Autophagy in Lysosomal Storage Disorders

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Autophagy in lysosomal storage disorders

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Keywords: autophagy, glycogenosis, Mucolipidosis Type IV, lysosomal storage disorders, mucopolysaccharidoses, lysosomes, sphingolipidoses

Lysosomes are ubiquitous intracellular organelles that have an acidic internal pH, and play crucial roles in cellular clearance. Numerous functions depend on normal lysosomes, including the turnover of cellular constituents, cholesterol homeostasis, downregulation of surface receptors, inactivation of pathogenic organisms, repair of the plasma membrane and bone remodeling. Lysosomal storage disorders (LSDs) are characterized by progressive accumulation of undigested macromolecules within the cell due to lysosomal dysfunction. As a consequence, many tissues and organ systems are affected, including brain, viscera, bone and cartilage. The progressive nature of phenotype development is one of the hallmarks of LSDs. In recent years biochemical and cell biology studies of LSDs have revealed an ample spectrum of abnormalities in a variety of cellular functions. These include defects in signaling pathways, calcium homeostasis, lipid biosynthesis and degradation and intracellular trafficking. Lysosomes also play a fundamental role in the autophagic pathway by fusing with autophagosomes and digesting their content. Considering the highly integrated function of lysosomes and autophagosomes it was reasonable to expect that lysosomal storage in LSDs would have an impact upon autophagy. The goal of this review is to provide readers with an overview of recent findings that have been obtained through analysis of the autophagic pathway in several types of LSDs, supporting the idea that LSDs could be seen primarily as “autophagy disorders.”

Introduction

Lysosomes are ubiquitous intracellular organelles that have an acidic internal pH, and have crucial roles in cellular clearance: Numerous functions have been shown to depend on normal lysosomes, including turnover of cellular constituents, cholesterol homeostasis, downregulation of surface receptors, inactivation of pathogenic organisms, repair of the plasma membrane and bone remodeling. Lysosomal biogenesis involves maturation of early endosomes to form multivesicular bodies within the cell due to lysosomal dysfunction. As a consequence, many tissues and organ systems are affected, including brain, viscera, bone and cartilage. Where clinical features of these disorders vary widely, most are fatal within the first two decades of life following many years of worsening disease. The progressive nature of phenotype development is one of the hallmarks of LSDs.

In spite of the clarity brought about by modern genetic and biochemical studies of storage diseases, a persisting conundrum is why defects in the lysosomal system per se ultimately cause cell and organ dysfunction, particularly for the brain. This question grows in part out of the realization that early on, cells and organs...
in most storage disorders appear to develop and function normally, and only later is this followed by insidious disease onset and progression. In recent years biochemical and cell biology studies of LSDs have revealed an ample spectrum of abnormalities in a variety of cellular functions. These include defects in signaling pathways, calcium homeostasis, lipid biosynthesis and degradation and intracellular trafficking (see ref. 6 for a review). Therefore, an emerging view to explain the disease cascade is one focused on the importance of the multiple endosomal and autophagosomal streams flowing into the lysosomal system for processing. Failure to degrade and recycle sequestered materials in lysosomal disease may also lead to deficiency states in which precursors for metabolic pathways in the cell are diminished, followed by altered synthetic pathways and an increased metabolic demand on affected cells. The lysosomal system has thus emerged from being considered only an end-organelle, to being at the very hub of metabolic regulatory control. Perhaps the best example of the interconnection of the lysosome with other cellular systems is autophagy. Lysosomes play a fundamental role in the autophagic pathway by fusing with autophagosomes and digesting their content. Recent evidence of the cooperative and integrated roles of lysosomes and autophagosomes comes from the discovery of an overarching regulatory gene network (CLEAR) and a master gene, transcription factor EB (TFEB), controlling the biogenesis and function of both lysosomes and autophagosomes. Considering the highly integrated function of lysosomes and autophagosomes comes from the discovery of an overarching regulatory gene network (CLEAR) and a master gene, transcription factor EB (TFEB), controlling the biogenesis and function of both lysosomes and autophagosomes.18

Autophagy in Glycogenosis Type II (Pompe Disease) and Danon Disease

Pompe disease. Pompe disease was the first recognized lysosomal storage disorder. The disease is caused by deficiency of acid maltase, also known as acid alpha-glucosidase (GAA). Clinical heterogeneity of the disease is a well-established phenomenon.4,5 In the most serious infantile form, the disease leads to profound weakness, heart failure, and if left untreated causes death within one year. Even in milder late-onset form the illness is relentless and debilitating: patients eventually become confined to a wheelchair or a bed and many die prematurely from respiratory failure. It took more than 30 y to define the cause of Pompe disease after its discovery in 1932,10,11 and even longer to develop a therapy. Only recently, enzyme replacement therapy (ERT) using recombinant human acid alpha-glucosidase designed to supplement the defective enzyme was approved for all forms of the disease. This therapy stemmed from a straightforward hypothesis to explain the disease pathogenesis, namely that progressive enlargement of glycogen-filled lysosomes would lead to lysosomal rupture and to release of glycogen and toxic substances into the cytosol.10-12 The assumption was that early treatment, initiated before lysosomal integrity was compromised, would reverse this pathogenic cascade. Now, after years of preclinical and clinical experience with this therapy it has become clear that this assumption is only partially correct: while cardiac muscle responds very well to therapy, skeletal muscle does not. The poor muscle response to therapy led to the need to revisit the pathogenesis of the disease, with increased attention to an involvement of the autophagic pathway in disease pathogenesis. Poor skeletal muscle response to ERT was initially shown in long-term preclinical studies in a mouse model of Pompe disease (GAA-knockout (GAA-KO)).14 The presence of large areas of autophagic accumulation detected by electron microscopy in the therapy-resistant fast muscle suggested that abnormal autophagy might be the culprit (Fig. 1A). Surprisingly, huge clusters of LAMP1 (a lysosomal marker) and LC3 (an autophagosomal marker)-positive vesicles are seen in the core of virtually every muscle fiber even in young Pompe mice. Only outside the core is the expected pathology of Pompe disease observed, namely individual or isolated groups of expanded lysosomes with clearly defined borders. The autophagic mass grows in size as the animals age, and from a morphological perspective, it is evident that abnormal autophagy, rather than lysosomal expansion, is what eventually causes muscle fiber destruction and the loss of muscle force.15 It appears that both ends of the autophagic process—the generation of autophagosomes and their resolution by lysosomal fusion—are impaired in Pompe skeletal muscle. The components of the system, such as Beclin1, GABARAP, ATG7 and LC3, are present in excess, but this excess is associated with functional deficiencies of autophagy. The phenotypic defect in fast muscle of the GAA-KO mice appears to arise not from an induction of autophagy but rather from a block in autophagosomal turnover (a defect in autophagosome-lysosome fusion) in the diseased muscle. Autophagy substrates, such as p62/SQSTM1 and ubiquitinated proteins5,10 accumulate in the core of Pompe muscle fibers. The formation of ubiquitin-positive protein aggregates in the GAA-KO mice precedes the development of clinical symptoms and parallels the progression of the disease.15 Autophagic buildup poses a significant problem for the lysosomal delivery of the therapeutic enzyme. The enzyme traffics to its destination, lysosomes, via mannose-6-phosphate receptor-mediated endocytosis. Autophagic and endocytic pathways converge at several steps along the way; autophagosomes fuse not only with lysosomes, but also with late and early endosomes.56 Therefore, it is perhaps not surprising that the recombinant enzyme ends up in the area of autophagosome accumulation.55 Thus, the removal of autophagic buildup seemed a reasonable approach to improve the therapy.

Indeed, ERT in muscle-specific Arg5– or Arg7–deficient Pompe mice results in near-complete glycogen clearance.10 This outcome observed in both young and older mice is never seen in Pompe mice in which autophagy is not tampered with. Of note, ERT plus suppression of autophagy converts Pompe mice into muscle-specific autophagy-deficient with type II muscle fibers of normal mobility and single fiber contractility of these mice is far better than the health of Pompe mice. The accumulation of dysfunctional mitochondria, mild atrophy and age-dependent decrease in

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force have been reported in muscle-specific autophagy-deficient wild-type mice,44,45 but these abnormalities seem to be a reasonable price to pay for the reversal of pathology in Pompe disease. In humans, autophagic buildup is present in many muscle cells in late-onset patients (both juvenile and adults), thus making the observations in the mouse model relevant to the human study. Furthermore, in many fibers autophagic accumulation is the overwhelming (and in some fibers the only) pathology, because the lysosomes that lie outside the autophagic region appear essentially normal.46,47 In contrast, the role of autophagy in the pathogenesis of infantile Pompe disease is much less obvious. Unexpectedly, the autophagic component which is so prominent in late-onset cases is insignificant in infants whose biopsies were analyzed within days after birth.47 Instead, the major characteristic of these fibers is the presence of hugely expanded lysosomes without clear borders, a finding consistent with the hypothesis of lysosomal rupture as a cause of muscle destruction.32,33

The difference between the relative contribution of the lysosomal and autophagic pathologies in untreated infants and adults presents a conundrum in Pompe disease. One thing appears to be clear: infants lacking the enzyme are born with already severely damaged muscle fibers filled with giant lysosomes with ruptured membranes and massive glycogen deposits. The lack of autophagic buildup in such infants suggests that the role of autophagy in muscle development is minimal, perhaps because of a constant supply of nutrients through the umbilical cord. This hypothesis is consistent with the data in mice showing a low level of autophagy throughout the embryonic period.48 Analysis of biopsies from infants receiving ERT shows that lysosomes shrink in some patients, but remarkably, autophagic buildup resembling that found in skeletal muscle from adults emerges.47 A long-term study and a larger number of samples are needed to evaluate the fate of autophagic buildup in ERT-treated infants.

Glycogen passage from the cytosol to lysosomes must involve some type of autophagic pathway since by definition autophagy is a process of transport and lysosomal degradation of any intracellular material. Early morphological data showing the presence of glycogen particles inside autophagic vacuoles in skeletal muscle, liver and heart of the newborn rats implied the involvement of macroautophagy.49,50 If this process operates later in life, then inhibition of macroautophagy would alleviate glycogen burden in lysosomes by preventing its transport from the cytosol. Indeed, suppression of autophagosome formation by inactivation of Atg5 or Atg7 in skeletal muscle in untreated Pompe mice results in reduction of accumulated glycogen; for reasons that are unclear, this reduction is much more pronounced in ATG7-deficient Pompe mice.44 Nevertheless, data from both strains suggest that at least some glycogen is delivered to the lysosomes via the

Table 1. The main results of the studies on autophagy in LSDs

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<tr>
<th>Disease</th>
<th>AV accumulation†</th>
<th>Defective AV degradation†</th>
<th>Increased AV formation†</th>
<th>Increased poly-ub proteins°</th>
<th>Increased dysfunctional mitochondria¹</th>
<th>Increased p62 NT</th>
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†Number of autophagic vesicles (AV) quantified by electron microscopy or LC3-immunofluorescence, amounts of LC3-II by western blotting. °Impaired autophagosome-lysosome fusion, defective degradation of long-lived proteins. †TITF3 downregulation, BECN1 activation. Poly-ubiquitinated proteins (poly-ub) revealed by immunofluorescence or western blotting using anti-ubiquitin antibodies. Polyfunctional mitochondria revealed by western blotting using mitochondrial markers. p62/SQSTM1 protein revealed by immunofluorescence or western blotting using anti-p62 antibodies.
macroautophagic pathway. However, it remains unclear how the remaining glycogen is transported to the lysosome. Yet another recent hypothesis suggests that the intracellular glycogen trafficking to lysosomes may proceed via a nonclassical LC3-independent autophagy mediated by glycogen-binding protein STBD1 (starch binding domain-containing protein 1), which anchors glycogen molecules to vesicular membranes.51

Danon disease. Danon disease (also called “glycogen storage disease due to LAMP2 deficiency” or “lysosomal glycogen storage disease with normal acid maltase activity”) is a lysosomal glycogen storage disease due to LAMP2 (lysosomal-associated membrane protein 2) deficiency.52 The disease is inherited as an X-linked trait and is extremely rare. The disease phenotype is characterized by severe cardiomyopathy and variable skeletal muscle weakness often associated with mental retardation.

Danon disease was the first LSD in which an involvement of autophagy was reported.52 Accumulation of autophagic vacuoles is detected in several tissues, particularly the muscle, from a mouse model of the disease.13

Autophagy in Mucopolysaccharidoses

Multiple sulfatase deficiency (MSD) and mucopolysaccharidosis type IIIA (MPS IIIA). The mucopolysaccharidoses (MPSs) are a group of lysosomal storage disorders caused by deficiency of enzymes catalyzing the degradation of glycosaminoglycans (GAGs), which are long, repeating chains of complex sugar molecules. When one of several enzymes is absent, a progressive buildup of GAGs occurs. Depending on the enzyme deficiency, catabolism of dermatan sulfate, heparan sulfate, keratan sulfate, chondroitin sulfate, or hyaluronan may be blocked, singly or in combination.53 Lysosomal accumulation of GAGs results in cell, tissue and organ dysfunction. There are 11 known enzyme deficiencies that give rise to 7 distinct MPSs. MPS III, also referred to as Sanfilippo syndrome, is caused by a deficiency of enzymes that are needed to break down heparan sulfate. MPS III is classified into four types (A,B,C and D), with each type caused by a deficiency of a different enzyme. MPS IIIA is due to deficiency of the heparan N-sulfatase enzyme, and is characterized by profound mental deterioration, hyperactivity, and relatively mild somatic manifestations.

Multiple sulfatase deficiency (MSD) is a rare but very severe disorder in which affected individuals present a complex multisystemic phenotype due to the impaired activity of all sulfatas. It is caused by mutations in the Sulfatase Modifying Factor 1 (SUMF1) gene, which is responsible for an essential
post-translational modification of all sulfatases. Lack of sulfatase activities in MSD patients leads to accumulation of sulfated lipids and mucopolysaccharides resulting in a clinical phenotype that combines the features of at least seven diseases, five of which are mucopolysaccharidoses. The sumf1/2 KO mouse model of MSD recapitulates most of the features of the human disease.

As for other types of LSDs, the pathogenic mechanisms that lead from enzyme deficiency to cell death in MSD and MPS IIIA are not completely understood. An impairment of autophagy is postulated to play a major role in disease pathogenesis. LC3 immunofluorescence reveals a higher number of autophagosomes in several brain regions of mouse models of MSD and MPS IIIA compared with wild-type mice. A decreased colocalization of LAMP1 with the autophagosomal marker LC3 in MSD and MPS IIIA cells compared with wild-type cells in vitro suggests the possibility of impaired lysosome-autophagosome fusion. A defective autophagic flux was also demonstrated by the accumulation of autophagy substrates, such as polyubiquitinated proteins and dysfunctional mitochondria (Fig. 1B and C), both of which are significantly increased in tissues from MSD and MPS IIIA mice. In addition, MSD cells show a decreased ability to degrade exogenously expressed aggregate-prone proteins, such as expanded huntingtin and mutated α-synuclein, which are responsible for Huntington and Parkinson disease, respectively.

Studies aimed at the identification of the mechanisms underlying the impairment of the fusion between lysosomes and autophagosomes in MSD and MPS IIIA point to abnormalities of membrane lipid composition and SNARE (Soluble NSF Attachment protein REceptor) protein distribution. In particular, a significant accumulation of cholesterol is found in the lysosomal membranes of both MSD and MPS IIIA cells. This is associated with a disorganization of the endolysosomal membrane and with disruption of "lipid rafts." Interestingly, wild-type cells "loaded" with cholesterol in vitro mirror the fusion defects observed in LSD cells. Conversely, lowering cholesterol by the use of methyl β-cyclodextrin in MSD and MPS IIIA cells rescues normal lysosomal function. The SNARE proteins, which are key components of the cellular membrane fusion machinery, are found aberrantly sequestered within cholesterol-rich regions of LSD lysosomal membranes. This abnormal distribution appears to lock these proteins in complexes and to impair their function and recycling, thereby directly affecting lysosomal membrane fusion capacities.

These studies provided evidence that a global lysosomal dysfunction leads to the impaired autophagy observed in the pathogenesis of MSD and MPS IIIA and possibly in other types of LSDs. A possible model for disease pathogenesis is depicted in Figure 2. According to this model, lysosomal accumulation of undegraded substrates results in impaired lysosome-autophagosome fusion and a block of the autophagic flux. This figure depicts a generalized mechanism that may apply to several LSDs, even though a reduced efficiency of autophagic degradation may not necessarily be due to impaired lysosomal fusion. The secondary accumulation of autophagic substrates, such as polyubiquitinated proteins and dysfunctional mitochondria, are a consequence of this block. This model places the emphasis on the secondary accumulation of autophagy substrates as a key determinant of cell death, rather than on the primary accumulation of lysosomal substrates.

Mucopolysaccharidosis type VI (MPS VI). Mucopolysaccharidosis VI (MPS VI), also known as Maroteaux-Lamy syndrome, is caused by deficiency of the lysosomal enzyme N-acetylgalactosamine-4-sulfatase (arylsulfatase B, ARSB). ARSB hydrolyzes sulfate esters from GAGs, mainly dermatan sulfate (DS), and a deficiency of the enzyme prevents the sequential degradation of DS leading to its accumulation in various cells and tissues. Clinically, MPS VI is characterized by coarse faces, short stature, dysostosis multiplex, stiffness and functional impairment of joints, hepatosplenomegaly, cardiac valve anomalies and corneal clouding. No evidence of CNS involvement is evident in clinically severe MPS VI, although scattered neuronal storage is evident in animal models lacking ARSB activity.

Studies using fibroblasts from MPS VI patients demonstrated that lysosomal storage in these cells results in impaired autophagy, accumulation of polyubiquitinated proteins and mitochondrial dysfunction.
disfunction. These studies also demonstrated that the extent of LAMP2-LC3 colocalization is similar between MPS VI and normal fibroblasts, indicating that autophagosome-lysosome fusion is not completely blocked in MPS VI fibroblasts. Since glycosaminoglycans are reported to inhibit cathepsin activity and cathepsin-activity deficiency results in impaired autophagy, Tesirote et al. suggest that this mechanism might play a role in autophagy impairment in MPS VI. Impaired autophagy is also observed in vivo in a rat model of MPS VI. Electroron microscopy in liver from affected mice reveals an accumulation of autophagy intermediates. Strikingly, autophagy induction, decreased clearance of autophagosomes, and an accumulation of autophagy intermediates results in the prevention of derman sulfite accumulation and in the rescue of the defects observed in the autophagic pathway, ubiquitination and mitochondrial function.

**Autophagy in Sphingolipidoses**

The sphingolipidoses are a heterogeneous group of inherited disorders of sphingolipid metabolism that often affect the nervous system. These diseases predominantly occur in the pediatric population, and the resulting neurodegeneration produces psychomotor retardation and myoclonus due to diffuse and progressive involvement of neurons, or weakness and spasticity due to involvement of white matter tracts. The underlying genetic defects are diverse and variable. Accumulation of sphingomyelin, glycolipids, glucocerebrosides, gangliosides, unesterified cholesterol, and sulfatide compounds. In some instances, this storage material results from hydrolytic enzyme deficiency, whereas in others its occurrence is less well understood and may be secondary to the accumulation of other lipids. In either case glycosphingolipids can alter macroautophagy. Recent studies demonstrate that loading cells with glycosphingolipids can alter macroautophagy. Recent studies demonstrate that loading cells with glycosphingolipids can alter macroautophagy.

**Niemann-Pick type C disease (NPC).** Niemann-Pick type C disease (NPC) is caused by mutations in the NPC1 or NPC2 genes, whose protein products are thought to act cooperatively in the efflux of cholesterol from late endosomes and lysosomes. NPC1 encodes a multipass transmembrane protein that contains a sterol-sensing domain, similar to that found in the regulators of cholesterol biosynthesis, HMG-CoA reductase, and 7DHCR. NPC2 is a soluble protein primarily localized to the late endosome/lysosome lumen, where it binds cholesterol in an orientation opposite that of the NPC1 N-terminal domain. NPC2 is a candidate of extracting cholesterol from lipid bilayers, and then transferring it to another bilayer or to the NPC1 N-terminal domain. As a result of NPC1 or NPC2 deficiency, unesterified cholesterol derived from receptor-mediated endocytosis of low-density lipoprotein (LDL) accumulates widely in cells throughout the body. A broad array of glycosphingolipids accumulates as well, although it is uncertain whether this latter phenomenon is attributable to a direct role for NPC1-NPC2 in glycosphingolipid trafficking or is secondary to cholesterol accumulation.

A marked accumulation of autophagosomes occurs in the brains of NPC mice and in skin fibroblasts from NPC patients. This is attributable, in part, to the induction of autophagy through BECN1, as of autophagic vacuoles, abnormal ubiquitination and abnormal mitochondrial function. Interestingly, gene transfer of wild-type ARSB results in the prevention of derman sulfite accumulation and in the rescue of the defects observed in the autophagic pathway, ubiquitination and mitochondrial function.

**Gaucher disease.** As in NPC, models of Gaucher disease show both an induction of autophagy and an accumulation of autophagosomes and autophagic substrates. Gaucher disease is caused by mutations in either glucocerebrosidase, the lysosomal enzyme that degrades glucosylceramide and glucosylsphingosine, or its activator protein saposin C. Fibroblasts from some patients deficient in saposin C show increased autophagy induction. Mice homozygous for mutant Y994L glucocerebrosidase and saposin C, used to model neuronopathic Gaucher disease, exhibit punctate p62 SQSTM1 accumulations in neurons and astrocytes, and subsequent undegraded material in vesicles within axons, consistent with an accumulation of autophagic substrates. These observations suggest that degradation of autolysosome cargo is deficient in Gaucher disease cells. Interestingly, an impairment of lysosomal protein degradation due to glucocerebrosidase haploinsufficiency was recently suggested to occur in carriers of the Gaucher disease mutation, leading to increased risk for Parkinson disease due to diminished α-synuclein degradation.

**Fabry disease and GM1 gangliosidosis.** Increased basal expression of the autophagosome marker LC3-II is observed in models of other sphingolipidoses, including GM1-gangliosidosis and Fabry disease. GM1-gangliosidosis is an autosomal recessive lysosomal lipid storage disorder caused by mutations of the lysosomal β-galactosidase (β-gal) and results in the accumulation...
of GM1 ganglioside. The disease phenotype is characterized by severe psychomotor delays, achlorhydria and visual abnormalities including retinal degeneration, corneal clouding, optic atrophy and strabismus.46-48 MLIV is caused by mutations in MCOLN1 (mucolipin 1, belonging to the transient receptor potential (TRP) superfamily) rectifying channel permeable to Ca2+, Na+, K+ and Cl-.90-92 MLIV inclusions are found in most tissues in MLIV patients. The composition of the storage material is heterogeneous and includes lipids and mucopolysaccharides forming characteristic multiconcentric lamellae, as well as soluble, granulated proteins.93-95 MLIV is caused by mutations in MCOLN1 (mucolipin 1, also known as TRPML1), an endolysosomal cation channel belonging to the transient receptor potential (TRP) superfamily of ion channels.93-95 Whole cell patch clamp, as well as recording of native endolysosomal membranes, have led to the conclusion that MCOLN1 functions as an inwardly (from lumen to cytoplasm) rectifying channel permeable to Ca2+, Na+, K+ and Fe3+/Mn2+ whose activity is potentiated by low pH.96-98

Although the cellular role of MCOLN1 is still under investigation, the current model suggests that this protein mediates Ca2+/Fe2+/Mn2+ whose activity is potentiated by low pH.91-93

MCOLN1 interacts with HSPA8 (HSC70) and DNAJB1 (HSP40), two components of the chaperone-mediated autophagy (CMA) molecular machinery.99 MLIV fibroblasts show defective CMA and decreased levels of LAMP2A resulting in increased levels of oxidized proteins.100 Finally, MCOLN1 has the ability to form heterologosomes with the two other members of the mucolipin family, MCOLN2 and MCOLN3.101,102 Depletion of endogenous MCOLN3 or expression of a channel-dead dominant negative MCOLN3 mutant inhibits starvation-induced autophagy.103-105 Therefore, MCOLN1 might also play an indirect role in the initiation of autophagy.

Autophagy has also been shown to be defective in primary neurons cultured from a murine model of MLIV. The molot7 mice provide an excellent phenotypic model of the human disease, and all of the hallmarks of MLIV are present in the mice with the exception of corneal clouding.106 At birth, the knockout animals display no obvious behavioral or morphological phenotypes when compared with wild-type littermates, but as they age they show progressive limb weakness, eventual limb paralysis, and death at approximately eight months. Analysis of the brain at 8 mo shows lysosomal inclusions in multiple cell types, including neurons, astrocytes, oligodendrocytes, microglia and endothelial cells, with larger inclusions present in neurons. The MLIV inclusions are unusual in their combination of dense lamella and granular matrices, and they do not resemble those typically seen in the glycosphingolipidoses, the mucopolysaccharidoses, or most other types of lysosomal disease.106,107 Electron microscopy of primary cerebellar neurons from Molot7-deficient mouse embryos demonstrates significant membranous intracytoplasmic storage bodies, despite the lack of gross phenotype at birth.108 Evaluation of macroautophagy in neurons by LC3-I/LC3-II immunoblot and electron microscopy (Fig. 1D)) shows increased levels of LC3-II, similar to what is seen in human MLIV fibroblasts. LC3-II clearance is also defective, as treatment of the molot7 neuronal cultures with protease inhibitors to stimulate autophagy does not result in increased LC3-II levels.109 Demonstration of defective autophagy in MCOLN1-deficient neurons suggests a possible mechanism underlying neurodegeneration, whereby increased protein aggregation and organelle damage lead to autophagic stress and eventual neuronal death.110 The MLIV mouse model provides an important tool for evaluating the complicated interplay between chaperone-mediated autophagy and macroautophagy and their role in neurodegeneration.

Mucolipidosis type II and Mucolipidosis type III. Mucolipidosis type II (MLII) and Mucolipidosis type III (MLIII) are autosomal recessive diseases caused by deficiency of the
enzyme N-acetylgalactosamine 1-phosphotransferase (GlcNAc-phosphotransferase).105,106 This enzyme modifies newly synthesized lysosomal hydrolases by attaching a molecule of mannose-6-phosphate (M6P) that functions as a tag for delivery to lysosomes.107 Mutations in GlcNAc-phosphotransferase result in the missing and cellular loss of lysosomal enzymes and lysosomal accumulation of storage material.108,109 MLII is characterized by missorting and cellular loss of lysosomal enzymes and lysosomal mental delays. MLIII is a late onset, milder form of MLII.110,111 Skeletal abnormalities, short stature, cardiomegaly and development delays. MLIII is a late onset, milder form of MLII.111 Alterations in autophagy have been reported recently in MLII and MLIII fibroblasts. This includes accumulation of autophagosomes, p62/SQSTM1, ubiquitin and fragmented mitochondrial. In contrast, no variations in the levels of BECN1 are observed, suggesting that formation of autophagosomes is not increased in these disorders.22 Accumulation of LC3-positive structures and ubiquitin aggregates is also reported in neuronal cells of dorsal root ganglions in a MLIII patient.23 Importantly, inhibition of autophagy restores mitochondrial alterations in MLII and MLIII cells, thus suggesting that increased autophagy might be detrimental for proper mitochondrial function.25

**Autophagy in Neuronal Cereoid-Lipofuscinoses**

The neuronal ceroid lipofuscinoses (NCLs) are the most common cause of neurodegeneration among children. These disorders typically manifest with blindness, seizures, progressive cognitive defects and motor failure. NCLs are both genetically and phenotypically heterogeneous.112 The juvenile onset NCL (JNCL), also known as Batten disease, is the most common form of NCL, and is due to mutations in the CLN3 gene.113 The congenital form of NCL is due to mutations in the cathepsin D gene (CTSD/CLN1).114 A significant increase in the number of autophagosomes is observed in patients affected by these two types of NCLs and in the murine models of these diseases.25,26 In addition, accumulation of dysfunctional mitochondria and downregulation of the MTOR pathway, a sign of activation of autophagosome formation, are detected in JNCL due to mutations of the Clcn3 gene.27

**Concluding Remarks**

Autophagy has been analyzed in a variety of LSDs with different severities of the phenotype, different tissues involved, and different types of storage molecules. Table 1 shows the main findings obtained and Figure 1 displays some examples of the results obtained by these studies. In spite of all the above-mentioned differences among the diseases and samples analyzed, a common theme can be recognized (see also ref. 115 for a further review). In most cases there is an impairment of autophagic flux, causing a secondary accumulation of autophagy substrates such as polyubiquitinated proteins, p62/SQSTM1 and dysfunctional mitochondria, on one end, and an increase in factors involved in autophagosome formation, such as BECN1, as an attempt to compensate for the impaired autophagic flux, on the other. Accordingly, LSDs can be seen primarily as “autophagy disorders.”130 Interestingly, a defect in autophagic lysosome formation, due to abnormal MTOR activation, is reported in several LSDs.131

Impairment of autophagy and accumulation of autophagy substrates in LSDs suggest that at least some mechanisms underlying the LSD phenotype may be similar to other diseases in which defective autophagy has been observed. In particular, many neurodegenerative diseases that affect the aging population including Alzheimer, Parkinson and Huntington diseases, exhibit the presence of intraneuronal accumulations of protein aggregates as key elements of their pathogenic cascades. Yet the potential importance of macroautophagy as a critical player in the formation of these aggregates was largely unappreciated prior to studies in which key autophagy regulatory proteins were conditionally knocked out in mouse models. Genetic ablation in the CNS of Aγt5 and Aγ7, each critical for the formation of autophagosomes in cells, was found to cause progressive neurological disease in mice accompanied the accumulation of protein aggregates and inclusion bodies, and by neuron death.132-135 Subsequent studies further revealed the critical role of AγT5 and AγT7 in maintaining normal integrity of axons, particularly for Parkin negative cells, which develop early and progressive neuroaxonal dystrophy characterized by accumulation of autophagosome-like membrane structures in swellings along the length of the axon.136,137

A further link between LSDs and neurodegenerative diseases comes from studies showing accumulation of phosphorylated-tau aggregates and neurofilamentary tangles, which are typically detected in patients with Alzheimer disease, in LSDs such as Niemann-Pick type C19 and mucopolysaccharidoses,138 and deficient degradation of amyloid precursor protein (APP) in sphingolipidoses.139 Parallels between the neuropathology of Niemann-Pick C and several age-dependent protein aggregation neurodegenerative disorders are striking, and include the accumulation of phosphorylated tau and β-amyloid,140,141 and in some cases amyloid β.142 The recent identification of a defect of lysosomal acidification in a murine model of Alzheimer disease143 and of pathogenic lysosomal depletion in a mouse model of Parkinson disease144 further support a connection between lysosomal dysfunction and neurodegenerative diseases.

The acknowledged importance of autophagy in maintaining normal bulk protein recycling in these diseases has led to interest in whether pharmacological stimulation of autophagy could provide therapeutic benefit by delaying or preventing protein aggregate accumulations in disorders such as Huntington disease.145 Rapamycin was demonstrated to protect against neurodegeneration in a fly model of Huntington and to improve neuropathology in a mouse model of Huntington disease by enhancing autophagy-mediated clearance of huntingtin accumulation.146,147 Rapamycin was also shown to have a clearing effect on a variety of aggregate-prone proteins with polyglutamine or polyalanine expansions, leading to an improvement in cellular phenotype.148 These data suggest that enhancement of autophagy can be an effective approach to reduce toxic protein accumulation and cell death also in LSDs. Trehalose, a disaccharide present in many nonmammalian species, is an mTOR-independent autophagy activator, that has an anti-apoptotic effect.
in cultured neurons and accelerates the clearance of mutant human α- and β-mannosidase.17 However, one should also take into consideration that the defect observed in most LSDs is not a dysfunction in the formation of autophagosomes, but a block in autophagic flux. Therefore, activation of autophagy in this scenario may have detrimental effects. This would be consistent with the observation that suppression of autophagy has a beneficial effect on ERT for Pompe disease.43

Recently, it was shown that cholesterol accumulation in the endosomal/lysosomal membranes in LSDs changes their organization and composition and reduces their fusion capacity.13 It is possible that drugs aimed at reducing cholesterol in membraneous, such as glycyrrhizin (MjGCD), can restore the fusion capacity of lysosomal membranes and release the block of autophagy in LSDs, as recently described for MSD and MPS IIIA.14,15 This compound is toxic in vivo, but FDA approved cyclodextrins (e.g., Kleptose, Trappsol and Captisol) may be used. Indeed, chronic treatment using hydroxypropyl-β-cyclodextrin in mice with NPC disease results in cholesterol and ganglioside storage reduction, normalization in the autophagy marker LC3-II and significantly increased survival, although similar studies in MPS IIIA and GM1 gangliosidosis mice do not show similar benefit.16,17 Finally, a potentially attractive possibility would be to induce a global enhancement of both the lysosomal and autophagic pathways by acting on the master gene TFE3.18 Further studies are needed to explore the effects of modulators of autophagy, which operate at different steps of the autophagic flux, on the LSD phenotype in cell culture and in animal models. Hopefully, these studies will lead to the development of effective treatments for several LSDs.

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