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The Autophagy Lysosomal Pathway and Neurodegeneration

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The autophagy lysosomal pathway (ALP) is a major mechanism for degrading intracellular macromolecules. The catabolic products can then be used by the cell for energy or as building blocks to make other macromolecules. Since its discovery, a variety of cellular pathways have emerged that target components with varying specificity for lysosomal degradation. Under some circumstances, lysosomes may release their contents into the extracellular space where they may serve signaling or pathogenic functions. The ALP is active in healthy cells, and the level of activity can be regulated by nutrient-sensing and metabolic signaling pathways. The ALP is the primary pathway by which lipids and damaged organelles are degraded and may be the only pathway capable of degrading aggregated proteins. As such, there has been intense interest in understanding the role of the ALP in the accumulation of aggregated misfolded proteins characteristic of many of the major adult-onset neurodegenerative diseases. This review focuses on recent advances in our understanding of the ALP and its potential relationship to the pathogenesis and treatment of neurodegenerative diseases.

HISTORY

The work of Drs. Christian de Duve and Yoshinori Ohsumi led to the discovery of the autophagy lysosomal pathway (ALP), and the contributions of each were recognized with the awards of the Nobel prize in physiology or medicine in 1974 and 2016, respectively. de Duve discovered the membrane-bound acidic compartment called the lysosome with biochemical approaches (De Duve and Wattiaux 1966). Ohsumi discovered the core machinery responsible for autophagy by identifying the genes in yeast that are necessary for survival in the setting of caloric restriction (Klionsky et al. 2003; Tooze and Dikic 2016).

LYSOSOME—THE HUB OF A PROTEOSTASIS NETWORK

The common way to portray the ALP is as a unidirectional pathway that begins with the de novo formation of double-membrane organelles called autophagophores and culminates in the fusion of autophagosomes and their contents with lysosomes to form autophagolysosomes, in which the contents of the autophagosomes are degraded. However, further study of the ALP has revealed multiple distinct pathways to the lysosome including nonspecific macroautophagy, substrate-specific forms of autophagy (e.g., mitophagy), chaperone-mediated autophagy (CMA), microautophagy, and micropinocy-

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tosis, to name a few (Fig. 1). One common feature of all these pathways is that degradation ultimately occurs in the lysosome. For this reason, it may be easier for the reader to understand the ALP using a hub and spoke model (Nixon et al. 2008; Perera and Zoncu 2016). Here, the hub, the

lysosome, will be introduced first and then the different pathways into and out of the lysosome will be described.

Lysosomes are defined as membrane-bound organelles delimited by a single-lipid bilayer and characterized by an acidified milieu ($\text{pH} \sim 4.5$).

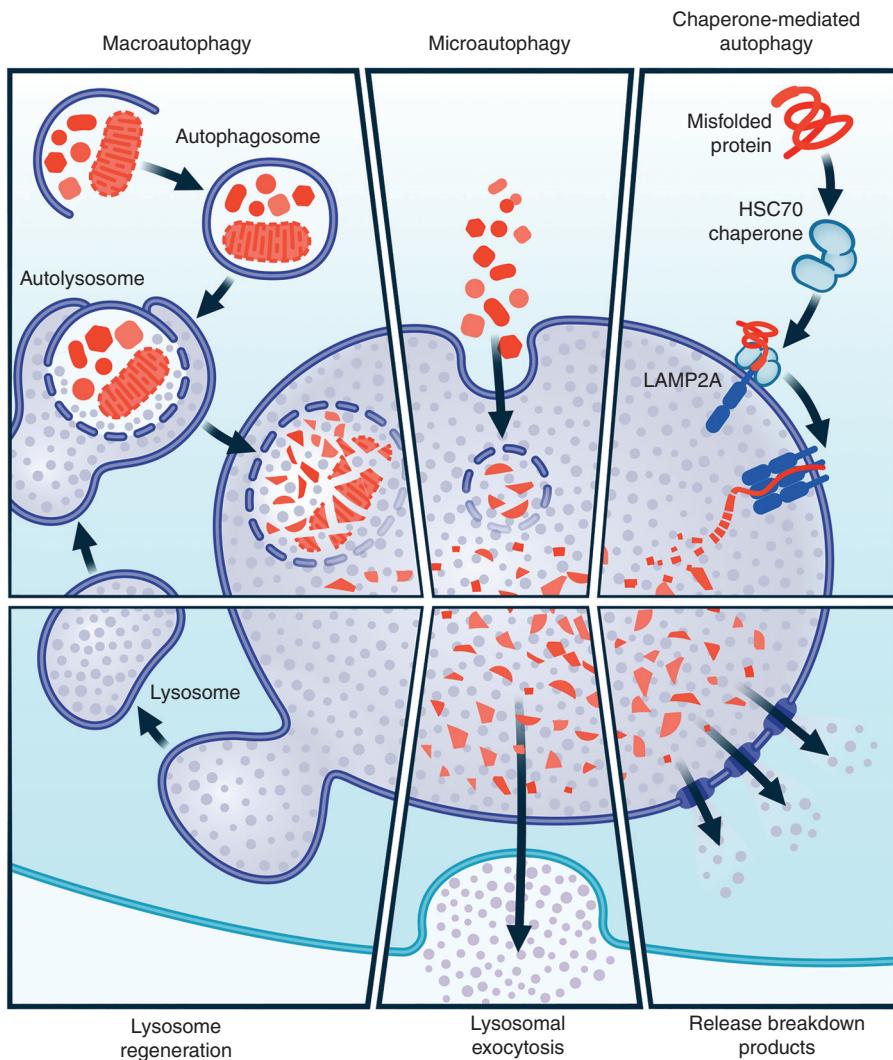


Figure 1. The autophagy lysosomal pathway. The lysosome is the hub of a network of pathways that feed cargo into its lumen for degradation. These include pathways depicted here to deliver intracellular cargo such as macroautophagy, chaperone-mediated autophagy and microautophagy, as well as others that deliver extracellular cargo to the lysosome including endocytosis and micropinocytosis (see text for details). Cargo delivered to the lysosome can undergo degradation into molecular building blocks that can return to the cytoplasm to be catabolized further to supply cellular energy needs or to be reused in the synthesis of new macromolecules. Contents of lysosomes can also be extruded extracellularly by a Ca^{2+} -dependent exocytic process. LAMP2A, lysosome-associated membrane glycoprotein 2; HSC70, heat shock cognate 71.

The membrane contains a variety of structural and signaling proteins, channels, transporters and trafficking, and fusion machinery. For example, the lysosomal membrane v-type ATPase (v-ATPase) pumps protons across the membrane and is the major mechanism for generating an acidic lumen and a pH gradient. Lysosomes are frequently located in the perinuclear area in the cell soma but undergo trafficking and fusion, mediated by a subset of membrane-associated RAB GTPases and SNARE proteins (Ao et al. 2014; Perera and Zoncu 2016). RAB5 and RAB7 function specifically to tether and dock endolysosomal membranes. LAMP1 makes up ~50% of the lysosomal membrane protein, and it couples lysosomes to transport machinery.

Lysosomes contain approximately 60 soluble hydrolases, which are active at acidic pH, and carry out the degradation of macromolecules transported from the cytoplasm to the lumen of the organelle. Membranes and lipids are degraded within intralysosomal vesicles that contain specialized hydrolases and activator proteins suited to the task. Lipid droplets shuttled to lysosomes are hydrolyzed into free fatty acids and glycerol. Catabolites such as short peptides, amino acids, and other molecules are translocated from the lumen to the cytoplasm or other cellular compartments for the cell to use.

Lysosome biogenesis is coordinated by transcription factors that belong to the microphthalmia-transcription factor E family (MiT), including transcription factor EB (TFEB) and TFE3 (Settembre et al. 2011). They bind to a DNA response element motif known as the coordinated lysosomal expression and regulation (CLEAR) element within genes that encode proteins required for lysosomal biogenesis, autophagy, exocytosis, and endocytosis. In effect, CLEAR-dependent transcription promotes processes that lead to the isolation from the cytoplasm of unwanted cytoplasmic macromolecules, and their permanent removal via degradation and/or exocytosis (Decressac et al. 2013; Polito et al. 2014). TFEB and TFE3 are normally located in the cytoplasm, bound to the scaffold 14-3-3 protein owing to phosphorylation of two serines in the transcription factors by TFEB kinases such as ERK2 or mTORC1. In response to stresses such

as starvation or lysosomal dysfunction, the lysosomal nutrient sensing (LYNUS) machinery, which sits on the cytoplasmic side of the lysosomal membrane, senses the nutrient content of the lysosome, and communicates the information to the nucleus (Alers et al. 2012; Inoki et al. 2012a; Lin et al. 2012; Settembre et al. 2013; Shanware et al. 2013). TFEB is dephosphorylated by mTOR, translocates to the nucleus, and drives the transcription of CLEAR-containing genes (Settembre et al. 2013). For example, TFEB induces expression of PPAR α and PGC1 α , which play a role in lipid oxidation and ketogenesis (Settembre et al. 2011, 2013; Tsunemi et al. 2012), emphasizing the tight integration of these catabolic processes. TFEB was also shown to be the main mediator of PGC1 α -induced improvement in a mouse model of Huntington's disease (Tsunemi et al. 2012). Transcription of TFEB itself is controlled via an autoregulatory loop (Settembre et al. 2013).

Although it is well established that the protein composition of lysosomes evolves during biogenesis and maturation, an important unanswered question in the field is whether functionally important subpopulations of mature lysosomes exist within different cell types or even within the same cell. Lysosomes uniformly express LAMP-1, but other lysosome-associated proteins are expressed more variably. For example, LAMP-2A, which is required for CMA, is absent from ~80% of lysosomes at the baseline (Cuervo et al. 1997; Kaushik and Cuervo 2012). It is unclear whether the heterogeneity reflects functionally distinct lysosomes in which production is regulated, or if it is related to stochastic variations in protein sorting or maturation. Lysosomes undergo "reformation" (Yu et al. 2010), suggesting that there is a lot of exchange between different endocytic compartments.

PATHWAYS TO THE LYSOSOME—MACROAUTOPHAGY

Macroautophagy is the major intracellular pathway by which intracellular cargo are delivered to the lysosome (Biswas et al. 2008). The complex biochemistry of the pathway is excellently reviewed elsewhere (Klionsky 2005, 2007; Ya-



mamoto and Yue 2014; Bingol 2018). Induction is governed by the Ulk1 complex, which induces the nucleation of the isolation membrane (IM) or phagophore. Then, the Beclin1-Atg14L-Vps34 lipid kinase complex catalyzes the production of PI3P at the IM, resulting in the recruitment of PI3P-binding proteins such as WIPI-1, -2, and DFCP1 (Ferguson et al. 2009). The sites of autophagy induction and the source of membranes has been controversial (Mari et al. 2011); endoplasmic reticulum (ER) and ER-mitochondrial contacts are likely sources but others have been suggested (Axe et al. 2008; Itoh et al. 2008). The IM expands and envelops the cargo in a process that requires Atg9 and two ubiquitin-like conjugation systems, which trigger the covalent attachment of the lipid phosphatidylethanolamine (PE) to Atg8 or its mammalian homolog, microtubule-associated protein 1 light chain 3 (LC3) (Nakatogawa et al. 2007; Fujita et al. 2008; Sou et al. 2008). Embedded into the autophagosome membrane via the PE moiety, LC3-II serves as an adaptor protein that binds cargo being engulfed by the autophagosome through other adaptor proteins described below (Tan et al. 2008; Tung et al. 2010). The mature autophagosome fuses with lysosomes by a mechanism that likely depends on SNAREs to form autophagolysosomes, exposing cargo to the lysosomal degradation machinery for digestion (Jäger et al. 2004; Stroikin et al. 2004; Cai et al. 2010; Yuzaki 2010; Itoh et al. 2011; Hyttinen et al. 2013; Albanesi et al. 2015; Murrow et al. 2015). Interestingly, although LC3 remains the most specific known marker of autophagosomes, LC3-independent forms of autophagy have been described (Kuma et al. 2007; Szalai et al. 2015; Engedal and Seglen 2016).

Initially, macroautophagy was thought to be nonselective, with phagophores scooping up and engulfing cytoplasm and cargo that happen to be in the neighborhood. Subsequently, a large number of adaptor proteins have been discovered, including p62/SQSTM1 (Sequestosome 1), NBR1, Nix, NDP52, Alfyl/WDFY3, and OPTN (optineurin), which play a role in targeting specific cargo for autophagic clearance including protein aggregates, mitochondria, other damaged organelles, etc. (Fortun et al. 2003; Komatsu

et al. 2007, 2010; Farré et al. 2008; Geisler et al. 2010; Brady et al. 2011; Matsumoto et al. 2011; Lim et al. 2015). Many of these adaptors contain ubiquitin- and LC3-interacting regions and often undergo oligomerization, which increases the avidity of their binding to cargo. In some cases, binding is regulated by clinically relevant modulators of these adaptor proteins such as TBK1, which phosphorylates OPTN (Wild et al. 2011). Defining the extent of substrate specificity and the associated mechanisms of regulation are a major focus of ongoing research in the field (Anding and Baehrecke 2017).

PATHWAYS TO THE LYSOSOME—MICROAUTOPHAGY, MULTIVESICULAR BODIES, AND PINOCYTOSIS

Another path to lysosomal degradation is microautophagy (Sahu et al. 2011; Shpilka and Elazar 2011) and the closely related endosomal microautophagy (Bingol 2018). These relatively less studied pathways begin with the invagination of the lysosomal membrane. Eventually, the invaginations, which contain contents from the cytoplasm, pinch off to form vesicles in the lysosomal lumen (Shpilka and Elazar 2011). The degree of substrate specificity and relative importance of microautophagy for physiology remains unclear.

PATHWAYS TO THE LYSOSOME—CHAPERONE-MEDIATED AUTOPHAGY

CMA is a pathway to translocate polypeptides with the KFERQ motif directly from the cytoplasm into the lumen of the lysosome (Olson et al. 1991; Kiffin et al. 2004). Translocation is mediated by LAMP-2A and HSP8A, a member of the HSP70 family. Interestingly, the KFERQ motif is found in ~30% of the proteome and in many proteins implicated in neurodegenerative diseases including α -synuclein (Olson et al. 1991; Cuervo et al. 2004; Martinez-Vicente et al. 2008). Importantly, and unlike macroautophagy, proteins evidently need to be translocated into the lysosome as monomers, so CMA may be less effective than autophagy at degrading aggregated protein. Nevertheless, induction of

CMA has been shown to accelerate the clearance of some disease-causing proteins (Massey et al. 2006; Bauer et al. 2010; Wang et al. 2010b), which presumably reduces their propensity to accumulate and aggregate.

OTHER PATHS TO THE LYSOSOME

Autophagy, microautophagy, and CMA are pathways to convey cytoplasmic contents to the lysosomal lumen for degradation. Additional pathways, including macropinocytosis, phagocytosis, and endocytosis can bring extracellular material to the lysosome for degradation (Binotti et al. 2015). In cancer cells, macropinocytosis may be a critical way to take up macromolecules for metabolic support, but relatively less is known about the role and importance of macropinocytosis in neurons. In the context of neurodegenerative disease, these pathways may be important routes by which extracellular aggregation-prone proteins enter neurons and transmit proteinopathy between neighboring cells. An important future direction will be to better understand mechanisms by which misfolded proteins are taken up by neurons and how they get access to the cytosol to template and propagate misfolded protein conformations.

PATHWAYS FROM THE LYSOSOME

Cargo delivered to the lysosome can be degraded into substituent molecular building blocks, then released into the cytoplasm to be metabolized or reused in the synthesis of new macromolecules. However, lysosomes or autolysosomes can also translocate to the plasma membrane, and fuse and release their contents into the extracellular space (Takenouchi et al. 2009; Settembre et al. 2013). This process of lysosomal exocytosis is believed to begin with activation of the lysosome, causing kinesin-associated lysosomes to be trafficked to the plasma membrane (Perera and Zoncu 2016). Ca^{2+} efflux from the lysosome mediated by the TRPML1 channel is likely critical for triggering SNARE-mediated plasma membrane fusion (Xu and Ren 2015; Perera and Zoncu 2016). TRPML1 gating is modulated by lysosomal pH and by phosphoinositides, such as

$\text{PI}(3,5)\text{P}_2$, $\text{PI}(4,5)\text{P}_2$, $\text{PI}(3,4)\text{P}_2$, and $\text{PI}(3,4,5)\text{P}_2$. Interestingly, lysosomal Ca^{2+} release and exocytosis may be triggered in neurons by back-propagating action potentials, and exocytosed proteolytic enzymes may play a role in synaptic plasticity (Padamsey et al. 2017). Fe^{2+} reportedly accumulates in lysosomes, likely as a consequence of degrading Fe^{2+} -containing cellular proteins, and abnormal neuronal accumulation of Fe^{2+} is a feature of neurodegenerative diseases (Kwan et al. 2012; Wang et al. 2016; van Duijn et al. 2017). Whether that is so because of lysosomal dysfunction is not known. How lysosomal exocytosis is related to other release mechanisms, including exosomes, is also not fully understood (Baixaulli et al. 2014; Poehler et al. 2014).

ALP IN THE CONTEXT OF THE PROTEOSTASIS NETWORK

It is important to remember that the ALP does not function in isolation. It exists within an elaborate proteostasis network and signaling system that enables cells to sense and respond to metabolic changes (Crighton et al. 2006; Maiuri et al. 2010; He et al. 2012). Although the ALP plays an important role in the turnover of proteins, other pathways including the unfolded protein response (UPR) and the ubiquitin proteasome system (UPS) are also critical (Webb et al. 2003; Keller et al. 2004; Kabuta et al. 2006; Wang et al. 2009, 2010a; Benbrook and Long 2012; Wang and Mandelkow 2012; Lee et al. 2013), and there is abundant evidence that there is cross talk between these pathways (Bernales et al. 2006; Pandey et al. 2007; Matus et al. 2008; Kirkin et al. 2009; Rouschop et al. 2010; Watanabe et al. 2010; Senft and Ronai 2015). For example, inhibitors of the UPR are capable of inducing autophagy, perhaps because they lead to ER-associated degradation and the extrusion of aggregated protein to the cytoplasm that must be cleared by autophagy (Høyer-Hansen and Jäättelä 2007; Hetz et al. 2009; Suh et al. 2012). Cross talk and redundancy between pathways probably explain how cells and organisms can survive at least some significant impairments in specific components of the proteostasis network.



ALP IN NEURODEGENERATIVE DISEASE—DO NEURONS MANAGE AUTOPHAGY DIFFERENTLY?

The genetics of autophagy were elucidated in yeast, and the majority of autophagy studies involve the use of nonneuronal cells (Kim and Klionsky 2000), raising the question of whether neuronal autophagy is unique (Larsen and Sulzer 2002; Boland and Nixon 2006; Moruno Manchon et al. 2016). Because neurons are postmitotic, they have lost one important mechanism to clear long-lived proteins—cell division and dilution (Eden et al. 2011). Neurons also have an elaborated morphology, with long dendrites and axons that can be a meter long or longer, and therefore must manage the degradation of cargo at distant sites (Shen and Ganetzky 2009; Bowling and Klann 2014; Tang et al. 2014). The cell biology of the autophagy pathways in neurons was initially characterized by Holzbaur and colleagues, who showed that autophagosomes are formed constitutively in axon terminals, and are trafficked to the cell body (Maday and Holzbaur 2014). En route, the protein composition gradually resembles mature lysosomes and the intraluminal pH drops. Eventually, in the soma, they fuse with lysosomes to form autophagolysosomes, and the degradation of their contents ensues.

In addition, neurons in the central nervous system are substantially buffered by astrocytes from large variations in nutrients that can occur elsewhere in the body and that can induce starvation-dependent activation of mTOR-dependent autophagy. Indeed, a number of studies have suggested that mTOR-dependent autophagy may be regulated in neurons differently than in nonneuronal cells (Boland et al. 2008). For example, inhibition of mTOR with rapamycin or sirolimus induces autophagy less effectively in neurons compared with nonneuronal cells (Tsvetkov et al. 2010; Krüger et al. 2012). Rapamycin binds FKB12, a nonobligate component of the mTORC1 complex, but not the mTORC2 complex, and one study has suggested that differences in the TORC complexes in neurons could contribute to the differences in reported efficacy of rapamycin (Roscic et al. 2011). There

is also evidence that subtypes of neurons may differ in their dependence on autophagy (Hara et al. 2006; Komatsu et al. 2006; Friedman et al. 2012).

ALP IN NEURODEGENERATIVE DISEASE—WHAT IS THE EVIDENCE?

A common thread cutting across multiple adult-onset neurodegenerative diseases, including Alzheimer's disease (AD), Parkinson's, Huntington disease, amyotrophic lateral sclerosis (ALS), and frontotemporal dementia, is the abnormal deposition of misfolded aggregated protein(s) (Friedman et al. 2012). Given the critical role of autophagy in the clearance of aggregated protein, this could indicate that autophagy dysfunction is a common mechanism in neurodegenerative disease.

That autophagy dysfunction may be a major mechanism in neurodegenerative disease is further suggested from the established role of mitochondrial damage and associated deficits in bioenergetics or excessive reactive oxygen species in these conditions (Beal et al. 2006; Lezi and Swerdlow 2012; Ryan et al. 2015; Wang 2017). Because autophagy is the principal pathway by which cells remove catastrophically damaged mitochondria (Youle and Narendra 2011), it stands to reason that impairment in this process may result in abnormal accumulation of deleterious mitochondria (Dagda et al. 2008; Narendra et al. 2008; Ferree et al. 2013; Lemasters 2014; Lazarou et al. 2015; Chen et al. 2017; Jinn et al. 2017).

More broadly, the link between autophagy and aging may be an important consideration (Meléndez et al. 2003; Bergamini et al. 2004; Rubinsztein et al. 2011; Inoue et al. 2012b; Carnio et al. 2014). Aging is the number-one risk factor for neurodegenerative diseases, and is associated with down-regulation of autophagy in the brain (Lipinski et al. 2010). Conversely, induction of autophagy has been shown in model organisms to increase their longevity (Simonsen et al. 2008; Zheng et al. 2010; Pyo et al. 2013). More importantly, autophagy induction is associated with an increase in their health span and quality of life, suggesting that the promotion of

autophagy may confer a more fundamental improvement in quality of the function of biological systems that could bring broad benefits (Cuervo et al. 2005; Levine et al. 2011; Oka et al. 2012; Kang et al. 2015).

Beyond the intuitive appeal of the pathway as a therapeutic target (Levine and Kroemer 2008; Nixon 2013), there is a remarkable genetic association between neurodegenerative disease and autophagy. Mutations in many different genes associated with different steps in autophagy have been linked to AD, Parkinson's, or Huntington's disease, as well as ALS, frontotemporal dementia, and others (Fig. 2; Table 1) (Kegel et al. 2000; Petersén et al. 2001; Skibinski et al. 2005; Ramirez et al. 2006; Cheung and Ip 2009; Ju et al. 2009; Montie et al. 2009; Winslow et al. 2010; Dehay et al. 2012; Lucin et al. 2013; Ochaba et al. 2014; Wong and Holzbaur 2014; Martin et al. 2015; Ciura et al. 2016; Sellier et al. 2016; Sullivan et al. 2016; Manzoni 2017; Fujikake et al. 2018), indicating that mutations and variants in genes associated with autophagy are sufficient to cause neurodegenerative disease in some cases. Indeed, mutations in some genes critical for lysosome function lead to lysosomal storage disorders that cause neurological symptoms in childhood (Nixon et al. 2008). The extent to which a mismatch between the production and autophagic clearance of misfolded proteins exists in the much more common cases of idiopathic or sporadic AD and Parkinson's disease or ALS is not known (Ahmed et al. 2012). However, recent studies in patients with AD and the dynamics of amyloid β turnover suggest the intriguing possibility that genetic forms of AD may cause an overproduction of misfolded proteins, whereas idiopathic forms may be associated with reduced clearance, with all forms of AD associated with a fundamental mismatch between production and clearance, and the same may hold for other common but idiopathic forms of neurodegenerative disease (Mawuenyega et al. 2010).

A number of studies have sought to further determine whether brains of patients with neurodegenerative disease exhibit morphological abnormalities that indicate autophagic malfunction. Although widespread abnormalities have

been reported, the nature of the morphological changes appear to be, at least partly, disease-specific (Anglade et al. 1997; Sikorska et al. 2004; Nixon 2007; Boland et al. 2008; Chu et al. 2009; Crews et al. 2010; Lucin et al. 2013; Yamamoto and Yue 2014; Martin et al. 2015; Fujikake et al. 2018). Some of these differences have been highlighted in excellent recent reviews (Nixon 2013; Yamamoto and Yue 2014). That different neurodegenerative diseases exhibit sometimes striking differences in patterns of autophagy-associated cytopathology underscores the importance of defining the underlying disease-associated mechanisms. This knowledge will help guide approaches to the development of effective therapeutics and for stratifying patient populations to do sensitive clinical trials.

Based in part on these lines of reasoning, many groups have found evidence in nonhuman models of neurodegenerative disease that autophagy modulation accelerates clearance of disease-causing proteins (Ravikumar et al. 2002; Sarkar et al. 2007a; Dolan and Johnson 2010; Tsvetkov et al. 2010; Wang et al. 2010a; Roscic et al. 2011; Congdon et al. 2012; Kruger et al. 2012; Barmada et al. 2014; Polito et al. 2014; Marrone et al. 2018) and improves disease phenotypes (Ravikumar et al. 2004; Jia et al. 2007; Sarkar et al. 2007b; Hetz et al. 2009; Montie et al. 2009; Spencer et al. 2009; Bauer et al. 2010; Rodriguez-Navarro et al. 2010; Tsvetkov et al. 2010; Watanabe et al. 2010; Schaeffer et al. 2012; Castillo et al. 2013; Decressac et al. 2013; Barmada et al. 2014; Höllerhage et al. 2014; Polito et al. 2014). It is worth noting that some important limitations apply to many of these studies. The assays available to measure autophagy induction are limited in their sensitivity. In general, these assays depend on making inferences about flux based on snapshots of levels of pathway intermediates, which can be prone to misinterpretation, even failing to distinguish upstream autophagy induction with downstream blockade (Klionsky et al. 2011, 2012, 2016). One assay that avoids this pitfall is the optical pulse labeling approach, which monitors the dynamic clearance of an autophagy substrate fused to a photo-switchable protein in live cells, allowing clearance to be calculated directly (Barmada



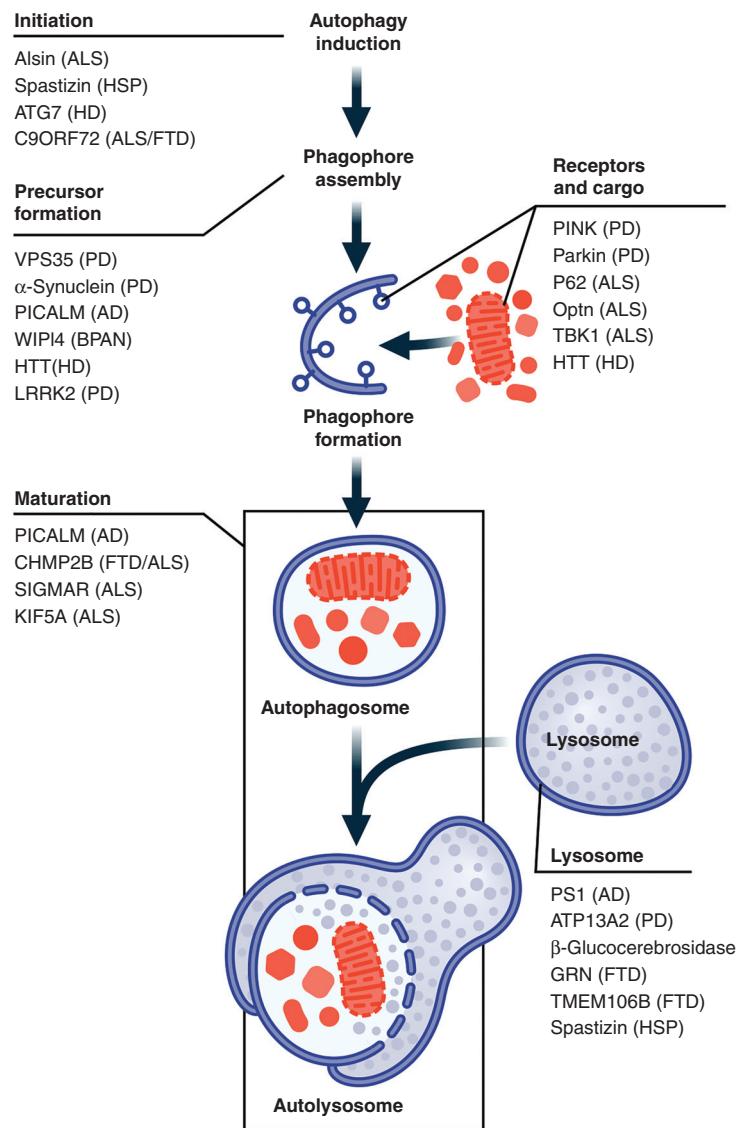


Figure 2. Genetic links between autophagy and neurodegenerative disease. Mutations in many genes that encode proteins that play a role in the autophagy lysosomal pathway (ALP) lead to neurodegenerative disease syndromes in humans, indicating that impairment of the ALP can be sufficient to produce neurodegenerative disease. Some examples are shown in this figure. AD, Alzheimer's disease; ALS/FTD, amyotrophic lateral sclerosis/frontotemporal dementia; BPAN, β -propeller protein-associated neurodegeneration; CMT2, Charcot-Marie-Tooth disease 2; HD, Huntington's disease; HSP, hereditary spastic paraparesis; PD, Parkinson's disease.

et al. 2014). Assays *in vivo* are even more limited (Mizushima et al. 2004), making it difficult to accurately assess the effects of putative autophagy inducers, and complicating any correlations seen with disease phenotypes. Very few studies that have reported positive effects of autophagy

induction on disease-associated phenotypes have done appropriate pharmacokinetic/pharmacodynamic studies. Without a direct demonstration that the intervention is, in fact, inducing autophagy, the exact relationship is difficult to determine.

Table 1. Autophagy lysosomal pathway and Parkinson's disease–associated genes

Genetic locus	Gene	Possible roles in autophagy
PARK1	SNCA (synuclein)	Blocks chaperone-mediated autophagy (CMA); may promote Atg9 mislocalization; vesicle fusion
PARK2	Parkin	Ubiquitin ligase that tags mitochondria for binding of adaptor proteins for mitophagy
PARK6	PINK1	Ubiquitin kinase whose accumulation on mitochondrial membranes is a marker for recruitment of Parkin to mediate mitophagy
PARK7	DJ-1	Works in parallel with PINK1/Parkin to play a role in mitophagy
PARK8	LRRK2	Kinase for key Rab proteins that may play a role in endosomal/lysosomal trafficking
PARK9	P-type ATPase ATP13A2	Essential for the maintenance of lysosomal pH and autophagosome–lysosome fusion
PARK14	PLA2G6	May play a role mediating mTOR-independent autophagy
PARK15	FBOX7	Mitophagy
PARK17	Vps35 (vacuolar sorting-associated protein 35)	Mutant Vps35 may mislocalize Atg9, leading to impaired autophagy
PARK19	DNAJC6	Endocytosis and endocytic trafficking
PARK20	SYNJ1	Endosomal trafficking and autophagy
PARK21	DNAJC13	Endocytosis
Unassigned	GBA	Lysosomal function, synuclein metabolism

Some studies have reported that interventions designed to modulate autophagy flux have unexpected effects (Zhang et al. 2011). Maniatis and colleagues tested whether genetic inhibition of the autophagy pathway would worsen disease-associated phenotypes in a mouse model of ALS based on mutations in superoxide dismutase 1 (Rudnick et al. 2017). They specifically knocked out Atg7, a gene required for autophagy, in motor neurons early in development in mice expressing a transgene encoding the ALS-associated mutant SOD1^{G93A}. Early on, denervation and behavioral deficits were accelerated compared with SOD1^{G93A} mice in which Atg7 was intact. But later, they observed that the loss of Atg7 was associated with less interneuron and astrocyte pathology and an extension of life span.

What could be happening? One possibility is that autophagy may play multiple roles in disease that differ depending on the stage of disease progression. For example, perhaps the initial and somewhat expected worsening of deficits in motor unit function and motor neuron-dependent phenotypes could result from an acceleration in

pathogenesis in motor neurons. But Cleveland and colleagues have shown by selectively reducing mutant SOD1 expression in a cell-type specific manner that motor neurons, astrocytes, microglia, and oligodendrocytes each contribute to different extents and in different ways to deficits exhibited by murine models of ALS (Ilieva et al. 2009). The exact nature and mechanisms of the cell-nonautonomous contributions to ALS pathogenesis still need to be worked out. But it is conceivable that if disease begins in motor neurons and if propagation of disease to neighboring nonneuronal cells depends on the release of misfolded proteins by lysosomal exocytosis, then blocking autophagy might actually mitigate the cell-nonautonomous component of disease at the expense of worsening the cell-autonomous component. It is interesting to note that whereas Maniatis and colleagues reported almost no effects of knocking out Atg-7 on baseline motor neuron structure or function (Rudnick et al. 2017), Komatsu found that disruption of Atg-7 and autophagy throughout the brain caused significant neurodegeneration (Komatsu et al. 2006).



But the explanation could be even more complicated. Others have shown that germline mutations that are designed to block specific arms of the protein homeostasis pathway, such as autophagy, are sufficient to induce neurodegeneration (Komatsu et al. 2005, 2006; Hara et al. 2006). Presumably, germline mutations in the autophagy pathway must induce widespread adaptive remodeling of other arms of the proteostasis network to compensate, possibly even in a complicated cell-specific way, which could confound the simple interpretation of the role of autophagy in disease. To what extent does the loss of autophagy at an early stage in development instruct us on the role of autophagy impairment in the aged brain when many neurodegenerative diseases develop? Answers to these questions will be critical for shaping our thinking about pathogenesis and treatment.

ALP AS A POTENTIAL THERAPEUTIC TARGET FOR NEURODEGENERATIVE DISEASE

The evidence suggesting that autophagy is a therapeutic target is intriguing and warrants further investigation. However, while it has been shown that it can be safe to chronically target a major protein homeostasis pathway (e.g., the drug bortezomib, which inhibits the UPS), there have as yet been no clinical trials of autophagy modulators in humans, and there are multiple caveats to consider.

The mechanisms by which disease-associated genetic mutations in the autophagy pathway cause neurodegeneration is a focus of ongoing research (Nixon 2006), and is critical to the design of therapeutic strategies. Deficits that attenuate the pathway might respond to interventions that stimulate the pathway to restore normal levels of activity (Bose et al. 2011), but that depends on the step in the process that is impaired and the nature of the impairment. For example, mutations in CHMP2B, which plays a role in autophagosome/lysosome fusion (Lu et al. 2013), cause frontotemporal dementia (Skibinski et al. 2005). If disease-causing mutations block that step completely, therapeutically stimulating autophagy might be detrimental, because induced

autophagosomes would accumulate without a path to clear them.

Unlike the UPS, autophagy is active basally and can be induced normally by caloric restriction, which can occur during fasting (Alirezaei et al. 2010). Chronic caloric restriction in non-human organisms has generally been associated with positive outcomes including increases in longevity and resistance to disease (Bergamini et al. 2007). However, the mechanism by which caloric restriction induces autophagy is thought to be via the inhibition of the mTOR kinase (Balgi et al. 2009; Inoki et al. 2012a). Whether mTOR could be a safe drug target is controversial (Zhang et al. 2011) because mTOR regulates other critical biological pathways in addition to autophagy (Inoki et al. 2012a), such as protein translation (King et al. 2008), and the mTOR inhibitor rapamycin is an immunosuppressant. mTOR inhibitors would be expected to have activity in the periphery, and it has been difficult to develop brain penetrant inhibitors. Partly for these reasons, a focus of the field has been on the development of autophagy inducers that act by mTOR-independent mechanisms (Hoyer-Hansen and Jäättelä 2007; Hoyer-Hansen et al. 2007; Williams et al. 2008; Lipinski et al. 2010; Decuypere et al. 2011; Bootman et al. 2017).

One additional concern with targeting this pathway has been the potential that systemic induction of autophagy might increase the risk of developing cancer (Shintani and Klionsky 2004; Amaravadi et al. 2007; Kimmelman 2011; Lock et al. 2011; Rosenfeldt et al. 2013; Cui et al. 2014; Rao et al. 2014; Galluzzi et al. 2015; Lévy et al. 2015; Perera et al. 2015; White 2015). Several studies suggest that cancers, particularly as they form tumors that outstrip their blood and nutrient supply, up-regulate the autophagy pathway, possibly in conjunction with macropinocytosis, to enable the cells to endure stress, scavenge nutrients, survive, and proliferate (Qu et al. 2003; Amaravadi and Thompson 2007; Mathew et al. 2007; Guo et al. 2011; Lopez et al. 2011; Yang et al. 2011, 2014, 2016; Amaravadi and Debnath 2014; Karsli-Uzunbas et al. 2014). It is important to note that although autophagy induction might enhance the growth of a preexisting cancer

by these mechanisms, there is also evidence that autophagy can function to suppress the initial development of cancer (Liang et al. 1999; Yue et al. 2003; Takamura et al. 2011; Wu et al. 2012; Guo et al. 2013). Interestingly, Levine and colleagues developed a cell-permeant version of beclin, an autophagy-inducing gene, and showed that chronic administration did not significantly increase the incidence of tumors in mice. In the end, it will be critical to do careful preclinical safety studies for any potential autophagy inducer before first-in-human trials. In addition, the field would benefit tremendously from the development of target-engagement biomarkers for autophagy to guide dosing regimens and to ensure that any clinical trial of a putative autophagy inducer is, in fact, inducing autophagy at the doses tested.

SUMMARY AND CONCLUSIONS

Previously relegated to a narrow role as the cell's trash bin, the lysosome has gained new prominence as an organelle centrally positioned to send and receive critical signals and to regulate cellular metabolism as well as catabolism of macromolecules and other organelles. Autophagy is one of several cellular pathways to deliver intracellular cargo to lysosomes for degradation, a process that depends in many cases on special sets of adaptor proteins that are specific for certain cargoes.

Autophagy may have particular importance for neurodegenerative disease given its demonstrated capacity to metabolize aggregated proteins, damaged organelles linked to neurodegenerative disease such as mitochondria, and its close association with aging, the most important risk factor for neurodegenerative diseases. The myriad mutations in genes with established or apparent roles in autophagy, which result in neurodegenerative disease underscore the conclusion that deficits in autophagy are sufficient to cause neurodegenerative disease and suggest that lysosomal dysfunction may be a common thread that even extends to the more common idiopathic forms of adult-onset neurodegenerative disease.

Nevertheless, it remains unclear whether modulation of autophagy and lysosomal function will be a successful strategy to treat one or more neurodegenerative diseases. Neuropathology studies support the conclusion that dysfunction in the ALP is a common feature of neurodegenerative diseases. However, the ALP is complex and our understanding of the nature of the impairments remains limited in most cases, making it uncertain whether the same type of intervention is likely to work in all diseases and at all stages of those disease. Some of these questions may be difficult to fully address in nonhuman models, given the poor predictive value many of these models have for results in human clinical trials. Frustratingly, knowledge of druggable targets in the pathway remains limited, and the throughput and resolution of current autophagy assays pose challenges for the effective prosecution of potential lead optimization programs. Finally, there is the question of whether and how modulation of the ALP could be achieved safely in humans. Good pharmacodynamic markers for the ALP would be invaluable to enable investigators to test the hypothesis in humans that modulation of the autophagy pathway could be a safe and effective treatment for neurodegenerative diseases.

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Autophagy Lysosomal Pathway and Neurodegeneration

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S. Finkbeiner

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