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The heart of autophagy: Deconstructing cardiac proteotoxicity

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Abstract

The heart is capable of robust structural remodeling, sometimes improving performance and sometimes leading to failure. Recent studies have uncovered a critical role for autophagy in disease-related remodeling of the cardiomyocyte. We have shown previously that hemodynamic load elicits a maladaptive autophagic response in cardiomyocytes which contributes to disease progression. In a recent study, we went on to demonstrate that protein aggregation is a proximal event triggering autophagic clearance mechanisms. The ubiquitin-proteasome-dependent pathways of protein clearance are similarly activated in parallel with processing of stress-induced protein aggregates into aggresomes and clearance through autophagy. These findings in the setting of pressure overload contrast with protein aggregation occurring in a model of protein chaperone malfunction in myocytes, where activation of autophagy is beneficial, antagonizing disease progression. Our findings situate heart disease stemming from environmental stress in the category of proteinopathy and raise important new questions regarding molecular events that elicit adaptive and maladaptive autophagy.

Keywords

cardiac hypertrophy; heart failure; cardiomyocyte; cardiac remodeling

A striking feature of the heart is its capacity for structural remodeling in response to environmental demands.¹ Indeed, the heart is a remarkably plastic organ, capable of growing or shrinking in the setting of a variety of physiological or pathological stimuli. In some instances, cardiac growth is beneficial, facilitating the organism's response to exercise, postnatal development or pregnancy. In other instances, such as the stress of hypertensive disease or infarction, cardiac remodeling is maladaptive, predisposing to arrhythmia and heart failure. In yet other situations, such as prolonged bedrest or weightlessness, the heart actually shrinks. There is great interest in developing therapeutic strategies that promote physiological cardiac remodeling and minimize the pathological variety.

Autophagy Contributes to Cardiac Remodeling

Growth and remodeling of the adult heart occur through changes in the balance between protein synthesis and protein degradation, as well as through the death (or survival) of individual myocytes. During hypertrophic growth, enhanced protein synthesis leads to an increase in the size of individual myocytes and heightened organization of intracellular force-generating units (sarcomeres). With time, decompensation ensues as the ventricular walls thin through a

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combination of proteolysis and/or myocyte death with subsequent replacement by fibrotic tissue. Numerous signaling pathways are implicated in stress-induced growth of the heart, several of which are further implicated in cell death.² However, mechanisms governing the transition from compensated hypertrophy to heart failure are incompletely characterized.

It has been known for 30 years that lysosomal pathways are activated in a variety of models of heart disease.^{3–7} Indeed, a number of groups report increases in lysosomal activity in tissue samples from diseased and failing human hearts.^{8–14} More recent studies reveal an important role for autophagy in the cardiomyocyte response to numerous types of stress, and compelling evidence has emerged that this autophagic response participates in the pathogenesis of disease. For example, pressure overload, chronic ischemia, ischemia-reperfusion and diphtheria toxin-induced injury each provokes an increase in autophagic activity in cardiomyocytes.^{15,16} Our group demonstrated recently that in pressure-overload heart failure, a common form of clinical disease, induction of autophagic activity is both robust and maladaptive.¹⁷ Work is underway now to identify molecular mechanisms governing autophagic activation in cardiac remodeling and to determine whether the autophagic response promotes disease progression or antagonizes it.

Protein Quality Control and Proteotoxic Disease

Strict regulation of proteolysis is critical in long-lived postmitotic cells such as cardiac myocytes, where the ability to replace cells is limited, yet intracellular proteins and organelles turn over continuously. Failure of this system leads to aggregation of misfolded proteins, which are toxic to the cell. In fact, proteinopathy, a disease characterized by toxic aggregations of misfolded proteins, is a growing family of human disorders, which includes Alzheimer disease, Parkinsonism, amyotrophic lateral sclerosis, and both poly-glutamine and polyalanine expansion disorders.¹⁸ Consistent with proteotoxicity being a mechanism contributing to heart disease, abnormal protein aggregation and accumulation of ubiquitinated proteins in the cytosol are sometimes detected in human hearts with idiopathic or ischemic cardiomyopathies.^{12,19,20}

Insoluble protein aggregates are processed by pathways that are just now being deciphered (Fig. 1). First, misfolded proteins can be degraded by proteasomes throughout the cytoplasm. However, as proteins begin to aggregate, they are delivered to the MTOC (microtubule organizing center) by dynein-dependent retrograde transport along microtubules. When the degradative capacity of the proteasome is exceeded, protein aggregates accumulate in perinuclear inclusions called aggresomes,²¹ organized structures surrounded by vimentin filaments that recruit chaperones, ubiquitin, proteasomes and mitochondria. Relatively little is known regarding whether intra-cellular inclusions are toxic themselves, or whether they represent a compensatory mechanism that sequesters harmful, soluble proteins within the cytoplasm. Whereas toxicity is sometimes disease-specific—related to loss of function of the mutated or misfolded protein—there is general agreement that early, still-soluble aggregates are potentially harmful.²² Indeed, evidence in neurons suggests that it is the soluble pre-amyloid aggregates that are the most toxic,²³ perhaps through the exposure of buried moieties such as main chain amino and carboxyl groups that could serve as hydrogen bond donors or acceptors in abnormal interactions with other proteins. Also, in many instances, mutations responsible for proteinopathies confer a toxic gain of function to the relevant protein.

Autophagy serves both to recycle cellular components and to eliminate damaged proteins or organelles that might otherwise be toxic or trigger apoptotic death. For example, targeted inhibition of *Atg7*, a gene required for autophagic activity, leads to accumulation of ubiquitin-positive aggregates.²⁴ Further, in the absence of basal levels of autophagic activity in the brain^{25,26} and the heart,²⁷ abnormal aggregates of intracellular proteins develop. In some

settings, however, autophagic activity is associated with the pathogenesis of disease, and unrestrained autophagic activity can cause cell death.²⁸

In many instances of proteinopathy, autophagy is activated as a clearance mechanism. For example, autophagy is activated in proteinopathic neuronal diseases, including Huntington's disease, amyotrophic lateral sclerosis, Parkinsonism and Alzheimer disease.²⁹ The prevailing notion is that autophagic pathways serve a beneficial function by facilitating removal of aggregates too large for efficient proteasome-mediated clearance.³⁰ In fact, in several neurodegenerative diseases, a strong association exists between induction of autophagy and the presence of protein aggregates.^{31,32} Further, pharmacologic or genetic induction of autophagy is sufficient to reduce polyglutamine-induced cytotoxicity in animal models of Huntington's disease.³³ That we and others do not detect membrane-bound inclusions, and the inclusions we detect are much larger than mammalian autophagosomes,^{34,35} suggests that autophagy serves to clear monomeric and oligomeric precursors of aggregates, rather than the large inclusions themselves. Taken together, these data are consistent with the notion that intracellular protein aggregates are capable of stimulating autophagic activity which serves, in turn, to facilitate clearance of the aggregates.

Proteotoxicity in Load-induced Heart Disease

Our group has focused recently on heart disease stemming from pressure overload, i.e., settings where the ventricle must work against, and generate, abnormally high levels of pressure. Common examples include hypertension, prior myocardial infarction (such that the myocardium which remains viable and functioning must perform the work of the tissue that has died), or stenotic aortic valvular disease. The public health significance of these diseases is highlighted by the fact that one-third of U.S. adults have hypertension.³⁶

We set out to determine the molecular events within the pressure-stressed cardiomyocyte that trigger autophagy. First, it is clear that numerous processes can trigger autophagy in a variety of settings.³⁷⁻⁴⁰ Among these, we established a link between protein aggregation and induction of cardiomyocyte autophagy,³⁴ finding that accumulation and aggregation of ubiquitinated protein is a powerful inducer of autophagy, capable of activating autophagy to levels comparable to pharmacologic induction. We also described the accumulation in vivo of ubiquitinated proteins in a spatial and temporal pattern consistent with our prior report of pressure overload-induced autophagy.¹⁷ In other words, the regions with maximal autophagic activity contained the highest density of ubiquitinated protein aggregates. We further characterized the organization of damaged proteins into vimentin associated, peri-nuclear, aggresome-like structures. We found that total proteasome activity is increased in heart failure, suggesting increased flux through proteasomal degradation pathways and consistent with similar findings in a model of desmin-related cardiomyopathy.⁴¹ Thus, proteasomal and autophagic activities increase in parallel, and the accumulation of ubiquitinated aggregates is not due to diminished proteasome-mediated degradation but rather stems from de novo protein synthesis.

Our findings are the first to describe aggresome formation in a common cardiovascular disorder, that is, load-induced heart disease, placing pressure-overload heart disease in the category of proteinopathies. Further, they are consistent with a model where autophagic activity is a general response to protein aggregation in the heart and point to a potential role for autophagy in cardiomyopathies of diverse etiology.

In another study,³⁵ we tested whether autophagy plays a role in a different form of proteotoxic heart disease, namely desmin-related myopathies (DRCM) where mutations in genes encoding desmin or the chaperone protein alpha-B-crystallin (CryAB) lead to accumulation of protein aggregates, profound heart failure, and eventually death.⁴²⁻⁴⁴ In that study, we also observed

robust activation of autophagic clearance pathways. In the context of this disease, however, we find that autophagy is a beneficial, adaptive response which serves to antagonize disease progression.³⁵

How do Protein Aggregates Trigger Autophagy?

In many instances, autophagy and the ubiquitin-proteasome system are activated in parallel as clearance mechanisms to eliminate aggregating (and aggregated) proteins. For example, atrophy of mammalian skeletal muscle depends on an increase in abundance of ubiquitin ligases, ubiquitination of myosins and other sarcomeric proteins, and then degradation via the proteasome,⁴⁵ whereas mitochondria and other organelles are engulfed in autophagic vacuoles. Many degenerative muscle diseases are associated with an increase in protein ubiquitination, protein aggregates and autophagic vesicles. If protein ubiquitination outpaces proteasome capacity, aggregates of ubiquitinated proteins may accumulate. Consistent with this, accumulation of ubiquitin aggregates is used as a marker for autophagocytosis in neurons and insect flight muscle.⁴⁶ Thus, activation of autophagy at early stages of the disease may be a protective mechanism to scavenge and eliminate misfolded, polyubiquitinated protein aggregates that have overwhelmed the degradative capacity of the proteasomal system.

Another way in which protein aggregates may elicit an autophagic response is through interaction with mitochondria. Some types of protein aggregates stain positive for Congo red, indicative of an amyloid protein configuration. This is true of protein aggregates found in a number of neurological diseases associated with increased autophagic activity²² and in the DRCM CryAB mutant heart.⁴⁷ Interestingly, amyloid proteins are capable of triggering mitochondrial permeability transition (MPT) by inserting into mitochondrial membranes.^{48–50} MPT can trigger either apoptosis or selective autophagic degradation of the affected mitochondria through a process termed mitophagy.⁵¹ Many other cellular stresses are capable of inducing MPT, including reactive oxygen species (ROS) and Ca²⁺ overload, processes frequently associated with cardiac stress. As a consequence of MPT, mitochondria depolarize, uncouple, swell and release cytochrome *c* as well as other pro-apoptotic proteins. Furthermore, uncoupled mitochondria are not only unable to generate ATP, they become a futile sink of ATPase activity. Thus, mitochondria that have undergone MPT must be repaired or removed to prevent a catastrophic loss of ATP, and consequent necrotic death, or triggering of apoptotic death. Mitophagy carries out this critical protective function. Ultimately, however, loss of too much mitochondrial content may be a key component of autophagic cell death.

Although protein aggregates accumulate in the myocardium in response to either hemodynamic stress or genetic mutation of critical proteins, experimental evidence indicates that autophagy is maladaptive in one context and beneficial in the other. Important questions for the future include whether there are inherent differences in the types of protein aggregates that form and/or in the associated autophagic response. What other factors stimulate autophagic activity in the heart? Is the pathophysiological outcome determined by severity of the autophagic response or the nature of the autophagy substrate?

Perspective

There is urgent need to identify mechanisms governing disease-related remodeling of the heart—and consequent systolic dysfunction, clinical heart failure, and arrhythmic sudden death—to improve treatment and prevention. It is apparent that cardiac autophagy is induced by diverse forms of cardiovascular stress, and the net effect of this activity, adaptive versus maladaptive, appears to be context dependent. A fundamental function of autophagocytosis is the removal of damaged protein aggregates,³⁰ a concept we recently extended to pressure-stressed myocardium³⁴ and to a genetic model of chaperone malfunction.³⁵ Further, our data point to a progression of protein damage, aggregation and coalescence into aggresomes as a previously

unrecognized mechanism of heart disease. As new advances emerge in deciphering molecular regulation of autophagy, it may soon be possible to enhance or inhibit autophagic activity selectively to have a meaningful impact upon heart disease.

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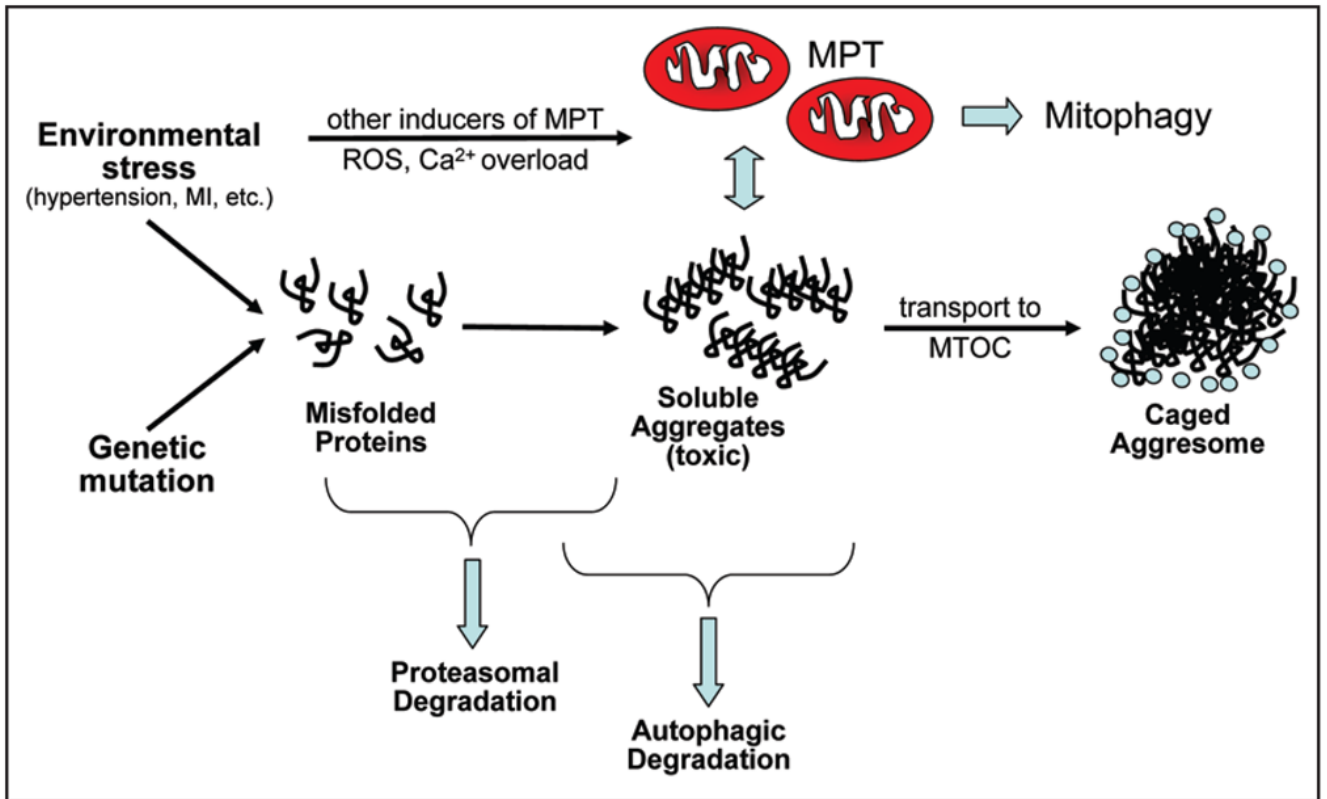


Figure 1.

Working model of the cellular response to proteotoxicity in cardiomyocytes. Misfolded proteins can arise as a consequence of either environmental cardiac stress or inherited genetic mutation. Accumulated proteins aggregate into soluble complexes that are then transported along microtubules toward the MTOC to form insoluble, caged aggresomes. Proteasomal and autophagic pathways are activated in parallel, targeting different but overlapping sets of substrates. Soluble aggregates are thought to be the toxic species and may induce a specialized form of autophagy called mitophagy by promoting MPT. MPT can also occur in response to aggregate-independent signals occurring in stressed myocardium. The pathophysiological consequences of cardiac autophagy likely depend upon both the rate of flux through these pathways and the cellular components being degraded.