-ori-3 cell) mediated by YBOX3/P21 pathway (Wen et al. [2021](#page-62-17)).

In cisplatin-resistant GC, Yao et al. manifested that the levels of exosomal circ-PVT1 and miR-30a-5p were respectively upregulated and downregulated, while the silence of Circ-PVT1 reversed cisplatin resistance via reducing autophagy alongside with increasing apoptosis through miR-30a-5p/YAP1 axis (Yao et al. [2021](#page-63-23)). Comincini et al. evaluated the expression levels of exosomal miR-17 and miR-30a to diagnose celiac disease and discovered that miR-17- and miR-30aregulated ATG7 and BECN1 known as two key executor of autophagy (Comincini et al. [2017](#page-49-11)).

Beclin-1 contains three main domains including coiled coil (CCD), evolutionarily conserved (ECD), and Bcl-2-homology-3 (BH3). Several proteins through binding to the various domains of Beclin-1 and forming different complexes regulate autophagy activity (Wirawan et al. [2012\)](#page-62-18). Beclin-1 is encoded by BECN1, which is located on chromosome 17q21 and was shown to be targeted via miR-30a (Zhu et al. [2009\)](#page-65-0). Exosomal miR-30a is capable of prohibiting autophagy via targeting the Beclin-1 pathway and maintains a

mandatory role in liver fibrosis and MI. It was revealed by Yang et al. ([2016b](#page-63-22)) that hypoxic cardiomyocytes prohibit autophagy through secreting miR-30a and, thereby, cause cardiomyocyte damage. So, it can be expected that autophagy level can be increased by targeting miR-30a, and, thereby, cardiomyocyte damage will be decreased. In contrast to findings of Yang et al., Zhang et al. found out that epigallocatechin gallate acts as a protective agent for MI through overexpression of exosomal miR-30a and, consequently, prohibiting autophagy and apoptosis (Zhang et al. [2020b\)](#page-64-17). An animal study that was conducted by Xu et al. $(2019c)$ also demonstrated that exosomal miR-30a through prohibiting autophagy decreased the level of cardiomyocyte apoptosis in rats with MI/reperfusion injury. Autophagy becomes active throughout hypoxia and displays protective effects by modifying cell survival. Nevertheless, as myocardial hypoxia continues, excessive autophagy occurs, which causes accumulation of a quite amount of toxic components and, as a consequence, cell death. In Yang et al.'s study, autophagy was inhibited by exosomal miR-30a; hence, there was a lack of protective autophagy in cardiomyocytes, which contributed to cardiomyocyte apoptosis. However, in other studies performed by Zhang and Xu, excessive autophagy was the reason behind cardiomyocytes damage. Exosomal miR-30a is able to decrease the level of cardiomyocyte apoptosis via prohibiting excessive autophagy. Moreover, it has been unveiled that excessive autophagy can induce liver fibrosis. It was shown that in a hepatic fibrosis model that was establish by Chen et al. ([2017c\)](#page-48-9), the expression level of exosomal miR-30a, secreting via hepatic stellate cells, was decreased. The upregulation of miR-30a may have the capacity to improve liver fibrosis through prohibiting autophagy mediated by the Beclin-1 pathway.

Li et al. [\(2021](#page-54-18)) revealed that osteosarcoma (OS)-secreted exosomal lncRNA OIP5-AS1 regulated autophagy and angiogenesis via reduction of miR-153 and enhancement of ATG5 expressions (Li et al. [2021\)](#page-54-18). In spite of pro-tumor effects of hBMSC-derived exosomes on OS progression via autophagy elevation, knockdown of

ATG5 in OS cells attenuated oncogenic effects of hBMSC exosomes (Huang et al. [2020\)](#page-52-13).

Reportedly, in osteoarthritis (OA) mice model, intra-articular administration of OA exosomes loaded with ATF4 had protective effects against chondrocyte apoptosis via activating autophagy (Wang et al. [2021b](#page-61-16)). Furthermore, in IVDD model, it was confirmed that normal cartilage end plate stem cell-derived exosomes (N-Exos) had a better therapeutic impact on stopping nucleus pulposus cell apoptosis and delay in IVDD progression in comparison with degenerated cartilage end plate stem cell-derived exosomes (D-Exos) via induction of PI3K/AKT/ autophagy pathway (Luo et al. [2021](#page-56-12)). Also, the effects of human umbilical cord mesenchymal stem cell-derived exosomes (hucMSC-ex) on tissue damages make them as a promising tool in the regenerative medicine. Based, Jia et al. [\(2018](#page-52-14)) discovered that hucMSC-ex enriched with 14-3- 3ζ reversed cisplatin-activated nephrotoxicity via interaction with ATG16L-induced autophagy (Jia et al. [2018](#page-52-14)).

It has been made clear that the levels of antiinflammatory cytokines and miR-30d-5p are reduced following acute ischemic stroke (AIS). Jiang et al. recognized that exosomes derived from miR-30d-5p-overexpressing ADSCs could overcome autophagy-induced cerebral damage via increasing polarization of M2 microglial/macrophage (Jiang et al. [2018\)](#page-52-9). Chen et al. [\(2020b](#page-49-12)) noticed that exosome-delivered circSHOC2 released from ischemic-preconditioned astrocyte (IPAS) potentiated neuronal protective effects against ischemic cerebral injury by affecting autophagy through the miR-7670-3p/SIRT1 axis (Chen et al. [2020b\)](#page-49-12). Recently, Pei et al. verified that astrocyte-released exosomes (AS-Exo) suppressed neuronal autophagy and alleviated neuronal injury and apoptosis in an in vitro model of ischemic injury via overexpression of miR-190b and downregulation of Atg7 (Pei et al. [2020\)](#page-57-8). It has been observed that hucMSC-ex could breakdown blood-brain barrier (BBB) and target substantia nigra leading to protection of dopaminergic neurons via activation of autophagy in a PD model (Chen et al. [2020c\)](#page-49-13). Ma et al. ([2021\)](#page-56-13) analyzed the amounts of lncRNA

LINC00470 in glioma-derived exosomes from patients and concluded that overexpressed LINC00470 could abrogate autophagy and raise glioma cells proliferation via binding to miR-580- 3p which in turn inactivated WEE1 and induced the PI3K/AKT/mTOR pathway (Ma et al. [2021\)](#page-56-13). Programmed death-ligand 1-containing exosomes (PD-L1-ex) derived from glioblastoma stem cell (GSC) enhanced autophagy and reduced apoptosis via AMPK/ULK1 pathway cascade resulted in enhanced resistance to TMZ, while knockdown of PD-L1 reversed these effects (Zheng et al. [2021\)](#page-65-5). There is line of evidence shown that Schwann cells (SCs) have regenerative role following peripheral nerve injury. In this context, Yin et al. discovered that ADSC-Exos loaded by miR-26b blocked SC autophagy and improved the myelin sheath regeneration in the sciatic nerve injury model via targeting Kpna2 (Yin et al. [2021](#page-63-24)). Due to the improvement of inflammation secondary to spinal cord injury (SCI) via anti-inflammatory effects of peripheral macrophages (PMs), Zhang et al. represented that PM-derived exosomes (PM-Exos) could promote spinal cord recovery via enhancement of microglial autophagy and anti-inflammatory microglia polarization mediated through PI3K/ AKT/mTOR pathway (Zhang et al. [2021b](#page-64-18)).

In type 2 diabetes mellitus (T2DM) rats, He et al. uncovered that hucMSC-ex promoted hepatic lipid and glucose metabolism potentially by enhancing the autophagosomes via AMPK pathway (He et al. [2020b\)](#page-51-14). Likewise, Zhang et al. reported that liver I-/R-induced injury could be alleviated by huMSC-ex-transmitted miR-20a via regulating apoptotic and autophagic genes including caspase-3, P62, mTOR, and LC3-II (Zhang et al. [2020c](#page-64-19)). Further, Zhu et al. [\(2020](#page-65-6)) verified that ADSC exosome carrying mmu_circ_0000623 inhibited liver fibrosis through autophagy induction (Zhu et al. [2020\)](#page-65-6). Since liver fibrosis can be driven by HSC activation, Wang et al. (Wang et al. [2020c\)](#page-61-5) displayed that natural killer (NK) cell-derived exosome (NK-Exo) attenuated HSC activation via inhibiting TGF-β1 mechanistically through overexpression of miR-223 and inhibition of ATG7-induced autophagy (Wang et al. [2020c](#page-61-5)).

All in all, studies have recently demonstrated that autophagy has regulatory properties in exosomal production and its release. The link between Atg5 and V1V0-ATPase and their role in induction of exosome production has been documented by Chen et al. ([2018\)](#page-48-4). They found that cells with Atg5 and Atg16L1 deficiency exhibit reduced exosome production, but it's not dependent on Atg7 and canonical autophagy. It has been shown that Atg5 affects the production of exosomes by reducing the acidifying of endosomes and disrupting the acidification of

V1V0-ATPase. Because of the role of autophagy and exosomes in metastasis, Atg5 is able to induce invasion and metastasis (Guo et al. [2017c](#page-51-8)). Abdulrahman et al. evaluated the role of autophagy in exosome production and processing. They found that the induction of autophagy by rapamycin, mTOR inhibitor, suppressed the release of exosomal prions; however, the inhibition of autophagy resulted in increased release of both exosomes and prions (Abdulrahman et al. [2018](#page-47-5)). Totally, further studies were collected in Table [3.](#page-29-0)

| | | Effect on | Type of | | |
|---------------|---|------------|--|---|-------------------------------|
| Type of cargo | Exosome source | autophagy | disease | Note | Ref |
| miR-146a-5p | Serum | Inhibition | Non-small- cell lung cancer (NSCLC) | miR-146a-5p upregulated and decrease level of Atg12 | Yuwen et al. (2017) |
| $miR-93-5p$ | Adipose- derived stromal cells (ADSCs) | Inhibition | Acute myocardial infarction (AMI) | | Liu et al. (2018b) |
| $miR-30d-5p$ | Adipose- derived stromal cells (ADSCs) | Induction | Acute ischemic stroke (AIS) | Enhancement of M2 microglial/ macrophage polarization and reduce of M1 microglial/macrophage polarization. Inhibition ischemia- induced neuronal damage via decreasing of TNF- α , IL-6, and iNOS secretion from M1 microglial cells. Downregulation of Beclin-1 and Atg5. Induction of expression anti-inflammatory cytokines IL-4 and IL-10 from M2 microglial cells | Jiang et al. (2018) |
| miR-181-5p | Adipose- derived mesenchymal stem cells (ADSCs) | Induction | Liver fibrosis | miR181-5p-ADSC block of STAT3/ Bcl-2/Beclin-1-dependent signaling pathway and decrease liver fibrosis | Qu et al. (2017) |
| $miR-30a$ | Serum H9c2 cell | Inhibition | Acute myocardial infarction (AMI) | Hypoxia promotes expression of miR-30a in cardiomyocytes and increases apoptosis and elevates Atg12 and Beclin-1 protein levels | Yang et al. (2016b) |
| m i $R-17$ | T98G cells | Induction | Celiac disease (CD) | miR-17 downregulated and increase of expression level of ATG7 | Comincini et al. (2017) |
| m iR-30 a | T98G cells | Induction | Celiac disease (CD) | miR-30a downregulated and increase of expression level of BECN1 | Comincini et al. (2017) |
| miR-221/222 | Human aortic smooth muscle cells (HAoSMCs) | Inhibition | $\overline{}$ | miR-221/222 upregulation in HUVECs, reduction of PTEN, LC3-II, ATG5, and Beclin-1protein levels. Increase of SQSTM1/p62 level and Akt signaling pathway | Li et al. (2016e) |

Table 3 Exosome and autophagy

| Type of cargo | Exosome source | Effect on autophagy | Type of disease | Note | Ref |
|---|---|------------------------|---|---|----------------------------|
| MSC exosome $(miR-125b)$ | Neonatal mice cardiomyocytes (NMCMs) cell | Inhibition | Myocardial infarction (MI) | Decrease of p53/Bnip3 signaling pathway and save myocardial from death | Monaco et al. (2017) |
| HucMSC exosome $(14-3-3\zeta)$ | NRK-52E cells | Induction | Acute kidney injury (AKI) | HucMSC exosome-delivered 14-3- 3ζ attached the ATG16L protein and induced autophagosome formation and as a result elevated cisplatin resistance and cell proliferation and reduced apoptosis | Jia et al. (2018) |
| Exosomes derived from gefitinib- treated $(Exo-GF)$ | PC9 cells | Induction | Non-small- cell lung cancer (NSCLC) | Enhancement cisplatin resistance, overexpression of Bcl-2 and LC3-II protein levels, decrease of Bax and p62 protein levels | Li et al. (2016f) |
| NA | H9C2 cells | Induction | Myocardial ischemia- reperfusion injury (MIRI) | Exosomes derived from mesenchymal Stem cells enhance cardiomyocyte autophagy, inhibit cell apoptosis and ROS production through H2O2, promote AMPK pathway and decrease Akt and mTOR pathways | Liu et al. (2017d) |
| HucMSC exosomes | NRK-52E cells | Induction | - | HucMSC exosomes block cisplatin- induced mitochondrial apoptosis and secretion of inflammatory cytokines, decrease of mTOR and NF-KB, increase levels of ATG5 and ATG7 | Wang et al. (2017c) |

Table 3 (continued)

4 Inhibition or Stimulation of Autophagy by the Virus

Viruses are known as intracellular parasites that are highly dependent on the host for their cell cycle. Hence, after entrance, they reprogram the target host cell to meet their basic needs (Fehr and Yu [2013](#page-50-11); Bagga and Bouchard [2014\)](#page-47-6). As we cited before, autophagy has a crucial role in preserving cellular hemostasis by participating in different physiological processes, such as, but not limited to, cell differentiation and development, starvation, and degradation of abnormal products. Additionally, it has been shown that autophagy is produced in response to stress conditions such as infection with viral viruses (Senft and Ze'ev [2015;](#page-58-13) Mizushima and Levine [2010\)](#page-56-14). Also, in response to viral infections, autophagy becomes active by innate immune system to degrade viruses (Deretic et al. [2013\)](#page-49-7).

Additionally, autophagy also takes part in activation of adaptive immune system by accelerating antigen processing (Paludan et al. [2005;](#page-57-9) Romao et al. [2013\)](#page-58-14). Xenophagy is a type of selective lysosomal degradation pathway that is vital for eliminating pathogens especially bacteria and viruses (Levine [2005](#page-53-12)). Although autophagosomes potentially are detrimental for invading viruses, several viruses have shown to be able to convert the autophagosome to their home during replication. The autophagosome provides a membrane-bound, protected site to produce their progeny, where their metabolites can be utilized as source of energy for viral replication. Another unique class of autophagy, called lipophagy, targets intracellular lipid droplets, and this process can also be captured by viruses. Lipid droplets are considered as the optimal source for viral assembly since the viruses have the potential to stimulate lipophagy provide the high values of

ATP needed for viral replication (Choi et al. [2018;](#page-49-14) Heaton and Randall [2011\)](#page-51-15). Taken together, according to recent findings, viruses are developing new strategies to fight or use autophagy to facilitate their replication. Herein, we sought to provide a brief review on how autophagy fights against viral viruses and, thereafter, how the viruses disrupt the autophagic pathway to escape form immune system reactions and prompt their replication.

Recently, several studies have reported that the aim of virus interference with host cell autophagy is to promote the life cycle of virus and avoid detection by the host immune system. The diverse set of viruses are able to dysregulated autophagy machinery (Glick et al. [2010](#page-50-0); Jackson [2015](#page-52-15)). The viral proteins directly or indirectly interact with autophagy components leading to enhance or block autophagy (Mack and Munger [2012\)](#page-56-15). For instance, coronavirus papain-like protease, termed PLP2, induces autophagy via interacting with Beclin-1 (Chen et al. [2014b](#page-48-2)). Although some viral proteins inhibit the autophagy via interaction with Beclin-1, HIV-Nef and HSV-1 ICP34.5 proteins are capable of inhibiting autophagydependent Beclin-1 (Orvedahl et al. [2007;](#page-57-11) Kyei et al. [2009a;](#page-53-13) Campbell et al. [2015a\)](#page-48-10). Beclin-1 has Bcl-2 homology 3 (BH3) domain and, through this domain, interacts with anti-apoptotic Bcl-2 family members (Oberstein et al. [2007\)](#page-57-12). This interaction inhibits Beclin-1 assembly to the pre-autophagosomal structure, thereby preventing autophagy (Liang et al. [1998\)](#page-54-19).

The importance of apoptosis and Bcl-2 proteins in immune system regulation and responses to stresses has provided evolutionary pressures on viruses to acquire the genes encoding pro-survival Bcl-2 proteins (Neumann et al. [2015](#page-57-13)). Large DNA viruses, such as γ-herpesviruses 68 (γ-HV68), adenovirus, Epstein-Barr virus (EBV), and Kaposi's sarcoma-associated herpesvirus (KSAH), mimic the pro-survival Bcl-2 proteins leading to hijack the intrinsic pathway of apoptosis for their purposes (Kvansakul et al. [2017\)](#page-53-14). Liang et al. [\(2008\)](#page-54-20) reported that murine gamma-herpesvirus 68 (MγHV68) Bcl-2 protected virus-infected cells against apoptosis, also repressed autophagy through its direct binding to Beclin-1 (Liang et al.

[2008\)](#page-54-20). In addition to suppressing autophagy by the vBcl2/Beclin-1 complex, KSHV also inhibits this process by viral homolog of cellular FLICE-like inhibitor protein (v-FLIP). Both KSHV v-FLIP and cellular FLIP directly interact with the autophagyprotein ATG3 in competition with LC3 protein. It has been demonstrated that, to suppress autophagic programmed cell death, this interacting ability of KSHV v-FLIP is required (Mack and Munger [2012;](#page-56-15) Irmler et al. [1997](#page-52-16); Thome et al. [1997;](#page-60-10) Lee et al. [2009](#page-53-15)). The biochemical evidences show interaction of different HCV and HBV proteins with autophagy machinery components. Nonstructural protein 3 (NS3) of HCV was found to co-localize and associate with the immunity-associated GTPase (IRG) family M that it known autophagy pathway regulator in response to the bacterial infection (Grégoire et al. [2011a;](#page-50-12) Singh et al. [2006\)](#page-59-10). Core protein of HCV activates autophagy through EIF2AK3and ATF6 UP pathway and/or upregulating Beclin-1 expression (Wang et al. $2014a$; Liu et al. $2015b$). Moreover, this core protein represses apoptosis and enhances autophagy in hepatocytes through upregulating Beclin-1 (Liu et al. [2015b](#page-55-21)). Small surface proteins of HBV interact with LC3 and HBV-HBx protein interacts with VPS34 (Sir and Tian [2010](#page-59-13); Li et al. [2011a\)](#page-54-4). Sir and colleagues reported that HBx through binding to phosphatidylinositol 3-kinase class III, a critical enzyme in the initiation of autophagy, leads to enhanced activity of this enzyme and thus activates the early autophagic pathway (Sir and Tian [2010\)](#page-59-13).

Espert et al. have shown that autophagydependent cell death is activated after binding of HIV envelope glycoprotein to CXCR4 on T cells (Espert et al. [2006](#page-50-13); Espert et al. [2007](#page-50-14)). Bcl-2 associated athanogene 3 (BAG3) is known as a pro-autophagic and anti-apoptotic factor in many normal and neoplastic cells (Rubinstein and Kimchi [2012](#page-58-15); Behl [2011](#page-48-11); Rosati et al. [2011\)](#page-58-16). Bruno and colleagues reported that transfection of HIV-1 trans-activator (Tat) protein into glioblastoma cells results in increasing BAG3 levels leading to stimulate the autophagic pathway, while silencing of BAG3 results in disrupted balance between autophagy and apoptosis (Bruno et al. [2014\)](#page-48-12). As mentioned earlier, autophagy process involves the formation and maturation of autophagosomes.

Recent studies have showed that interferon-γ (IFN-γ) activates autophagosomes to participate in immunity defense (Deretic [2006\)](#page-49-15). HIV-Tat protein suppresses the formation of autophagosome. In other words, this protein disrupts the IFN- γ signaling pathway through repression of STAT1 phosphorylation and, consequently, inhibits the IFN-γ-induced autophagy (Li et al. [2011b](#page-54-21)). Additionally, influenza matrix protein 2 and human parainfluenza virus Type 3 phosphoprotein interrupt the maturation of autophagy through blocking autophagosome degradation (Ding et al. [2014;](#page-49-16) Gannagé et al. [2009\)](#page-50-15).

One of the most important regulators of autophagy is the mammalian target of rapamycin (mTOR), which moderates the balance between autophagy and growth in response to environmental stress and physiological conditions (Cuyàs et al. [2014\)](#page-49-17). Kinase mTOR is the downstream target of PI3K-Akt signaling pathway, which is activated by growth factor receptors and neurotropism as well as promotes cell differentiation, growth, and survival and also reduces apoptosis (Manning and Cantley [2007](#page-56-16); Brunet et al. [2001;](#page-48-13) Hanada et al. [2004\)](#page-51-16). It has been observed that suppression and activation of PI3K/AKT/mTOR pathway lead to promote and inhibit autophagy, respectively (Heras-Sandoval et al. [2014\)](#page-51-16). Surviladze et al. reported that contamination of HaCaT cells with HPV-16 pseudovirions activates thePI3K/Akt/mTOR signaling pathway leading to autophagy inhibition (Surviladze et al. [2013](#page-60-12)). KSHV-K1, a viral protein, activates thePI3K/Akt/mTOR signaling pathway in endothelial cells and B lymphocytes (Mack and Munger [2012](#page-56-15); Tomlinson and Damania [2004](#page-60-13); Wang and Damania [2008\)](#page-60-14). Also, HBV induces autophagy in HepG2 cells transfected with HBx through regulating the PI3K/Akt/mTOR pathway (Wang et al. [2013a\)](#page-60-15). It is believed that autophagy plays an important role in the regulation of cancer progression and development and in determining of tumor responses to anticancer treatments. It has been observed that oncolytic viruses (OVs) interact with autophagy in infected tumors to ensure their own survival and replication advantage (Jiang et al. [2011](#page-52-17)). While an increasing number of OVs are reported to induce autophagy in infected tumors, some OVs choose to subvert or evade it (Zhang et al. [2006](#page-64-18); Moloughney et al. [2011\)](#page-57-14). For instance, Rodriguez-Rocha et al. showed that adenoviruses induce autophagy to promote virus replication and oncolysis in lung cancer A549 and H1299 cells (Rodriguez-Rocha et al. [2011](#page-58-17)). This concept suggests an insightful indication to OV therapy to improve the quality of life and survival of patients with cancer. Therefore, viruses and viral products can effect on the stimulation or inhibition of autophagy. Searching for using these agents to control stress conditions should be more focused.

HCMV belongs to β-herpesvirus family, which has shown to be transmissible via different body fluids. HCMV is known as one of the biggest viruses since its genome contains of 236 kilobases (Plotkin and Boppana [2019](#page-57-6)). Albeit it has been demonstrated that primary infection mainly is asymptomatic, the congenital form of the virus can be accompanied by several complications including, but not limited to, disabilities and death. HCMV was shown to have the potential to favor cancer through transformation of infected cells when infecting normal tissues by regulating several signaling pathways (Herbein [2018\)](#page-51-17). The virus modulates autophagy in a dual fashion (Joseph et al. [2017](#page-52-18); Nahand et al. [2021\)](#page-57-15). At early phases of infection, it contributes to autophagic vesicle formation. On the contrary, later, it inhibits autophagy via producing some proteins (Chaumorcel et al. [2012](#page-48-14)). By far, two viral proteins, namely, TRS1 and TRS2, that participate in autophagy prohibition in cooperation with Becline-1 have been explored. It has been demonstrated that simultaneous expression of TRS1 and IRS1 is necessary for prohibition of autophagy in virus infection (Mouna et al. [2016\)](#page-57-16). Recently, viral components with the ability of regulating latency and lytic reactivation, especially those in the uLb' gene region, have been at the center of focus. These viral components are capable of limiting virus replication via moderating immune system response and viral latency through expressing quite a few virus proteins. For instance, a viral protein, namely, UL138, through autophagy machinery, can

modulate adaptive immunity of fibroblast when it presents to MHC-1 (Tey and Khanna [2012](#page-60-16); Mlera et al. [2020](#page-56-17)). However, recent evidence clarified that prohibition of autophagy is associated with extreme CD8 + T-cell response because of the internalization of molecules in MHC-I (Loi et al. [2016\)](#page-55-21). Expressing viral proteins derived from HMCV genes 1 and 2 (IE1 and IE2) is essential for immunomodulation and reactivation of host cell virus (Suares et al. [2021](#page-59-14); Reddehase and Lemmermann [2019\)](#page-58-18). IE2 is able to modulate gene expression by interacting with UL84 and itself along with a number of cell transcription factors. IE2 protein has a mandatory role in synthesis of viral DNA and was shown to have the potential to counteract host responses (Li et al. [2020f](#page-54-10); Møller et al. [2018](#page-56-18)). Lately, it has been shown that upregulation of IE2 can contribute to autophagy in cells infected with the virus (Zhang et al. [2021c\)](#page-64-20). Briefly, it has been found out that when a cell is infected with HMC, viral proteins result in autophagosomal vesicle formation. Later, the proteins prohibit vesicle-to-lysosome binding, which leads to loss of their degradative capability.

HTLV-1 is a complex type C virus belongs to Retroviridae family and contains an envelope which derived from the cell membrane of host (Martin et al. [2016\)](#page-56-19). The virus first was extracted from patients who were suffering from rapidly growing T-cell lymphoma (ATLL) with cutaneous involvement (Martin et al. [2016\)](#page-56-19). Additionally, it has been shown that HTLV-1 has a major role in other diseases including development of poliomyelitis, arthropathy, HTLV-1-associated myelopathy, facial nerve palsy, and infectious dermatitis (Futsch et al. [2018](#page-50-16)). It has been reported that approximately 5–20 million individuals carry the virus globally; however, a small proportion (3–5%) of them progress secondary ATLL (Gessain and Cassar [2012;](#page-50-17) Schierhout et al. [2020\)](#page-58-19). Tax is known as a regulatory protein maintaining a crucial role in HTLV-1 replication and, hence, is needed for the virus propagation. It also plays a crucial role in ATLL development since it cooperates with more than 100 cellular proteins to increase cell signaling, inhibit apoptosis, contribute to cell cycle dysregulation, disrupt DNA repair, and

stimulate proto-oncogenes (Mui et al. [2017\)](#page-57-5). It was shown that the virus is able to prohibit the binding between autophagosomes and lysosomes through a mechanism involving tax. As a result, quite a few autophagic vesicles, which are not degraded, appear, and these vesicles are great for virus replication (Tang et al. [2013\)](#page-60-17). Hence, Tax protein combines with the IKK complex to induce NF-kB and Beclin-1 activity. Cell adhesion molecule 1 (CADM1) is a glycoprotein belonging to the type 1 transmembrane cell adhesion family, which is part of immunoglobulin superfamily and is taken into account as a marker of T cells infected with HTLV-1 in (Nakahata et al. [2021](#page-57-17); Chen et al. [2015\)](#page-48-15). Tax and NF-kB stimulation and degradation of NF-kB negative regulator, namely, p47, are necessary for CADM1 expression. The main mechanism behind p47 degradation is autophagy, and autophagy can be detected in the majority of HTLV-1 infected ATLL cells (Sarkar et al. [2019\)](#page-58-20). HBZ is another crucial essential viral protein for progression of ATLL (Akram et al. [2017\)](#page-47-7). Recent evidence found out that HBZ can prohibit autophagy as well as apoptosis and, in contrast, stimulate brain-derived neurotrophic factor (BDNF) and its receptor expression (Baratella et al. [2017](#page-47-8); Mukai and Ohshima [2014\)](#page-57-18). HBZ can exert different effects based on its location; its expression in cell nucleus and cytoplasm is associated with tumor development and stimulation of inflammation, respectively. Its entry to cytoplasm from nucleus is associated with activation of mTOR via PPP1R15A expression, which is a regulator subunit of protein phosphatase1 (Mukai and Ohshima [2014\)](#page-57-18). Same to other viruses, infection with HTLV-1 is associated with formation of autophagosomes and prohibition of binding to lysosomes so as to inhibit degradation. As a consequence, a great amount of autophagosome vesicles will appear, which provides a suitable environment for the virus formation and, moreover, a physical barrier, which limits the progression of cellular processes (Ren et al. [2015](#page-58-21)).

Since 2019, the world is witnessing a pandemic caused by a new virus called SARS-CoV-2, causing COVID-19 infection (Khatami et al. [2020\)](#page-53-16). It has been reported that at least 270 million individuals infected with SARS-CoV2 and near 5.3 million people have died because of that (Worldometer [2020\)](#page-62-20). Although its mortality rate is not considerably high, it is highly infectious (Sanche et al. [2020](#page-58-22)). COVID-19 infection symptoms are broad ranging from fatigue, fever, tiredness, and cough to acute respiratory distress syndrome, MI, stroke, renal injury, and death (Xu et al. [2020b\)](#page-63-25). Albeit some mechanisms have been proposed for sever form of the disease, the exact mechanism behind the diseases pathology is yet not clarified and required more studies (Gorshkov et al. [2020](#page-50-11)). It has been demonstrated that for the virus replication and transcription, there is a need to DMVs to be formed, indicating the fact that the virus may hijack the autophagosomal machinery to assist DMV formation (Carmona-Gutierrez et al. [2020\)](#page-48-16). Hence, autophagosomes play a crucial role in infection replication by using viral replicase proteins (Cottam et al. [2011\)](#page-49-18). In support of that, also, it was found out that NSP6, a viral replicase protein, colocalized with DMVs positive for LC3, showing a probable correlation between the virus replication and autophagy (Cottam et al. [2011](#page-49-18); Bello-Perez et al. [2020\)](#page-48-17). Furthermore, Fulvio et al. designed a study to explore the mechanism that coronaviruses such as mouse hepatitis virus and SARS hijack the formation of EDEMosome, and vesicles participate in the regulation of endoplasmic reticulum degradation, in order to produce the DMVs needed for the virus replication. They declared that mouse hepatitis disrupts two endoplasmic reticulum-associated degradation (ERAD) regulatory proteins, namely, EDEM1 and OS-9, degradation via trapping them into DMVs (Reggiori et al. [2010](#page-58-23)). This represents that SARS-CoV2 is able to facilitate the virus replication within the infected individual by escaping from autophagy.

Enhanced amount of processed form of LC3B and LC3B-II and an accumulation of SQSTM1, supporting the fact that SARS-CoV2 infection contributed to decreased autophagic flux (Hayn et al. [2021\)](#page-51-18). An experimental study illustrated that although stimulation of autophagy using rapamycin cannot affect the virus considerably, activation of innate immune using interferons keeps the virus sensitive. Therefore, the virus escapes from antiviral mechanism of autophagy. In order to understand the mechanism behind anti-autophagy effects of SARS-CoV2, Hayn et al. [\(2021](#page-51-18)) evaluated the effect of 29 of the 30 SARS-CoV-2 proteins on autophagy. They found out that while NSP15 expression is associated with reduced number of autophagosomes positive for LC3B, ORF3a, E, M, and ORF7a expression was associated with accumulation of LC3B. Moreover, the authors showed that E, M, ORF3a, and ORF7a inhibit autophagic flux. It is of importance to note that the reduction of autophagosomes for Nsp15 expression was improved following administration of rapamycin, proposing that possibly Nsp15 impacts mTOR axis. While upon E, ORF3a, and ORF7a expression, the values of processed LC3B-II enhanced, Nsp15 expression led to decrease but not substantial in LC3B-II values. In consistent with this finding, ORF3a, ORF7a, E, and Nsp15 expression is associated with higher values of SQSTM1. Noteworthy, while M expression is associated with higher values of processed LC3B, it was not able to prohibit the degradation of SQSTM1, showing that M cannot inhibit autophagy. Immunofluorescence assay demonstrate that although overexpression of ORF3a, E, and ORF7a is associated with higher numbers of LC3B-positive puncta, M expression is associated with elevated LC3B localization. Also, following Nsp15 expression, decrease in number of autophagosomes was observed. Moreover, the authors proposed that the role of SARS-CoV2 proteins including M, ORF3a, ORF7a, and Nsp15 in autophagy is virtually similar to their function in SARS-CoV-1 and bat coronavirus RaTG13 (Hayn et al. [2021;](#page-51-18) Koepke et al. [2021\)](#page-53-17). A very recent study showed that ORF3a can intensely prohibit autophagic flux by preventing the fusion of autophagosomes with lysosomes (Zhang et al. [2021d\)](#page-64-12). It was shown that ORF3a colocalized with lysosomes and interacted with VPS39, which is a subunit of the homotypic fusion and protein sorting (HOPS) complex. The interaction between VPS39 and ORF3a contributes to inhibition of -HOPS binding to RAB7, which inhibited the assembly of a fusion

machinery, contributing to increase levels of autophagosomes. These findings shed light on the mechanism behind the virus escape degradation, which is disrupting the fusion of autophagosomes with lysosomes (Zhang et al. [2021d\)](#page-64-12). Taken together, the spread of SARS-CoV-2 virus can be limited with using approaches targeting autophagy.

Several drugs, for instance, azithromycin, chloroquine, and hydroxychloroquine, have been considered since these drugs are capable of modulating autophagy signaling pathways (Gao et al. [2020b\)](#page-50-18). The fact that the mentioned medications are able to inhibit endocytic pathway and, thereby, inhibit SARS-CoV2 replication constitute a rational for considering using these drugs in patients who are infected with the virus (Gao et al. [2020b](#page-50-18)). In clinical settings, inconsistent findings regarding the benefits of these drugs in COVID-19 patients have been reached. Some studies revealed that hydroxychloroquine administration is associated with lower mortality rate in severe COVID-19 patients (Yu et al. [2020;](#page-64-14) Meo et al. [2020](#page-56-20)); however, several studies demonstrated that these medications were not able to decrease mortality from infection with SARS-CoV2 (Molina et al. [2020](#page-56-21); Singh et al. [2020\)](#page-59-15). Noteworthy, it has been found that these medications are associated with prolonged QT interval, which can lead to cardiac arrhythmia and sudden cardiac death (Chorin et al. [2020;](#page-49-19) Jankelson et al. [2020](#page-52-19)). Thus, more investigations are warranted to evaluate the advantageous and disadvantageous of autophagy modulator drugs to limit the virus infection progression. Table [4](#page-36-0) lists the effects of viral infection on the regulation of autophagy during some viral diseases.

5 Autophagy Supporting Viral Replication

RNA viruses hijack autophagy for replication. During the autophagy process, DMVs are formed, which maintain a crucial role in poliovirus replication by creating a promising environment for poliovirus replication and keeping polioviruses RNAs away from innate immune receptors recognition and degradation.

Polioviruses, a member of picornavirus family, lack a membrane envelope. Autophagy was shown to be inducer of poliovirus replication, and its inhibition was shown to associated with reduced virus replication (Jackson et al. [2005;](#page-52-20) Dales et al. [1965](#page-49-9)). Besides, infection with poliovirus increases the level of LC3 in puncta and expresses two nonstructural poliovirus proteins 2BC and 3A, contributing to lipidation and formation of LC3 and DMVs, respectively, which makes link between the virus replication and autophagy. Similar to polioviruses, foot-andmouth disease virus and CVB3 exploit autophagy for replication (Berryman et al. [2012](#page-48-18); Robinson et al. [2014](#page-58-24)).

Hepatitis C virus also can trigger autophagy via increasing levels of autophagosomes and using autophagosomal membranes, which is the site for the virus replication (Shrivastava et al. [2011;](#page-59-16) Dreux and Chisari [2009](#page-49-3); Ait-Goughoulte et al. [2008\)](#page-47-9). Nonetheless, the capacity of HCV in stimulating the fusion of lysosome with autophagosomes is still the matter of debate. Several studies have claimed that the virus stimulates autophagosomes and inhibits the autophagosome and lysosome fusion to enhance viral replication and limit virus degradation (Taguwa et al. [2011;](#page-60-18) Sir et al. [2008a,](#page-59-4) [b\)](#page-59-17). A study stated that HCV enhances the levels of autophagosomes without any change in the levels of autophagy protein degradation, which is (Sir et al. [2008b\)](#page-59-17). Dreux et al. demonstrated that although the autophagy proteins are key components in the translation process of incoming HCV genome, it is not essential for maintenance of the infection (Dreux et al. [2009\)](#page-49-20). However, Ke et al. revealed that the viral replication is totally dependent on the whole autophagic process through complete autolysosome maturation (Ke and Chen [2011b\)](#page-53-18). At early phase of infection with HCV, the interaction between the HCV RNA-dependent RNA polymerase NS5B and ATG5 was observed, which highlights the importance of ATG5 for infection initiation. Blocking ATG5 expression was shown to be associated with the virus replication and maintenance (Guévin et al. [2010\)](#page-51-19).

HCV dynamically modulates autophagy by expressing ultraviolet radiation resistanceassociated gene protein (UVRAG) and Rubicon to increase its replication (Wang et al. [2015c](#page-61-21)). At the early stages of viral infection, upregulation and downregulation of Rubicon and UVRAG, respectively, by the virus inhibit the autophagosomes maturation and thereby increase the levels of autophagosomes, leading to virus replication (Wang et al. [2015c\)](#page-61-21). Additionally, immunity-related GTPase family M protein (IRGM), an IFN-inducer GTPase, was shown to be able to modulate autophagy process by interacting with several autophagic proteins (Grégoire et al. [2011b](#page-50-24)). Hansen et al. showed that IRGM by promoting autophagy and Golgi fragmentation induces the virus replication. IRGM stimulates Golgi fragmentation via modulation of Golgi apparatus-specific brefeldin A-resistant guanine nucleotide exchange factor 1 (GBF1) and AMPKα (Hansen et al. [2017](#page-51-21)). In summary, HCV is able to regulate autophagy process to induce the virus replication.

According to findings of related studies, it can be concluded that flaviviruses take benefits from the close connection between ER and autophagy processes. At first, it was believed that stimulation of autophagy in those infected with flaviviruses is only related to the ER stress-related UPR signaling pathway. On the other hand, it was shown that several nonstructural proteins of West Nile virus (WNV) and DENV are able to stimulate autophagy irrespective of the UPR (Blázquez et al. [2014](#page-48-23); Miller et al. [2007\)](#page-56-25). Analyses of neural progenitor cells infected with Zika virus (ZIKV) disclosed that the infection causes a huge remodeling of ER and, moreover, vesicular packet formation, which are assumed to be the spots of ZIKV replication (Offerdahl et al. [2017;](#page-57-24) Cortese et al. [2017\)](#page-49-25). Infection of skin fibroblast is associated with autophagosomes formation, leading to higher levels of ZIKV replication (Hamel et al. [2015](#page-51-22)). Furthermore, enhancement in lapidated form of LC3 along with decrement in ATG16L1 expression, a vital autophagy gene, in placentae infected with ZIVK, indicates the fact that autophagy plays a crucial role in vertical transmission of ZIKV (Cao et al. [2017\)](#page-48-24). Liang et al. clarified the mechanism responsible for fetal neurological defects causing by ZIKV. They found out that two proteins exist in ZIKV, namely, NS4A and NS4B, in cooperation with each other inhibit the Akt-mTOR signaling pathway, which contributes to autophagy activation and defective neurogenesis (Liang et al. [2016\)](#page-54-22). Upon early phase of ZIKV and DENV infection, inhibition of FAM134B, which acts as an autophagy receptor, enhances the virus replication. The viruses use their NS3 protease to cleave FAM134B, leading to limit ER and autophagosomes formation (Khaminets et al. [2015;](#page-53-25) Lennemann and Coyne [2017\)](#page-53-26).

It was shown that two HIV proteins Gag and Nef modulate the autophagy process through interacting with LC3 and Beclin-1, which, finally, causes higher viral replication. During early phase of autophagy, Gag protein interacts with C3, which leads to higher levels of Gag processing and HIV levels in macrophages (Kyei et al. [2009b\)](#page-53-27). Also, during the maturation stage of autophagy, Nef protein of HIV inhibits autophagy maturation via binding to Beclin-1 and, thereby, keeps the virus safe from degradation. Thus, the interaction between the virus and autophagy increases HIV load and replication through inducing early-stage autophagy but prohibits late stages (Kyei et al. [2009b](#page-53-27)). Nevertheless, it has been detected that during permissive infection, the virus inhibits autophagy so as to prevent the degradation of proteolytic. In the normal situation, mTOR by phosphorylating transcription factor EB (TFEB) limits TFEB translocation. TFEB is able to induce autophagy and lysosomal activation when it transfers to the nucleus. In doing so, TFEB should become dephosphorylated, which is dependent upon mTOR inhibition. For stimulating autophagy within macrophages infected with HIV, the interaction between TLR8 and HIV should be occurred, which is dependent on the dephosphorylation and nuclear translocation of TFEB. The authors also observed that during permissive infection, the interplay between Nef and Beclin-1 contributed to phosphorylation of TFEB, mTOR activation, cytosolic sequestration, and, thereby, autophagy inhibition (Campbell et al. [2015b\)](#page-48-25).

A number of experimental studies have declared that autophagy inhibition causes

prohibition of HBV replication, which represents the fundamental role of autophagy in HBV life cycle (Table [3\)](#page-29-0). The studies have utilized cells that were infected with HBV, or transfected with HBV, or exhibiting HBV DNA replication. It was found out by Sir and his colleagues that triggering autophagy by HBV is dependent on the presence of HBx, which increases its activity through binding to PI3KC3. Therefore, autophagy along with PI3KC3 modulates the majority of HBx impacts on HBV replication (Sir et al. [2010a,](#page-59-24) [b](#page-59-25)). Either inhibition of PI3KC3 or Atg7 contributes to decrease in HBV replication (Sir et al. [2010b\)](#page-59-25). A study found out that autophagy inhibition decreases pgRNA packaging and HBV RNA values to some extent while inhibited HBV DNA replication remarkably (Tang et al. [2009b\)](#page-60-27). Therefore, it can be concluded that this phenomenon indicates that autophagy exerts its effects on HBV replication mainly at the viral DNA replication stage of the viral life (Sir et al. [2010b\)](#page-59-25). Another study similarly found positive effects of autophagy on HBV replication; however, the effects were mostly seen at the stage of envelopment (Rautou et al. [2010](#page-58-25)). Li et al. designed a study to evaluate the association between autophagy and HBV by suppressing autophagy using 3-methyladenine and siRNA duplexes that suppress fundamental genes need for autophagosome formation. The investigators explored that autophagy inhibition is able to suppress the virus replication notably and stimulating autophagy using starvation and/or rapamycin increases the virus replication (Li et al. [2011c\)](#page-54-24). These inconsistent findings can be explained by using different HBV strains or sublines of Huh7 cells in the relevant studies. Also, a study unveiled ROS HBV capsid assembly in the existence of Hsp90; however, it was observed that ROS without Hsp90 decreases the virus assembly (Kim et al. [2015](#page-53-28)). Another pathway responsible for HBV-induced autophagy is ROS/JNK signaling pathway. In doing so, ROS/JNK signaling pathway modulates the interaction between Beclin-1 and Bcl-2, which is crucial for activation of autophagy (Zhong et al. [2017](#page-65-11)). Additionally, it has been shown that HBV has the potential to favor its replication by subverting autophagy Atg5-12/16L1 complex, without any need for Atg8/LC3 lipidation, which is a vital process for autophagosomes maturation (Döring et al. [2018\)](#page-49-26). At the same time, several studies have claimed that autophagy triggered by HBV inhibits the virus replication. Wu et al. demonstrated that autophagy following infection with HBV is able to degrade envelope proteins (Wu et al. [2016d\)](#page-62-3). For the first time, Lazar et al. demonstrated that HBV decreases the level of envelope protein through that the ERAD signaling pathway. Simultaneous expression of the virus envelope proteins and EDEM1 caused huge envelope protein degradation, which was blocked through EDEM1 inhibition (Lazar et al. [2012](#page-53-16)). Furthermore, a study revealed that AMPK activation is able to limit the virus production by inducing autophagy, suggesting the therapeutic value of targeting AMPK for HBV management (Xie et al. [2016](#page-62-22)). Collectively, it can be said that the precise relationship between the virus replication and autophagy merits extra studies.

Also, infection with influenza A virus (IAV) is able to induce enhanced levels of autophagosomes that needed for viral replication (Zhou et al. [2009\)](#page-65-12). A study showed that the virus increases the levels of autophagosomes by inhibition of their fusion with lysosomes, and the presence of matrix 2 (M2) ion-channel protein for prohibition of autophagosomes degradation is pivotal (Gannagé et al. [2009\)](#page-50-15). Another research displayed that M2 escapes from autophagy using its LC3-interacting region (Beale et al. [2014](#page-48-19)). M2 interacts with LC3 and induces LC3 re-localization to the plasma membrane, and disruption of this interaction downregulates virion budding and stability. The NS1 is another IVA protein that induces autophagy via overexpression of M2 and hemagglutinin (HA) (Zhirnov and Klenk [2013b](#page-65-13)). Recently, the interplay between M2 protein and MAVS signaling pathway was demonstrated, which leads to MAVS aggregation and, thereby, stimulates MAVS-mediated antiviral innate immunity. Furthermore, it was shown that M2 triggers ROS generation, which is a crucial factor for autophagy activation (Wang et al. [2019f\)](#page-61-18). Additionally, H5N1, a major avian pathogen, has the potential

to induce autophagy via prohibiting mTOR (Ma et al. [2011b](#page-56-0)).

As we mentioned before, Beclin-1 is a fundamental modifier of autophagy process that forms two distinct complexes, one with Atg14 that is needed for autophagosome formation and the other with UVRAG, which is essential for autophagosome maturation (Levine et al. [2015\)](#page-53-3). In a study that was conducted by Qu and his associates, it was demonstrated that infection with SARS-CoV-2 is associated with incomplete autophagy response, which was shown to be needed for effective virus replication. Moreover, the investigators disclosed that although infection with SARS-CoV-2 stimulates autophagosomes formation, the infection contributes to prohibition of autophagosome maturation and block autophagy by inhibiting fundamental genes involved in the virus replication (Qu et al. [2021\)](#page-58-26). They analyzed expression of 26 proteins expressing by the virus and found out that ORF3a expression is associated with incomplete autophagy. The ORF3a interplays with UVRAG to promote and prohibit expression of PI3KC3- C1 (Beclin-1-Vps34-Atg14) and PI3KC3-C2 (Beclin-1-Vps34-UVRAG), respectively. In summary, the authors shed light on how ORF3a inhibits autophagy and, thereby, prompts SARS-CoV-2 replication, which provides a therapeutic potential of targeting autophagy for COVID-19 treatment (Qu et al. [2021](#page-58-26)).

6 Conclusion

Autophagy is known as conserved intracellular process which transfers cytoplasmic materials to lysosomes for degradation though autophagosomes. This process emerges to be relevant to the pathogenesis of various diseases, and its regulation could have therapeutic value. It has been indicated that a sequence of cellular and molecular signaling pathways by several internal and external factors is involved in initiation and progression of autophagy. Viruses are one of main factors which exert their pathogenesis effects via affecting on autophagy processes.

Besides viruses, a wide range of internal factors including genetic and epigenetic factors could influence on underlying pathways involved in autophagy processes. Very recently, microRNAs and exosomes have been emerged as critical players in the autophagy processes, given that exosomes and microRNAs are able to change behavior of host cells via targeting of a large number of cellular and molecular signaling pathways. Hence, more insights into the various signaling pathways that are targeted by exosomes and microRNAs could pave the way to the finding and designing new therapeutic approaches.

Conflicts of Interest The authors have declared that no competing interest exists.

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