

Mitophagy in Hypertension-Associated Premature Vascular Aging

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Hypertension has been described as a condition of premature vascular aging, relative to actual chronological age. In fact, many factors that contribute to the deterioration of vascular function as we age are accelerated and exacerbated in hypertension. Nonetheless, the precise mechanisms that underlie the aged phenotype of arteries from hypertensive patients and animals remain elusive. Classically, the aged phenotype is the buildup of cellular debris and dysfunctional organelles. One means by which this can occur is insufficient degradation and cellular recycling. Mitophagy is the selective catabolism of damaged mitochondria. Mitochondria are organelles that contribute importantly to the determination of cellular age via their

production of reactive oxygen species (ROS; Harman's free radical theory of aging). Therefore, the accumulation of dysfunctional and ROS-producing mitochondria could contribute to the acceleration of vascular age in hypertension. This review will address and critically evaluate the current literature on mitophagy in vascular physiology and hypertension.

Keywords: blood pressure; hypertension; mitophagy; premature vascular aging

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While the increased incidence of cardiovascular events as we age is generally attributable to the natural decline in organ function, in hypertension, dysfunction is premature in its onset and particularly pronounced. As a result, hypertension has been classified as a condition of premature aging.¹ In particular, arteries from hypertensive patients and animals present a range of phenotypes including, hypercontractility, stiffening and remodeling, inflammation, oxidative stress, and cellular senescence which are all relatively early in their onset compared with age-matched normotensive controls.² Clinically, vascular age determination, as opposed to chronological age *per se*, has now been introduced into guidelines for cardiovascular disease prevention.³ Nonetheless, a critical barrier to our progress in reducing the morbidity and mortality of hypertensive patients is our lack of understanding of the mechanisms that cause arteries to prematurely age.

The aged phenotype is classically viewed as the accumulation of cellular debris and dysfunctional organelles. Normally, endogenous cellular recycling mechanisms function to repair or clear damaged macromolecules. The two major pathways by which eukaryotic cells perform degradation and cellular recycling are autophagy and the ubiquitin–proteasome system.⁴ While both systems function to eliminate cellular debris and dysfunctional organelles, there are mechanistic differences between the two proteolytic pathways.

For example, the proteasome system functions primarily to degrade single proteins, while autophagy specializes in the degradation of larger cellular materials indiscriminately (e.g., protein aggregates, organelles, and pathogens).⁴ However, if either one of these systems is dysregulated, cellular debris can accumulate and confer the classical “aged” phenotype. Given that several recent publications have revealed that autophagy is downregulated in the vasculature of old animals,^{5–8} new and exciting questions have emerged regarding the connection between impaired autophagic mechanisms and premature vascular aging observed in hypertension.⁹ Therefore, the broad focus of the following review is on the emerging role of autophagy in the etiology of premature vascular aging in hypertension, with a particular emphasis on the organelle-specific autophagic mechanism, mitophagy.

AUTOPHAGY AND VASCULAR AGING

Autophagy is the evolutionarily conserved catabolic process essential for maintaining homeostasis via the removal of cellular debris and dysfunction organelles, to provide micro- and macronutrients during times of stress (e.g., prolonged fasting or extreme exercise), and to initiate cell death pathways (e.g., apoptosis or necrosis). Broadly, autophagy can be classified by three unique subclasses: microautophagy,

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chaperone-mediated autophagy, and macroautophagy, and it can be further refined based on the constituents being degraded.¹⁰ These classes have been shown to include different initiation markers, materials being catabolized, and the cell type in which the degradation occurs.¹⁰ Microautophagy involves the lysosomal membrane folding inwards to directly internalize cytosolic constituents to be degraded.¹¹ In contrast, the chaperone-mediated autophagy mechanism includes the chaperone protein heat shock cognate 71 kDa protein (Hsc70), a member of the heat shock protein 70 family. Hsc70, along with cochaperones, can recognize and unfurl substrate proteins containing the KFERQ amino acid sequence.¹² After unfolding, substrates adhere to lysosome-associated membrane protein-2 isoform A (Lamp-2A) and are subsequently translocated across the lysosomal membrane for hydrolysis.¹² Perhaps the most described type of autophagy is macroautophagy, which is evolutionarily conserved from single-cell organisms to whole animals. Macroautophagy is further divided into bulk autophagy or selective autophagy, each with different initiating conditions.¹³ For example, starvation of the cell and a lack of vital nutrients initiates bulk autophagy; whereas selective autophagy occurs to clear damaged, dysfunctional, or otherwise extraneous organelles, including mitochondria. Macroautophagy commences when an isolation membrane termed the phagophore engulfs a portion of the cytosol or an entire organelle. This subsequently forms a double membrane structure termed an autophagosome and the autophagosome then merges with the lysosome to form an autolysosome. The autolysosome is the structure within which the hydrolytic degradation of the contents of the autophagosome occurs, completing the macroautophagy mechanism.¹¹ Uniquely, mitochondria are removed by a special form of macroautophagy called mitophagy, which will be discussed more below.

Autophagy has long been associated with longevity for multiple, compelling reasons,¹⁴ including the lengthening of lifespan,¹⁵ and it has been well established that induction of autophagy reduces the “aged” vascular phenotype.^{16,17} Currently, our understanding of how autophagy exerts a beneficial effect on the vasculature centered on the premise that reduced autophagy leads to the accumulation of damaged cellular debris and dysfunctional organelles. If undegraded, this buildup results in a proinflammatory/prooxidative milieu that promotes the generation of vasoconstricting factors,⁹ quenching of nitric oxide bioavailability,^{6,7} and uncoupling of endothelial nitric oxide synthase.¹⁸ Therefore, upregulation or reconstitution of autophagy decreases these vascular dysfunctions.

MITOPHAGY IN PHYSIOLOGY

Mitophagy is the selective elimination of dysfunctional, damaged, or superfluous mitochondria, requiring the two major degradation systems: autophagy and the ubiquitin–proteasome system, working separately or in concert.¹⁹ It has been well established that disruptions to mitophagy contribute to disease, including age-associated pathologies.²⁰ Therefore, it is tempting to rationalize that

decreased mitophagy, resulting in oxidative stress and inflammation from residual and dysfunctional mitochondria, may be a novel mechanism of premature vascular aging in hypertension (Figure 1). We briefly introduce some of the normal molecular pathways of mitophagy to provide context for which dysfunctional mitophagy may promote pathophysiology.

Phosphatase and tensin homolog-induced putative protein kinase 1 (PINK1) is a nuclear encoded, mitochondrial targeted serine/threonine-protein kinase. PINK1 is involved in mitochondrial quality control by identifying dysfunctional mitochondria and targeting these mitochondria for degradation. Healthy mitochondria maintain a membrane potential that can be used to import PINK1 via the translocase of the outer membrane and translocase of the inner membrane complexes at the outer and inner mitochondrial membrane, respectively. The mitochondrial targeting sequence is then cleaved off by the mitochondrial processing peptidase located in the matrix. Subsequently, the inner mitochondrial membrane protease presenilin-associated rhomboid-like protease (PARL) cleaves PINK1. The resulting peptide is then retrotranslocated to the cytosol, where it is subjected to constitutive degradation via the proteasome through the N-end rule pathway²¹ (Figure 2a).

On the other hand, in severely damaged mitochondria that lack sufficient membrane potential, PINK1 accumulates on the outer membrane. As a result, PINK1 interacts with the translocase of the outer membrane complex, dimerizes, and PINK1 kinase activity becomes activated through autophosphorylation.²¹ PINK1 phosphorylates ubiquitin, which triggers recruitment of Parkin to the outer mitochondrial membrane and activation of its E3 ligase activity. At the same time, phosphoubiquitin recruits autophagy receptors to initiate autophagosome formation. Parkin acts as an enhancer of this signaling through further ubiquitination of mitochondrial proteins²² (Figure 2a). This mitochondrial ubiquitination acts as the autophagic signal and adaptor proteins, such as adaptor p62/SQSTM1 via its ubiquitin-binding domain, recognizes and initiates autophagosome formation.²³ If all components are functional, the PINK1–Parkin-mediated mitophagic pathway is the major mechanism by which damaged mitochondria are marked for degradation and cleared from cells before causing deleterious downstream effects.

Another major pathway by which mitochondria are cleared after being damaged is Parkin-independent mitophagy.²⁴ In contrast to PINK1–Parkin-mediated mitophagy, which requires the translocation of Parkin to the damaged mitochondria followed by recruitment of autophagic receptors, there exist several light chain 3 (LC3)-interacting region containing autophagic receptors (e.g., FUN14 domain-containing protein 1 (FUNDC1), BCL2-interacting protein 3 (BNIP3), and NIP3-like protein X (NIX)) that are constitutively expressed on the outer membrane of mitochondria and can bind to microtubule-associated protein 1A/1B LC3 proteins anchored in the membrane of the phagophore. As a result, the autophagosome engulfs the mitochondria for degradation and recycling²⁴ (Figure 2b). Interestingly, it has been proposed that basal mitophagy

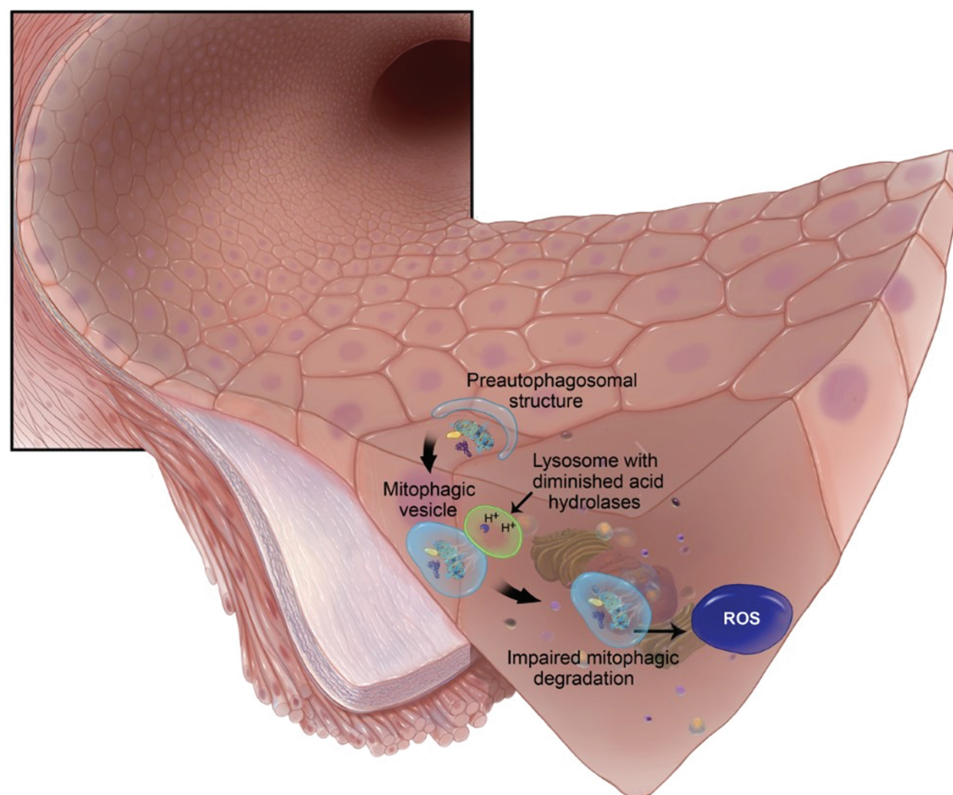


Figure 1. Impaired mitophagic degradation of damaged mitochondria leads to oxidative stress. In endothelial cells this prooxidative milieu promotes the release of contractile factors, quenches nitric oxide bioavailability, and uncouples endothelial nitric oxide synthase (eNOS). Abbreviation: ROS, reactive oxygen species.

occurs in a Parkin-independent manner within tissues of high metabolic demand, including the vasculature.²⁵

DYSFUNCTIONAL MITOPHAGY AND HYPERTENSION

It is clear that dysfunction in the mitophagy process can cause the accumulation of dysfunctional mitochondria that can contribute to a diverse range of pathologies. However, much of the breadth of pathophysiological research on mitophagy pertains to (age-related) neurodegenerative diseases.^{20,26} Conditions, such as Huntington's disease, Parkinson's disease, and Charcot-Marie-Tooth 2A, have been linked to altered, damaged, or absent mitophagy mechanisms, usually due to genetic mutations. For example, deleterious mutations in Parkin and PINK1 are linked with familial forms of Parkinson's disease.²⁷ Additional pathologies that are linked to dysfunctional mitophagy include cancers,²⁸ lysosomal storage disorders (e.g., Pompe disease),²⁹ Duchenne muscular dystrophy,³⁰ and innate immune defense.³¹

Although mitophagy has been measured *in vivo* in several different hypertensive models including, spontaneously hypertensive rats,³² Goldblatt two-kidney, one-clip (2K1C) hypertension,³³ unilateral renal artery stenosis,³⁴ and *in vitro* after cellular exposure to hypertensive stimuli (e.g., elevated angiotensin II,^{35–39} a high fat diet,⁴⁰ reactive oxygen species (ROS),⁴¹ pressure overload,^{42,43} ischemia,^{44,45} oxidized low-density lipoprotein,⁴⁶ and high glucose and free fatty

acids^{47,48}), our understanding of mitophagy in hypertension is still nascent. Indeed most of this literature has focused on cardiomyocytes,^{32,34,37–40,42–45} and only a few studies have investigated mitophagy in response to prohypertensive factors in arteries,⁴⁹ vascular smooth muscle cells,^{35,46} or endothelial cells^{36,44,47,48} (Table 1). Moreover, the direction of change in mitophagy activity varies between these studies, and this may be model-, stressor-, or tissue-dependent (e.g., in the heart, inhibition of mitophagy ameliorates pressure overload induced heart failure⁴³ and conversely, mitophagic activity is protective against angiotensin II-induced cardiac injury³⁸) (Figure 3). Therefore, it is still premature to conclude whether mitophagy is in fact a cause or an effect of hypertension, as no one has directly manipulated mitophagy status in hypertensive animals *in vivo*.

It has also been well established that mitochondrial dynamics (fusion, fission, and biogenesis) regulates mitophagy status. It is widely considered that mitochondrial fission precedes and facilitates mitophagy by dividing elongated mitochondria into a manageable size for autophagosome encapsulation,⁵⁰ while fusion protect elongated mitochondria from mitophagy.⁵¹ In relation to hypertension, it has been reported that prohypertensive stimuli such as elevated levels of aldosterone,⁵² ROS,⁵³ angiotensin II,⁵⁴ dietary salt,⁵⁵ and calcium⁵⁶ can mediate mitochondrial fission, and inhibition of fission is cardioprotective.^{57,58} Interestingly, acute inhibition of mitochondrial fission in vascular smooth muscle cells can antagonize contractile

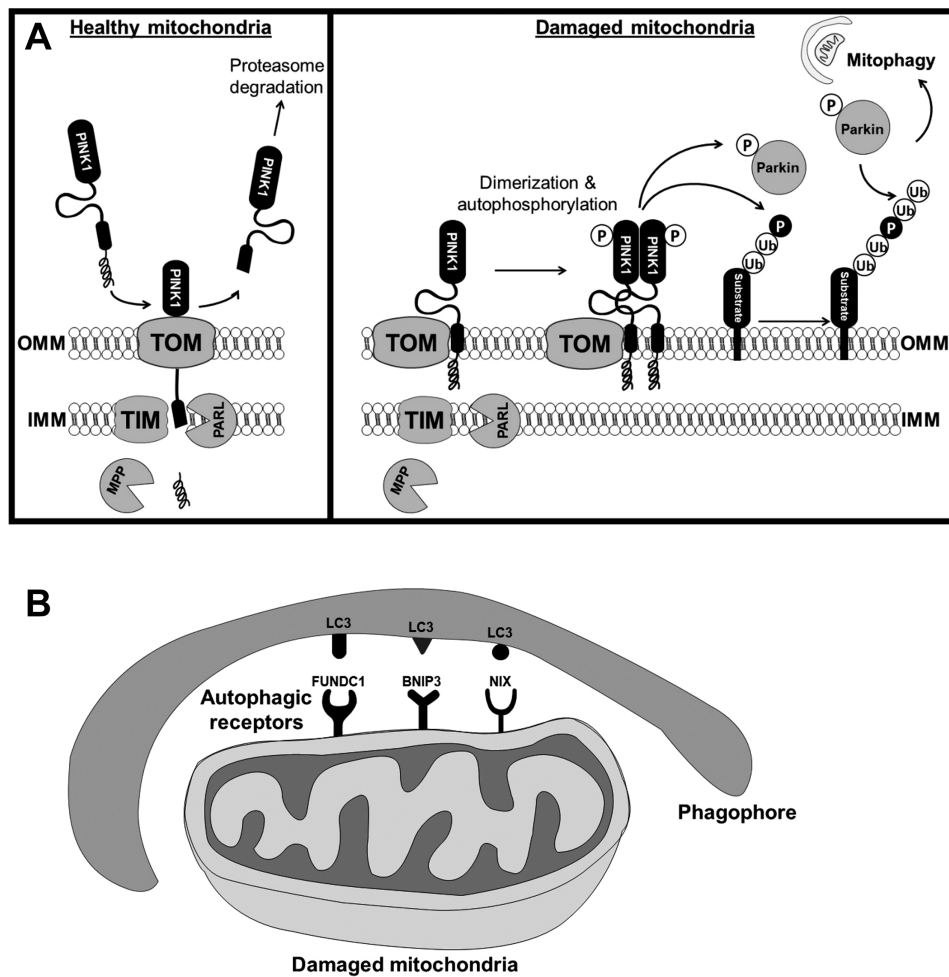


Figure 2. Mitophagy signaling pathways. (a) Parkin dependent mitophagy: healthy mitochondria import PINK1 via the translocase of the outer membrane (TOM) and translocase of the inner membrane (TIM) complexes. The mitochondrial targeting sequence is then cleaved off by the mitochondrial processing peptidase (MPP) and the inner mitochondrial membrane protease presenilin-associated rhomboid-like protease (PARL) cleaves PINK1. The resulting peptide is then retrotranslocated to the cytosol, where it is subjected to degradation via the proteasome. However, when mitochondria are damaged, PINK1 accumulates at the outer mitochondrial membrane bound to the TOM complex. As a result, PINK1 dimerizes and is activated by autophosphorylation. PINK1 subsequently phosphorylates Parkin and ubiquitin chains, resulting in Parkin activation and relocation to the mitochondria where it further ubiquitinates mitochondrial substrates and signals the removal of the damaged organelle. (b) Parkin-independent mitophagy: microtubule-associated protein 1A/1B light chain 3 (LC3) proteins anchored in the membrane of the phagophore can bind to LC3-interacting region (LIR) containing autophagic receptors (e.g., FUNDC1, BNIP3, and NIX) that are constitutively expressed on the outer membrane of mitochondria. Subsequently, the autophagosome can engulf the damaged mitochondria for degradation.

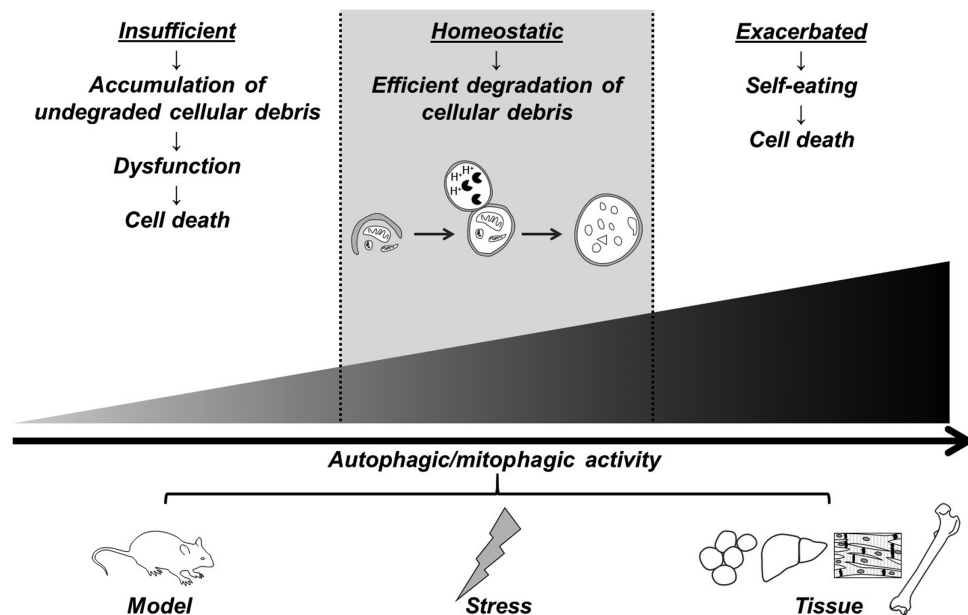
responses, and vasoconstriction stimuli induce mitochondrial fission.⁵⁹ Moreover, hyperhomocysteinemia increased mitochondrial fission, causing endothelial cell damage, and collagen deposition in the mesenteric arteries.⁴⁹ Nonetheless, the cause-and-effect relationship between mitochondrial dynamics and mitophagy is difficult to discern because fission is not only essential for the removal of damaged mitochondria, it can facilitate cell death during high levels of stress, and it can also stimulate creation of *de novo* mitochondria.⁶⁰

Given the importance of mitophagy in maintaining cellular homeostasis and its participation in a number of pathophysiological conditions, there are numerous clinical and experimental drugs that have shown efficacy at activating and inhibiting mitophagy (Table 2).

These drugs include classical autophagy activators such as mammalian target of rapamycin inhibitors (e.g., rapamycin), inositol monophosphatase inhibitors (e.g., carbamazepine), and epigenetic mediators (e.g., spermidine) and classical autophagy inhibitors such as lysosomal alkalizers (e.g., chloroquine) and phosphatidylinositol 3-kinase inhibitors (e.g., 3-methyladenine). Table 2 also contains a number of novel mitophagy drugs. These drugs offer the opportunity to therapeutically manipulate the mitophagy pathway a number of different ways and depending on the conditions. However, caution needs to be observed when proposing the use of these drugs as mediators and modulators of mitophagy (and autophagy), as these drugs have a number of known and unknown pleiotropic effects.

Table 1. Investigations that have reported changes in mitophagy in vascular cells, including the model (or stressor to induce mitophagy) and the direction of mitophagy change (increased or decreased)

Model	Tissue/cell type	Mitophagy status	Reference
Angiotensin II	Endothelial cells	↓	36
	Vascular smooth muscle cells	↓	35
Glucose and palmitate	Endothelial cells	↓	48
Ischemia	Endothelial cells	↓	44
Oxidized low-density lipoprotein	Vascular smooth muscle cells	↑	46
Palmitic acid	Endothelial cells	↑	47

**Figure 3.** Autophagy and mitophagy activity spans a continuum, where too much or too little is detrimental to homeostasis and health. Differences between studies indicate that increases or decreases in activity are model-, stressor-, or tissue-dependent. We hypothesize that decreases in mitophagy confer an aged phenotype in the vasculature of hypertensive patients and animals.

HARMAN'S FREE RADICAL THEORY OF AGING: A POTENTIAL LINK BETWEEN MITOPHAGY AND VASCULAR AGE

First described over 60 years ago, one of the most prominent theories on aging is Harman's free radical theory of aging. This theory postulated that decreased cellular longevity is caused by increased ROS.^{92,93} ROS are highly reactive and short lived due to their unpaired valence shell electron. While ROS occur as a consequence of normal cellular metabolism, when ROS formation overwhelms antioxidant defenses, it is defined as oxidative stress. Oxidative stress can cause damage to cellular constituents (e.g., lipids, proteins, and nucleic acids), and has been suggested to lead to a variety of pathophysiological conditions. Hence, an ideal balance between ROS production and antioxidant defense is paramount for maintenance of physiological homeostasis. Harman's theory held that these nonspecific, essentially irreversible oxidative reactions with cellular macromolecules over time are likely involved in the chronological aging process, and conversely, the longevity of an organism can be

increased by slowing the incidence of ROS.^{92,93} Progressively, the understanding of ROS reactions has evolved and extended Harman's initial theory^{94,95}; however, the basis of the senescence-promoting nature of ROS, remains consistent.

More recent work has implicated the role of mitochondria as a primary target of ROS-mediated damage.⁹⁶ It is well known that mitochondria are a major source of intracellular ROS as a natural byproduct of mitochondrial respiration and energy production. Exacerbated ROS production causes damage to certain macromolecules, most notably mitochondrial DNA, which can then induce an amplification and further buildup of ROS within cells.⁹⁶ Recently, it was confirmed that vascular mitochondrial respiratory capacity significantly deteriorates with advancing age as a result of declining mitochondrial content.⁹⁷ Despite this decline, aging also resulted in greater mitochondrial-derived ROS.⁹⁷ These findings are a direct application of Harman's theory to the aging vasculature and support the idea that increasing the degradation of damaged mitochondria can prevent age-related vascular dysfunction.⁸ Nonetheless, if decreased mitophagy is also involved in exacerbated mitochondrial

Table 2. Clinical and experimental drugs that that shown efficacy at activating and inhibiting autophagy and mitophagy, including the putative mechanism of active, and mitophagy-specific reference

Drug	Putative autophagic action	Reference
Autophagy/mitophagy activators		
AICAR	AMPK-dependent inhibition of mTOR	61
Betulinic acid	AKT-mTOR inhibitor	62
BEZ235	mTOR inhibitor	63
Carbamazepine	IMPase inhibitor and mTOR-independent activator	64
3-Carboxyl proxyl nitroside	AMPK-dependent inhibition of mTOR	65
CCI-779	mTOR inhibitor	66
Ceramide	(i) AKT-mTOR inhibitor	67
	(ii) Dissociation of the Beclin 1:Bcl-2 complex	
Lithium chloride	IMPase inhibitor and mTOR-independent activator	68
Metformin	AMPK-dependent inhibition of mTOR	69
MDL-28170	Inhibition of calpains I and II and subsequent cleavage of autophagic machinery	70
Mitochondrial toxins	ROS-induced translocation of Parkin to mitochondria	71,72
Mito-metformin	AMPK-dependent inhibition of mTOR	65
Nicotinamide derivatives	SIRT1 activators	73
Olanzapine	(i) ROS-induction of FoxO transcription factor	74
	(ii) AMPK-dependent inhibition of mTOR	
p62-mediated mitophagy inducer (PMI)	Parkin-dependent and -independent mitophagy	75
Phenanthroline	Mitochondrial fission	76
Rapamycin	mTOR inhibitor	77
RAD001	mTOR inhibitor	63
Resveratrol	NAD ⁺ -dependent deacetylase and mTOR-independent activator	78
Rilmenidine	mTOR inhibitor	79
Selenite	Superoxide-induced mitochondrial damage	80,81
Spermidine	Acetyltransferase inhibitor and mTOR-independent activator	82
Trehalose	mTOR-independent activator	83
Urolithin A	(i) Mitochondrial fission	84
	(ii) AMPK-dependent inhibition of mTOR	
Autophagy/mitophagy inhibitors		
Acid protease inhibitors	Lysosomal alkalisers	85
Ammonium chloride	Lysosomal alkalisers	86
Antioxidants (butylated hydroxyanisole, <i>N</i> -acetylcysteine)	(i) Protection of mitochondrial from ROS-mediated damage	87
	(ii) Inhibition of the MPTP	
Bafilomycin A1	Vacuolar-type H ⁺ -ATPase inhibitor	88
Brefeldin A	Inhibitor of intracellular protein transport and alternative (Atg5/Atg7-independent) autophagy	89
Chloroquine	Lysosomal alkalisers	88
Cyclosporine A	Inhibition of the MPTP	85,87
Idebenone	(i) Protection of mitochondrial from ROS-mediated damage	90
	(ii) Inhibition of the MPTP	
Liensinine diperchlorate	Inhibition of autophagosome-lysosome fusion	91
LY294002	Class III PI3K inhibitor	85
3-Methyladenine	Class III PI3K inhibitor	77,85
Mitochondrial division inhibitor 1 (Mdivi-1)	Inhibition of mitochondrial fission	43
Wortmannin	Nonspecific PI3K inhibitor	85

Abbreviations: AKT, protein kinase B; AMPK, 5'AMP-activated protein kinase; Atg, autophagy-related gene; Bcl-2, B-cell lymphoma 2; IMPase, inositol monophosphatase; MPTP, mitochondrial permeability transition pore; mTOR, mammalian target of rapamycin; PI3K, phosphatidylinositol 3-kinase; ROS, reactive oxygen species; SIRT, sirtuin.

ROS production in the vasculature of hypertensive patients or animals is yet to be determined.

Mitophagy is the selective catabolic process for removing damaged mitochondrial. Insufficient mitophagy would lead to the accumulation of dysfunctional mitochondria. Given that mitochondria are a prominent source of intracellular ROS in all cell types, including cells of the vasculature, and our knowledge of Harman's free radical theory of aging,^{92,93} we hypothesize that diminished mitophagy in the vasculature contributes to oxidative stress and the vascular aging phenotype associated with hypertension. This hypothesis is supported by studies which showed an upregulation of autophagy and mitophagy reversed several phenotypes of vascular aging in old mice⁶⁻⁸ and premature vascular aging in spontaneously hypertensive rats.⁹

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DISCLOSURE

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