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Lysosomes: regulators of autophagy in the retinal pigmented epithelium

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Abstract

The retinal pigmented epithelium (RPE) is critically important to retinal homeostasis, in part due to its very active processes of phagocytosis and autophagy. Both of these processes depend upon the normal functioning of lysosomes, organelles which must fuse with (auto)phagosomes to deliver the hydrolases that effect degradation of cargo. It has become clear that signaling through mTOR complex 1 (mTORC1), is very important in the regulation of lysosomal function. This signaling pathway is becoming a target for therapeutic intervention in diseases, including age-related macular degeneration (AMD), where lysosomal function is defective. In addition, our laboratory has been studying animal models in which the gene (*Cryba1*) for β A3/A1-crystallin is deficient. These animals exhibit impaired lysosomal clearance in the RPE and pathological signs that are similar to some of those seen in AMD patients. The data demonstrate that β A3/A1-crystallin localizes to lysosomes in the RPE and that it is a binding partner of V-ATPase, the proton pump that acidifies the lysosomal lumen. This suggests that β A3/A1-crystallin may also be a potential target for therapeutic intervention in AMD. In this review, we focus on effector molecules that impact the lysosomal-autophagic pathway in RPE cells.

Keywords

AMD; Autophagy; β A3/A1-crystallin; Lysosome; mTORC1; Oxidative stress; RPE; V-ATPase

Lysosomes are cellular organelles that modulate various processes such as autophagy and heterophagy, plasma membrane repair, cholesterol homeostasis and cell death (Xu and Ren, 2015). The number, size and content of lysosomes vary in different cell types. The distribution of lysosomes within the cell is determined by the nutrient sensing machinery at

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the lysosomal membrane, and is an important factor in lysosomal catabolic function. In this review, we focus on the effector molecules present in retinal pigmented epithelial (RPE) cells that impact the lysosomal-autophagic pathway.

Retinal Pigmented Epithelium (RPE)

The RPE is a single layer of cells interposed between the neurosensory retina and Bruch's membrane (Strauss, 2005). En face, RPE cells assume a hexagonal, cobblestone-like appearance. The cells are highly polarized and contain abundant melanin granules that absorb scattered light, thereby reducing photo-oxidative stress on the retina (Beatty et al., 1999). In addition, the RPE has several other functions that are crucial to the retina's functional integrity. Perhaps its most important function is the phagocytosis of shed photoreceptor outer segments (POS) and the subsequent degradation and recycling of their molecular components for re-use in the visual cycle (Young and Bok, 1969 and Bok, 1993). Apical microvilli of the RPE extend around the POS and ingest shed rod and cone outer segment discs into the RPE as membrane bound phagosomes. These phagosomes fuse with lysosomes to form phagolysosomes. The acid hydrolases from the lysosomes digest the outer segment material, critical components of which are returned to the photoreceptors for re-use. In a related process, called autophagy, damaged intra-cellular components including organelles, protein aggregates, and membranes are packaged into autophagosomes, which like phagosomes, fuse with lysosomes to effect cargo degradation.

Lysosomes and Autophagy

Much is now known about the molecular mechanisms of autophagosome formation (Mizushima and Kamatsu, 2011, Yang and Klionsky, 2010 and Rubinsztein et al., 2012), however, we know less about the end stages of macroautophagy, particularly the role of lysosomes in the degradation of autophagosome contents (Shen and Mizushima, 2014). The process is different from microautophagy and chaperone-mediated autophagy, where cellular materials to be degraded are directly delivered to the lysosomes, independent of autophagosomes (Kaushik and Cuervo, 2012). Therefore, lysosomes are indispensable in the degradation and recycling processes of all three major autophagy types.

Lysosomes are the major digestive organelle in eukaryotic cells (Saftig, 2006). They have a lipid bilayer membrane with an acidic lumen containing over 60 acidic hydrolases, each capable of degrading specific substrates (Settembre et al., 2013). The acidification of lysosomes is established by vacuolar-type H⁺-ATPases (V-ATPase) (Sun-Wada et al., 2003 and Mindell, 2012) which are multi-subunit complexes, composed of a peripheral V₁ domain that hydrolyzes ATP and an integral V₀ domain, that translocates protons from the cytoplasm to the lumen (Toei et al., 2010).

Lysosomal dysfunction may result from abnormal functioning of any of the myriad of proteins required for maintaining lysosomal homeostasis. However, in each case, the disease phenotype and tissue (s) affected can be different. Therefore, the mechanisms by which lysosomal function is regulated in the RPE may be unique. RPE cells are not only among the most active phagocytic cells in the body, continuously phagocytosing shed POS, but also are post-mitotic cells with high metabolic activity, where a high rate of autophagy would be

expected. Therefore, lysosomal-mediated removal of waste products in the RPE is essential to insure functional integrity of the neural retina. The lysosomal degradation pathway declines with age in the human brain, contributing to the pathogenesis of neurodegenerative diseases (Cuervo and Dice, 2000 and Nixon, 2013). While RPE lysosomal dysfunction is now thought to be a significant risk factor for age-related macular degeneration (AMD), our knowledge of how such abnormalities contribute to the disease process remains limited (Kaarniranta et al., 2013). In 1 year old rats with a spontaneous mutation in the *Cryba1* gene (encoding for β A3/A1-crystallin) (Sinha et al., 2008), electron microscopy (EM) showed large aggregates of lipofuscin-like material (arrows in Figure 1A) and large vacuoles containing many degenerated cellular organelles (arrowheads in Figure 1A) indicative of inefficient lysosomal clearance (Zigler et al., 2011). Interestingly, similar structures are also seen in EM sections of the fovea from a 95-year old male patient with geographic atrophy (Figure 1B). Therefore, understanding the lysosomal-mediated clearance mechanisms in the RPE may help to understand the pathophysiology of AMD.

In the RPE, lysosomes degrade both extracellular (POS) and intracellular (autophagy) material. Recently, it has become very clear that lysosomes and mTORC1 signaling are interconnected (Bar-Peled and Sabatini, 2014, Betz and Hall, 2013 and Puertollano, 2014). An elegant study demonstrated that lysosomal positioning within the cell regulates mTORC1 signaling (Korolchuk et al., 2011) while another showed that long starvation periods lead to mTORC1 reactivation and, thereby, formation of proto-lysosomes that develop into mature lysosomes (Yu et al., 2010).

mTOR Signaling and Autophagy

The mammalian target of rapamycin (mTOR), now officially known as the mechanistic TOR, is an atypical serine/threonine kinase that has been conserved throughout evolution. It interacts with many other proteins to form at least two distinct multiprotein complexes, namely mTORC1 and mTORC2 (Laplante and Sabatini, 2013). The mTOR complexes have different upstream inputs and downstream outputs (Zoncu et al., 2011). mTORC1 integrates multiple signals either to promote cellular growth when growth factors, nutrients and energy are available, or to induce catabolic processes during stress. Active mTORC1 has a number of downstream biological effects, including suppression of autophagy (Zoncu et al., 2011).

Several studies have shown that inhibition of mTORC1 activity is crucially important for autophagy induction in eukaryotic cells subjected to nutrient deprivation (Yang and Klionsky, 2010 and Laplante and Sabatini, 2012). Although mTORC1 is inhibited by both glucose/growth factor and amino acid deprivation, the signalling mechanisms involved are different. In the presence of glucose and growth factors, the TSC1/2 (tuberous sclerosis complex), a heterodimeric complex, which is a negative regulator of mTORC1 is phosphorylated and inactivated by several growth factor effector kinases such as Akt/PKB (protein kinase B) and ERK1/2 (extracellular-signal-regulated kinase 1/2). This leads to activation of mTORC1 (Wullschleger et al., 2006), and inhibition of de novo autophagosome formation (Kim et al., 2011 and Ganley et al., 2009). In contrast, glucose starvation activates AMPK (5'-AMP-activated protein kinase), which inhibits mTORC1 by phosphorylation and activation of its negative regulator, TSC1/2 (Inoki et al., 2003b).

Recent studies showed that amino acid- mediated activation of mTORC1 is dependent on formation of a four component super complex with V-ATPase, Ragulator and members of the Rag family of GTPases (Sancak et al., 2010 and Efeyan et al., 2013). V-ATPase is crucial to this process, functioning as a sensing device that responds to the lysosomal amino acid content by activating the Rag family GTPases. Upon activation, the Rag GTPases regulate the translocation and activation of mTORC1 on the lysosomal surface (Settembre et al., 2012).

Although the mTOR signaling pathway is highly conserved and ubiquitously expressed, its regulation is cell and tissue specific. RPE cells express both mTORC1 and mTORC2 complexes that are functionally active (Chen et al., 2010). Increased mTORC1 activation in senescent RPE cells leads to age-related decline in RPE cell function and rapamycin-mediated inhibition of mTORC1 prevents replicative senescence in cultured RPE cells (Yu et al., 2014 and Chen et al., 2010). In mouse models of retinal degeneration, rapamycin treatment prevented photoreceptor dysfunction (Zhao et al., 2011). In our *Cryba1* cKO (conditional knockout) mouse model, where *Cryba1* is knocked out specifically in the RPE, we have recently shown that mTORC1 activation leads to impaired lysosomal function and decreased autophagy in the RPE (Valapala et al., 2014). We demonstrated that β A3/A1-crystallin regulates lysosome-mediated degradation in the RPE by modulating V-ATPase via the AKT/mTORC1 signaling cascade. We also reported that β A3/A1-crystallin binds to the V_0 domain of V-ATPase, the first such binding partner in a mammalian system (Valapala et al., 2014). V-ATPase is a master regulator for amino acid sensing in lysosomes and for translocation of amino acids into the lumen, a requirement for mTORC1 activation (Zoncu et al., 2011). These findings suggest that β A3/A1-crystallin is essential for mTORC1 signaling in the lysosomes of RPE (Figure 2). Our mouse models, both *Cryba1* cKO (Valapala et al., 2014b) and *Cryba1* KO develop a slowly progressive AMD-like pathology that is associated with inefficient lysosomal clearance (Figure 3).

Oxidative Stress and Autophagy

Postmitotic RPE cells in the macula are constantly exposed to a high metabolic and oxidative stress environment (Bok 1993 and Decanini et al., 2007). During RPE cell aging, the capacity to neutralize mitochondrial-derived ROS diminishes due to decreased anti-oxidant production, reduced ability to repair DNA or protein damage, and disturbed proteolysis (Kaarniranta et al., 2009 and Blasiak et al., 2013). The inadequately neutralized ROS damage cellular proteins, leading to detrimental protein aggregation. Lipofuscin is one consequence of this aggregation because oxidized PUFAs are not efficiently digested in lysosomes of aged RPE cells (Schutt et al., 2002, Bergman et al., 2004, Vives-Bauza et al., 2008, Krohne et al., 2010 and Valapala et al., 2014). Lipofuscin is an autofluorescent heterogeneous mixture of lipid-protein aggregates, which sensitizes RPE cells to light induced oxidative stress, ultimately evoking further protein misfolding (Figure 4). In all cells, the heat-shock protein (Hsp) stress response is capable of refolding misfolded proteins, thereby improving cellular survival under oxidative stress (Ryhänen et al., 2009). Upregulation of Hsps has been detected in RPE homogenates isolated from human donor AMD samples (Schutt et al., 2002 and Decanini et al., 2007). This is an indication of stressed RPE cells, but importantly, it also reveals dysfunction in proteasomal clearance

(Kapphahn et al., 2007, Li et al., 2008, Fernandes et al., 2008 and Ryhänen et al., 2009). Once Hsp repair capacity is exceeded, individual polypeptides can be degraded by either the proteasome or by chaperone-mediated autophagy, while aggregates are degraded by selective macroautophagy, also called aggrephagy (Hytinen et al., 2014). In aggrephagy, cellular organelles and protein aggregates are encapsulated from the cytoplasm into autophagosomes, which then fuse with lysosomal vesicles for degradation (Lamark and Johansen, 2012). However, autophagy activity decreases with aging in RPE cells (Rodríguez-Muela et al., 2013, Viiri et al., 2013, Ferguson and Green, 2014 and Toops et al., 2015). One explanation for this decreased autophagy might be the accumulation of lipofuscin, a hallmark of aging, because it suppresses lysosomal function and autophagic clearance in RPE cells (Ryhänen et al., 2009, Krohne et al., 2010, Viiri et al., 2013, Mitter et al., 2014 and Valapala et al., 2014). Lipofuscin components have also been shown to inhibit V-ATPase, thereby elevating lysosomal pH and impairing the digestion of phagocytosed POS (Finnemann et al., 2002, Bergmann et al., 2004, Lamb and Simon 2004, Vives-Bauza et al., 2008 and Guha et al., 2014).

The p62 protein sorts proteins between the proteasomal and autophagic clearance pathways (Kirkin et al., 2009). In this process, p62 selectively targets ubiquitinated protein aggregates for autophagic degradation. First, it binds to the perinuclear protein aggregates and undergoes autophagic clearance, making it a useful biomarker of autophagy activity (Bjørkøy et al., 2006, Clausen et al., 2010, Larsen et al., 2010 and Viri et al., 2013). Its accumulation in macular RPE cells rather than in the cells of the periphery suggests that autophagy activity declines in AMD (Viiri et al., 2013 and Valapala et al., 2014). Second, p62 interacts with the Nrf2/ARE (nuclear factor-erythroid 2-related factor-2/antioxidant response element) pathway by disrupting the cytoplasmic Nrf2-Keap1 complex to regulate antioxidant production (Jain et al., 2010 and Wang et al., 2014). A functional ARE element is located in the p62 gene promoter (Jain et al., 2010 and Hirotsu et al., 2012). Nrf2 and p62 create a regulatory loop where Nrf2 activates p62 expression, while Nrf2 nuclear localization is facilitated by p62 (Lau 2010). In addition, Keap1 elimination is processed by p62 dependent autophagy (Taguchi et al., 2012). Nrf2 signaling dysfunction plays an important role in the oxidative stress response (Sachdeva et al., 2014) of RPE cells, and been found to decline in the RPE of AMD samples (Wang et al, 2014). With decreased Nrf2 signaling, p62 can decrease and thus, impair aggrephagy during AMD.

Autophagy in Retinal Diseases

Autophagy clearly plays a protective role against disease in the retina and RPE. It has recently been found that the retina, and in particular the photoreceptors and RPE, of wild-type mice have constitutive autophagic events and that light exposure induces an additional autophagic response (Chen et al., 2013). Mice deficient in Beclin 1 or Atg7 develop severe retinal degeneration upon light exposure, indicating that autophagy is important for maintaining retinal homeostasis. Furthermore, impaired mitophagy, with Park2 deficiency, results in mitochondrial dysfunction and retinal degeneration. Given the highly abundant mitochondria in photoreceptors, mitophagy in addition to macroautophagy, plays an essential role in photoreceptor homeostasis. Since autophagy in photoreceptors is covered in another review in this issue, we will not discuss it further here.

In general, autophagy decreases with aging (Cuervo and Dice, 2000); further, decreased autophagy with aging in retinas of C57BL6 mice has recently been described (Rodriguez-Muela et al, 2013). The aging retinas did not have an increase in autophagy related compartments, suggesting that the defect occurs during autophagosomal formation and not during degradation. The decline in macroautophagy was partially compensated by chaperone-mediated autophagy, where several rate-limiting components were upregulated, such as Lamp2A and Hsc70. Similarly, in mice deficient of Atg5 specifically in rod photoreceptors, retinas displayed increased TUNEL positive rods, coincident with decreased scotopic vision. Because the decreased rod mediated vision with impaired autophagy mirrors that of age-related vision loss, the authors speculated that impaired autophagy contributes to decreased vision with aging. The reduction in retinoids from impaired autophagy is perhaps a specific aspect of autophagy that explains the decreased vision during aging (Kim et al., 2013), especially because the visual function can be recovered to some extent, with vitamin A supplementation (Owsley et al, 2006).

Autophagy appears to have a biphasic response in AMD. Autophagy is increased in the RPE in aging and early AMD to compensate for oxidative stress and damaged organelles (Mitter et al., 2014). In two AMD mouse models and human AMD samples, LC3, ATG7 and ATG9 were increased in the RPE and retinal layers. Likewise, Wang et al. reported that Atg12 immunolabeling and Atg12-Atg5 and LC3 proteins were increased in the RPE/Bruch's membrane of elderly mice (Wang et al., 2009). However, LC3, ATG7, and ATG9 are decreased in advanced AMD samples, suggesting that autophagy failure contributes to late disease (Mitter et al., 2014).

Dysregulated inflammation contributes to AMD pathology. In addition to genetic variants in multiple complement factors being associated with AMD risk (Edwards et al., 2005, Haines et al., 2005, Klein et al., 2005, Yates et al., 2007, Maller et al., 2007 and Kondo et al., 2010), the NLRP3 inflammasome has been implicated in geographic atrophy development (Tarallo et al, 2012). A decrease in Dicer causes an increase in Alu RNAs, oxidative stress, mitochondrial dysfunction, oxidized mitochondrial DNA, and lysosomal permeability, all of which can activate the inflammasome and are relevant stimulants in AMD (Halle et al., 2008, Hornung et al., 2008, Tschopp et al., 2010, Zhou et al., 2011, Kauppinen et al., 2012 and Shimada et al., 2012). Autophagy controls NLRP3 inflammasome activation by degrading inflammasome components and effector molecules (Shi et al., 2012 and Harris et al., 2011). With an autophagy decline, inflammasome control can be compromised, resulting in excessive activation and potential tissue injury (Zhou et al., 2011 and Nakahira et al., 2011). Given the role of the inflammasome in AMD, impaired inflammasome control by decreased autophagy in the RPE may contribute to an exaggerated inflammatory response during late AMD.

Perspective

Lysosomes are a heterogeneous collection of distinct organelles, specialized for intracellular digestion. mTORC1 regulates the biogenesis, distribution, and activity of lysosomes. In neurodegenerative diseases, such as Alzheimer's and Parkinson's, several studies suggest that defective lysosomal clearance is involved in disease pathogenesis (Bergamini et al.,

2004, Keller, 2004 and Shintani and Klionsky, 2004). We believe that prolonged impairment of lysosomal clearance in the RPE, as seen in our *Cryba1* genetic animal models, can lead to pathological changes reminiscent of AMD. The mTORC1 pathway regulates many major cellular processes and is implicated in an increasing number of pathological conditions, including cancer, obesity, type 2 diabetes and neurodegeneration (Efeyan et al., 2012). A multicenter study (Interventions Testing Program) conducted by the National Institute of Aging, reported that mTOR inhibition with rapamycin extends the life span of mice (Harrison et al., 2009). While rapamycin or rapalogs (Lamming et al., 2013) have shown therapeutic efficacy for age-related pathologies in animal models, significant side effects limit their use in humans. Therefore, selective targeting of the mTORC1 signaling pathway may offer a safe mode for the treatment of age-related diseases, such as AMD. A better understanding of the functions of the mTOR interacting proteins would allow for the development of novel modulators of mTOR complexes that perturb their function in specific ways. The mTORC1 signaling pathway in the lysosome is becoming a legitimate target for developing therapeutic approaches for human diseases, such as AMD, where dysfunction of the lysosomal–autophagic pathway is apparent. We are optimistic that β A3/A1-crystallin represents a potential avenue of targeting the autophagic-lysosomal process in RPE in an effort to restore or maintain normal lysosomal function in human AMD disease.

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- In the RPE, lysosomes modulate both heterophagy and autophagy to maintain retinal homeostasis.
- The mTORC1 signaling pathway regulates the biogenesis, distribution and activity of lysosomes.
- β A3/A1-crystallin is a novel target for restoring normal lysosome function in human AMD disease.

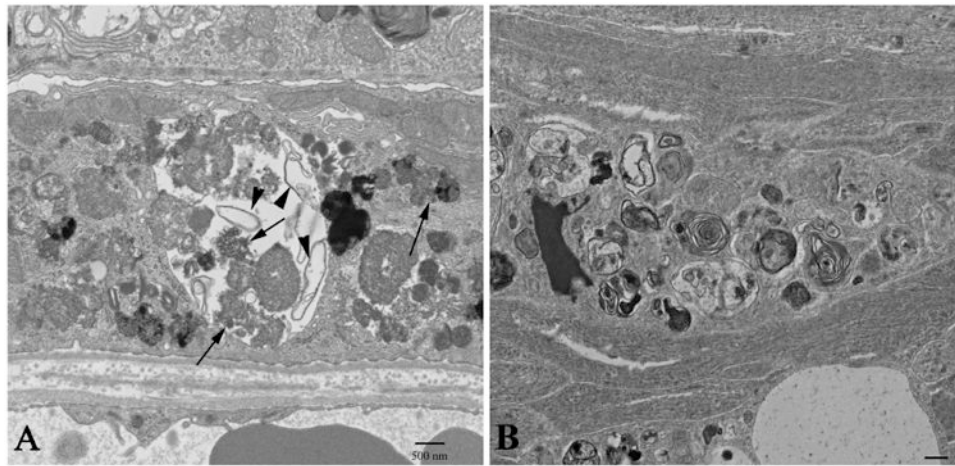


Figure 1. Effects of Lysosomal dysfunction on RPE cell ultrastructure

Transmission electron microscopy (TEM) was used to compare the cellular ultrastructure of the RPE in the Nuc1 rat (A) and a 95-year old human subject with geographic atrophy (B). Nuc1 is a spontaneous mutation in *Cryba1*, the gene encoding β A3/A1-crystallin, a lysosomal protein in RPE cells that participates in lysosomal-mediated clearance. The Nuc1 RPE at 1 year of age shows a large vacuole containing both partially degraded cellular organelles (arrowheads) and lipofuscin-like aggregates (arrows). The RPE from the foveal region of a 95-year old geographic atrophy subject (B) shows similar changes in the fibro-cellular formation located above Bruch's membrane near the area of atrophy. Scale bar= 500nm.

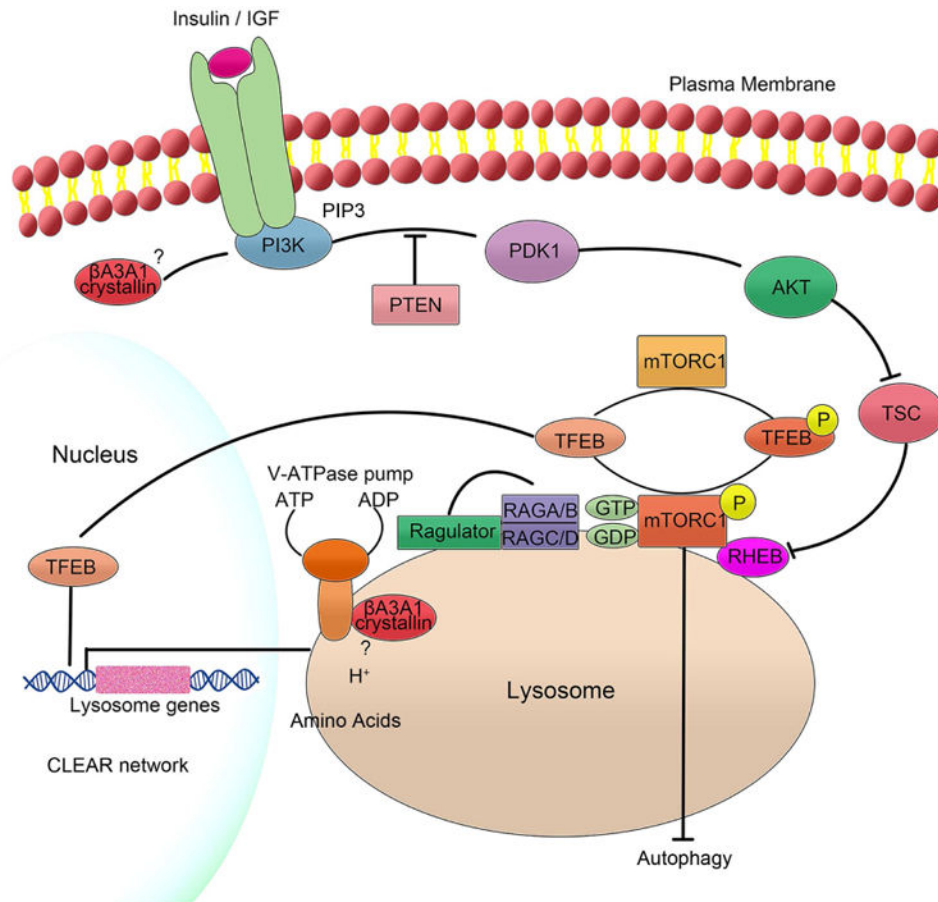


Figure 2. A schematic diagram showing activation of mTORC1 and a possible role for β A3/A1-crystallin

mTORC1 has been shown to integrate inputs from extracellular signal proteins, such as growth factors as well as amino acids and other nutrients. It is now known that V-ATPase interacts in an amino acid sensitive manner with pentameric Ragulator, a scaffolding complex that anchors the heterodimeric Rag GTPases to the lysosomes. This leads to the translocation of the inactive mTORC1 to the lysosomal surface. Once mTORC1 is on the surface of the lysosomes, it is activated by Rheb that is also localized to the lysosomal surface. It has been postulated that amino acids are probably translocated to the lysosomal lumen by V-ATPase and that amino acid signaling from the lysosomal lumen plays an important role in the complex process of recruiting mTORC1 to the lysosomal surface and activating it. We have recently shown that β A3/A1-crystallin is localized to the lysosomal lumen of RPE cells and is a binding partner of V-ATPase. It is also known that in the presence of growth factors or insulin, Akt inhibits Tsc, which releases its inhibitory activity on Rheb, thus allowing the activation of mTORC1. We have previously shown that β A3/A1-crystallin regulates cell survival in astrocytes through PI3K/Akt/mTOR. Further, following autophagy induction both *in vivo* and *in vitro*, phospho-Akt and phospho-Raptor decrease, while phospho mTOR increases in RPE cells, inhibiting autophagy and Akt/mTORC1. mTORC1 also regulates lysosomal function by directly preventing autophagy and Transcription factor EB (TFEB) activation. Unphosphorylated TFEB accumulates in the

nucleus, where it activates genes in the Coordinated Lysosomal Expression and Regulation (CLEAR) network (such as V-ATPase) that act to support lysosomal function. Once TFEB is phosphorylated by mTORC1, TFEB transiently binds to the lysosomal surface and is also retained in the cytoplasm. It is possible that upstream inputs, such as from β A3/A1-crystallin to mTORC1 can contribute to novel regulation of TFEB in RPE cells. β A3/A1-crystallin produces two closely related proteins, β A3 and β A1, differing only in 17 amino acids in their amino termini from a single *Cryba1* mRNA using an alternative translation by leaky scanning. It is possible that β A3- and β A1-crystallins exert their functions independently in the activation of mTORC1 in RPE, e.g. via modulation of V-ATPase/mTOR and PI3K/Akt/mTOR.

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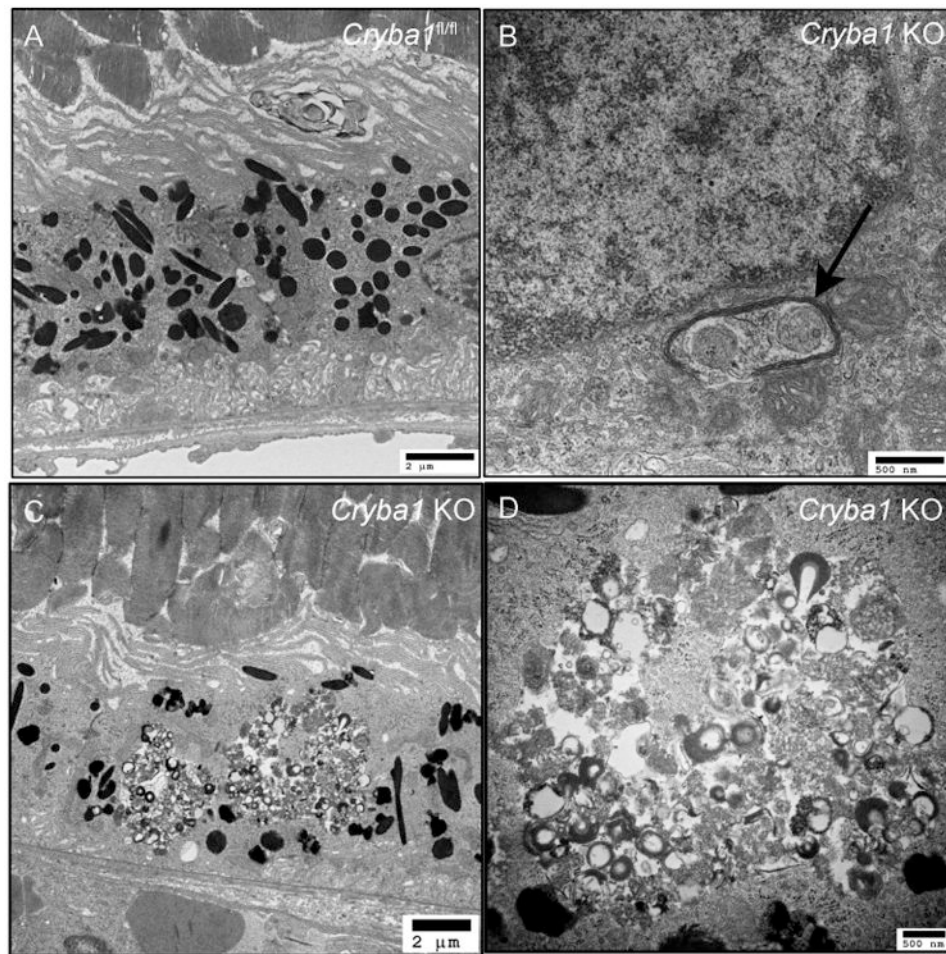


Figure 3. Lysosomal dysfunction inhibits organelle clearance by selective autophagy
Transmission electron microscopy showing RPE in a 20 month old *Cryba1* floxed (wild type) mouse (A). The *Cryba1* knockout mouse at the same age shows degenerative changes in the RPE (C), including accumulation of undigested material (D is higher magnification of C). Inefficient lysosomal clearance affects mitophagy as seen in (B). Damaged mitochondria are enclosed by an autophagosome (arrow), but not cleared.

