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## Shared and Distinct Mechanisms of Skeletal Muscle Atrophy: A Narrative Review

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### Abstract

Maintenance of skeletal muscle mass and function is an incredibly nuanced balance of anabolism and catabolism that can become distorted within different pathological conditions. In this paper we intend to discuss the distinct intracellular signaling events that regulate muscle protein atrophy for a given clinical occurrence. Aside from the common outcome of muscle deterioration, several conditions have at least one or more distinct mechanisms that creates unique intracellular environments that facilitate muscle loss. The subtle individuality to each of these given pathologies can provide both researchers and clinicians with specific targets of interest to further identify and increase the efficacy of medical treatments and interventions.

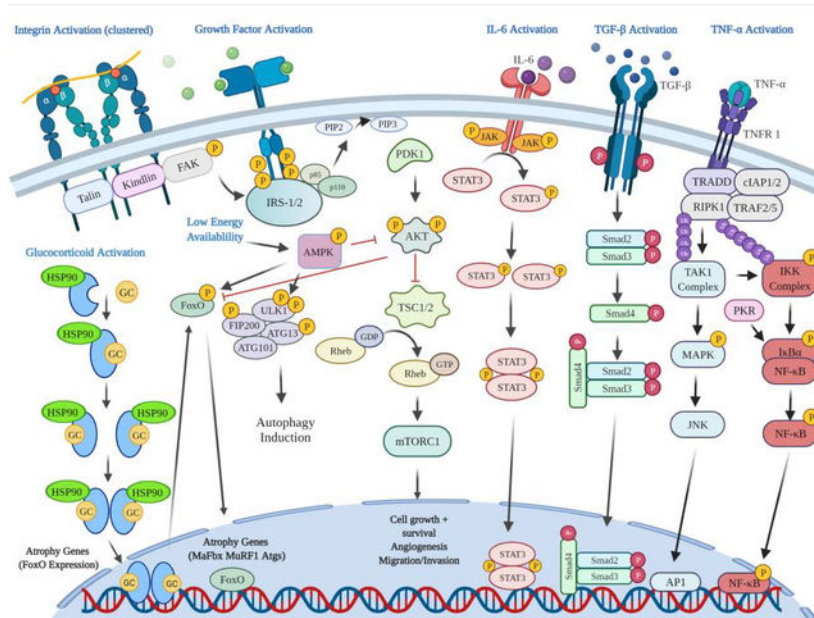
### Graphical Abstract

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Above shows varying signaling pathways that regulate both skeletal muscle anabolism and catabolism. Focal Adhesion Kinase (FAK) is shown activate mammalian target of rapamycin (mTOR) in response to mechanical load through the phosphatidylinositol 3 kinase (PI3K), protein kinase B (AKT) pathway. Insulin or insulin-like growth factor (IGF) stimulation can activate mTOR through the same cascade. Also shown are the catabolic pathways related to inflammatory cytokines such as tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ), and interleukin-6 (IL-6). TNF- $\alpha$  receptor 1 (TNFR1) ligand binding activates nuclear factor kappa-light-chain-enhancer of activated B cells (NF- $\kappa$ B) and c-Jun N-terminal kinase (JNK) pathway increasing rates of proteolysis. Protein Kinase R (PKR) can also stimulate the activation of NF- $\kappa$ B. IL-6 receptor binding activates the Janus Kinase (JAK) Signal Transducer and Activator of Transcription (STAT) signaling that can increase rates of muscle loss. Transforming Growth Factor-beta (TGF-  $\beta$ ) receptor binding facilitates small mothers against decapentaplegic (SMAD) homologs 2 and 3 (SMAD2/3) phosphorylation, and subsequent SMAD 4 phosphorylation, upregulating genes related to collagen synthesis and fibrosis. Additionally, glucocorticoid (GC) receptor activation, dimerization, and DNA binding subsequently facilitates increases in FOXO expression which can increase the expression of UPS related E3 ligases. During low energy availability, increased 5' adenosine monophosphate-activated protein kinase (AMPK)- Unc-51 like autophagy activating kinase 1 (ULK1) phosphorylation induces the activation of autophagy related processes.

**Keywords**

Muscle Protein Degradation; Sarcopenia; Muscle Loss; Atrophy; Cachexia; Catabolism

**Introduction**

Skeletal muscle is a dynamic tissue that is remodeled through a balance of anabolic and catabolic processes that are governed by a variety of factors (McCarthy and Esser,

2010). Increased rates of muscle protein synthesis (MPS) by anabolic processes maintains correct skeletal muscle architecture and contractile properties by creating new functional proteins. Conversely, catabolic processes increase muscle protein degradation (MPD), which is a normal process for removal of damaged or inadequately functioning proteins. Both anabolism and catabolism exist in a harmonious balance that is controlled by diet and exercise within normal populations (Tipton et al., 2004). Muscle loss or dysfunction is observed in various situations such as: cancer cachexia, obesity related chronic inflammation, ageing sarcopenia, immobilization, muscular dystrophy, and peripheral artery disease (PAD) (Collins et al., 2018; Dirks et al., 2016; English and Paddon-Jones, 2010; Penet and Bhujwala, 2015; Pipinos et al., 2008a, 2008b; Rolland et al., 2008). Within each of these situations, shared and distinct signaling cascades that result in negative protein balance function to ultimately decrease the mass and function of skeletal muscle tissue. In this review, we aim to discuss and examine the varying situational mechanisms of skeletal MPD. The purpose of the review is to discuss the cellular and molecular mechanisms controlling skeletal muscle atrophy induced by various pathological conditions. Specifically, we discuss both shared pathways as well as condition-specific differences associated with muscle atrophy. We begin by providing an overview of catabolic and anabolic systems regulating MPD and MPS. This is followed by a discussion of the specific pathophysiological mechanisms that have been identified to play a role in muscle atrophy from both preclinical studies as well as human studies.

## The Skeletal Muscle Proteolytic Systems

### Calpains

There are three proteolytic systems that function to remove and breakdown protein from skeletal muscle tissue: the calpain, ubiquitin-proteasomal, and autophagy lysosomal systems. Calpains are intracellular calcium ( $\text{Ca}^{2+}$ )- dependent cysteine proteases that belong to the papain protease superfamily (Ono and Sorimachi, 2012; Sorimachi et al., 1989). Three separate calpains exist within skeletal muscle, which include;  $\mu$ - and m- (or calpain-1 and calpain-2, respectively) and muscle specific calpain-3 (formally known as CAPN3[p94]) (Ono and Sorimachi, 2012; Sorimachi et al., 1989). In order to become active, calpain-1 and calpain-2 must form a heterodimer with calpain small subunit-1 (formally known as CAPNS1[30k]) producing either calpain-1/S1 or calpain-2/S1 conformations within the cytosol, respectively (Ono and Sorimachi, 2012). Calpain-1 and calpain-2 activity is dependent on the formation of a heterodimer with calpain small subunit-1 which acts as a regulatory subunit (Ono and Sorimachi, 2012). Muscle specific calpain-3, however, forms a homodimer and interacts with connectin/titin between the Z- and M-lines within muscle (Hayashi et al., 2008; Ono and Sorimachi, 2012; Sorimachi et al., 1995). Calpain activation occurs allosterically with increased  $\text{Ca}^{2+}$  concentration within the cytosol of the myofibril (Byrd, 1992; Takekura et al., 2001). Increased intracellular  $\text{Ca}^{2+}$  concentration can occur from excitation-contraction coupling or myofibrillar damage to the t-tubule and sarcoplasmic reticulum (Byrd, 1992; Takekura et al., 2001). Calpains are activated in both rats and humans in response to exercise and are currently thought to help with the early stages of myofibrillar remodeling (Belcastro, 1993; Hsieh et al., 2008; Huang and Forsberg, 1998). Interestingly, activated calpains *in vivo* exhibit selective proteolysis of

receptor proteins, membrane proteins such as protein kinase A and C, cytoskeletal proteins, and contractile proteins (Belcastro et al., 1998; Busch et al., 1972; Saido et al., 1994). Additionally, this selectivity to cleave specific protein sites enables calpains to cleave and release proteins inaccessible by other proteolytic systems (Goll et al., 2008; Hyatt and Powers, 2020; Neti et al., 2009). Therein, it appears that the calpain system does also appear to work in concert with the other proteolytic systems, complementing them to cleave and degrade proteins in an organized and somewhat sequential fashion.

### Ubiquitin Proteasomal System

Another major proteolytic system used to disassemble proteins into their individual amino acid constituents is the ubiquitin proteasomal system (UPS). This system uses a series of cytosolic enzymes to tag and chaperone proteins to a large proteasome complex that subsequently degrades the protein. The tagging and chaperoning of proteins occurs through a series of steps that are regulated by a ubiquitin activating enzyme (E1), a ubiquitin conjugating enzyme (E2), and a ubiquitin ligase (E3) (Kleiger and Mayor, 2014). E1 enzymes initiate this cascade by creating a thioester bond with the ubiquitin molecule's C-terminal glycine residue and the E1's catalytic cysteine residue, activating the ubiquitin protein (Hann et al., 2019; Kleiger and Mayor, 2014). The activated ubiquitin (now bound to the E1 activating enzyme) is then subsequently transferred to the E2 conjugating enzyme's catalytic cysteine residue (Hann et al., 2019; Kleiger and Mayor, 2014). The ubiquitin-bound E2 enzyme then binds a class of E3 ligases; either a Really Interesting New Gene/U-box-type (RING), Homologous to E6AP C-Terminus-type (HECT), or a RING Between RING (RBR) E3 ligase (Weber et al., 2019; Ye and Rape, 2009). Once bound to one of these E3 ligases, the ubiquitin is then subsequently transferred from the E2 to the E3, and then bound to a lysine residue on the target protein (Hann et al., 2019; Kleiger and Mayor, 2014; Weber et al., 2019; Ye and Rape, 2009). Following the initial ubiquitination, formation of a poly-ubiquitin chain of at least four ubiquitin molecules must be formed before a protein will undergo degradation (Kleiger and Mayor, 2014). Once the protein reaches sufficient ubiquitin chain length, it is transported to the 26S proteasome (comprised of a core 20S subunit and two 19S regulatory subunits that form two caps on the 20S core). The ubiquitin chain on the target protein docks to the 19S subunit of the 26S proteasome by anchoring to the receptor's proteasome regulatory particle base subunit 10 (Rpn10) and Rpn13 (Elsasser et al., 2004; Kleiger and Mayor, 2014). Once bound to the 19S receptors, the entire ubiquitin chain is cleaved which creates enough space for the target protein to enter the 20S core for degradation (Kleiger and Mayor, 2014). The 20S core is comprised of four heptameric rings, two outer  $\alpha$  rings that function as gate keepers, and two inner  $\beta$  rings that carry out the proteolytic functions (Ben-Nissan and Sharon, 2014). Within the heptameric  $\beta$  rings, there are three  $\beta$  subunits that are catalytically active and contain caspase-like, trypsin-like and chymotrypsin-like proteases, which are responsible for breaking down the target protein into oligopeptides (Ben-Nissan and Sharon, 2014). These small amino acid chains are currently thought to either be recycled for the creation of other proteins, used for energy metabolism, or removed from the cell.

Glucocorticoids and proinflammatory cytokines such as tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ), and various interleukins (IL) such as IL-1 are known to increase ubiquitin proteasomal

activity within skeletal muscle (Lecker et al., 2006; McElhinny et al., 2002). For example, the membrane permeable glucocorticoid is able to bind its intracellular receptor within muscle, form a homodimer with another activated glucocorticoid receptor and bind the glucocorticoid response element, upregulating the expression the muscle specific E3 ligase, muscle RING finger protein 1 (MuRF1) as well as O-type forkhead transcription factors (FOXO) and kruppel-like factor-15 (KLF-15) (Bodine and Baehr, 2014). The increased expression of FOXO's or KLF-15 then subsequently binds to the promoter region of the other muscle specific E3 ligase, muscle atrophy F-box (MaFbx), and induces its expression (Bodine and Baehr, 2014). Similarly, TNF- $\alpha$  binds to its transmembrane receptor and subsequently leads to the activation of the transcription factor nuclear factor kappa-light-chain-enhancer of activated B cells (NF- $\kappa$ B), which also increases the expression of MuRF1 and MaFbx, thus increasing MPD (Glass, 2005). Although other homologs of MuRF1 exist, such as MuRF2 and MuRF3, current evidence suggests muscle atrophy is only associated with MuRF1 (Baehr et al., 2011; Bodine and Baehr, 2014). Interestingly, MuRF1, MuRF2, and MuRF3 have been shown to localize at the M-lines, while MuRF1 and MuRF3 have been found at the Z-lines of sarcomeres (Bodine and Baehr, 2014; Centner et al., 2001; McElhinny et al., 2002). This would seem to indicate that the contractile apparatus of skeletal muscle are the target proteins for these E3 ligases. However, the ubiquitin proteasome system cannot degrade intact myofibrils, and it has been speculated that calpains work synergistically to allow contractile proteins to be bound and ubiquitinated for degradation (Goll et al., 2008; Jackman and Kandarian, 2004; Neti et al., 2009).

### Autophagy Lysosomal System

The third intracellular proteolytic pathway which coordinates protein breakdown in skeletal muscle is the autophagy lysosomal system. Autophagy is the only mechanism able to degrade large structures and, in the absence of stress, serves a house keeping function, eliminating damaged components that could become detrimental to the cell. There are three different defined types of autophagy: macro-autophagy, micro-autophagy, and chaperone-mediated autophagy (Glick et al., 2010). All three types result in the lysosomal degradation of proteins by various acid hydrolases such as cathepsins, carboxypeptidases, and aminopeptidases (Glick et al., 2010; Kaushik and Cuervo, 2018; McEwan and Dikic, 2010; Oku and Sakai, 2018). Macro-autophagy is a process that allows larger cytosolic proteins, such as organelles, to be degraded within cells. Macro-autophagy begins with the creation of a membrane known as a phagophore, that expands to surround proteins, organelles, and ribosomes eventually creating a double-membrane autophagosome (McEwan and Dikic, 2010). The autophagosome acts as a transport vehicle that fuses with a lysosome allowing for the degradation of the encased proteins by lysosomal acid proteases (Glick et al., 2010). In micro-autophagy, cytosolic components are directly engulfed by the lysosome without requiring the fusion of an autophagosome by various mechanisms such as lysosomal wrapping, lysosomal invagination, or endosomal invagination (Oku and Sakai, 2018). Chaperone-mediated autophagy is a process where specific proteins that contain the pentapeptide KFERQ-like motif are bound to heat shock cognate 71 kDa protein (HSC70) and shuttled to the lysosome for degradation (Kaushik and Cuervo, 2018). Approximately 25–30% of all cellular proteins contain a homologous pentapeptide sequence that enables binding and translocation to the lysosome by HSC70 and its co-chaperones (Kaushik

and Cuervo, 2018; Knecht and Salvador, 2013). At the lysosomal membrane, the target protein and HSC70 bind to a lysosome-associated membrane protein type 2A (LAMP2A), which initiates the unfolding of the target protein by the chaperone proteins (Kaushik and Cuervo, 2018). An isoform of HSC70 is present within the lysosome and helps facilitate the movement of the unfolded target protein from the cytosol through the translocation complex at the membrane and into the lysosome for degradation (Kaushik and Cuervo, 2018).

Macro-autophagy is suspected to be the responsible for most intracellular MPD and will be the predominant autophagy pathway discussed throughout the remainder of this review. Macro-autophagy is stimulated by energy depletion, low glycogen concentration, low intracellular amino acid content, hypoxia, and inflammation. On the contrary, macro-autophagy is inhibited by insulin signaling, as well as by activation of mammalian target of rapamycin complex 1 (mTORC1) (Rabinowitz and White, 2010). The molecular studies which characterized macro-autophagy initiation found that proteins created from autophagy-related genes (Atg), such as Atg1, coordinate the formation of autophagosomes in yeast and fungus (He and Klionsky, 2009; Rabinowitz and White, 2010). In nutrient depleted conditions, Atg1 forms a protein complex with Atg13, Atg17, Atg29, and Atg31, and is thought to stimulate autophagosome formation (Kabeya et al., 2005). In mammals, Atg1 has a homologous protein known as Unc-51 like autophagy activating kinase 1 (ULK1) that helps facilitate the autophagy cascade (He and Klionsky, 2009; Rabinowitz and White, 2010). ULK1 forms a complex with mammalian Atg13 (mAtg13), focal adhesion kinase (FAK) family-kinase interacting protein of 200 kDa (FIP200), and Atg101 (Hara et al., 2008; Hosokawa et al., 2009; Mercer et al., 2009; Park et al., 2016). Under nutrient deprivation, 5' adenosine monophosphate-activated protein kinase (AMPK) phosphorylates ULK1 on multiple residues, resulting in ULK1 activation and the subsequent phosphorylation of both FIP200 and mAtg13 in the bound complex (Mao and Klionsky, 2011; Park et al., 2016). This complex is then thought to be translocated to the endoplasmic reticulum tubulovesicular membranes, which are tagged with Atg9-containing vesicles to help facilitate autophagosome membrane formation (Zachari and Ktistakis, 2020). The process of autophagosome formation is incredibly detailed and is thoroughly reviewed elsewhere (Galluzzi et al., 2017; Yu et al., 2018; Zachari and Ktistakis, 2020).

## Apoptosis

In addition to these proteolytic systems, apoptosis, or programmed cell death, may also be an important contributing factor for muscle atrophy in certain conditions, although its role is less well-defined (Dupont-Versteegden, 2006). The main enzymes thought to be involved in apoptosis are the caspases; caspase-8, 9, and 12 are involved in the initiation process, while caspase-3, 6, and 7 play a role in apoptosis execution (Dupont-Versteegden, 2006). Caspase activation occurs following changes in the ratio of pro- and anti- apoptotic proteins of the B-cell lymphoma (Bcl)-2 family. Specifically, Bcl-2 is considered anti-apoptotic and Bcl-2-associated X protein (Bax) is pro-apoptotic. High levels of calcium can initiate signaling that activates Bax and leads to its association with the mitochondrial membrane, where it is believed to play a role in promoting permeabilization and the release of important apoptotic signals such as cytochrome C (Garrido et al., 2006). However, Bax function can be inhibited by Bcl-2; thus an elevated Bax/Bcl-2 ratio can up-regulate caspase-3-induced

apoptosis (Garrido et al., 2006). Caspase-induced apoptosis is reviewed in detail elsewhere (Primeau et al., 2002a).

## Muscle Protein Synthesis

### PI3K-AKT-mTOR Pathway

In addition to enhanced MPD, muscle breakdown can also be potentially explained by reduced MPS. Research has demonstrated that signaling by mTOR plays a central role in the regulation of MPS (Laplante and Sabatini, 2012; Sengupta et al., 2010). Specifically, mTOR-mediated phosphorylation of the eukaryotic initiation factor 4E binding protein 1 (4E-BP1) results in recruitment of the initiation factor eIF4G to the 5' end of mRNA, promoting the initiation of protein synthesis (Haghighat et al., 1995). In addition, mTOR can phosphorylate and activate the p70 ribosomal protein S6 kinase (p70S6K), which can promote an increase in the activity of another initiation factor, eIF4A, providing an additional stimulus for initiation (Raught et al., 2004). The mTOR pathway can be activated by insulin binding to its receptor, triggering tyrosine kinase activity via insulin receptor substrate-1 (IRS-1), and subsequent activation of phosphatidylinositol 3 kinase (PI3K), which phosphorylates phosphatidylinositol-4,5-bisphosphate (PIP2) into phosphatidylinositol-3,4,5-triphosphate (PIP3). This results in the recruitment of phosphoinositide-dependent protein kinase-1 (PDK1), which phosphorylates and activates protein kinase B (Akt), which further activates mTOR (Goodman et al., 2010). Akt can also phosphorylate glycogen synthase kinase 3 $\beta$  (GSK-3 $\beta$ ), which can increase protein synthesis by increasing eukaryotic initiation factor 2B (eIF2B) activity (Welsh et al., 1998). Likewise, insulin-like growth factor-1 (IGF-1) can also bind to the insulin receptor or the IGF-1 receptor; however, the anabolic effects of IGF-1 are not demonstrable except in the presence of insulin (which mediates increased glucose and amino acid transport), consistent with the role for IGFs as permissive factors that augment signals of other factors (Biagetti and Simó, 2021; Hakuno and Takahashi, 2018; Musaro, 2010).

## Sarcopenia Age-Related Loss of Muscle

The term sarcopenia, coined by Irwin Rosenberg in 1989, refers to the age-associated loss of muscle mass. Sarcopenia is thought to affect up to 29% of older adults, with some estimates as high as 60%, depending on the definition and measure of muscle mass used (Mayhew et al., 2019). This natural loss of muscle mass and concomitant function can occur at a rate of 0.64–0.7% per year and 0.8–0.98% per year, in women and men over the age of 75, respectively (Mitchell et al., 2012). Epidemiological studies suggest that total lean body mass declines by ~18% in men and ~27% in women from the second to the eighth decade of life (Janssen et al., 2000). Reductions in muscle strength and general function are more rapid than the loss of muscle mass, occurring at a rate between 2.5–4% per year (Mitchell et al., 2012). This decrease in both size and strength increases the morbidity risk of older individuals, while decreasing their quality of life and independence. Interestingly, in sarcopenia, both a decrease in muscle fiber size as well as fiber number may be evident. Specifically, some studies have observed a preferential atrophy of Type II fibers with ageing, which results in a greater ratio of Type I to Type II fiber area (Klein et al.,

2003; Larsson, 1978). This may result from a loss of myosin heavy chain (MHC)IIa and IIx isoform expression, which contributes to weaker, slower, and less powerful whole muscle contractile properties (D'Antona et al., 2007). A higher relative MHCI content and lower relative MHCIIa and IIx content was also shown in muscles from elderly individuals who were physically active, removing the confounder of impaired physical function (Brocca et al., 2017a). Despite this shift in MHC isoform, however, myosin content was not different between younger and older groups. Thus, it was suggested that while a fast- to- slow shift may be occurring, there may be no down-regulation of myofibrillar proteins (i.e., myosin) in healthy ageing without disuse atrophy. Researchers also saw no difference in the myosin: actin ratio. Instead, there was evidence of MHC oxidation, which may be a factor in reduced force generation (Brocca et al., 2017a). A study by Marx et al. also supports the findings of the previous study at both the mRNA and protein level. In this investigation, there were no differences in myosin gene or protein expression between younger and older healthy individuals (Marx et al., 2002). In fact, the expression of the MHC isoforms was also not different between groups, and both younger and older muscles were predominantly type II (Marx et al., 2002). Some researchers have proposed that these inconsistencies in the findings related to myosin content during ageing may be due to other factors that may influence muscle loss. For example, it appears that when individuals are physically active throughout their life, myosin content may not be affected. Data such as these have led to the characterization of sarcopenia as either primary (due to no other factors other than ageing itself) or secondary (due to multiple factors associated with the ageing process, such as inactivity) (Cruz-Jentoft et al., 2010).

There are many potential mechanisms underlying sarcopenia and the loss of muscle function. For example, a recent review lists increased fat deposition in skeletal muscle, dysregulation of proteasomal pathways, mitochondrial dysfunction, reduced satellite cell number, increased ROS production, and increased inflammation as possible associated mechanisms (McCormick and Vasilaki, 2018). One of the major hypotheses surrounding sarcopenia is age-associated anabolic resistance, or the idea that the normal exercise and nutrient responses to increase MPS and inhibit MPD are blunted with age (Cuthbertson et al., 2005; Kumar et al., 2009; Wilkinson et al., 2018). Studies have shown that, although basal protein synthesis and degradation do not seem to be greatly affected, there are major differences in MPS in response to anabolic stimuli such as feeding and exercise between young and older individuals (Volpi et al., 2001; Volpi and Rasmussen, 2000). For example, the increase in MPS is blunted by ~40% in response to acute amino acid feeding and ~30% in response to acute exercise (Cuthbertson et al., 2006; Volpi and Rasmussen, 2000). Likewise, reduced MPS and blunted muscle mass accretion was found in older individuals in response to 6 weeks of unilateral resistance exercise when compared to younger individuals, but a clear cause was not determined (Matthew S. Brook et al., 2016; M. S. Brook et al., 2016). The anabolic resistance to exercise that is associated with ageing is likely a factor of altered signaling responses. For example, Akt is a serine/threonine protein kinase involved with regulating anabolic and catabolic processes related to growth factors, nutrients, cytokines, and mechanical tension (Bodine et al., 2001b; Miyazaki et al., 2008; Wu et al., 2011). In aged mice, Akt phosphorylation (Ser<sup>473</sup> and Thr<sup>308</sup>) was significantly greater in old mice compared to younger mice in response to exercise but did not equate



to similar elevations of mTOR phosphorylation (Ser<sup>2448</sup>) and subsequent formation of eukaryotic initiation factor-4 (eIF4E) eukaryotic initiation factor-4G (eIF4G) complexes post exercise (Hwee and Bodine, 2009; Wu et al., 2009). Additionally, higher quantities of Akt phosphorylation in aged mice did not relate to GSK-3 activity (phosphorylation of Ser<sup>9</sup>), indicating there may be impaired Akt kinase function with age (Hwee and Bodine, 2009; Wu et al., 2009). The higher amount of Akt signaling that is occurring in older mice may be an ineffective compensatory mechanism in an attempt to elevate downstream signaling proteins. In humans, the activation of Akt and subsequent inhibition of proteolysis and MPD after feeding is also blunted in older compared to younger participants (12% decrease vs. 47% decrease in MPD, respectively) (Wilkes et al., 2009). In addition to its roles with intracellular nutrient regulation and mTOR activation, Akt also serves as an inhibitor of UPS and autophagy by phosphorylation of FOXO transcription factors and beclin 1, respectively (Brunet et al., 1999a; R. C. Wang et al., 2012). Interestingly, even in organs other than skeletal muscle, such as liver, adipose, or heart, reduced catalytic activity of Akt does not explain decrease in proteolytic activity found in aged muscle (Altun et al., 2010; Fernando et al., 2019; Höhn et al., 2016; Strucksberg et al., 2010). Despite direct evidence of anabolic resistance, it is not readily apparent that the UPS is the most influential proteolytic system that facilitates muscle tissue loss during sarcopenia. Finally, there does not seem to be a major role for the activation of the ubiquitin ligases (MuRF1 or MAFbx) in ageing independent of other conditions or illness (Greenhaff et al., 2008).

Other mechanisms attempting to explain the effects of sarcopenia stem from age-related alterations to the neuromuscular system. The major noticeable change to the neuromuscular system with ageing is the loss of contractile strength and muscle mass, some of which occurs via loss of motor units (MUs) (Campbell et al., 1973). Age related MU loss has been hypothesized to occur via distinct mechanisms known as the “dying-back” or “dying-forward” phenomena. The “dying-back” hypothesis states that the integrity of the MU is lost first at the distal end near the neuromuscular junction (NMJ). The “dying-forward” hypothesis suggests that pathological MU loss is initiated at the proximal sites of the motor neuron (MN) near the ventral root. Comparisons of the distal end of the MU between old and young mice show unconventional acetylcholine receptor localization without the formation of NMJs and fragmented motor endplates in older mice. This aberrant NMJ structure is coupled with significant reductions in relative limb strength (Chung et al., 2017). Additionally, the ventral roots on the proximal end of the MU did not show significant differences in axon diameter, total axon count per root, or G-ratio (ratio of axon diameter to fiber diameter) between old and young mice. These data in animals indicate that MU loss and early decreases in strength may therefore be occurring by the “dying-back” phenomenon (Chung et al., 2017). Similarly, studies have shown that beyond the 7<sup>th</sup> decade of life, there is a clear loss of MNs, and it seems that the loss of functioning MUs precedes the death of the MN at the spinal cord (Tomlinson and Irving, 1977). This loss of the MUs at the distal NMJ site is referred to as denervation. Collateral sprouting and regeneration of nerve fibers from surviving MUs can remodel the MU, increase MU territory, and increase the number of muscle fibers per MU, seen as fiber grouping (Gordon, 2017; Hepple and Rice, 2016; McComas, 1977). Skeletal muscle is known to undergo repeated cycles of denervation and reinnervation during adulthood to old age (Hepple and Rice, 2016). The cyclical process of

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denervation and reinnervation can occur earlier in the development of sarcopenia, resulting in decreases in strength with little changes in muscle mass. Notably, these changes in NMJ structure also occur at an earlier age than myofiber atrophy in rats (Hepple and Rice, 2016). However, once the process of denervation outpaces re-innervation in old age, complete loss of MU integrity and death of MUs at the NMJ occurs (Gordon et al., 2004). Following the death of MN in the spinal cord, or axonal degeneration, muscle fibers that are no longer part of an operating MU will atrophy and become non-functional unless they are reinnervated (Doherty and Brown, 1997). Without reinnervation, the muscles experience atrophy and the mechanisms responsible have only partly been elucidated. For example, in denervated mice, inhibition of NF- $\kappa$ B leads to protective effects against denervation-induced loss of muscle mass and tetanic force production (Mourkioti et al., 2006). Similarly, mice deficient in MuRF1 or MaFbx show significant muscle preservation in response to denervation (Bodine et al., 2001a). In addition, muscle fibers positive for a denervation-specific sodium channel demonstrate higher levels of MuRF1 and MaFbx (Rowan et al., 2012). Furthermore, mice that are deficient in small mothers against decapentaplegic (SMAD) homologs 2 and 3 (SMAD2/3) show resistance to denervation induced muscle atrophy (Tando et al., 2016). Thus, it appears that skeletal muscle catabolism in response to MU loss is globally increased through several signaling cascades in a nonspecific manner.

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It is currently thought that one of the factors that may be associated with the initiation of denervation may be enhanced ROS production. Ageing has been linked to elevated production of ROS that may overwhelm intracellular antioxidant defense mechanisms (Fulle et al., 2004; Jackson and McArdle, 2011). Superoxide dismutase (SOD) knockout mice have been shown to display both denervation and axonal sprouting between one and four months of age (Fischer et al., 2012, 2011). Similarly, SOD-null mice also display large amounts of intramuscular protein carbonylation and altered excitation-contraction coupling mechanisms that mirror old wild-type mice (Ivannikov and Van Remmen, 2015). The similarities between the SOD-null and aged mice indicate uncontrolled ROS production may play a large role in mediating the initial steps of denervation with age (Fischer et al., 2012, 2011; Ivannikov and Van Remmen, 2015). However, it is still unclear if NMJ deterioration is facilitated primarily by the muscle, axon or some synergistic mechanism involving both. The amount ROS produced by the muscle is likely far greater than that produced from the axon due to the sheer size and metabolic activity of the tissue. However, other mechanisms primarily involving the function of the MU have been recently reported as well, which suggest that apparent loss of homeostatic functions of the MU itself may play a role in the acceleration of muscle catabolism (Cisterna et al., 2020). For example, increased proteolysis may involve connexin hemichannels, which are non-selective membrane channels that decrease resting membrane potential through altered ion influx. These transmembrane proteins, also known as gap junction proteins, play an important role in electrical coupling between cells by conducting ion currents (Fiori et al., 2012). Calcium is known to permeate through connexin hemichannels, and increased intracellular calcium may stimulate calcium-dependent proteolysis in response to denervation (Cisterna et al., 2020). In mice and in *in vitro* assays, repression of connexin-43 and connexin-45 (via acetylcholine receptor activation) prevented muscle atrophy induced by denervation, (Cisterna et al., 2020, 2016). It has thus been postulated that both enhanced ROS production

and frequent excitation-contraction coupling mechanisms may work synergistically to regulate denervation/reinnervation during sarcopenia. Importantly, high levels of life-long physical activity can mitigate the loss of MUs and maintain the amount of excitable muscle mass, and this has been shown to be based on activation of the MN specific to the muscle action trained (Brocca et al., 2017a; Power et al., 2012).

Mitochondrial dysfunction has also emerged as a central factor in sarcopenia progression (Romanello and Sandri, 2010). There are several mechanisms that have been found to link dysfunctional mitochondria with muscle atrophy, which include increased mitochondrial ROS production, mitochondrial release of pro-apoptotic factors, and signaling events that are driven by diminished ATP production (Hyatt and Powers, 2021). For example, permeabilization of the outer mitochondrial membrane can result in cytochrome c release, which can activate caspase-3 (Hyatt and Powers, 2021). Interestingly, mitochondrial sensitivity to permeability transition is increased in both older humans as well as in a murine model of sporadic denervation (Gospillou et al., 2014; Spendiff et al., 2016). Even in physically active older individuals showing no changes in mitochondrial ROS or maximal respiratory capacity, increased sensitization to mitochondrial permeability transition is still observed (Gospillou et al., 2014; Spendiff et al., 2016). Furthermore, reduced ATP production by dysfunctional mitochondria can result in the activation of AMPK, which is associated with both MPS suppression (via mTOR inhibition) as well as enhanced MPD (via an AMPK-FOXO3-MuRF1/MAFbx axis) (Hyatt and Powers, 2021). With relevance to ageing specifically, several lines of evidence implicate mitochondrial dysfunction in sarcopenia. First, there are clear morphological alterations in aged muscles (Leduc-Gaudet et al., 2015). Additionally, ageing is characterized by perturbations in the expression of proteins that control mitochondrial dynamics (i.e., fusion and fission) (Tezze et al., 2017). Likewise, mitophagy regulators are also reduced in aged muscles, which could result in the accumulation of dysfunctional mitochondria (Gospillou et al., 2014). Finally, further evidence for a relationship between mitochondrial dysfunction and sarcopenia is that in aged animals, treatment with compounds that improve mitochondrial function, such as SS-31 (elamipretide) (Campbell et al., 2019; Siegel et al., 2013) or sulforaphane (Bose et al., 2020) have been shown to prevent age-associated muscular deficits.

Notably, in sarcopenia there is also a loss of contractile function, even when normalized to muscle mass, which suggests that ageing may also be associated with impairments in cross-bridge force generation kinetics. For example, there is an evident loss of myosin content relative to cross-sectional area that results in less actomyosin interactions as well as decreased actin sliding speed (D'Antona et al., 2003). Functionally, there is a decline in muscle strength, shortening velocity, and power output during natural ageing (Frontera et al., 2000). The loss of strength may be attributed to structural changes in the muscle rather than an inability to activate the muscle. Older individuals tend to also be slower for voluntary angular contraction velocities of muscles, and the loss of strength and shortening velocity leads to alterations in the force-velocity relationship, impairing power production. These slower contractile properties may be a mechanism to achieve the same contraction at a lower firing rate (Raj et al., 2010). Older adults are also more fatigable for tasks relative to maximal force production (Dalton et al., 2010). Interestingly, eccentric contraction efficiency and strength are relatively maintained compared to isometric

and concentric actions, which suggests that there may be reduced agonist and increased antagonist activation during concentric contractions, or that increases in muscle passive stiffness enhance lengthening actions (Hasson et al., 2011; Phillips et al., 1992). Finally, there is a reduction in the amount of calcium released from the SR and reduced calcium sensitivity associated with ageing (Ingalls et al., 1998).

The research on satellite cells in ageing have not led to consistent results. Some studies have shown that satellite cells decrease in number during ageing, but other studies have found no reduction (Renault et al., 2002; Roth et al., 2000). However, the overwhelming evidence remains that there is no reduction in myonuclei number with ageing; and despite a lower number of satellite cells, myonuclei number may actually be higher in aged muscle (Kadi et al., 2004). Therefore, satellite cells may have decreased functional ability regardless of the effect on their number, which can influence the ability of the satellite cells to proliferate and fuse, therefore potentially influencing changes seen in sarcopenia (Gallegly et al., 2004). An increased myonuclear number with decreased fiber size suggests decreased myonuclear efficiency in ageing, which contradicts the concept of a constant nuclear domain, since each myonucleus would instead have less cytoplasm to control (predicting a decrease in myonuclear domain) (Kadi et al., 2004). More recent evidence also supports a flexible myonuclear domain. For example, in studies in both rats and humans, muscle hypertrophy (especially in Type 2 fibers) has been demonstrated in the absence of myonuclear accretion (Murach et al., 2018a). This suggests satellite cell density can possibly increase in the absence of myonuclear accretion, which implies an expansion of the myonuclear domain.

Recent studies point to age-related differences in satellite cell requirements for skeletal muscle hypertrophy (Murach et al., 2018b). In a model of conditional satellite cell depletion, Murach et al. showed that adolescent mice (2–2.5 months), but not mature mice (>4 months), require satellite cells for overload-induced hypertrophy (Murach et al., 2017). In fact, hypertrophic growth still occurred in mature adult mice, even in the absence of satellite cells. In contrast, a previous study in aged mice (>24 months) found that overload-induced hypertrophy is impaired, regardless of satellite cell content (Lee et al., 2016). However, in this study, satellite cell depletion in aged muscle was also shown to result in increased skeletal muscle fibrosis (Lee et al., 2016). Interestingly, the breaking of satellite cell quiescence and proliferation initiation are driven by Notch, and Notch activation declines with ageing as a result of depressed mitogen-activated protein kinase (MAPK) activity, which may reduce satellite cell activation (Caldeira, 2009). Furthermore, transforming growth factor-beta (TGF- $\beta$ ) levels are also increased with ageing, which can lead to activation of cyclin-dependent kinase, which additionally inhibits satellite cells and prevents their regenerative response. Elevated levels of TGF- $\beta$  may also play a role in the infiltration of non-contractile tissue into whole muscle with age (Ismaeel et al., 2019; Overend et al., 1992).

Despite the effects of satellite cells on acute muscle size, more recently, satellite cells have been shown to play an important role in physical activity-driven adaptations. In satellite cell-depleted adult mice assigned to wheel-running for 13 months (as a model of life-long physical activity), the adaptations to exercise, including balance, coordination, and running volume were all reduced (Englund et al., 2020). Thus, satellite cells may be critical

for the maintenance of physical function and for preserving exercise adaptations during the ageing process. These adaptations may occur via recently discovered novel secretory and communication functions of satellite cells, which are independent from their better understood fusion roles (Murach et al., 2021).

## Mechanical Unloading

In healthy individuals, muscle atrophy can occur independent of disease conditions due to mechanical unloading. In fact, one of the best human models of mechanical unloading is spaceflight. For example, one study showed that prolonged spaceflight (115–197 days) led to significant reductions in gastrocnemius, soleus, and quadricep muscle volume of 10–17% (LeBlanc et al., 2000). Other studies have also shown that this atrophy is greatest in type I fibers (Fitts et al., 2010). A method that is commonly used to model spaceflight is bed rest, especially prolonged bed rest with a 6° head down bed rest (HDBR). This model has consistently shown large reductions in muscle mass, which is also greater in type I fibers (Brocca et al., 2012). Other forms of immobilization, such as casting, have also been used to study mechanical unloading. Even as little as five days of casting can lead to significant declines in muscle cross-sectional area of ~4% (Wall et al., 2014). In addition, reducing daily step count for two weeks also has been shown to lead to ~3% losses in leg lean mass (Krogh-Madsen et al., 2010). Animal models used to study mechanical unloading include rodent hind limb unloading (HLU). For example, two weeks of HLU can lead to muscle mass losses of up to 34%, with the most rapid atrophy in slow muscles such as the soleus (Ohira et al., 1992). However, the mechanisms underlying unloading-induced muscle atrophy seem to differ between rodents and humans (Crossland et al., 2019). These differences are likely due to metabolic dissimilarities, including a higher relative MPS rate and basal metabolic rate in rodents. In addition, age differences between studied species may also play a role, as rodent models often use young animals that are still growing and in development (Crossland et al., 2019). This may explain the discrepancies noted above in the time-matched magnitude of muscle mass loss between animal and human unloading models. Thus, in this section, we begin by discussing the mechanisms of mechanical-unloading-induced muscle atrophy based on rodent data, followed by focusing on the impact of unloading in humans.

### Animal Studies

A decrease in MPS is believed to be a major factor in muscle atrophy during unloading conditions (Gao et al., 2018). In a study by Baehr et al., MPS was shown to decrease in nearly all skeletal muscles in response to HLU, and changes in MPS were muscle-specific (Baehr et al., 2017). Notably, the Akt-mTOR pathway may play a role in HLU-mediated muscle atrophy, as there is evidence for reduced phosphorylation of Akt, S6K1, and 4E-BP1 in a model of HLU (Bodine et al., 2001b). HLU was also shown to increase binding of 4E-BP1 to eIF4e (inhibitory association) in just three days (Liu et al., 2012). HLU has also been shown to reduce the activation of mTORC1-independent MPS signaling pathways, as evidenced by reduced phosphorylation of GSK-3 $\beta$  (Mirzoev et al., 2016). More recently, mRNA levels of the mTOR signaling repressor, regulated in DNA damage and development 1 and 2 (REDD1/2), were significantly elevated in response to HLU (Kelleher et al., 2015,

2013). In addition to the regulation of translation initiation, mechanical unloading may also affect MPS at the level of elongation of mRNA translation and translational capacity. After two weeks of HLU phosphorylated (inactive form) levels of eukaryotic elongation factor 2 (eEF2), which plays a role in the elongation of translation, were doubled (Lomonosova et al., 2017). Furthermore, HLU has been shown to decrease total RNA and 28S rRNA content in rat muscle (markers of ribosome content, the main component of translational capacity) (Bajotto et al., 2011; Mirzoev et al., 2016).

With respect to MPD, all the MPD pathways seem to be involved in mechanical unloading-induced atrophy in rodents. For example, inhibition of either calpain or caspase-3 prevented immobilization-induced atrophy in rats (Talbert et al., 2013). However, the UPS is likely the most important. Gene expression of both MuRF1 and MAFbx have been shown to rapidly increase in mice in response to spaceflight (Allen et al., 2009; Gambaro et al., 2017), rats in response to HLU (Baehr et al., 2017), and rats in response to both immobilization and HLU (Bodine et al., 2001a). Further evidence comes from the fact that mice deficient in MAFbx or MuRF1 are resistant to HLU-induced muscle atrophy (Bodine et al., 2001a; Labeit et al., 2010). Notably, MuRF-1 and MAFbx are regulated by upstream FOXO transcription factors, FOXO1 and FOXO3. FOXO are also controlled by Akt; phosphorylation of the transcription factors by Akt retains them in the cytosol, preventing nuclear translocation (Brunet et al., 1999b). However, when dephosphorylated, FOXO can translocate to the nucleus and upregulate the expression of MuRF-1 and MAFbx. Cast immobilization and spaceflight have been shown to increase FOXO3 and FOXO1 expression, respectively, in mice (Allen et al., 2009; Okamoto and Machida, 2017). Moreover, inhibition of FOXO3 during disuse in rats prevented increases in MuRF-1 and MAFbx (Senf et al., 2008).

In addition to the aforementioned effects on MPS and MPD, there is evidence that mechanical unloading leads to oxidative stress (Powers et al., 2012, 2007, 2005). The first evidence for this comes from a study in which rats subjected to immobilization demonstrated increased muscle lipid peroxidation, and vitamin E administration partially attenuated muscle atrophy (Kondo et al., 1991). Other studies, especially those focusing on mechanical ventilation-induced diaphragm muscle atrophy (a specific model of disuse) have demonstrated a link between increased oxidative stress and muscle loss. Powers and colleagues were able to show that in rats, mechanical ventilation led to increased mitochondrial ROS production and that using a mitochondrial-targeted antioxidant decreased ROS, with concomitant protection against diaphragm myofiber atrophy (Powers et al., 2011a). Furthermore, in mice, two weeks of hindlimb immobilization was shown to increase mitochondrial ROS production and muscle oxidative damage, measured as 4-HNE-conjugated proteins (Min et al., 2011). Notably, in this study, a mitochondrial-targeted antioxidant was also effective in preventing myofiber atrophy (Min et al., 2011).

Mechanical unloading is also associated with mitochondrial dysfunction and reduced mitochondrial quality. For example, expression of peroxisome proliferator-activated receptor gamma coactivator 1 alpha (PGC-1 $\alpha$ ), the transcriptional coactivator that regulates mitochondrial biogenesis, is reduced up to 40% following HLU (Rosa-Caldwell et al., 2020a). Earlier studies have shown that PGC-1 $\alpha$  overexpression blunts decreases in muscle fiber diameter in mice induced by denervation and fasting (Sandri et al., 2006) and

HLU (Cannavino et al., 2015, 2014) via reduced proteasomal degradation (MuRF1 and MAFbx induction) and reduced autophagy. In contrast to these studies, however, a recent study showed that PGC-1 $\alpha$  overexpression does not protect against HLU-induced muscle atrophy (Rosa-Caldwell et al., 2020b). Although mice overexpressing PGC-1 $\alpha$  had blunted expression of MuRF1 and MAFbx, these mice had an increase in MPD via autophagic mechanisms. In contrast, overexpression of mitochondrially targeted catalase (MCAT) did mitigate the response to HLU; however, this effect was shown to be sex specific, only protecting against muscle atrophy in female mice (Rosa-Caldwell et al., 2020b). Notably, this may be due to an augmented catabolic response reported in female mice (Rosa-Caldwell et al., 2021). The earlier studies (Cannavino et al., 2015, 2014; Sandri et al., 2006) all used male mice. However, the study by Rosa-Caldwell et al. included both males and females to investigate how interventions may impact males and females separately (Rosa-Caldwell et al., 2020a). Interestingly, recent data suggest a sex difference in the etiology of disuse muscle atrophy in rodents. Following 7 days of HLU, female mice had an average of 33% lower type IIB cross-sectional area, while male mice did not lose any significant type IIB fiber area (Rosa-Caldwell et al., 2021). Reductions in MPS were also more pronounced in female mice compared to male mice (40% reduction and 23% reduction, respectively) (Rosa-Caldwell et al., 2021). Finally, the differences could also be due to the differing ages of the mice. The studies by Cannavino and Sandri et al. (Cannavino et al., 2015, 2014; Sandri et al., 2006) used six-month old mice, while in Rosa-Caldwell et al.'s study, disuse atrophy was induced at ten weeks of age (Rosa-Caldwell et al., 2021). Overall, these data suggest that sex and age differences in muscle pathologies may exist and highlight the importance of investigating these mechanisms in both sexes and in different age groups.

Another final mediator that may be involved in unloading-induced muscle atrophy is calcium. An early study in 2001 by Ingalls, Wenke, and Armstrong showed that hindlimb suspending mice leads to significant increases in skeletal muscle intracellular calcium levels (up to 117% after just one week) (Ingalls et al., 2001). More recently, tetramethylpyrazine, which has been described as a calcium antagonist, was shown to suppress intracellular calcium and attenuate HLU-induced muscle atrophy in rats (Hu et al., 2017). Interestingly, calpains are calcium-dependent, and calpain1 and calpain2 have been shown to be activated by increased intracellular calcium following HLU (Matsumoto et al., 2014). Furthermore, an overload of intracellular calcium can activate caspase-12, which activates caspase-3 (Primeau et al., 2002b), and after HLU in rats, the Bax/Bcl-2 ratio has been shown to be significantly elevated (Hu et al., 2017).

It is important to note that despite the muscle mass losses observed during mechanical unloading, studies have also shown that reloading may restore these losses. For example, a study by Shimkus and colleagues showed that HLU-induced reductions in MPS, and the accompanying losses in muscle mass, are repeatable with serial reloading-unloading bouts (Shimkus et al., 2018). Specifically, after 28 days of HLU, a 56-day recovery period recovered the MPS rate and muscle size. However, exposure to a subsequent HLU period once more decreased MPS and muscle size, which again recovered after a final reloading period (Shimkus et al., 2018).

## Human Studies

Although results in animal models have been consistent, the results of human models of mechanical unloading remain less clear. In a human model of disuse atrophy (lower leg suspension), rates of both myofibrillar and tendon protein synthesis rates progressively decreased over a three-week period (de Boer et al., 2007). More specifically, the reduction in MPS may involve attenuated activation of the Akt-mTOR pathway, as unloading is also associated with insulin resistance. For example, just five days of bed rest has been shown to lead to 67% increases in the insulin response to glucose (Hamburg et al., 2007). Likewise, seven days of immobilization also decreased insulin action on glucose uptake and MPS (Richter et al., 1989).

Still, the mechanistic drivers of possible MPS suppression in humans are unresolved. For example, following lower leg suspension for three weeks, although significant atrophy occurred and MPS rates decreased, there were no changes observed in the activation of any of the mTOR pathway components (de Boer et al., 2007). Similarly, following knee immobilization, although MPS rates were reduced, there were no differences in mTOR, GSK-3 $\beta$ , or eEF2 activation (Glover et al., 2008; Marimuthu et al., 2011). One pathway that may instead be involved in the MPS reduction in response to unloading in humans is focal adhesion kinase (FAK), a non-receptor protein tyrosine kinase that is sensitive to mechanical loading (Graham et al., 2015). For example, in de Boer et al.'s study, FAK activation was reduced by 30% after ten days of lower leg suspension (de Boer et al., 2007). Likewise, in another study unilateral immobilization for 14 days reduced FAK activation by 23% with a concomitant reduction in MPS in the restricted leg after amino acid infusion (Glover et al., 2008). While plasma insulin concentrations and fractional synthetic rates increased with higher amino acid doses, MPS rates were still lower in the muscles of the immobilized limb (Glover et al., 2008). Investigation of signaling proteins showed no differences between limbs in the phosphorylation of mTOR or downstream targets, suggesting this immobilization-induced suppression of MPS may be independent of mTOR activation (Glover et al., 2008). These data support prior *in vitro* studies demonstrating that FAK is co-immunoprecipitated with IRS-1 without catalytic activation, and FAK inhibition results in insulin resistance despite insulin administration (Bisht et al., 2007; Lebrun et al., 1998). There appears to be a degree of cross-talk regulation between the insulin signaling pathway and FAK, which could be a target for investigation in studies assessing inactivity-induced insulin resistance. Importantly, other etiological factors such as loss of muscle mass alone can also decrease the body's ability to store and utilize glucose, which may contribute to insulin resistance from altered glucose homeostasis. However, this idea of altered glucose and protein metabolism in response to immobilization needs further investigation.

While increased MPD likely plays a major role in muscle mass loss in rodents in response to mechanical unloading, the involvement of MPD in human muscle atrophy is less clear. For example, gene expression of MuRF-1 and MAFbx were elevated in humans after three days of lower limb suspension (Gustafsson et al., 2010) and five days of immobilization (Dirks et al., 2014). In two other studies, however; one using a 20-day bed rest model, and the other two weeks of limb immobilization, only MAFbx increased, with no change in MuRF-1 (Jones et al., 2004; Ogawa et al., 2006). In contrast, in de Boer et al.'s study using lower



leg suspension, after 10 days, there were significant increases in MuRF-1 mRNA expression, but no changes in MAFbx (de Boer et al., 2007). It is important to note that these differences between studies may be due to the varying timelines. Notably, other studies suggest that the effects of FOXO, MuRF-1, and MAFbx are muscle- and time course- specific and may explain the discrepancies reported between different studies (Atherton et al., 2016; Brocca et al., 2017b). Furthermore, in the context of the role of ROS in unloading, in humans, prolonged mechanical ventilation was shown to increase oxidative stress, measured as protein carbonyls and hydroxynonenal (HNE)-protein adducts (Hussain et al., 2010). However, results of other studies have been contradictory. For example, in one study in humans, two weeks of immobilization did not affect levels of the markers of oxidative stress, 4-HNE or protein carbonyls (Glover et al., 2010). Thus, whether unloading-induced ROS production does indeed play a role in muscle atrophy remains debated (Powers et al., 2012). Despite this, mechanistically, there is strong evidence that ROS can indeed lead to muscle atrophy. For example, exposure of myotubes to ROS leads to fiber atrophy (Gilliam et al., 2012). This is most likely due to allosteric regulation of proteases, via increased FOXO3 signaling, and thus expression of MuRF-1 and MAFbx (Min et al., 2011). Additionally, ROS may also activate calpain and caspase-3 (Powers et al., 2011a). Further, ROS can inhibit insulin action and may play a role in the development of insulin resistance (Di Meo et al., 2017), and oxidation of proteins is known to increase unfolding and proteolytic degradation (Powers et al., 2011b; Smuder et al., 2010).

While muscle mass loss is a known endpoint of immobilization in humans, there is still a lack of understanding of the mechanisms responsible for this, and a gap in the understanding of the pathophysiology of mechanical unloading exists. Due to important clinical ramifications (i.e., intensive care), future studies are necessary to clarify these mechanisms. These studies should be conducted in humans, include several time-points, and incorporate various assessments including functional deficit measures in addition to muscle size, muscle protein turnover and nutrient uptake measurements, and insulin sensitivity/resistance measures, in addition to molecular biology assays of signaling pathways. Furthermore, while muscle mass recovery has been demonstrated in humans after reloading as well, most studies have shown this in young, healthy individuals (Seene et al., 2012). Therefore, future work should assess the recovery potential of older and clinical populations.

## Cancer Cachexia

Cachexia refers to the progressive atrophy of adipose tissue and skeletal muscle that leads to progressive loss of body weight (Tisdale, 2009). Weight loss is thought to occur in 30–80% of cancer patients, and 15% of these patients may lose more than 10% of their initial body weight (Dewys et al., 1980). The extent of weight loss varies between patients and between tumor types; pancreatic cancer and gastric cancer patients experience the most dramatic losses in body weight, reaching a median of 24.5% weight loss in pancreatic cancer patients before death (Dewys et al., 1980; Wigmore et al., 1997). Importantly, weight loss is an important prognostic factor in survival, as a greater amount of weight loss is associated with a reduced survival time (Dewys et al., 1980; Tisdale, 2009). In addition, loss of skeletal muscle leads to reductions in mobility and quality of life in cancer patients (Tisdale, 2009).

Anorexia is highly prevalent among cancer patients, even independent of chemotherapy and other treatments. In one study, 61% of cancer patients nearing end-of-life were shown to display anorexia (Tranmer et al., 2003). Several factors may lead to these findings, and possible causes of this include psychological depression, tumor encroachment on the gastrointestinal tract, and tumors affecting the mucosa (Knox et al., 1983). Furthermore, cytokines, including IL-1, IL-6, and TNF- $\alpha$  can suppress appetite (Banks, 2001). There is some evidence that there may also be an imbalance between orexigenic, or appetite-inducing, (i.e., neuropeptide Y (NPY)) and anorexigenic, or appetite-suppressing (i.e., proopiomelanocortin (POMC) signals in cancer (Jatoi et al., 2001; Wisse et al., 2001). Despite these links, anorexia does not fully explain body mass losses in cachexia; diminished caloric intake has been shown to not affect weight lost in patients (Bosaeus et al., 2001), and greater amounts of muscle mass are lost in cancer cachexia than can be explained by anorexia alone (Fearon, 1992).

In addition to decreased energy intake, cancer patients are also known to exhibit decreases in physical activity levels. Despite this, however, several types of cancers have been associated with an increased resting energy expenditure (REE), which may also contribute to cachexia. For example, in pancreatic, lung, and GI cancers, REE has been shown to be elevated in association with an elevated acute phase response (McMillan et al., 1998). One potential explanation for an elevated REE in cancer patients is increased thermogenesis in brown adipose tissue (BAT) and skeletal muscle due to uncoupling proteins (UCPs), which mediate proton leakage across the inner mitochondrial membrane, reducing the level of coupling of respiration to ATP synthesis. Interestingly, gene expression of UCPs have been shown to be elevated in tumor-bearing mice (Bing et al., 2000) as well as in cancer patients with weight loss compared to controls and cancer patients that did not lose weight (Collins et al., 2002). Additionally, futile cycles may play a role in increasing the energy expenditure of cancer patients. Notably, tumor hypoxia, which is induced by tumor growth beyond the vascular supply, activates the transcription factor hypoxia-inducible factor-1 (HIF-1). HIF-1 acts to increase glucose uptake via increased transcription of the glucose transporter GLUT1. Additionally, HIF-1 activates pyruvate dehydrogenase kinase (PDHK), which inactivates pyruvate dehydrogenase (PHD), the enzyme responsible for catalyzing the conversion of pyruvate into acetyl-CoA. This results in accumulation of pyruvate and subsequent conversion into lactate (Kim et al., 2006). Notably, this is an energy inefficient process compared to oxidative phosphorylation. Furthermore, the lactate is also inefficiently converted back to glucose in the liver via the Cori cycle. Overall, this process is thought to account for a loss of ~300 extra kcal/day in cancer patients (Edén et al., 1984).

The loss of muscle mass in cancer cachexia may also be attributed to a substantial decrease in MPS. Although a decrease in MPS may be attributed to anorexia, some animal studies suggest that cancer cachexia may be accompanied by depressed MPS independent of anorexia. For example, in mice with adenocarcinoma that lost 15–30% of their weight, MPS was reduced by 60% (Smith and Tisdale, 1993). Similarly, in a mouse model of colorectal cancer, MPS was reduced by 19% during cachexia initiation, with further reductions of up to 50% demonstrated with intermediate weight loss of 6–19% (White et al., 2011). Muscle mass was also significantly associated with MPS rates in these mice. Interestingly, in another murine model of colorectal cancer, although basal MPS was suppressed in cachectic

mice, these mice still demonstrated a normal response of activated MPS after a single eccentric contraction bout, and the relative induction of MPS by eccentric contraction was not different from control mice (Hardee et al., 2018). Finally, in mice injected with Lewis lung carcinoma, MPS was reduced by 40% (Brown et al., 2018). However, results in humans have been less consistent. An early landmark study by Emery and colleagues showed that MPS was significantly reduced in patients with cancer (Emery et al., 1984). However, other more recent studies have shown no evidence of MPS suppression in patients with cancer cachexia (MacDonald et al., 2015). Several studies have also assessed markers of MPS to identify potential mechanisms affecting the protein synthetic machinery. In a murine model of cancer cachexia as well as in weight-losing cancer patients, there is evidence for elevated levels of phosphorylated, active double-stranded RNA-dependent protein kinase (PKR), which phosphorylates and inactivates eIF2 (which results in inhibition of translation initiation) (Helen L. Eley et al., 2007; H. L. Eley et al., 2007; Eley et al., 2008; Eley and Tisdale, 2007a). Additionally, mice with a cachexia-inducing tumor demonstrated an increase in eIF4E-4E-BP1 binding, a decrease in the active eIF4E-eIF4G complex, and a 5-fold increase in the phosphorylation of eEF2 (Helen L. Eley et al., 2007; H. L. Eley et al., 2007; Eley et al., 2008; Eley and Tisdale, 2007a). In the mouse models of colorectal cancer demonstrating reduced MPS, mechanistically, IGF-1 mRNA expression was shown to be reduced, and mTOR signaling was suppressed (reduced Akt, p70, and 4EBP1 phosphorylation) (Hardee et al., 2018; White et al., 2011). Despite this basal reduction, however, these mechano-sensitive signaling pathways were still induced following eccentric contractions (White et al., 2011).

With respect to MPD, the UPS seems to play a major role in cancer cachexia-induced muscle atrophy. In the common murine model of cancer cachexia of adenocarcinoma, proteasome proteolytic activity was increased in parallel with increasing weight loss (Chand et al., 2005). Furthermore, gene and protein expression of the proteasome subunits were shown to be elevated in cancer patients that lost >10% of their body weight (Khal et al., 2005). Expression of both MuRF-1 and MAFbx have also been shown to be elevated in several models of cancer cachexia (Bodine et al., 2001a; Gomes et al., 2001). In White et al.'s study of colorectal cancer in mice, MPD was increased by 45% in mice that lost 5% of their body weight. Further, mice that lost between 6–19% of their body weight, or 20% of their body weight, demonstrated elevations in MPD of 134% and 188%, respectively (White et al., 2011). These elevations in MPD were accompanied by significant and progressive (with weight loss severity) increases in MAFbx and MuRF1 expression (White et al., 2011). In mice injected with Lewis lung carcinoma, muscle protein ubiquitination was increased by around 50%, with concomitant increases in FOXO1 (50%) as well as MAFbx and MuRF1 (two to four-fold increase) (Brown et al., 2018). Likewise, apoptosis may also play a role in MPD. In the murine model of cancer cachexia, there were significant increases in the proteolytic activity of several of the caspases, including caspase-3 (by 151%) and caspase-9 (177%) (Belizário et al., 2001). Finally, in patients with upper GI cancer, skeletal muscle apoptosis was observed, measured as DNA fragmentation (Busquets et al., 2007).

Glucocorticoids are commonly used in the setting of cancer to aid with the symptoms; however, these compounds are known to induce skeletal muscle atrophy. Specifically, glucocorticoids attenuate activation of the PI3K/Akt pathway and augment the activity of

forehead box (FOXO) transcription factors, which results in increased MAFbx expression (Hasselgren, 1999; Sandri et al., 2004). Another interesting link is the increase in intramuscular myostatin expression in response to glucocorticoids (Gilson et al., 2007a). Myostatin is a myokine and secreted growth differentiation factor that reduces myogenic gene expression, inhibits Akt, and increases FOXO1 expression (McFarlane et al., 2006). Interestingly, myostatin gene deletion actually prevents muscle atrophy in response to glucocorticoids (Gilson et al., 2007b). Furthermore, proteolysis-inducing factor (PIF) is a glycoprotein which has been identified in mice and humans with cancer cachexia, that has been speculated to also upregulate the UPS (Williams et al., 2004). In fact, a longitudinal study established a relationship between the presence of PIF in urine and weight loss in cancer patients (Williams et al., 2004). Interestingly, administration of PIF isolated from the urine of cancer cachexic patients to mice was shown to induce cachexia by reducing MPS, seemingly by PKR activation, and increasing MPD, seemingly by increasing UPS (Cariuk et al., 1997).

Several cancers are also associated with an excessive production of TNF- $\alpha$ , and in animal studies, there is ample evidence that TNF- $\alpha$  plays a role in the induction of cachexia. For example, in a murine Lewis lung carcinoma model, mice deficient in the TNF- $\alpha$  receptor exhibited reduced skeletal muscle wasting (Llovera et al., 1998). Notably, TNF- $\alpha$  treatment has been shown to decrease MPS and enhance MPD in rats (García-Martínez et al., 1993). The link between TNF- $\alpha$  and muscle wasting may also involve reactive oxygen species (ROS), as TNF- $\alpha$  has been shown to induce oxidative stress (Buck and Chojkier, 1996). Either by an ROS-dependent or independent mechanism, TNF- $\alpha$  leads to increased expression of MAFbx (Li et al., 2005). Moreover, there is evidence that at least *in vitro*, TNF- $\alpha$  can suppress MyoD mRNA at the posttranscriptional level (Guttridge et al., 2000). However, it is important to note that the involvement of TNF- $\alpha$  in human cancer cachexia is less clear, as some studies show no elevations of TNF- $\alpha$  in patients (Iwase et al., 2004). In contrast to TNF- $\alpha$ , there is much stronger evidence for the involvement of IL-6 in cancer cachexia in humans (Carson and Baltgalvis, 2010; White, 2017). IL-6, which can act as both a pro- or anti-inflammatory myokine, has been described as a predictor of weight loss in patients with cancer cachexia (Scott et al., 1996). In a model of murine colorectal cancer and cachexia, mice with the highest circulating IL-6 levels showed the most severe cachexia (Baltgalvis et al., 2008). Furthermore, IL-6<sup>-/-</sup> mice did not experience muscle wasting (Baltgalvis et al., 2008). Likewise, in a mouse model of colorectal cancer, administration of an IL-6 receptor antibody attenuated cachexia progression by suppressing MPD, without affecting MPS (White et al., 2011). Similarly, in murine colorectal cancer, NF $\kappa$ B was activated in response to cachexia and further induced by eccentric contractions (Hardee et al., 2018). Inhibition of NF $\kappa$ B improved both basal MPS and MPS in response to eccentric contractions (Hardee et al., 2018). These mechanism may involve MPD by both proteasomal and lysosomal pathways, as *in vitro*, IL-6 and NF $\kappa$ B have been shown to activate both (Cuervo et al., 1998; Ebisui et al., 1995). Finally, angiotensin II (Ang II) has been shown to be elevated in several cancers (Sanders et al., 2005). Ang II has been shown to both increase MPD by activation of PKR (Eley and Tisdale, 2007b; Russell et al., 2007) and the UPS (Sanders et al., 2005), as well as inhibit MPS by reducing levels of IGF-1 (Brink et al., 2001).

Abnormal mitochondrial morphology has been displayed in cancer cachexia, along with altered expression of mitochondrial fusion/fission proteins (de Castro et al., 2019; Marzetti et al., 2017). Furthermore, cachexia-associated muscle wasting is correlated with reductions in mitochondrial respiration and electron transport chain complex activity (Padrão et al., 2013). Interestingly, in murine models of lung and colorectal cancer, Brown et al. showed that mitochondrial degeneration actually precedes muscle atrophy (Brown et al., 2017). However, increasing mitochondrial biogenesis by transgenic PGC-1 $\alpha$  overexpression was shown to have no effect on muscle atrophy in a mouse model of lung cancer (X. Wang et al., 2012).

## Obesity-Related Chronic Inflammation

Obesity is defined as having a body mass index equal to or greater than 30 kg/m<sup>2</sup> and is an epidemic primarily affecting developed countries. The CDC: National Center for Health Statistics reported that 39.8% of American adults and 18.5% of American children were obese in 2016 (Hales et al., 2017). Several health problems are related to obesity such as cardiovascular disease, cancer, insulin resistance, dyslipidemia, sleep apnea, and osteoarthritis. In addition, obesity is also a disease of low-grade chronic inflammation, which is likely due to the accumulation of excess adipose tissue (Lee et al., 2013). It is important to note that adipose tissue is not an inert energy storage depot; it is an endocrine organ that has been shown to have diverse roles within the body and has demonstrated communication with muscle (Coelho et al., 2013; Li et al., 2017). White adipose tissue secretes a variety of signaling molecules that are now commonly referred to as adipokines that function as hormones (Waki and Tontonoz, 2007).

As adipocytes hypertrophy and undergo hyperplasia, they secrete an increased amount of the hormone leptin, which upregulates monocyte chemoattractant protein-1 expression, causing adipose tissue to become infiltrated with pro-inflammatory macrophages. These macrophages also release their own pro-inflammatory molecules, which exacerbates the inflammatory cascade (Burhans et al., 2018; Chawla et al., 2011; Haase et al., 2014; Lumeng et al., 2007; Monteiro et al., 2019; Weisberg et al., 2003). Therefore, adipose tissue expressing this inflammatory phenotype, can serve as a source of chronic low-grade inflammation, whereby inflammatory cytokines and chemokines are secreted into the blood to have negative effects on surrounding tissues. Once fat begins to display an inflammatory phenotype, it can stimulate an increased release of TNF- $\alpha$ , IL-6, leptin, visfatin, and resistin into systemic circulation, which may have negative influences on skeletal muscle (Makki et al., 2013). TNF- $\alpha$  is known to stimulate the UPS through NF- $\kappa$ B signaling and increased concentrations in circulations could stimulate muscle catabolism, but this direct mechanism has yet to be proven in the context of obesity in humans. Under normal conditions TNF- $\alpha$  and IL-6 can help promote muscle regeneration in an acute short-term inflammatory response such as during the post-exercise recovery; however, chronic exposure has been shown to induce muscle atrophy (Akhmedov and Berdeaux, 2013). This would seem to indicate that with obesity mediated low-grade chronic inflammation, muscle tissue could be chronically exposed to TNF- $\alpha$  and IL-6 and may have altered catabolic and anabolic activity.

The crosstalk between adipocytes and muscle cells has been investigated using an *in-vitro* co-culture model consisting of primary human satellite cells and mature adipocytes, isolated from subcutaneous adipose tissue from lean and obese individuals as well as visceral adipose tissue from obese subjects (Pellegrinelli et al., 2015). The researchers observed that the secretome of the obese visceral adipose tissue displayed a more pronounced inflammatory profile, while the lean, subcutaneous adipose tissue had the lowest inflammatory profile measured (Pellegrinelli et al., 2015). These findings support the idea that there is a spectrum of adipocyte cell size that may be related to inflammatory phenotype. When cocultured with muscle cells, the obese visceral adipose tissue decreased the expression of: MyoD, myogenin, titin,  $\alpha$ -sarcoglycan, and caveolin-3, while disturbing the sarcomere structure (Pellegrinelli et al., 2015). The cell co-culture findings were supported by histological analysis of obese mice gastrocnemius muscle that showed abnormal muscle fiber sizes and adipocyte accumulation (Pellegrinelli et al., 2015). Additionally, the obese mice had increased expression of leptin and fatty acid binding protein-4 within the skeletal muscle, indicating a large amount of fat infiltration (Pellegrinelli et al., 2015). These results indicate a spectrum of inflammatory signaling can emerge from various adipose tissue locations and has the potential to influence muscle remodeling. *In-vivo*, leptin-deficient obese and leptin receptor-mutant diabetic mice have been found to have reduced muscle regenerative capacity several days after cardiotoxin injection (Nguyen et al., 2011). While the reduced regenerative capacity could potentially have been influenced by a dysregulated inflammatory response, the wild type mice fed a high fat diet to induce obesity and diabetes did not show any impairment in muscle regeneration or alterations in inflammatory cell accumulation as seen in the leptin-deficient or receptor-mutant mice (Nguyen et al., 2011). Notably, leptin has been previously found to stimulate muscle hypertrophy and can initiate the inflammatory process of macrophages to promote their M1 pro-inflammatory phenotype (Hamrick et al., 2010; Loffreda et al., 1998; Nguyen et al., 2011; Santos-Alvarez et al., 1999; Weisberg et al., 2003). These studies indicate that leptin may have a mediating role in muscle regeneration that could be a target of interest in obese populations.

Research in animal models of obesity and insulin resistance suggest varying effects on MPS at rest and in response to exercise (Nilsson et al., 2013, 2010). Basal mixed protein synthesis rates of sedentary obese Zucker rats were greater than lean rats in the quadriceps, red gastrocnemius, and white gastrocnemius muscles (Nilsson et al., 2013). Investigation of MPS-related signaling pathways showed that at rest, sedentary obese rats displayed decreased expression of both mTOR and DEP domain-containing mechanistic target of rapamycin (mTOR)-interacting protein (DEPTOR), a negative regulator of mTOR, coupled with significant elevations in p70S6k activation. In response to resistance exercise, there was an increase in mixed, myofibrillar, and cytosolic fractions of MPS in the lean rats that appeared to be blunted with obesity (Nilsson et al., 2013). This desensitization to the anabolic stimulus of resistance exercise was postulated to also be impacted by dysregulated mTOR signaling, since DEPTOR expression decreased after exercise in lean rats, but remained unchanged in obese rats (Nilsson et al., 2013). Additionally, despite the increased basal MPS seen in the obese rats, the muscle wet mass and total protein content of the of

the quadriceps were significantly lower in the obese rats when compared to the lean rats, potentially indicating greater protein turnover with obesity.

Microscopy studies have found that intramyocellular lipid droplet content, size, and subsarcolemmal localization are directly associated with impaired insulin sensitivity in obesity. The impaired insulin sensitivity has been postulated to decrease fractional MPS rates through the dysregulation of mTOR signal transduction (Beals et al., 2019; Daemen et al., 2018; Nielsen et al., 2010; Smeuninx et al., 2017). However, there have been inconsistencies in findings related to mTOR activation in obesity, which may be due to variations between individuals (Beals et al., 2018; Tran et al., 2018). Despite this, the effects of obesity-induced anabolic resistance to exercise and dietary amino acids have also been displayed in humans (Beals et al., 2018; Smeuninx et al., 2017). Interestingly, the attenuated MPS response to exercise does not appear to be directly related to increased intramuscular NF- $\kappa$ B signaling (Beals et al., 2018). Instead, attenuated myofibrillar protein synthesis rate responses to nutrient ingestion are associated with large increases in serum insulin (Smeuninx et al., 2017). This association has been posited to suggest that obesity-induced insulin resistance may be a factor contributing to anabolic resistance (Smeuninx et al., 2017). While this mechanism of insulin resistance-induced anabolic resistance has been consistently linked to aberrant mTOR signaling in murine models, whether this mechanism involves dysregulated mTOR activation in humans is still unclear. Unlike animal models that give a more uniform presentation of obesity and insulin resistance, humans can display a range of obesity with or without metabolic disease (Jais et al., 2014; Stefan et al., 2013). This apparent difference in obesity severity or obesity-induced alterations in insulin sensitivity may be partially responsible for the inconsistent findings in human studies (Beals et al., 2019; Daemen et al., 2018; Nielsen et al., 2010; Smeuninx et al., 2017)(Beals et al., 2018)(Beals et al., 2018; Tran et al., 2018).

Overall, the collection of studies discussed indicate that obesity may influence skeletal muscle remodeling in a negative manner. Interestingly, while pro-inflammatory adipokines and signaling pathways may have the potential to alter muscle remodeling based on *in vitro* studies, the effects *in vivo* are less clear. Further, alterations in the regulatory mechanisms controlling mTOR (i.e., DEPTOR) due to obesity-induced insulin resistance may compromise skeletal muscle remodeling, leading to muscle atrophy. Still, a more concise characterization of obesity may be needed to distinguish between the divergent results of the different human studies. Further research is also needed to investigate how obesity alters adipocyte secretome, and the subsequent effects these signaling molecules have on regulating skeletal muscle mass in both animal models and humans.

## Muscular Dystrophy

Muscular dystrophy refers to a group of diseases that lead to progressive skeletal muscle degeneration, disability, and eventually death (Emery, 2002). Muscular dystrophies are caused by mutations in genes that encode for proteins including extracellular matrix (ECM) or nuclear matrix proteins (Blake et al., 2002). The most severe of muscular dystrophies result from mutations in the dystrophin-glycoprotein complex (DGC), the scaffold which localizes to the sarcolemma, providing mechanical stability to muscle (Hoffman et al.,

1987). For example, one of the most common types of muscular dystrophy is Duchenne muscular dystrophy (DMD), which results in a lack of functional dystrophin protein, an important component of the DGC. Dystrophin plays a critical role in linking the cytoskeleton of muscle fibers to the ECM and transmembrane complexes (Prins et al., 2009). Without the presence of dystrophin, the mechanical stress from muscle contractions leads to damage of the sarcolemma and muscle fiber necrosis (Petrof et al., 1993). In addition to the direct effects of mechanical injury, the progression of muscular dystrophies also involves the activation of several pathological signaling pathways and cascades (Shin et al., 2013).

Studies have shown that cytosolic calcium concentrations are increased in *mdx* mice, the animal model of DMD, especially in the subsarcolemmal space (Mallouk et al., 2000). There is evidence that this may be associated with increased calcium uptake into the cells by both passive mechanisms, by increased leakage across channels, as well as active mechanisms, via physical openings of the sarcolemma (Mallouk et al., 2000; Wang et al., 2005). The role of calcium may be independent of membrane fragility, as studies have shown that increasing cytosolic influx by overexpressing transient receptor potential canonical 3 (TRPC3), an intracellular calcium release channel, results in a muscular dystrophy phenotype (Millay et al., 2009). Furthermore, inhibition of TRPC channels reduce dystrophic features of *mdx* mice (Millay et al., 2009). Notably, increased calpain activity has been shown in dystrophic muscle fibers, and inhibiting calpains reduces dystrophic pathology in *mdx* mice (Spencer and Mellgren, 2002).

Several studies analyzing muscle biopsies from humans with DMD as well as myofibers of *mdx* mice have demonstrated an enhanced inflammatory gene profile (Haslett et al., 2002; Porter et al., 2004). The source of the inflammatory molecules and cytokines is mostly attributed to immune cell infiltration by macrophages, T cells, and neutrophils (Evans et al., 2009). In fact, macrophage depletion has been shown to ameliorate muscle injury and muscle lesions in *mdx* mice (Wehling et al., 2001). Specifically, macrophages can exist either as M1, a proinflammatory state, or M2, which are generally anti-inflammatory (Tidball and Villalta, 2010). Activation of M1 macrophages is mediated by inflammatory cytokines such as TNF- $\alpha$  and interferon- $\gamma$  (IFN- $\gamma$ ), and these cytokines also inhibit the transition to M2 macrophages (Tidball and Villalta, 2010). In contrast, anti-inflammatory cytokines such as IL-4 and IL-10 promote activation of M2 macrophages (Villalta et al., 2011). Furthermore, CD4<sup>+</sup> T cells can produce inflammatory cytokines, and CD8<sup>+</sup> T cells can trigger perforin-mediated muscle cell death; ablation of perforin or depletion of CD4<sup>+</sup>/CD8<sup>+</sup> T cells resulted in reduced fiber necrosis and decreased pathology in *mdx* mice (Spencer et al., 2001, 1997). Finally, analysis of muscle biopsies from DMD patients have shown increases in these immune cells, in addition to neutrophils and mast cells (Evans et al., 2009). Finally, elevated levels of activated NF- $\kappa$ B and NF- $\kappa$ B-regulated inflammatory cytokines TNF- $\alpha$  and IL-1 $\beta$  have been shown in DMD patients as well as in different animal models of muscular dystrophy (Acharyya et al., 2007; Lammerding et al., 2004).

Increased oxidative stress, as assessed by lipid and protein oxidation, has also been reported in muscle of patients with DMD as well as in several animal models of muscular dystrophies (Haycock et al., 1996; Terrill et al., 2013). The major source of ROS in dystrophic muscle seems to be NADPH oxidase (NOX), which is upregulated in *mdx* muscle (Whitehead



et al., 2010). Pharmacological inhibition of NOX protects against muscle damage in *mdx* mice (Whitehead et al., 2010). However, other sources of ROS exist, and include infiltrating neutrophils, which produce myeloperoxidase (MPO), mitochondria, and nitric oxide synthase (NOS) (Lawler, 2011). One of the mechanisms by which oxidative stress may be related to muscle loss in muscular dystrophy is via ROS-induced activation of NF- $\kappa$ B (Tidball and Wehling-Henricks, 2007). Interestingly, antioxidant treatments have been shown to reduce NF- $\kappa$ B activation and attenuate muscle wasting and myopathy in *mdx* mice (Hnia et al., 2007; Messina et al., 2006). Mitochondrial dysfunction is also a well-known feature of muscular dystrophies, resulting in up to 50% reductions in ATP production (Timpani et al., 2015). The connection between muscular dystrophy and mitochondrial dysfunction is thought to involve the increased calcium permeability, which can lead to calcium overload in the mitochondria, swelling, and enhanced opening of the mitochondrial permeability transition pore (Timpani et al., 2015). PGC-1 $\alpha$  overexpression has been studied in murine models of muscular dystrophy as well, and has been shown to ameliorate muscle damage and improve muscular dystrophy (Chan et al., 2014).

Matrix metalloproteinases (MMPs) are zinc-dependent endopeptidases that are important for regulating ECM degradation, inflammation, fibrosis, and activation of cytokines and cell adhesion molecules (Page-McCaw et al., 2007). The most widely studied MMPs in skeletal muscle are MMP-2 and MMP-9. It has been suggested that increased levels of MMP-9 can target (proteolyze)  $\beta$ -dystroglycan in *mdx* mice, thus disrupting the link between the ECM and cell membrane (Matsumura et al., 2005; Roma et al., 2004). Serum levels of MMP-9 have been shown to be significantly higher in patients with DMD and to be linked to disease progression (Nadarajah et al., 2011). Several other MMPs have also been shown to be elevated in *mdx* muscle, and treatment with a broad spectrum inhibitor of MMPs reduced pathological features (Kumar et al., 2010). In addition to the effects of MMPs on breakdown of the cytoskeleton-ECM network causing sarcolemmal damage and fiber necrosis, MMPs can also activate latent inflammatory molecules and interfere with the process of muscle regeneration (Kumar et al., 2010; Li et al., 2009; Page-McCaw et al., 2007).

Furthermore, one of the major features of muscular dystrophies is fibrosis, or an excessive deposition of ECM proteins such as collagens and fibronectin, which impairs tissue function (Mann et al., 2011). Tissue fibrosis is also characterized by chronic inflammation and persistent production of pro-inflammatory cytokines (Mann et al., 2011). Endomysial fibrosis is the only pathological feature that significantly correlates with poor motor outcome (Desguerre et al., 2009). Cytokine members of the TGF- $\beta$  superfamily play a role in the pathogenesis of fibrosis in most organs, including in skeletal muscle myopathies such as muscular dystrophy (Burks and Cohn, 2011). TGF- $\beta$ 1, for example, can promote fibrosis by enhancing collagen synthesis, promoting fibroblast growth and differentiation, and reducing expression of ECM degradation proteins (Biernacka et al., 2011). TGF- $\beta$ 1 can convert myoblasts into fibroblasts, suggesting that although satellite cells are activated, they can still differentiate into noncontractile tissue (Li et al., 2004). Several studies have shown that TGF- $\beta$  levels are elevated in *mdx* mice and in several animal models of muscular dystrophies (Onofre-Oliveira et al., 2012), as well as in DMD patient muscle, in association with fibrosis, degree of pathology and clinical severity (Bernasconi et al., 1995; Song et al., 2017).

Apoptosis seems to be a relevant mechanism of muscle wasting in some muscular dystrophies, such as Bethlem myopathy and congenital muscular dystrophy; however, it does not appear to play a role in DMD pathogenesis (Miller and Girgenrath, 2006). For example, muscle from patients with merosin-deficient congenital muscular dystrophy type 1 A (MDC1A), caused by mutations in a laminin gene, exhibits signs of extensive apoptosis (Miller and Girgenrath, 2006). In a mouse model of laminin-deficient muscular dystrophy, overexpression of Bcl-2 (apoptosis inhibitor) or deletion of Bax (apoptosis inducer) reduced disease severity (Dominov et al., 2005; Girgenrath et al., 2004). *In vitro*, disruption of the binding of laminin- $\alpha$ 2 to  $\alpha$ -dystroglycan activates apoptosis via Akt inhibition (Langenbach and Rando, 2002). Likewise, in a mouse model of Bethlem myopathy and Ullrich congenital muscular dystrophy (*Col6a1*-knockout), there is an increased number of apoptotic nuclei. Treatment with cyclosporine A, an inhibitor of mitochondrial permeability transition pore opening, or inhibition of apoptosis with doxycycline attenuate disease progression (Davies et al., 2005; Irwin et al., 2003). However, in DMD, necrosis is primarily responsible for the death of myofibers (Tidball et al., 1995).

Interestingly, autophagy is impaired in muscle of *mdx* mice as well as DMD patients, which leads to accumulation of damaged organelles (De Palma et al., 2012). This attenuation of autophagy occurs along with activation of the Akt-mTOR pathway in *mdx* mice, and restoration of autophagy by chronic low-protein feeding improves pathological features (De Palma et al., 2012). Similarly, activation of AMP-activated protein kinase (AMPK) (which activates autophagy by activation of ULK1, a key initiator of autophagy, and inhibition of mTOR) by the agonist AICAR also improves pathology in *mdx* mice (Pauly et al., 2012). However, in other types of muscular dystrophy, such as in MDC1A, autophagy is actually highly upregulated, and inhibition of autophagy using 3-methyladenine has been shown to reduce dystrophic features in laminin-deficient mice (Carmignac et al., 2011).

## Peripheral Artery Disease

Peripheral artery disease (PAD) refers to a group of diseases that affect arteries other than those supplying the brain or heart (Kullo and Rooke, 2016). PAD affects up to 27% of 45- to 74-year-olds, and with the expected increases in the elderly population, it is quickly becoming a major cause of morbidity (Wang et al., 2016). The most common cause of PAD is atherosclerosis, which most commonly affects the femoropopliteal or infrapopliteal arteries of the legs (Chen et al., 2013). Cycles of ischemia-reperfusion in PAD are thought to lead to significant muscle atrophy and degeneration. The earliest detailed report demonstrating that PAD is associated with abnormal skeletal muscle histology was published in 1977 (Mäkitie and Teräväinen, 1977). In this study, histochemical analysis of muscle biopsies obtained from the gastrocnemius and rectus femoris of PAD patients demonstrated myofiber atrophy, myofibrillar disorganization, and myofiber necrosis and phagocytosis (Mäkitie and Teräväinen, 1977). This was followed by a light- and electron microscopy study of gastrocnemius biopsies from PAD patients demonstrating significant morphological abnormalities characteristic of skeletal muscle myopathies, including angular fibers, fiber type grouping, central nuclei, and abundant connective tissue, or endomysial fibrosis (Hedberg et al., 1988). At the ultrastructural level, abnormalities in the contractile elements of myofibers have also been shown, such as Z-line disorganization

and fragmentation as well as disintegration of the myofilaments (Hedberg et al., 1988). More recently, the use of quantitative fluorescence microscopy has allowed for more detailed studies of the changes that occur in PAD skeletal muscle. These studies have demonstrated that the average cross-sectional area of PAD myofibers is reduced ~30% compared to non-PAD controls (Weiss et al., 2013). There are also significant reductions in major and minor axes, equivalent diameter, perimeter, and density, and a significant increase in roundness of myofibers (Koutakis et al., 2015b). There is also evidence that there is selective degeneration of type II myofibers in PAD, as type II fibers demonstrate significantly greater reductions in CSA compared to type I and type I/II fibers (Koutakis et al., 2014). There is also a lower relative frequency of type II fibers compared to type I and type I/II fibers (Koutakis et al., 2014). In addition to the morphometric changes in skeletal muscle, PAD patients have also been shown to have significantly lower knee extension/flexion force-velocity parameters compared to non-PAD controls, assessed by isokinetic dynamometry, and lower limb muscle strength correlated with maximum walking distance (Dziubek et al., 2015). Likewise, PAD patients demonstrated reduced peak torque during isometric plantar flexion contractions compared to non-PAD controls, even at baseline and before the onset of ischemic pain (Schieber et al., 2017).

Interestingly, despite altered hemodynamics, elderly PAD patients have been shown to have similar basal MPS rates as healthy, non-PAD control elderly individuals. Furthermore, PAD patients were also shown to have a normal anabolic response to amino acid ingestion (Killewich et al., 2007). Thus, the skeletal muscle myopathy of PAD may not involve MPS-related mechanisms. Instead, the myopathy of PAD is believed to involve increases in ROS production and oxidative stress. Several studies have consistently demonstrated that PAD patients exhibit higher levels of oxidative stress markers in circulation compared to non-PAD controls at rest as well as in response to exercise. Likewise, there is clear evidence of oxidative stress in skeletal muscle as well (Koutakis et al., 2018). Following hindlimb ischemia (HLI) in mice, myofibers of ischemic skeletal muscle demonstrate increased levels of 4-HNE, a marker of lipid peroxidation, as well as carbonyl groups, a measure of protein oxidation (Pipinos et al., 2008c). Similarly, myofibers of gastrocnemius muscle from PAD patients also demonstrate greater labeling of carbonyl groups (30%) and HNE adducts (40%) compared to non-PAD control muscle (Weiss et al., 2013). Furthermore, the extent of oxidative damage is associated with significant atrophy of the myofibers, and oxidative stress markers are also correlated with walking distances of PAD patients (Dopheide et al., 2013; Weiss et al., 2013). PAD is also associated with mitochondrial dysfunction, and a number of studies in both human patients as well as murine models of hindlimb ischemia have shown impairments in skeletal muscle mitochondrial respiration and electron transport chain complex activity (Pipinos et al., 2008d, 2006, 2003). Importantly, skeletal muscle mitochondrial dysfunction in PAD is also associated with myofiber atrophy and abnormal myofiber morphology (Koutakis et al., 2015a).

## Discussion

Muscle protein metabolism is an ever-changing dynamic system that involves both anabolic and catabolic mechanisms. When this equilibrium is altered to favor catabolic pathways, skeletal muscle atrophy occurs. This perturbation in protein balance can arise in response to

various pathophysiological processes and conditions (Table 1). The proteolytic systems that govern MPD (i.e., the UPS, autophagy-lysosomal, caspase, calpains) appear to differentially upregulate in response to different atrophic conditions, as discussed in this review. In addition, skeletal muscle atrophy associated with certain catabolic states may also involve inhibition of MPS or resistance to anabolic stimuli (such as exercise and nutrient intake). Other factors that have also been implicated in muscle atrophy across certain pathological and physiological conditions include mitochondrial dysfunction, enhanced ROS production, and enhanced inflammatory processes.

In 2001, Bodine and colleagues identified the mTOR pathway as a crucial regulator of muscle hypertrophy (Bodine et al., 2001b) as well as the involvement of the ubiquitin ligases, MuRF1 and MAFbx, in the muscle atrophy induced by different atrophic conditions (Bodine et al., 2001a). Since then, the primary focus during the past 20 years in the field of skeletal muscle atrophy has been to further identify and elucidate the molecular mechanisms that lead to muscle atrophy under different conditions. However, most researchers have focused on investigating the mechanisms of muscle atrophy in specific, isolated conditions. It is important to note, however, that there is significant overlap in many of the conditions associated with muscle atrophy. For example, PAD prevalence increases with age, and individuals with PAD may be at a greater risk for sarcopenia. Both sarcopenia and PAD are conditions that lead to significant losses of physical function (mechanical unloading), and notably, PAD patients with sarcopenia have also been shown to have decreased function compared to PAD patients without sarcopenia (Addison et al., 2018). Therefore, disuse atrophy is also strongly implicated in both PAD and sarcopenia development (Bell et al., 2016). Due to these overlapping etiologies, it is important to differentiate between the underlying factors that may be secondary to the condition of interest (Nishikawa et al., 2021). Additionally, most of the research has involved reductionist experiments, focused on specific proteins and pathway components. Despite new innovations in techniques and the identification of novel regulators of molecular signaling pathways, these factors are still understudied in humans. While mechanisms have been more clearly defined *in vitro* and in animal models, there have been inconsistencies related to the involvement of different factors in the muscle atrophy induced by different conditions in clinical populations. Due to the complexity of the signaling pathways involved and the plethora of factors that contribute to atrophy in response to varying catabolic stimuli, future studies are required to better define the involved pathogenesis. These studies should contain a human component and include larger sample sizes to account for large inter-personal variability in the responses to these stimuli.

Currently, physical exercise and nutritional strategies are considered the best approaches to attenuate muscle atrophy across various catabolic circumstances (Magne et al., 2013; Shen et al., 2018). Beyond this, considerable research has identified several novel drug targets to counter muscle atrophy induced by different conditions. However, no efficacious drug counteracting muscle atrophy has yet to reach the clinic. Although many *in vitro* and animal studies have demonstrated that various investigational drugs can protect against muscle atrophy, human clinical trials often result in important side effects or no significant improvements (Chen et al., 2021; Sartori et al., 2021). Only a limited number of therapeutics have been shown to be safe and effective in clinical trials. This highlights the importance

of future development of novel therapies. In addition, new methods of combination therapy may be worthwhile since several intracellular degradation pathways may be upregulated simultaneously. Despite diverse etiology, muscles atrophying in response to different catabolic conditions share many common features. Thus, in the journey for the development of rational treatment strategies, targeting shared mechanisms and pathways associated with muscle wasting in a wide variety of atrophy conditions is logical when considering the potential impact.

Anabolic resistance seemingly afflicts individuals who are obese, sarcopenic, or are experiencing immobilization. One of the common lifestyle factors that is predominant within each of these populations is physical inactivity and mechanical unloading (muscular disuse). Anabolic resistance in each of these conditions appears to be partially mediated by the impaired integration of both mechanical load and nutrient signals, referred to as anabolic or inactivity-induced insulin resistance. It is possible that physical inactivity itself is one of the main contributors to anabolic resistance that is independent from the other factors such as age or body composition. Recently, researchers have indicated a necessity in separating the effects of ageing and disuse to specifically isolate the negative effects of age (Brocca et al., 2017a). It was found that the atrophic effects of age are exacerbated with disuse, indicating that physical inactivity is a major contributor to the loss of mass and anabolic resistance in this population. Like the age specific findings of Brocca et al., (2017a), the individual effects of obesity with and without chronic physical activity need to be elucidated to distinguish if separate mechanisms such as increased intramuscular ROS facilitate anabolic resistance in these populations as a separate mechanism.

Caspase-mediated apoptosis appears to be confined to cachexia and DMD and does not appear to play a major role in the other conditions discussed in this review. Additionally, increases in MPD via the UPS has been shown to occur with inflammatory signaling cascades induced by TNF- $\alpha$ , IL-6, and INF- $\gamma$  in both cancer cachexia and DMD patients. These signaling molecules are primarily released from macrophages that infiltrate into the tissue to degrade cancer cells or the mutated dystrophin proteins. It has been hypothesized that macrophage-infiltrated, hypertrophied adipose tissue can secrete TNF- $\alpha$  and IL-6 into circulation and induce UPS-mediated MPD of skeletal muscle tissue. However, a definite link between adipocyte-associated inflammatory phenotypes and skeletal muscle atrophy has yet to be established in wild-type animals or in humans.

Increased ROS production and associated mitochondrial dysfunction appear to be the main mechanisms that are shared between all the reviewed conditions. However, despite this similar presentation of increased ROS, the mechanism for the increase and the sequential effects are somewhat distinct for various pathologies. For example, ROS production associated with cachexia and DMD has been shown to be modulated by TNF- $\alpha$  and the infiltration of immune cells, leading to UPS-mediated MPD. In sarcopenia, increased ROS production is mainly associated with mitochondrial dysfunction and has been postulated to be partially responsible for inducing denervation of MUs. In PAD, ROS production is thought to be driven by cycles of ischemia-reperfusion. It is important to note, however, that the majority of PAD patients are also elderly and may be sarcopenic; thus, large increases in ROS production in PAD could also increase the rate of ROS-driven denervation

and MU loss. Therefore, the combination of distinct factors could mediate muscle atrophy via several mechanisms within the same condition, further highlighting the complexity of skeletal muscle atrophy research.

## Conclusion

In each of the conditions listed throughout the review there is an overall shift in the protein regulation within skeletal muscle that favors MPD. Despite the shared atrophic effect these conditions have on muscle, the mechanisms in which they operate are somewhat distinct. Regardless of their apparent uniqueness, these situational conditions and signaling events are not mutually exclusive and multiple overlapping circumstances can augment protein breakdown in a synergistic manner. This review highlights the major mechanisms involved to better summarize the current understanding of the role the individual complex proteolytic events play across disease conditions. Future interventions that target the specific mechanisms will be critical in the development of novel treatments for patients suffering from these conditions.

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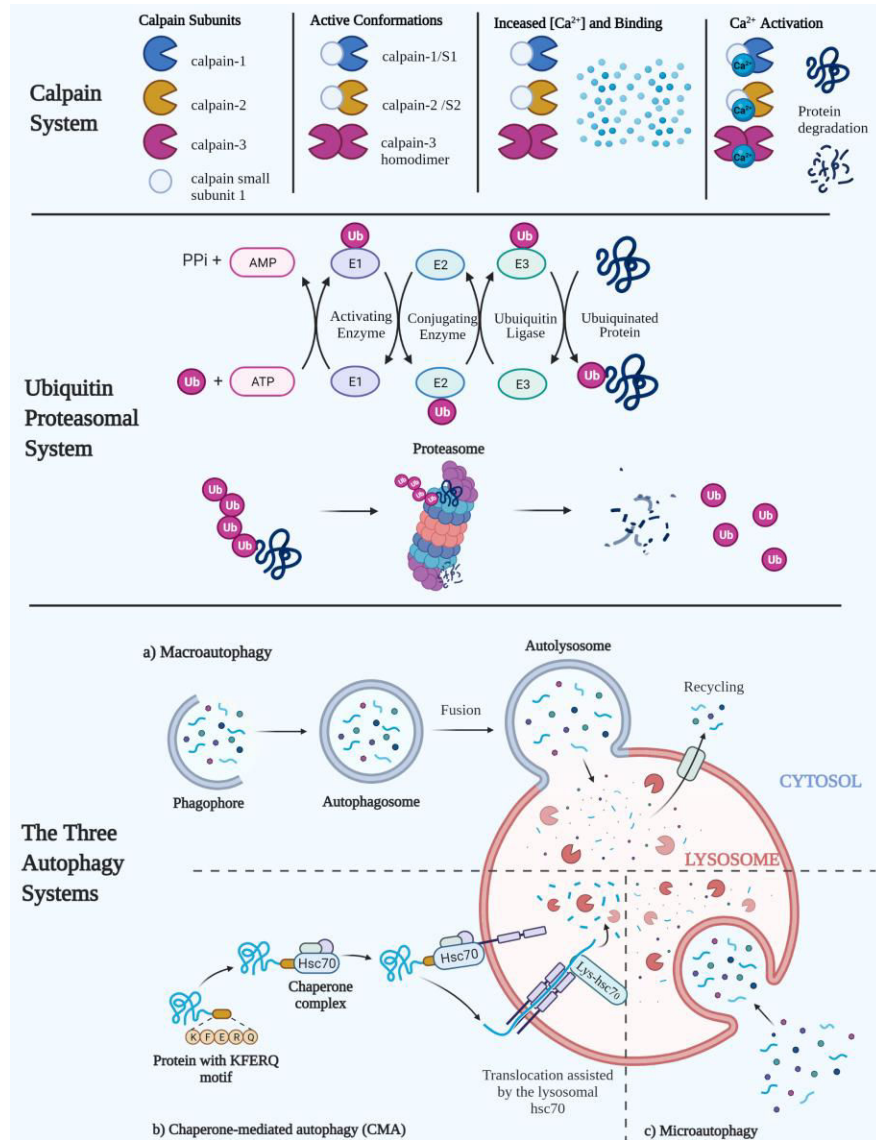
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### Highlights

- The ubiquitin-proteasome is involved in muscle degradation in cachexia and unloading.
- Co-morbid conditions such as obesity and PAD increase ROS and muscle loss with ageing.
- Without co-morbidities, anabolic resistance leads to muscle loss in ageing.



**Figure 1:** Above indicates the three major proteolytic systems that regulate skeletal muscle atrophy. Calpain activation can induce protein degradation by calcium dependent binding. The ubiquitin proteasomal system can degrade proteins through post-translational polyubiquitination through a series of E1, E2, and E3 relaying mechanisms. The polyubiquitinated protein is then subsequently shuttled into the 26S proteasome for degradation. The three autophagy pathways degrade polypeptides, proteins, and organelles by integrating substrates into the lysosome. Macro-autophagy and micro-autophagy are non-specific in their degradation targets, but chaperone-mediated autophagy uses the specific pentapeptide sequence (KFERQ) to selectively bind, shuttle, and translocate proteins into the lysosome with the help of cytosolic and lysosomal heat shock cognate 71 kDa protein (Hsc70).

**Table 1:**

The major mechanisms of skeletal muscle degradation are outlined for each condition visually in the table above.

Overview of Skeletal Muscle Atrophy Mechanism by Condition						
	Cancer Cachexia	Obesity-Related Chronic Inflammation	Sarcopenia	Mechanical Unloading	Muscular Dystrophy	Peripheral Artery Disease
UPS	X			X		
Reduced MPS	X		X	X		
Inflammatory cytokines	X	X	X		X	X
ROS	X	X	X	X	X	X
Mitochondrial dysfunction	X	X	X	X	X	X
Apoptosis	X				X	
Motor unit loss			X			
Reduced myonuclear efficiency			X			
Calpains				X	X	
Autophagy dysregulation					X	
Anabolic Resistance		X	X	X		

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