REVIEW

The role of autophagy and apoptosis in early brain injury after subarachnoid hemorrhage: an updated review

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Abstract

Subarachnoid hemorrhage (SAH) is a worldwide devastating type of stroke with high mortality and morbidity. Accumulating evidence show early brain injury (EBI) as the leading cause of mortality after SAH. The pathological processes involved in EBI include decreased cerebral blood fow, increased intracranial pressure, vasospasm, and disruption of the blood–brain barrier. In addition, neuroinfammation, oxidative stress, apoptosis, and autophagy have also been proposed to contribute to EBI. Among the various processes involved in EBI, neuronal apoptosis has been proven to be a key factor contributing to the poor prognosis of SAH patients. Meanwhile, as another important catabolic process maintaining the cellular and tissue homeostasis, autophagy has been shown to be neuroprotective after SAH. Studies have shown that enhancing autophagy reduced apoptosis, whereas inhibiting autophagy aggravate neuronal apoptosis after SAH. The physiological substrates and mechanisms of neuronal autophagy and apoptosis by which defects in neuronal function are largely unknown. In this review, we summarize and discuss the role of autophagy and apoptosis after SAH and contribute to further study for investigation of the means to control the balance between them.

Keywords Subarachnoid hemorrhage · Early brain injury · Autophagy · Apoptosis · Caspase

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Introduction

Subarachnoid hemorrhage (SAH), a disease that primarily occurs secondary to aneurysm rupture, afects 1 in 10,000 people annually, and is one of the most severe types of brain hemorrhage [[1,](#page-5-0) [2\]](#page-5-1). Early brain injury (EBI) and delayed cerebral vasospasm are the main contributors impacting the poor outcomes of SAH patients [[3](#page-5-2)]. However, treatments toward ameliorating cerebral vasospasm outcomes after SAH have been underwhelming. Recent studies have shifted focus from cerebral vasospasm to EBI which was frst coined in 2004 to explain the acute pathophysiological event that occurs within the frst 72 h after SAH. EBI accounts for brain injury, and is characterized by elevated intracranial pressure, autoregulation dysfunction, and brain edema within the frst 72 h after SAH.

Autophagy is a cellular defense and survival mechanism under physiological conditions. The autophagy pathway is activated and lasts up to 3 days after SAH [[4\]](#page-5-3). Meanwhile, the activation of the autophagy process has been shown to be neuroprotective [\[5](#page-5-4)]. Apoptosis is the most well-characterized type of programmed cell death. Apoptosis after SAH is one kind of important intracellular pathways, which leads to cell death in EBI [\[6](#page-5-5)]. Compelling evidence indicated that autophagy and apoptosis play important roles in EBI after SAH [[7,](#page-5-6) [8\]](#page-5-7). Autophagy can precede apoptosis, and exerts a protective role in the early stages of programmed cell death [\[9](#page-5-8), [10\]](#page-5-9). However, it can promote apoptosis under some circumstances [\[11\]](#page-5-10).

In this review, we attempt to emphasize autophagy and apoptosis interplay after SAH, and we discuss several molecular and cellular mechanisms that are potential candidates for novel treatment options.

The autophagic process

Autophagy is a programmed cell death pathway in mammalian cells that is essential for elimination of obsolete cellular proteins and damaged organelles to maintain homeostasis [\[12,](#page-5-11) [13](#page-5-12)]. There are three primary types of autophagy process: macroautophagy chaperone-mediated autophagy, and microautophagy [\[14,](#page-5-13) [15\]](#page-5-14).

Macroautophagy is the most demonstrated pathway in SAH and intracerebral hemorrhage [[16](#page-5-15), [17](#page-5-16)]. There are five stages in the macroautophagy process, including initiation, elongation, closure, maturation, fusion, and degradation (Fig. [1\)](#page-1-0). To begin, an isolation membrane called the phagophore engulfs a portion of the cytoplasm, resulting in the formation of a double-membrane known as the autophagosome. After autophagosome formation, the autophagosome will deliver its cargo to the lysosome and the outer autophagosomal and lysosomal membranes will fuse [\[18](#page-5-17)]. Macroautophagy is regulated by evolutionarily conserved autophagy related genes (ATG) in yeast. There are more than 40 ATG genes identifed in yeast. Of which, 15 are known for their core ATG genes. They are involved in both selective and nonselective autophagy [\[19](#page-5-18)]. ATG1-ATG13-ATG17-ATG31-ATG29 assemble into a kinase complex to induce the formation of the autophagosome. In mammalian cells, the UNC-51-like kinase family comprise a complex, which includes ULK1, ATG13, ATG101, and FIP200. It plays a critical role in the induction of autophagy [[20,](#page-5-19) [21](#page-6-0)]. Under nutrient-rich conditions, the serine/threonine kinase mammalian Target of rapamycin (mTOR) associates with the complex and phosphorylates, as well as inactivates ULK1/2 and ATG13. Meanwhile, when cells are starved for nutrients, the mTOR complex 1 dissociates, leading to the dephosphorylation of ULK1/2 and ATG13 and initiation of macroautophagy [\[22](#page-6-1), [23](#page-6-2)].

The apoptotic process

Apoptosis is a programmed cell death process by which a cell ceases to grow and enters a controlled cell death stage without any spillage of its contents into the surrounding environment. There are two main apoptotic pathways: the intrinsic or mitochondrial pathway and the extrinsic or death receptor pathway [\[17](#page-5-16), [24](#page-6-3)] (Fig. [2\)](#page-2-0). The intrinsic pathway, which is mediated by the mitochondrial release of cytochrome c, activates diferent caspases as downstream signals [\[25](#page-6-4), [26\]](#page-6-5). The extrinsic pathway originates from the activation of cell death receptors [\[27,](#page-6-6) [28](#page-6-7)]. Both pathways share the fnal caspase activation step after the activation of diferent intermediate molecules by the signaling cascade, leading to the cleavage of diferent proteins.

The intrinsic pathway involves a series of molecular events occurring entirely within cells. Many stimuli, such as toxins, DNA damage, trophic factor deprivation, ionizing radiation, and other cellular stress, could trigger the intrinsic pathway. As the core of the intrinsic pathway, mitochondria release a number of pro-apoptotic factors into the cytoplasm to induce or regulate the intrinsic apoptosis pathway [\[25,](#page-6-4) [29\]](#page-6-8). Among the pro-apoptotic factors, the most important is cytochrome c. In normal cells, the mature form of cytochrome c is remained in an enclosed space between the

Fig. 1 The autophagic process. Five stages in the macroautophagy process, including initiation, elongation, closure and maturation, fusion, and degradation

inner and outer mitochondrial membranes (IMM and OMM) where it functions to remove electrons from respiratory complex III (BCL complex) to complex IV (cytochrome oxidase) in the electron-transport chain. The release of cytochrome c is positively regulated by pro-apoptotic BCL-2 family members, including BAX (BCL-2 associated X protein), BAK (BCL-2 antagonist killer 1), BID, BIM, and PUMA, and is negatively regulated by anti-apoptotic BCL-2 family members, including BCL-XL, BCL-2, BCL-W, and MCL1. Once they receive the apoptotic signals, the pro-apoptotic BCL-2 family oligomerizes and inserts into the outer mitochondrial membrane, leading to permeabilization of the outer mitochondrial membrane and allowing the redistribution of cytochrome c into the cytoplasm [[30](#page-6-9), [31](#page-6-10)]. Cytochrome c binds to APAF-1 in the cytoplasm and induces oligomerization of APAF1 molecules. This binding induces the conformational change in APAF1, exposing its caspase recruitment domain (CARD domain) and its oligomerization domains, thereby assembling APAF1s and caspase-9 into a complex

known as the apoptosome [[32\]](#page-6-11). Caspase-9 cleaves and activates the downstream efector caspases, such as caspases-3 and -7, which will cleave many protein substrates and cause cell death [[33\]](#page-6-12). The activation of caspase-3 is negatively regulated by the inhibitory apoptosis (IAP) protein family, such as XIAP, c-IAP1, and c-IAP2. Other proteins released from mitochondria, such as apoptosis-inducing factor (AIF) and SAC, also have pro-apoptotic functions [\[34](#page-6-13)].

The extrinsic pathway is also called the death receptor pathway. The pro-apoptotic death receptors include TNFR1, TNFR2, Fas, and TRAIL receptors, DR4 and DR5 [[35\]](#page-6-14). When pro-apoptotic ligands bind to cell surface death receptors, the extrinsic pathway is activated. There is one conserved protein–protein interaction domain, known as the death domain, in the intracellular domains of the proapoptotic death receptors. Upon binding to the ligands, the adaptor protein, FADD (Fas-associated protein with death domain), forms a complex with the initiator 8 or 10, called the DISC (death-inducing signaling complex) [[36\]](#page-6-15). The formation of this complex activates caspase-8, which in turn, cleaves and activates downstream efector caspases-3, -6, and -7, as well as BID cleavage [\[37](#page-6-16)].

The relationship between autophagy and apoptosis

The relationship between autophagy and apoptosis is relatively complex, including the physical and functional interactions between the several proteins (Fig. [3](#page-3-0)). Autophagy and apoptosis are regulated by various transcription factors [\[38\]](#page-6-17). They share some same triggering by different protein kinase cascades. While apoptosis is invariably involved in cell death, autophagy plays dual roles in cell death and survival, depending on the cellular context [\[39](#page-6-18)].

As important regulatory factors in cell apoptosis, an increasing number of studies have revealed the importance of BCL-2 family members in autophagy. As pro-apoptotic proteins, BCL-xl and BCL-2 can bind to the BCL-2 homology (BH) 3 domain of Beclin 1 through their BH3 receptor domain [[40](#page-6-19), [41](#page-6-20)]. The regulation of the BCL-2-Beclin 1 has been demonstrated by the competitive substitution of the Beclin 1 BH3 domain by other BCL-2 family proteins, such as BNIP and BAD, but not by BAK and BAX [[42,](#page-6-21) [43](#page-6-22)]. When the BH3 domain of Beclin 1 or the BH3 receptor domain of BCL-xl is mutated, BCL-xl is unable to inhibit Beclin 1-induced autophagy [\[44](#page-6-23)]. The phosphorylation of BCL-2 blocks its binding to Beclin-1, meaning that phosphorylated BCL-2 loses its ability to inhibit autophagy

[[45\]](#page-6-24). AMPK can dissociate the BCL-2-Beclin 1 complex and promote the formation of the Beclin 1- PI3K complex to enhance autophagy [\[46\]](#page-6-25). Phosphorylation of BCL-2 at multiple sites by c Jun N terminal protein kinase 1 (JNK1) and extracellular signal related kinase (Erk) has been shown to reduce binding of BCL-2 to Beclin, causing the activation of autophagy [\[46–](#page-6-25)[48\]](#page-6-26). There are two cellular resources of BCL-2, the endoplasmic reticulum and the mitochondria, and both can regulate apoptosis and autophagy. Endoplasmic reticulum proteins and nutrient deprivation autophagy factor 1 facilitate the binding of BCL-2 to Beclin at the endoplasmic reticulum to inhibit autophagy, while endoplasmic reticulum localized BH3-only protein and B cell interacting killer (BIK) [[49](#page-6-27)].

There is another regulation between apoptosis and autophagy in spatial separation of proteins to cellular compartments. MCL1, the anti-apoptotic protein, has been proven to regulate autophagy. The degradation is an early event in nutrient deprivation condition and apoptosis induction. Under nutrient deprivation conditions, MCL1 levels regulate activation of autophagy [[50,](#page-6-28) [51](#page-6-29)]. The mammalian target of rapamycin (mTOR) kinase plays an important role in the interplay between apoptosis and autophagy as well. The deletion of Raptor, a positive regulator of mTOR, promotes both apoptosis and autophagy by activating caspase-3, leading to abnormal mitochondria [\[52](#page-6-30), [53\]](#page-6-31). Under hypoxic conditions, the mTOR pathway is inhibited by BNIP3, which directly binds to and inactivates Rheb. Therefore, mTOR induces a positive relationship of apoptosis and autophagy in a caspase-dependent manner [[54,](#page-6-32) [55](#page-6-33)]. The death-associated

Fig. 3 The relationship between autophagy and apoptosis. The physical and functional interactions between autophagy and apoptosis

protein kinase (DAPK) is a calcium/calmodulin-regulated Ser/Thr kinase that mediates cell death induced by diverse death signals. DAPK has also been proven to be related to cellular autophagy and apoptosis [\[56](#page-6-34)]. DAPK is activated in ER stress conditions to trigger a mixed reaction of cellular autophagy and apoptosis [[57](#page-6-35)]. In times of ER stress, DAPK integrates signals from apoptotic and autophagic pathways to induce cell death [\[58\]](#page-6-36). As a classic ligand that participates in activation of the extrinsic apoptotic pathway, TRAIL promotes an autophagic program while activating caspasemediated apoptosis during the process of lumen formation in human mammary epithelial cells [[59\]](#page-6-37). Moreover, TRAIL induces FADD, which in turn activates cellular apoptosis and autophagy. TRAIL supports the positive relationship between apoptosis and autophagy [\[60](#page-6-38)].

Reactive oxygen species (ROS) are classifed as a heterogeneous group of molecules naturally generated in cellular metabolism of diatomic oxygen [[61](#page-7-0)]. The relationship between ROS and autophagy represents an adjusted negative feedback mechanism by which autophagy eliminates the source of oxidative stress and protects the cells from oxidative damage [[62\]](#page-7-1). ROS induces cellular autophagy, whereas autophagy reduces the levels of ROS as it consumes the major source of ROS, damaged mitochondria. Many factors, including hypoxia, TNF-α, starvation, and nerve growth factor deprivation, simultaneously trigger both autophagic fux and an increase in intracellular ROS [[63,](#page-7-2) [64](#page-7-3)]. Several environmental endocrine-disruptors can increase oxidative stress and ROS production, which can ultimately lead to the activation of cell death processes, such as apoptosis. Several apoptotic efectors, including caspases, BCL-2, and cytochrome c, are signifcantly regulated by cellular ROS [[65,](#page-7-4) [66](#page-7-5)]. Licarin A induces autophagy and apoptosis in non-small cell lung cancer cells by ROS. Furthermore, upregulation of autophagy by mTOR-dependent pathways appears to be cytoprotective in preventing CYT997-induced excessively high levels of ROS [\[67](#page-7-6)].

To sum, autophagy and apoptosis are connected by several molecules in order to keep the coordinate regulation in survival and death.

The roles of autophagy and apoptosis interplay in SAH

The pathophysiological mechanism of SAH is complicated and remains incompletely understood. SAH causes a sudden increase in intracranial pressure, which causes a decrease in blood perfusion pressure. The following events, such as acute hydrocephalus, platelet aggregation, microvascular alterations, reperfusion injury, and acute vasospasm, may contribute to EBI after SAH [\[68](#page-7-7)[–70](#page-7-8)]. Cellular apoptosis may be seen in endothelium, cortical, subcortical, or hippocampal neurons after SAH [\[71](#page-7-9)[–73\]](#page-7-10). The mechanisms, that initiate apoptosis after SAH, include global ischemia, decreased cerebral perfusion pressure, microcirculatory disturbance, transient global ischemia, and blood toxicity [[68](#page-7-7)[–70](#page-7-8)]. There are several apoptotic pathways that are believed to be important in relation to SAH. First, the death receptor pathway: SAH can activate many death receptors including Fas, P2X7R, TNF receptor, and death receptor 4/5, leading to the activation of caspase-3, and thus activating apoptosis [[74,](#page-7-11) [75](#page-7-12)]. Second, the mitochondrial pathway: after SAH, mitochondrial matrix releases cytochrome c, which binds with APAF-1 and pro-caspase-9 to form the apoptosome [[76](#page-7-13)]. The Cytochrome c-procaspase-9-APAF-1 complex further activates downstream efector molecules to trigger apoptosis. Third, the p53 pathway in response to SAH: p53 regulates the apoptotic cascade [\[77](#page-7-14)–[79\]](#page-7-15). Last, the caspaseindependent pathway: after SAH, p53 regulates the release of apoptosis-inducing factor in the absence of APAF-1, and then activates the caspase-independent pathway [\[30](#page-6-9)]. Inhibition of apoptosis has been proven to have a neuroprotective efect after SAH, and has become a key target in preventing and treating EBI after SAH.

After SAH, the levels of the autophagy marker proteins, such as Beclin-1 and LC3, were significantly increased in the ipsilateral region and persisted for 3 days. It was shown that autophagy activity peaks at 24 h after SAH. However, the role of autophagy remains controversial. After SAH, autophagic activation is accompanied by inhibition of apoptosis and improvement of EBI [\[80](#page-7-16), [81](#page-7-17)]. Study has reported gradually increased levels of autophagy-related proteins, such as Beclin-1 and LC3- II, over 24 h after SAH. The expression of Beclin-1 and LC3- II in the basilar artery wall is upregulated during the first 48 h after SAH [\[82](#page-7-18), [83](#page-7-19)]. Lee et al. found out that Beclin-1, LC3- II, and cathepsin-d gradually increased within 24 h after SAH induction, but decreased at 72 h. Beclin-1 and cathepsin-d are expressed in neurons, but not in astrocytes [\[84\]](#page-7-20).

Shao et al. reported that 3-MA inhibition of class III PI3K activity and autophagy activation resulted in increased cell apoptosis after SAH [[85,](#page-7-21) [86\]](#page-7-22). In contrast, treatment with RAP, inducing autophagy by inhibiting mTOR, signifcantly reduced apoptosis in the EBI phase [\[87](#page-7-23), [88](#page-7-24)]. To investigate the interaction or balance between autophagy and apoptosis after SAH at the histological level, dual immunofuorescence staining was performed with apoptotic marker, cleaved caspase-3, and autophagy marker, p62 to show that resveratrol could upregulate autophagy while inhibiting apoptosis after SAH in rats [[87\]](#page-7-23). Sun et al. found that after SAH, caspase-3 expression was concentrated closely around the injured core, whereas Beclin 1 expression could only be observed at a small distance from the blood clot area, but not at the injured core [[89](#page-7-25)]. They also found that cells were either stained with caspase-3 or with Beclin 1, but not both. This led to

the observation of a "confrontation line" between caspase-3-positive cells and Beclin 1-positive cells, suggesting that when a cell expressed a large amount of autophagy-initiating protein, Beclin 1, it would not enter late phase apoptosis [\[90\]](#page-7-26). In conclusion, autophagy and apoptosis might be two opposing processes for individual cells after SAH. In addition, administration of osteopontin improved neurobehavioral dysfunction, enhanced autophagy while inhibiting apoptosis, and regulated autophagy-apoptosis interaction [\[91,](#page-7-27) [92\]](#page-7-28).

Conclusion

Autophagy exerts critical roles in maintaining intracellular homeostasis within the brain in the setting of SAH. Proper functioning of autophagic mechanisms has a pro-survival efect and reduces apoptotic cell death after SAH. However, if SAH exceeds a certain stress threshold, autophagic mechanisms lead to increased apoptotic cell death. Therefore, regulation of the autophagic and apoptotic interplay processes in the setting of SAH will likely lead to a benefcial efect that will allow us to develop effective therapeutic strategies for SAH patients.

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Declarations

Conflict of interest The authors declare no confict of interest, fnancial or otherwise.

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