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**Review**


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# Autophagy in aging and in neurodegenerative disorders

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## ABSTRACT

**Autophagy (ATG) is the process of bulk degradation and recycling of long-lived proteins, macromolecular aggregates, and damaged intracellular organelles. Cellular homeostasis requires continuous removal of worn-out components and replacement with newly synthesized ones.** Studies in yeast and other mammalian systems have increased our knowledge of the molecular mechanism of autophagy and the role of autophagy in various pathological conditions. Discovery of the genes involved in the process of autophagy has provided insight into the involvement of various molecular pathways. **Growing evidence has indicated that diminished autophagic activity may play a pivotal role in the aging process.** Cellular aging is characterized by a progressive accumulation of nonfunctional cellular components owing to oxidative damage and a decline in turnover rate and housekeeping mechanisms. Lysosomes are key organelles in the aging process due to their involvement in both macroautophagy and other housekeeping mechanisms. Autophagosomes themselves have limited degrading capacity and rely on fusion with lysosomes. Accumulation of defective mitochondria also appears to be critical in the progression of aging. Inefficient removal of nonfunctional mitochondria by lysosomes constitutes a major issue in the aging process. **Autophagy has been associated with a growing number of pathological conditions, including cancer, myopathies, and neurodegenerative disorders.** In this review, we discuss the cellular and molecular mechanisms involved in autophagy, the mechanisms of aging, and the possible role of autophagy in this process. **Understanding the mechanisms by which autophagy impacts aging may provide useful molecular targets for pharmaceuticals designed to delay aging or correct conditions of premature aging.**

**Key words:** Aging, Alzheimer's disease, Autophagy, Lifespan, Lipofuscin, Lysosomes, Mitochondria, Neurodegenerative diseases, Neuronal aging, ROS

## INTRODUCTION

Homeostasis in living cells requires continuous removal of damaged and worn-out components and

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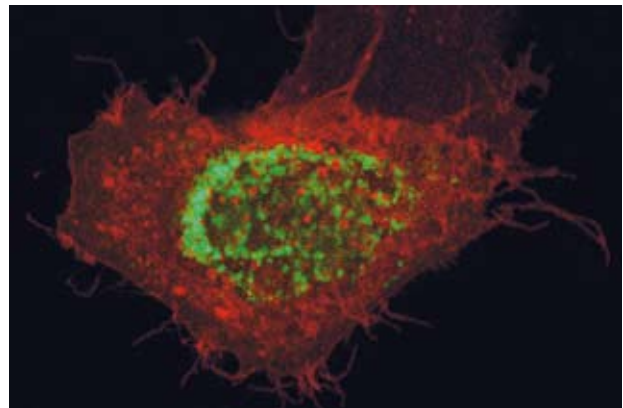
replacement by newly synthesized ones.<sup>1</sup> Turnover of all cellular components is accomplished by different degradative and synthetic pathways, which are usually complementary to each other. Different types of proteolytic systems are present in the intracellular environment that replace or repair the damaged proteins.<sup>2</sup> These systems ensure that sufficient amounts of protein exist for the proper functioning of cells. Short-lived nuclear and cytoplasmic proteins

are degraded by multicatalytic proteinase complexes (proteasomes)<sup>3</sup> and by calcium-dependent neutral proteases (calpains).<sup>4</sup> More than 90% of cellular proteins are long-lived. Turnover of most long-lived proteins, macromolecules, biological membranes, and whole organelles, including mitochondria, ribosomes, endoplasmic reticulum, and peroxisomes, is mediated by autophagy.<sup>5</sup> Unlike the proteasome, autophagy not only degrades proteins but can also eliminate unwanted, damaged, or redundant cell organelles or structures. Mitochondria can autonomously turn over certain defective proteins, because they possess their own proteolytic systems.<sup>6,7</sup> Therefore, the autophagic machinery can mediate major intracellular housekeeping tasks.

Autophagy (derived from the Greek meaning “to eat oneself”) is present in all eukaryotic cells and is evolutionarily conserved from yeast to humans.<sup>8</sup> Bulk proteins and organelles are degraded by autophagy and the degradation products are recycled for the synthesis of new molecules.<sup>9</sup> In the process of autophagy, defective and worn-out structures are sequestered into double-membrane vesicles, which are called autophagosomes. These structures are transported to and fuse with lysosomes (forming the autophagolysosome) for proteolytic degradation. The process of autophagy begins with cargo selection. After selection, the material to be degraded is engulfed in the double-membrane vesicles. Microtubule-associated protein Light Chain 3 (LC3) is recruited on the surface of the double-membrane vesicles, which subsequently surround proteins and organelles that are to be degraded. For that reason, LC3 is widely used as a marker for visualizing autophagosomes.<sup>10</sup> Autophagosome-lysosome fusion is a multi-step process. The autophagolysosomes are very short-lived structures and no reliable markers exist to visualize them (Figure 1). After being transported into the vicinity of lysosomes, the outer membrane of the autophagosome fuses with the lysosomal limiting membrane. The contents of the autophagosome are released into the lysosomal cavity, where degradation takes place by the action of hydrolytic enzymes, which is facilitated by the acidic lysosomal environment.<sup>11</sup>

### Forms of autophagy

Eukaryotic cells are equipped with several deg-



**Figure 1.** Autophagosomes and lysosomes. LC3 (green), a marker of mature autophagosomes, is not localized on CD63 (red) labeled organelles. CD63 primarily resides on lysosomes and plasma membrane. As yet, no reliable markers exist to monitor the transition to autophagolysosomes.

radation systems, the predominant system being the process of autophagy. Autophagy is responsible for the degradation of whole organisms and structures (bacteria, viruses), whole organelles, as well as long-lived soluble proteins.<sup>12,13</sup> Three forms of autophagic processes are currently known: classic autophagy (also called macroautophagy to distinguish it from other processes), chaperone-mediated autophagy, and microautophagy.<sup>14</sup>

Classic autophagy is an inducible form of autophagy that becomes activated under stress conditions (nutrient starvation, infections, and toxins).<sup>15</sup> Most eukaryotic cells are equipped with another form of autophagy, known as Chaperone-Mediated Autophagy (CMA).<sup>16</sup>

CMA is selective for a particular group of soluble cytosolic proteins that contain a specific sequence signature. Unlike autophagy, CMA does not require intermediate vesicle formation.<sup>17</sup> Once the specific signature sequence is identified, these soluble proteins are directly translocated to the lysosomal membrane. The specific signature sequence, which is present in all CMA substrates, is biochemically related to the pentapeptide KFERQ.<sup>18</sup> All substrates with this sequence are then targeted to lysosomes. The cytosolic molecular chaperone heat shock protein 70 (hsp70) and its co-chaperones recognize the signature motif in substrate proteins.<sup>19</sup> The substrate/chaperone complex is then targeted to the lysosomal membrane, where it

binds to a receptor protein, the Lysosome-Associated Membrane Protein type 2a (LAMP-2a).<sup>20</sup> A second chaperone, lysosomal hsc73 (lys-hsc70), is required for complete translocation of the substrate protein/hsc70 complex into the lysosomal matrix, where it is completely degraded by lysosomal proteases.<sup>21</sup>

The third form of autophagy is microautophagy.<sup>14</sup> The characteristic feature of the microautophagy process is that the lysosomal membrane itself either invaginates or exvaginates to engulf an organelle. Unlike macroautophagy, there is no sequestering double-membrane formed in the cytoplasm.<sup>22</sup> Pexophagy<sup>23</sup> and Mitophagy<sup>24</sup> involve the selective sequestration or engulfment of peroxisomes and mitochondria, respectively, and their delivery to lysosomes.

There is one more pathway, found in the yeast *S. Cerevisiae*, which is closely related to the process of autophagy, called cytoplasm-to-vacuole targeting (Cvt) pathway.<sup>25</sup> The major function of this pathway, which plays a pivotal role in the biosynthetic and physiological role of yeast cells, is to deliver the enzymes aminopeptidase I and alpha-mannosidase to the yeast vacuole.<sup>26</sup> Several genes that are involved in the Cvt pathway are also involved in the classic autophagy pathway.<sup>27</sup>

### ***The autophagy process***

The stages involved in the process of autophagy have not as yet been precisely delineated, especially for mammalian cells. Studies in the yeast *S. Cerevisiae* have provided insight into the mechanisms involved and, based on these studies, the following steps of ATG are largely accepted.<sup>28</sup>

#### ***Induction and cargo selection***

Autophagy may be either a selective or nonselective process.<sup>29</sup> In *S. Cerevisiae*, Cvt is a transport mechanism involved in the recognition and packaging of cargo and is considered a selective process. However, this pathway is limited only to yeast; it is not present in any other organism.<sup>30</sup> At present, autophagy is viewed as a nonselective process, where cytoplasmic structures and organelles are randomly enwrapped into double-membraned structures.<sup>31</sup> Nonetheless, the possible presence of a mechanism like Cvt in mammalian cells cannot be excluded. At the molecular level (Figure 2), the serine/threonine protein kinase

TOR (Target Of Rapamycin) is involved in the induction of autophagy.<sup>31</sup> Activated TOR (phosphorylated form) is part of the induction complex and acts as a negative regulator of autophagy.<sup>32</sup> Phosphorylated Tor negatively controls autophagy, primarily by acting on the signaling cascade that controls general translation and transcription. In addition, activated Tor induces hyperphosphorylation of Atg13, which lowers its binding affinity to other Atg interacting proteins, thereby inhibiting autophagy.<sup>33</sup>

#### ***Vesicle nucleation***

The initial formation of an autophagosomal membrane takes place by enwrapping the degradative cargo within a double membrane, which eventually elongates to form a vesicle called an autophagosome. The exact origin of autophagosomal membranes is controversial. Studies in mammalian cells have suggested that autophagosomal membranes originate from the ribosome-free region of the rough endoplasmic reticulum.<sup>34</sup> Alternatively, a poorly-characterized organelle, called a phagophore, has also been suggested as the origin of autophagosomes and other vesicular structures.<sup>35</sup> In yeast, a unique perivacuolar structure, called PAS (preautophagosomal structure), has been proposed as the precursor of autophagosomes due to the transient association of several Atg proteins with it.<sup>36</sup> A PAS-like structure has not yet been identified in any other endomembrane system.<sup>37</sup>

#### ***Vesicle expansion and retrieval***

Vesicles will elongate and extremities will fuse to complete the double-membraned structure. Phagophores elongate and completely encircle the cargo to form an 'autophagosome' or 'autophagic vacuole'.<sup>12</sup> Most of the proteins involved in vesicle expansion and maturation steps are retrieved to the original pool because they do not associate with the complete and mature autophagosome.<sup>8,12,14</sup> Therefore, it has been suggested that the proteins involved in autophagosome formation are retrieved for future use. Atg8 (LC3) is the exception; it is found on the mature autophagosome and can be used as a valuable marker to track these structures<sup>38</sup> (Figure 1).

#### ***Vesicle targeting, docking, and fusion with lysosomes***

The next critical step is transport and fusion of the

autophagosome with the lysosomes. The outer membrane of the autophagosome completely fuses with the outer membrane of the lysosome to make a path for the inner membrane bound autophagic vacuole. The inner membrane and its enclosed cytoplasmic contents, which together are called an 'autophagic body', are released into the lumen of the lysosome. The machinery required for the process of vesicle fusion includes SNARE proteins and the class C Vps/HOPS complex.<sup>13</sup>

#### *Vesicle breakdown and recycling*

The ultimate step in the autophagic process is degradation of the autophagic body content by lysosomal enzymes, which ensures recycling of essential cytoplasmic contents.

#### ***Molecular machinery involved in autophagy***

Various extracellular and intracellular stimuli can induce and modulate autophagy, including nutrient regulation, cell proliferation, cell size regulation, differentiation, apoptosis, hormone or therapeutic treatment, accumulation of misfolded proteins and damaged organelles, and invasion of microorganisms. Discovery of the *ATG* genes in yeast has greatly advanced our understanding of the molecular mechanisms involved in autophagosome biogenesis and the various pathways that regulate autophagic activity.<sup>39</sup> Most yeast *ATG* genes have mammalian homologues, which suggests that the basic machinery for autophagy has been evolutionarily conserved in eukaryotic organisms. These genes, also called APG/AUT/CVT, were initially identified from studies that investigated defects in the formation of autophagic vacuoles and protein degradation in *S. Cerevisiae*.<sup>40,41</sup> In these studies, knockout strains of individual *ATG* genes showed defects of starvation-induced autophagy. It is now widely accepted that at least 28 yeast genes are actively involved in autophagy. More than 50 additional yeast genes may be required for autophagy, which also play key roles in other pathways.<sup>42</sup> The precise cellular and biochemical function of these genes in the autophagic pathway remains to be elucidated.

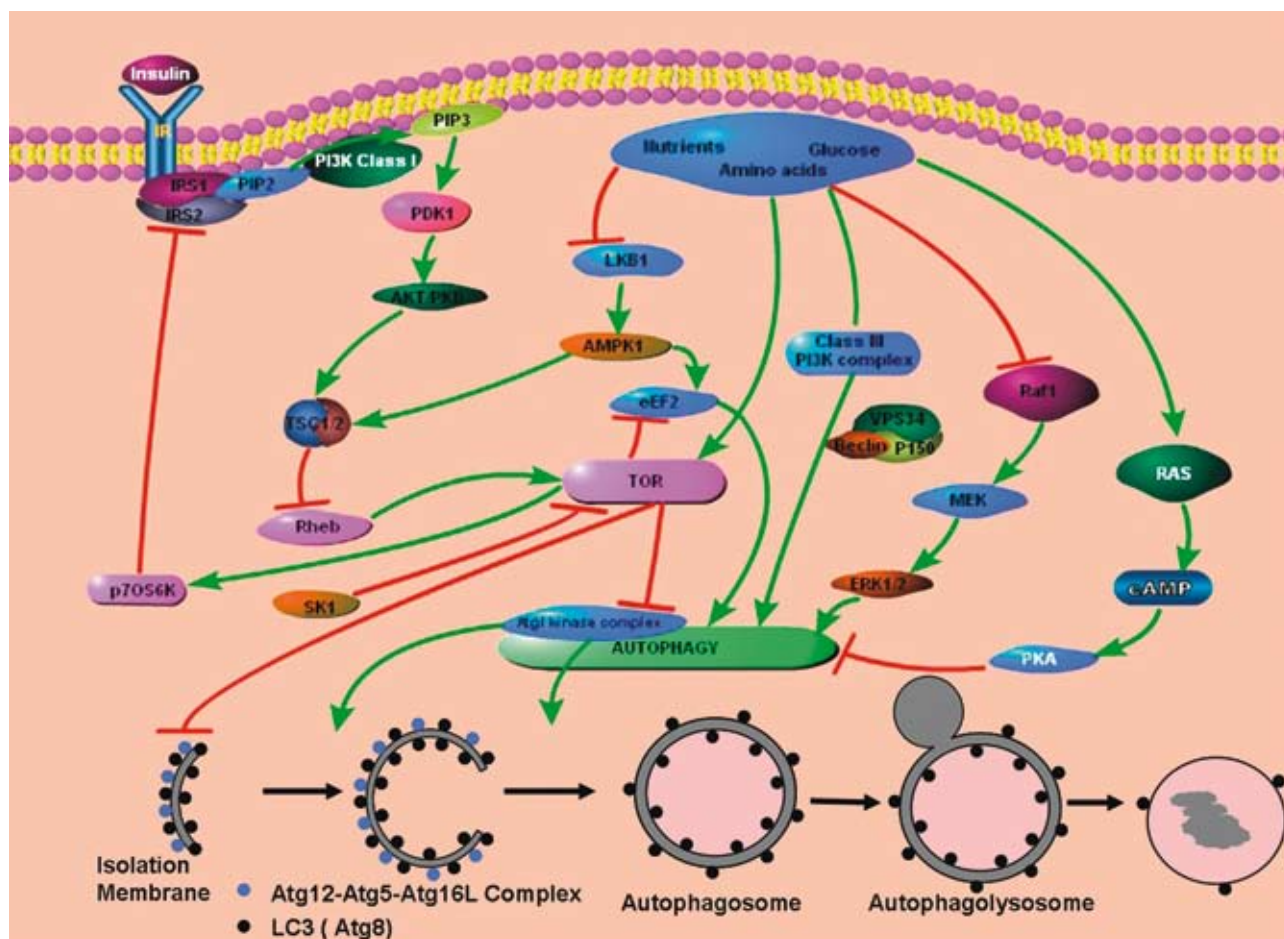
Regulation of autophagosome biogenesis, maturation, and fusion with lysosomes is a complicated process, a number of diverse signaling complexes and pathways being involved (Figure 2). Many signaling

pathways, including Tor or mammalian Target Of Rapamycin (mTOR), Phosphatidylinositol 3-Kinase-I (PI3K-I)/PKB, Class III PI3K, Akt-PTEN-TSC1/2-Rheb-mTOR circuit, the Insulin Receptor and downstream targets, GTPases, calcium, and protein synthesis all play important roles in regulating autophagy.<sup>43</sup> In general, Class I PI3K, Akt, Rheb and mTOR components inhibit autophagy, while Class III PI3K, PTEN and TSC1 and 2 positively regulate autophagy. Cross-talk between these regulatory pathways mediates the response of cells to various challenges that affect autophagy.<sup>44</sup>

The Tor signaling pathway, the Atg1 complex, and the Vps34/class III PI3K complex are critical in initiating an autophagic response. TOR is a classic serine/threonine kinase. Nutrient starvation or treatment of yeast cells with rapamycin (a specific inhibitor of TOR) rapidly induces an increase in autophagosome biogenesis and autophagic activity.<sup>45</sup> Inhibition of Tor results in dephosphorylation of Tap,<sup>42</sup> causing its dissociation from PP2A. PP2A becomes activated, causing dephosphorylation of downstream targets, which leads to a variety of anti-proliferative responses and induction of autophagy. In mammalian cells, mTOR appears to modulate autophagy in a manner similar to that observed in yeast. Likewise, the activity of the mammalian PP2A orthologue is strongly correlated to induction of autophagy.<sup>46</sup> Recently, association of protein kinase A components with mTOR in regulation of autophagy has been observed. Depletion of the type IA regulatory subunit (RIalpha) of Protein Kinase A (PKA) in mammalian cells and tissues activates mTOR and causes autophagic deficiency.<sup>47</sup> Further, it has been shown that mTOR and the regulatory subunit of protein kinase A (PRKAR1A) spatially and functionally interact during autophagosome maturation.<sup>48</sup> However, the response of mammalian cells to rapamycin is more diverse; certain cell types respond but others do not.

A second autophagy signaling complex includes Atg1, a protein kinase involved in both yeast Cvt and autophagic pathways, Atg11, and Atg13.<sup>49</sup> Under nutrient-rich conditions, Tor activation causes hyperphosphorylation of Atg13 that prevents its association with Atg1, which subsequently enables interaction of Atg1 with Atg11; this may determine the use of the





**Figure 2. Pathways Regulating Autophagy:** TOR (Target Of Rapamycin) is at the center of the diverse pathways linked to autophagy. The PI3K signaling pathway has been extensively characterized and involves the class I and class II PI3Ks. The class I PI3K kinases link autophagy to cancer through the AKT/PKB pathway. The class II PI3K pathway, which is mediated by beclin1, also plays an important role in regulation. MAPKinase pathway is also involved in regulation of autophagy through Raf-1 and Ras.

autophagic machinery in the Cvt pathway. Under **nutrient** starvation or treatment with rapamycin, Atg13 becomes partially dephosphorylated, leading to an Atg1-Atg13 interaction, which subsequently triggers autophagy and generation of autophagosomes instead of Cvt vesicles. In mammalian cells, GATE-16 (Golgi associated ATPase enhancer of 16 kDa) and GABARAP ( $\gamma$ -aminobutyric acid type A receptor-associated protein)<sup>50</sup> were found to interact with the ULK1 kinase. Since GATE-16, GABARAP, and MAP-LC3 (microtubule-associated protein light chain 3) are putative orthologues of yeast Atg8a (essential for autophagosome formation), it has been postulated that ULK1 may be the mammalian orthologue of Atg1.<sup>51</sup>

The third major autophagy signaling pathway involves the Vps34/class III Phosphatidylinositol 3-Kinase (PI3K) complex. The observation that 3-methyladenine (PI3K inhibitor) inhibits autophagy was the first evidence that implicated this family of kinases in the process.<sup>52</sup> In addition, other PI3K inhibitors, such as wortmannin and LY294002, have also been found to inhibit autophagy. In yeast, Vps34 is primarily involved in vacuolar protein targeting, through the endosomal/prevacuolar compartment, to form a complex with Vps15-Vps38-Atg6.<sup>53</sup> At the same time, Vps34 has been found to associate with Vps15-Atg6-Atg14 on pre-autophagosomal membranes. However, the mechanism by which Vps34 affects autophagosome formation is largely unknown.

In mammalian cells, there are three classes of PI3Ks. So far, only Class I and Class III PI3K have been implicated in autophagy, primarily in the early steps of autophagosome formation.<sup>54</sup> Class III PI3K has been found to associate with beclin-1 and p150, which are the orthologues of yeast Atg6 and Vps15, respectively. Class III PI3K regulates diverse molecular pathways, including several involved in tumor formation. The first autophagy-related tumor suppressor gene reported was *Beclin-1*, the mammalian orthologue of yeast Atg6, which showed a relationship between autophagy and cancer.<sup>55</sup>

### **Aging**

Aging is an essential, inevitable physiological phenomenon characterized by the accumulation of deleterious changes in cells and tissues during the post-maturational deterioration, which decreases the ability to survive and increases risk of death.<sup>56</sup> Aging changes are the result of predetermined genetic factors, environmental influences, and certain diseases. Aging is grossly characterized by an accumulation of worn-out organelles and various cellular substructures over time. These progressive accumulations reduce cellular efficiency in various biological processes that are required to maintain homeostasis and survival. Malfunctions in the biological processes required for the maintenance, repair, and turnover pathways may be the main cause of the cumulative cellular damages during aging.<sup>57</sup> The balance between synthetic and catalytic pathways controls the turnover rate of cellular components, which in turn depends on the physiological condition of the cells.

A general consensus on the fundamental mechanism of aging exists. During the lifespan of an organism, cells are subjected to various destructive forces, which may originate from either internal or external sources. The result of continuous exposure to these harmful forces is progressive accumulation of lesions. Over time, these lesions become detrimental to cell and tissue survival. The precise molecular mechanism of aging is not yet completely understood, but the elements that are responsible for oxidative damage and improper housekeeping are considered the main contributory causes. These two factors are considered to play pivotal roles in cell survival.<sup>58</sup>

We cannot point out a single factor responsible

for the process of aging, due to the complexity of the whole process. For proper functioning, adaptation, and survival in harsh environments, various cells have to function in unity. These types of cells have diverse kinds of machinery which accomplish their assigned functions and several pathways are involved. Aging is thus seen to be a complex, interwoven, multi-factorial process that depends on the cross-talk between different cells and different molecular pathways within the cells. Several theories of the aging process have been proposed, the fundamental concept behind these theories being the build-up of “damage” that occurs throughout the entire lifespan of cells. Such damage may accumulate from toxic byproducts of routine metabolism or inefficient repair/defensive systems. It is apparent that in long-lived cells, such as neurons or cardiomyocytes, accumulation of lesions can be more detrimental. In proliferating cells, lesions rarely accumulate with age while the process of cell division seems to efficiently remove damaged structures.<sup>59</sup>

Current theories of aging cannot in themselves completely explain the entire process; however, each one of them can partially contribute to the overall understanding of the phenomenon. Notwithstanding that these various theories cannot as yet be clearly demarcated, they have been categorized as evolutionary, molecular, cellular, and systematic.<sup>60</sup>

### **Theories of aging**

First proposed in 1956,<sup>61</sup> the “oxidative damage” theory of aging postulates that an accumulation of oxidized macromolecules causes a progressive functional deterioration of cells, tissues, and organ systems, which subsequently may lead to cell death. Reactive Oxygen Species (ROS) are generated in the normal oxygen metabolism of cells. If not neutralized or eliminated, these harmful free radicals may cause deleterious effects, such as DNA-strand breaks, DNA-protein cross-linking, protein fragmentation, and lipid oxidation, which in turn results in formation of hydroperoxides, alkyl radicals, and aldehydes. Normally, cells have their own protective mechanisms (superoxide dismutase, catalase, glutathione peroxidase, vitamin E) whose function is to reduce the formation of free radicals. However, total elimination cannot be accomplished. Basically, the oxidative damage theory proposes that

ROS formation is inherent in biological systems and causes cumulative damage and senescence.<sup>62</sup>

The oxidative damage theory can be further categorized based on the individual role of certain organelles in the aging process. The mitochondrial theory of aging proposes that it is the accumulation of damage to mitochondria and mitochondrial DNA (mtDNA) that leads to aging in humans and animals.<sup>63,73,74</sup> Mitochondria, the powerhouse of cells, produce the energy (in form of ATP) required for all cellular functions. During the process of energy production, mitochondria also produce superoxide ions, hydrogen peroxide, hydroxyl radicals, and iron-centered free radicals.<sup>64</sup> These free radicals, as well as ROS, produced inside the mitochondria via the Electron Transfer Chain (ETC), make them prone to damages, both at the level of protein and mtDNA. In addition, mtDNA has properties that make it susceptible to deleterious mutations. mtDNA lacks introns and has no efficient DNA repair mechanisms. These characteristics increase the possibility that random mutations cannot be repaired and that they are more deleterious.<sup>65</sup> Another phenomenon frequently observed in aging cells is the accumulation of mitochondria with mutated DNA. Often, complete replacement of normal mitochondria with mutated mitochondria is observed (homoplasmy).<sup>66</sup> It has been proposed that mutated mtDNA may have a replicative advantage over normal mtDNA; consequently, there will be increased replication (clonal expansion) of defective mitochondria.<sup>65</sup> Occurrence of homoplasmic mtDNA mutations in normal intestinal epithelial,<sup>67</sup> as well as in neoplastic cells,<sup>68</sup> provides support for this concept. Development of premature aging in different organs of homozygous mtDNA polymerase gamma knockout mice provides further support for the role of mitochondrial damage in aging.<sup>69</sup>

Despite the presence of various protective proteases (membrane-bound AAA<sup>6</sup> and matrix Lon-proteases<sup>7</sup>), mitochondria are unable to effectively degrade damaged proteins. During aging, the change in morphology and function of mitochondria is remarkable. Mitochondria become excessively enlarged (in this form usually referred to as giant mitochondria) and exhibit complete loss of cristae and destruction of inner and outer membranes. These altered mitochondria cannot perform ETC or respiratory chain func-

tions, a phenomenon which results in the formation of amorphous electron-dense material.<sup>70</sup> Autophagy is the protective mechanism used by cells to remove damaged mitochondria and mutated mtDNA.<sup>71</sup> In younger organisms, most defective mitochondria are removed by autophagy. As mitochondrial damage progressively increases with age, the accumulation of defective and enlarged mitochondria becomes more prominent. Recent experiments have indicated that small mitochondria are degraded more efficiently by autophagy than larger ones.<sup>70</sup> The decline in autophagic activity with age plus the inability to efficiently remove large mitochondria provide an explanation for the apparent accumulation of giant mitochondria in postmitotic aging cells.<sup>72</sup>

Significant changes have been observed in peroxisomes during aging and it has been hypothesized that peroxisomes may be involved in the process of aging.<sup>75</sup> Increased generation of peroxisomal ROS and alterations in fatty acid oxidation activity are the two major observations that implicate peroxisomes in the aging process. Changes in fatty acid oxidation may lead to altered membrane lipid composition. Several investigators have suggested the essentiality of various membranes in maintaining intracellular homeostasis and that deterioration of membrane integrity is the underlying cause of the aging process.<sup>76</sup> Many age-related membrane alterations have been reported, including lipid peroxidation,<sup>77</sup> as well as accumulation of the lipid dolichol, which can greatly impair transmembrane signaling.<sup>78</sup> Interestingly, the degree of dolichol accumulation in the liver of growing rats is highly correlated with levels of autophagic activity (both macroautophagy and pexophagy) in the same organ.<sup>79</sup>

The glycation/cross-linking hypothesis of aging is based on observations that our proteins, DNA, and other structural molecules develop cross-links to one another with age.<sup>80</sup> The main way cross-linking occurs is through a process called glycation. Posttranslationally processed proteins contain sugar moieties. These glycated molecules can be reduced through a complex series of reactions (Maillard reaction) to yield a multitude of end-products known as Advanced Glycation End-products (AGEs). When both of the sticky ends of AGEs adhere to neighboring proteins, they form permanent, disabling cross-links. Damaged proteins

are normally broken down by proteases; however, in the presence of cross-linkages, proteases are inhibited and, as a result, damaged proteins accumulate.<sup>81</sup>

Several studies have strongly suggested involvement of glycation/cross-linking in aging. Cross-linking of collagen has been shown to be at least partially responsible for some age-related changes in skin.<sup>82</sup> Cross-linking of proteins in the lenses of the eyes plays a significant role in age-related cataract formation.<sup>83</sup> Cross-linking of proteins in arterial walls may account for at least some forms of atherosclerosis, like diabetic angiopathy<sup>84</sup> as well as age-related decline in kidney function. Recent evidence has also indicated that glycation contributes to the formation of beta-amyloid, the protein that clumps together in the brains of Alzheimer's patients.

## LYSOSOMAL FUNCTION DURING AGING

Lysosomes are the major organelles responsible for proteolytic degradation and recycling. The term lysosome derives from the Greek words lysis (dissolution or destruction) and soma (body). After the discovery of lysosomes by the Belgian cytologist Christian de Duve in 1959,<sup>85</sup> lysosomes have been described as the cellular demolition crew or garbage disposal system. They are frequently nicknamed "suicide-bags" or "suicide-sacs" by cell biologists due to their role in autolysis. The main function of these microscopic organelles is the digestion of macromolecules derived from phagocytosis, endocytosis, and autophagy (Figure 2). As mentioned earlier, autophagy is a catabolic process that eliminates aggregates of aberrant proteins, superfluous or damaged organelles, and sometimes even entire organisms such as invading bacteria. Although autophagosomes possess some hydrolytic activity, this activity is insufficient to complete proteolytic degradation. Thus, fusion of autophagosomes with lysosomes can be viewed as the Achilles' heel in the process of autophagy.

There are various pathways by which lysosomes receive the extracellular and intracellular material that is to be degraded.<sup>86</sup> Endocytosis can internalize extracellular proteins, as well as integral membrane proteins, and sequester them in endosomes. Subsequently, these endosomes fuse with lysosomes and deliver the cargo. Crinophagy is the process by which

secretory proteins are delivered to lysosomes by fusion with secretory vesicles. Autophagy is the bulk degradation of cytoplasm and organelles by promoting the transfer of material from one, topologically distinct compartment, to another—from the cytosol to the vacuole in yeast, or to lysosomes in eukaryotic cells. Chaperone-Mediated Autophagy (CMA) is a more selective degradation process of autophagy in which a specific sequence in the target substrate protein is recognized by cytoplasmic molecular chaperones. Subsequently, the substrate-chaperone complex is delivered to lysosome for degradation.

The activity of lysosomes is pivotal in aging cells. Age-related decline in overall proteolytic activity has been observed in almost all organisms that have been studied, and specific age-related defects in the different proteolytic systems have been reported.<sup>87</sup> Reduced proteolysis with aging is most evident for long-lived proteins, some of which are known substrates for lysosomal pathways of degradation. Non-lysosomal proteolytic pathways either show very little change (ubiquitin-proteasome pathway)<sup>88</sup> or increase (calpains)<sup>89</sup> with age. Therefore, the lysosomal pathway has become the focus of investigations in pursuit of likely explanations for reduced proteolysis with age.

Age-related alterations in the lysosomal system are clearly noticeable in the form of a pigmented product (lipofuscin) that accumulates in lysosome-related vesicles as a result of incomplete digestion of engulfed components. The lysosomal compartment is rich in iron molecules. Diffusion of cytoplasmically produced peroxides into the lysosome could result in Fenton-type reactions and hydroxyl radical production, which in turn can lead to peroxidation of the lysosomal protein content and formation of lipofuscin. Lipofuscin is a yellowish-brown, autofluorescent, non-degradable polymeric substance.<sup>90</sup> Accumulation of lipofuscin reduces the degradative capacity of lysosomes,<sup>91</sup> which in turn results in further accumulation of waste material inside the lysosome. The rate of lipofuscin formation is inversely related to age, and lysosomes filled with lipofuscin have a reduced ability to fuse with autophagic structures.<sup>92</sup> The molecular basis of the age-related decline in different autophagic pathways is the subject of intense investigation.<sup>8</sup>



As mentioned earlier, lipofuscin is non-degradable and cells cannot get rid of it.<sup>93</sup> However, actively dividing and growing cells can partially eliminate lipofuscin by diluting the pigment in each mitotic cycle. Post-mitotic cells do not have this capability. It has previously been observed that while accumulation of lipofuscin in postmitotic cells of short-lived animals is very rapid, in long-lived animals it is very slow.<sup>94</sup> This finding suggests a relationship between lipofuscin accumulation, function of the lysosomal compartment, and cell survival. It is also worth mentioning that mitochondria of long-lived animals tend to produce significantly less superoxide and hydrogen peroxide than short-lived ones.<sup>95</sup>

The presence of undigested materials in lysosomes could be responsible for their impaired ability to fuse and/or degrade the autophagosome contents. A decrease in the lysosomal levels of the CMA receptor (LAMP-2A) is the primary defect responsible for the diminished CMA activity during aging.<sup>92</sup> Normal CMA activity is initially maintained (during middle age) by increasing the amount of luminal chaperone. At advanced ages, the levels of the receptor are so low that compensation by the chaperone is no longer possible.<sup>96</sup> The reasons behind the decline in receptor numbers are not known and are currently under investigation.

### **Role of autophagy in diseases**

Several human diseases are associated with decreased autophagic activity, particularly in nondividing cells of the nervous and muscle systems where turnover of intracellular proteins may be critical. Muscular disorders, known as vacuolar myopathies, are associated with massive accumulation of imperfect autophagic or lysosomal vacuoles.<sup>97</sup> Danon disease is characterized by cardiomyopathy and mild mental retardation and is caused by a deficiency in LAMP-2, the transmembrane protein involved in endosomal and lysosomal fusion during the late maturation phase of the autophagosome.<sup>98</sup> Accumulation of aberrant autophagosomes has also been associated with X-linked myopathy (X-MEA),<sup>99</sup> inclusion body myositis,<sup>100</sup> and Marinesco-Sjögren syndrome.<sup>101</sup>

Reduced autophagic activity is also associated with neurodegenerative disorders, such as Parkinson's (PD),<sup>102</sup> Alzheimer's (AD),<sup>103</sup> Huntington's (HD),<sup>104</sup>

and transmissible spongiform encephalopathy (prion disease).<sup>105</sup> Altered activity of proteolytic systems and the occurrence of intracellular protein aggregates (inclusion bodies) are characteristic of these neurodegenerative diseases. The protein that accumulates in PD is mutated  $\alpha$ -synuclein,<sup>106</sup> in HD the protein is an abnormally expanded form of huntingtin,<sup>107</sup> and in AD, protein deposits of overproduced  $\beta$ -amyloid precursors. Reduced autophagy has also been associated with chronic liver disease and hepatocellular carcinoma due to retention of mutant alpha (1)-Anti-Trypsin Z (ATZ) protein in the ER and mitochondria of hepatocytes.<sup>108</sup> One could hypothesize that perturbations at any stage of autophagosome biogenesis, maturation, or fusion with lysosomes would result in progressive accumulation of these aggregates and lead to disease progression.

In addition to the classic aging disorders and those of premature aging, autophagy has also been implicated in pathogenesis of infectious diseases. In general, autophagy functions as a protective mechanism against infections. Most foreign invaders (bacteria, parasites, viruses) must actually bypass the autophagic line of defense before they can establish infections. In certain cases, some microorganisms have developed strategies to manipulate the autophagic machinery to their own advantage. After escaping the endophagocytic pathway and preventing fusion with lysosomes, the bacterium *Brucella abortus* shelters and replicates itself in autophagosome-like vesicles.<sup>109</sup> *Legionella pneumophila* secretes a product that activates autophagy and allows it to replicate itself directly inside autolysosomes.<sup>110</sup> Likewise, a virulence protein, ICP34.5, in the *Herpes simplex* virus antagonizes the autophagic pathway and allows the virus to escape degradation.<sup>111</sup> Recent immunological studies have also indicated the importance of autophagy in antigen presentation and successful cellular defense. It can be speculated that the decline in autophagic activity with age may contribute to the apparent increased risk of infectious disease in the elderly.

Since autophagic elimination of aggregated proteins and damaged organelles preserves cells from further damage, autophagy could serve a protective role. Enhancement of autophagic activity in aging organisms can have preventive or therapeutic potential. Caloric restriction-induced autophagy has a

well-documented effect in extending life expectancy, at least in lower eukaryotic organisms and some laboratory mammals.<sup>112</sup> The mTOR inhibitor and autophagy promoter, rapamycin, has shown promising anticancer activity in clinical trials.<sup>113</sup> Bacterial and viral proteins that modify autophagosome formation could also be harnessed to modulate this degradative pathway for therapeutic purposes.

## AUTOPHAGY AND NEURONAL AGING

Autophagy has primarily been implicated in various neurodegenerative disorders because of the apparent accumulation of aberrant structures and macromolecules in neuronal cells. Since neurons have very limited capabilities for cell replication and renewal, one would anticipate that any perturbations in autophagic activity would first affect the neuronal tissues. Autophagy dysfunction is emerging as a theme in neurodegenerative diseases in which mis-aggregated proteins accumulate. It has long been puzzling why protein aggregation and neurotoxicity develop so late in life, even in familial forms of diseases where the mutant protein is present throughout life. It now seems likely that declining efficiency of protein turnover is partly responsible. Both macroautophagy and CMA slow considerably during normal aging, contributing directly in the declining of tissue performance.<sup>87</sup> Genetic ablation of autophagy in mice has recently been shown to induce neurodegeneration and accumulations of ubiquitinated proteins.<sup>114</sup> Moreover, some gene mutations that cause neurodegenerative diseases directly impair the proteolytic systems responsible for degrading the mutant protein.

### *I) Parkinson's disease*

Parkinson Disease (PD) is characterized by progressive death of dopaminergic neurons in the substantia nigra. Accumulation of  $\alpha$ -synuclein, a cytosolic protein with synaptic functions, takes place within intracellular inclusion bodies called Lewy bodies. The presence of Lewy bodies is a hallmark feature of this disorder. Neuronal cell death in PD is more complex. In addition to the accumulation of aberrant autophagosome-like structures, there is apoptosis and necrosis.<sup>115</sup> CMA is considered the rate-limiting degradative mechanism in neuronal cells, but both macroautophagy and proteasome pathways might

be involved in  $\alpha$ -synuclein turnover.<sup>114,115</sup> In cases of familial PD, mutant  $\alpha$ -Synuclein cannot efficiently enter lysosomes because of abnormally high affinity to lysosomal receptor LAMP-2A. Due to high binding affinity for the receptor, the substrate to be degraded cannot be translocated properly. The high affinity of mutant  $\alpha$ -synuclein to LAMP-2A also blocks uptake of other CMA substrates and thereby prevents their degradation.<sup>5,117</sup> Impaired CMA is usually accompanied by accumulation of abnormal autophagic vacuoles and subsequent cell death. It has been hypothesized that when macroautophagy is induced to compensate for the CMA defect, impaired autophagosome-lysosome fusion and incomplete lysosome acidification occur.<sup>116</sup>

### *II) Alzheimer's disease*

Alzheimer's Disease (AD) is characterized mainly by gradual neuronal loss and progressive dementia. The observed cell damage is associated with intraneuronal fibrillary tangles and extracellular senile plaques. In addition to the well-documented lysosomal dysfunction in AD,<sup>119</sup> significant alteration in autophagic activity has recently been indicated.<sup>118</sup> The hallmark feature of AD pathology is the presence of enormously swollen 'dystrophic' neuritis in which autophagic vacuoles progressively accumulate and become the predominant organelle.<sup>118</sup> In normal brain cells, autophagosomes are usually found in low numbers. However, in a large number of brain cells from AD patients, autophagosomes are very prominent. This probably indicates activation of autophagy but with impaired maturation and/or impaired autophagosome-lysosome fusion,<sup>120</sup> which eventually leads to apoptosis. A key pathogenic factor in AD is generation of Amyloid- $\beta$  peptide ( $A\beta$ ) by the activity of autophagosome hydrolases.<sup>119</sup>  $A\beta$  is the proteolytic product of a transmembrane protein that actually resides in autophagosome membranes. In the normal brain, most  $A\beta$  formed during normal autophagosome biogenesis is degraded within the lysosomes. In AD brains, diminished autophagosome-lysosome fusion results in accumulation of  $A\beta$ -filled autophagosomes, which constitute a major intracellular reservoir of the toxic peptide.<sup>121</sup>

Excessive generation of  $A\beta$  in AD brain cells is also driven by increased levels of the  $\gamma$ -secretase

complex within autophagosomes. The  $\gamma$ -secretase complex mediates the cleavage of APP to A $\beta$  within autophagosomes. Most familial, early-onset cases of AD are due to mutations on the Presenilin-1 gene, a component of the  $\gamma$ -secretase complex. Mature autophagosome membranes are highly enriched with Presenilin-1. During the early stages of induction and autophagosome biogenesis, presenilin-1 translocates to the immature autophagosomal vesicles and is suspected of being involved in regulation of autophagosome maturation. Mutations of presenilin-1 in early-onset AD accentuates lysosomal pathology and promotes A $\beta$  pathology and neuronal cell loss.<sup>122</sup> In support of this possibility are observations that the turnover of several proteins is impaired in blastocysts that lack the genes encoding presenilins-1 and -2, leading to the increased appearance of these proteins within autophagic vacuoles.<sup>123</sup>

### III) Huntington's disease

Huntington's Disease (HD) is one of the best characterized polyglutamine-expanded diseases. These diseases are caused by mutations that result in abnormally long sequences of polyglutamine residues, which make proteins aggregation-prone and toxic. Polyglutamine disorders also include spinal and bulbar atrophy, spinocerebellar ataxia, and dentatorubral-pallidoluysian atrophy.<sup>124</sup> Autophagy plays a crucial role in the pathogenesis of HD, as polyglutamine sequences are poor substrates for the proteasome degradation pathway. Degradation of proteins that contain polyglutamine sequences is dependent largely on autophagy.<sup>125</sup> Dependency on autophagy is evidenced by the accumulation of highly ubiquitinated aggregates of huntingtin (htt) in the endosomal-lysosomal organelles of neurons<sup>126</sup> and lymphoblasts<sup>127</sup> in patients with HD. When over-expressed in cells, htt accumulates in autophagic compartments, the degree of accumulation being proportional to the length of the polyglutamine sequence in the protein.<sup>128</sup> Experimental inhibition of autophagosome biogenesis and/or fusion with lysosomes increases htt aggregation in cells both *in vitro* and *in vivo*.<sup>129</sup> In contrast, rapamycin treatment reduces htt accumulation and neurodegeneration in cell and fly models of polyglutamine disease and reduces neurological deficits and htt aggregation in a mouse model of HD.<sup>130</sup> This strongly suggests that inadequate levels

of autophagy contribute to the complex neuronal cell death pattern in this disease.<sup>131</sup> The mechanism by which htt aggregates inhibit autophagy is not known. However, sequestration of endogenous autophagy inhibitors (mTOR) to the sites of autophagosome maturation has been speculated.<sup>48,132</sup>

## CONCLUSIONS AND FUTURE PROSPECTS

Over the last four decades, our understanding of the autophagic process has increased enormously. Genetic screening approaches using yeast have addressed many questions concerning the molecular mechanisms of autophagy. Nevertheless, the interplay between the different signaling complexes involved in the process and the specific mechanisms of autophagosome biogenesis, transport, and fusion warrant further exploration. Despite recent findings that have shed some light on the major cellular and molecular events involved in mammalian autophagy, our knowledge regarding the autophagic pathway in mammalian cells remains rather limited. Discovery of a larger number of Autophagy-related genes (*ATG* genes) in mammals compared to those in lower eukaryotes suggests that autophagy is a much more complex process in higher organisms. Generation and analysis of transgenic and knockout animal models will be essential to understand the evolutionarily acquired complexity of autophagy mediated processes in mammals.<sup>133</sup> Longevity studies on these animal models would also help to assess components of the aging phenotype and directly link them to autophagic malfunction.

A decrease in the autophagic activity has been convincingly demonstrated in older organisms. It has been proposed that accumulation of aberrant or functionally disabled mitochondria and other damaged structures is a consequence of an age-related decline in autophagic and lysosomal activity.<sup>134</sup> Furthermore, it has been reported that the decline of autophagy with age is affected by alterations in glucose metabolism and hormone levels which are inherent to aging.<sup>135</sup> These observations, together with the finding that autophagy genes are essential for lifespan extension in *Caenorhabditis elegans*,<sup>136</sup> and that inhibition of Tor kinase (whose activity inhibits autophagy) doubles the lifespan of this nematode,<sup>137</sup> support the idea that dysfunction of the autophagic

pathway may induce premature aging.

Considerable advances have been made in our understanding of the defective steps that lead to dysfunction of autophagy during aging. However, most of the molecular components responsible for diminished autophagic activity with aging still remain elusive. Age-related research should very soon benefit from current advances in the molecular dissection of macroautophagy and CMA and from the availability of novel autophagic markers and better functional tests. Critical at this point is the understanding of how age-related changes in different hormonal and metabolic environments contribute to the diminished autophagic activity. The growing number of large-scale proteomic and metabolomic-based studies on aging models should provide valuable clues on this matter.

Several studies analyzing autophagy in pathological conditions have concomitantly expanded our knowledge regarding the physiological roles of autophagy in multi-cellular organisms. However, a better understanding of the connections between autophagy and processes such as programmed cell death, malignant transformation, and tumor growth would be of particular interest. Pharmacological modulation of the disrupted autophagic process could be a very promising strategy for future therapies within a wide spectrum of pathological situations including cancer, neurological diseases, and premature aging.

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