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REVIEW

Longevity and skeletal muscle mass: the role of IGF signalling, the sirtuins, dietary restriction and protein intake

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Summary

Advancing age is associated with a progressive loss of skeletal muscle (SkM) mass and function. Given the worldwide aging demographics, this is a major contributor to morbidity, escalating socio-economic costs and ultimately mortality. Previously, it has been established that a decrease in regenerative capacity in addition to SkM loss with age coincides with suppression of insulin/insulin-like growth factor signalling pathways. However, genetic or pharmacological modulation of these highly conserved pathways have been observed to significantly enhance life and healthspan in various species, including mammals. This therefore provides a controversial paradigm in which reduced regenerative capacity of skeletal muscle tissue with age potentially promotes longevity of the organism. This paradox will be assessed and considered in the light of the following: (i) the genetic knockout, overexpression and pharmacological models that induce lifespan extension (e.g. IRS-1/6K KO, mTOR inhibition) versus the important role of these signalling pathways in SkM growth and adaptation; (ii) the role of the sirtuins (SIRTs) in longevity versus their emerging role in SkM regeneration and survival under catabolic stress; (iii) the role of dietary restriction and its impact on longevity versus skeletal muscle mass regulation; (iv) the crosstalk between cellular energy metabolism (AMPK/TSC2/SIRT1) and survival (FOXO) versus growth and repair of SkM (e.g. AMPK vs. mTOR); and (v) the impact of protein feeding in combination with dietary restriction will be discussed as a potential intervention to maintain SkM mass while increasing longevity and enabling healthy aging.

Key words: AKT; AMPK; cachexia; calorie restriction; FOXO; high-protein diets; IGF-I; IRS-1; lifespan; longevity; MAFBx; mTOR; MURF; regeneration; sarcopenia; satellite cells; SIRT; SkM; TSC.

Sarcopenia: demographics and impact on quality of life in humans

Life expectancy is increasing rapidly in many countries. As a consequence, there are a greater proportion of older people making up our global population. In the UK, 10 million people are currently over 65 years of age, with the latest projections suggesting that this will increase to 19 million people by 2050 (Cracknell, 2013). Age is the primary risk factor for a multitude of pathological conditions, including Alzheimer’s disease, cardiovascular disease, type II diabetes and sarcopenia. Sarcopenia is the age-related loss of skeletal muscle (SkM) mass and function (Rosenberg, 1997). Muscle loss is evident in sedentary humans at 25 years of age, with a 10% loss in peak lean SkM mass at 40 years of age, which increases to 40% at 70 years of age (Porter et al., 1995). Indeed, from age 50, muscle mass is lost at a rate of 1–2% per year (Hughes et al., 2001). This loss impacts negatively on functional and metabolic performance, maximal strength and muscle quality (Renault et al., 2002; Morse et al., 2005a,b; Rossi et al., 2008). Importantly, loss of functional capacity in skeletal muscle with age is strongly correlated with decreased quality of life and increased frailty, morbidity and early mortality (Rantanen et al., 2003). Given that approximately 40–50% of the population over 80 years of age suffers from sarcopenia, this condition has been recognized as a major geriatric clinical disorder (Cruz-Jentoft et al., 2010). Thus, ameliorating age-related SkM wasting is of high clinical importance if we are to improve quality of life and ultimately reduce the socio-economic impact of sarcopenia.

Overview and Rationale

This review will focus on the cellular and molecular mechanisms that underpin age-related muscle loss and will debate the trade-off that may occur between skeletal muscle maintenance and survival into old age versus whole organism life/healthspan. This concept emerges from the body of research investigating the molecular modulators of aging. It focuses on genetic knockout (KO) of IRS-1 and p70S6K1 as well as transgenic models such as FOXO, SIRT1 and finally pharmacological modulation including mTOR inhibition and sirtuin activation. All of these models have been shown to extend both lifespan and healthspan. Importantly however, all of these pathways are also inextricably shared with those that modulate skeletal muscle mass maintenance. Therefore,
this review will seek to discuss the hypertrophic, degradative and sirtuin pathways in relation to their modular regulation of lifespan, healthspan and muscle cell survival particularly in inflamed aged environments. Finally, the potential importance of optimizing dietary restriction and amino acid uptake to ameliorate the reduction in SkM mass while promoting healthy aging will be discussed.

### Insulin-like growth factors (IGFs) and skeletal muscle

#### Overview of IGF’s and their role in skeletal muscle mass regulation

The insulin-like growth factor (IGF) family consists of the ligands, IGF-I and IGF-II, the type I and type II IGF cell surface receptors, six specific high-affinity binding proteins (IGFBP-1 to IGFBP-6), IGFBP proteases and other IGFBP-interacting molecules (Holly et al., 2000). They have a wide range of biological functions including embryonic, foetal and adult SkM development (reviewed in Stewart & Rotwein, 1996a). In vivo rodent studies have shown that KO of IGF-I, IGF-II or the IGF-I receptor (IGF-IR) results in animals that are phenotypically small for their gestational age with significant decreases in SkM mass and neonatal lethality (Nabeshima et al., 1993; Lau et al., 1994; Stewart & Rotwein, 1996a,b). Alternatively, increasing circulating IGF-I expression in transgenic mice results in SkM hypertrophy (Matthews et al., 1988). Furthermore, KO of IGF-IIR also results in SkM overgrowth; as IIR acts as a clearance receptor for IGF-II, thus its removal leads to an increase in circulating IGF-II and subsequent hypertrophy (Lau et al., 1994). Our group has extensively characterized the multifaceted roles of the IGF system where they are fundamental in the proliferation, survival, differentiation and hypertrophy of primary human and mouse SkM cells (Stewart et al., 1993; James et al., 1996; Stewart et al., 1996; Stewart & Rotwein, 1996b; Stewart et al., 1999a,b; Foulstone et al., 2001, 2003a,b, 2004; Grohmann et al., 2005; Saini et al., 2008; Stewart & Pell, 2010; Al-Shanti & Stewart, 2011; Saini et al., 2012; Sharples et al., 2013; Player et al., 2014) (Reviewed in Scime & Rudnicki, 2006). Skeletal muscle-derived IGF-I is also important in adult muscle hypertrophy, as demonstrated using liver IGF-I-deficient (LID) mice (Matheny et al., 2009). In this study, despite an 80% reduction in total circulating levels of IGF-I in LID versus control (L/L) mice, following 16 weeks of hypertrophy inducing resistance exercise there was no difference in locally produced IGF-I mRNA or IGF-IR activation between groups (Matheny et al., 2009). Despite these compelling data, the importance of IGF-I in mechanical load-induced hypertrophy following resistance exercise and the development of animal models of nonphysiological hypertrophy have been recently debated. This controversy is reviewed by our group elsewhere, and it not the focus of this current review (Stewart & Pell, 2010; Sharples & Stewart, 2011).

#### Reducions in IGF-I and associated signalling in aging skeletal muscle

With sarcopenia, a 33% reduction in circulating IGF-I (Benbassat et al., 1997) and a 45% decline in SkM-derived IGF-I mRNA are observed in older (70 ± 0.3 years) vs. younger (20 ± 0.3 years) human males (Leger et al., 2008). A corresponding attenuation in downstream intracellular signalling targets involved in protein synthesis with age has also been described. These include reductions in the activity of PI3K, Akt, mTOR, p70S6K1, 4E-BP1 and EIF28 in older vs. younger counterparts (Terada et al., 1994; Welsh et al., 1997; Pallafacchina et al., 2002; Cuthbertson et al., 2005; Leger et al., 2008). With impairments of these signalling pathways also observed with age following muscle contraction (Fry et al., 2011), a recent study using mouse models attempted to recapitulate declining human serum IGF-I concentrations with age. It should be noted that in rodents, serum IGF-I levels are consistently high and do not decrease until very old age when sarcopenia is observed, whereas in humans, serum IGF-I is highest during adolescence and declines earlier in the life course, starting in middle age and paralleling the onset of sarcopenia. This study suggested that mice with reduced serum IGF-I at 1 year of age had significantly deteriorated healthspans. They exhibited increased liver weight and inflammation and increased incidence of hepatic tumours. Importantly, in SkM tissue, increased oxidation of proteins was observed, indicative of increased oxidative stress (Gong et al., 2014), overall suggesting an important role for IGF-I in reducing some, but not all (see below), age-associated pathologies.

We have recently developed and begun to characterize the roles of the IGFs, their receptors and modulatory binding proteins in an in vitro murine cell model of SkM aging via the following: (i) comparisons of parental (older) vs. daughter (younger) cell populations and (ii) multiple population doublings as a way of artificially aging cells (Sharples et al., 2010, 2011, 2012, 2013). These studies demonstrated that IGF binding protein levels increases in cells that display aging phenotypes via mechanisms that ultimately reduce the activity of Akt (Sharples et al., 2011, 2013). These observations correspond with impaired differentiation and hypertrophy of myotubes (Sharples et al., 2010, 2011, 2012; Deane et al., 2013). These phenotypes are also observed in primary human SkM cells isolated from aged vs. young donors (Collins et al., 2007; Bigot et al., 2008; Pietrangelo et al., 2009; Beccafico et al., 2010). These effects correspond with a loss of myogenicity (Hidestrand et al., 2008) in the face of unchanged telomere length and telomerase activity (O’Connor et al., 2009). Together, the majority of evidence (both in vitro and in vivo) therefore points towards the need for IGF-I and activation of its downstream signalling pathways to maintain skeletal muscle mass across the lifespan.

#### Reduced Insulin/Insulin-like-Growth Factor Signalling (IIS): enhanced longevity vs. reduced muscle mass in aging skeletal muscle

**IGF and Insulin Receptor Substrate (IRS-1)**

Reductions in IGF-I activity with age are associated with reductions in SkM size and function. However, reduced signalling through the IIS pathway is also associated with increased lifespan and healthspan in model organisms (Clancy et al., 2001; Holzenberger et al., 2002; Barbieri et al., 2003; Tatar et al., 2003; Giannakou & Partridge, 2007; Piper et al., 2008; Selman et al., 2008; Vallejo et al., 2009; Kenyon, 2011; Selman et al., 2011). For example, both female and male mice globally lacking insulin receptor substrate 1 (Irs1−/−) are long lived (Selman et al., 2008, 2011). Female mice lived 32% longer compared to wild-type controls, equating to a mean lifespan of 971 days in the Irs1−/− mice compared with 738 days in wild-type control animals. Interestingly, Irs1−/− mice showed resistance to several parameters associated with aging, including bone, skin, metabolic, immune and motor dysfunction (Selman et al., 2008). Thus, Irs1−/− mice, in common with several other long-lived models, enjoy a greater period of their life free from various age-associated pathologies (Selman and Withers, 2011). Importantly, Irs1−/− mice display reduced growth compared to wild-type animals perhaps due to the important role for IRS-1 in embryonic and postnatal growth (Withers et al., 1998, 1999). Furthermore, mice with growth hormone (GH)/IGF-I defects, while phenotypically growth retarded compared with wild-type littermates, also exhibit enhanced longevity, lower DNA mutation frequencies, higher...
DNA excision repair and secondary attenuation of IIS (Bates & Holder, 1988; Pell & Bates, 1992; Bartke & Brown-Borg, 2004; Bartke, 2005; Garcia et al., 2008; Garinis et al., 2009; Masternak et al., 2009; Page et al., 2009).

While there are clear benefits of reduced IIS signalling for lifespan and aspects of healthspan, as eluded to above, reductions in SkM mass correspond with decreases in IGF-I with age. Indeed, some studies suggest that bone, cardiac muscle and other tissues display aged characteristics when IGF-I is impaired (Adamo and Farrar, 2006; Anversa, 2005; Ceda et al., 2005; Geusens and Boonen, 2002). Indeed, Irs1−/− mice have reduced body weight and fat mass compared to age-matched controls (Pete et al., 1999; Selman et al., 2008) with reduced gastrocnemius SkM weight that is proportionately greater than the decrease seen in total body weight (Pete et al., 1999). Irs1−/− mice are, however, more resilient to age-associated osteoporosis compared to controls, which may account somewhat for this discrepancy. A recent study using an inducible liver-derived IGF KO mouse, allowing temporal reductions of IGF of 70% in the serum, showed that lower IGF from the age of 1 year resulted in greater oxidative stress in SkM, accelerated bone loss and reduced lifespan (Gong et al., 2014). Indeed, across 31 genetically diverse inbred mouse strains, lower serum IGF-I was associated with enhanced longevity (Yuan et al., 2009). Furthermore, human population studies suggest that reductions in IGF-I at young age but elevations at old age might maximize healthy lifespan, reviewed in Yang et al. (2005). To the authors’ knowledge, the only study to investigate potential mechanisms of SkM adaptation with Irs-1 loss suggested that it did not affect glucose uptake or GLUT1/4 function in electrically stimulated mouse muscle (Dumke et al., 2001). Skeletal muscle mass or synthetic/degradative signalling was, however, not investigated in this study. Overall, it is clear that reductions in IIS enhance lifespan and delay some aging-associated parameters yet perhaps results in small body size that is characterized by both reduced fat mass and potentially, proportionally smaller SkM mass. However, more investigation into SkM mass and the corresponding cellular signalling in Irs1−/− mice into old age is required in the near future to understand the potential crosstalk between the mechanisms that control increased lifespan and healthspan while contributing to reductions in SkM mass with age.

Mammalian target of Rapamycin (mTOR)

In addition to reduced IIS, reduced signalling through the target of rapamycin (TOR) signalling pathway has also been shown to modulate lifespan and increase healthspan in model organisms (Kapahi et al., 2004; Kaebelerin et al., 2005; Powers et al., 2006; Hansen et al., 2007; Harrison et al., 2009; Anisimov et al., 2010; Bjedov et al., 2010; Miller et al., 2011; Robida-Stubs et al., 2012; Zhang et al., 2014). Longevity in humans is also associated with reduced mTOR signalling (Slagboom et al., 2011; Passtoors et al., 2013). The TOR or mTOR (mammalian target of rapamycin) is, however, a key regulator of SkM growth where it also plays a central role in the crosstalk between growth and metabolism in a wide variety of cell types (Inoki et al., 2003) and SkM (most recently see Hamilton et al., 2014). Mammalian target of rapamycin regulates its hypertrophic effects in SkM through the phosphorylation of downstream effectors such as P70S6 kinase 1 (S6K1) and eIF4E-binding protein 1 (4E-BP1) (reviewed in Schiaffino et al., 2013). Their roles in SkM growth following contraction and mechanical load-induced hypertrophy, synergistic ablation, myotube hypertrophy and amino acid sensing are also well defined (Fujita et al., 2007; Drummont et al., 2009; Willett et al., 2009; Goodman et al., 2011; Miyazaki et al., 2011; Philip et al., 2011; Jacobs et al., 2013; Hamilton et al., 2014). In older people, mTOR becomes less responsive to contraction-induced activation (via resistance exercise), compared with young adults (Fry et al., 2011). The activity of mTOR in response to amino acid feeding is also impaired in older individuals, a phenomenon known as ‘anabolic’ resistance (Cuthbertson et al., 2005).

Rapamycin-induced inhibition of mTOR has, however, been shown to increase lifespan in yeast, drosophila and mice (Powers et al., 2006; Harrison et al., 2009; Anisimov et al., 2010; Bjedov et al., 2010; Miller et al., 2011; Robida-Stubs et al., 2012; Wilkinson et al., 2012). Further, rapamycin diminishes a range of age-related pathologies (reviewed by Johnson et al., 2013b), and despite a contentious study claiming that it does not (Neff et al., 2013), the wide consensus is that appropriate modulation of mTOR signalling could be an important route of intervention to slow aging and increase healthspan (reviewed by Johnson et al., 2013a). However, in skeletal muscle rapamycin-induced inhibition of mTOR has been shown to impair myogenic differentiation (Willett et al., 2009), blunt the anabolic response to overload and nutrients (Goodman et al., 2011), with muscle-specific inactivation of mTOR leading to myopathy (Risson et al., 2009). These data therefore suggest, perhaps paradoxically, that despite inhibition of mTOR increasing lifespan and improving many age-related pathologies, mTOR signalling plays a critical role in maintaining SkM mass and anabolism. Despite this, the only study that has so far investigated muscle size and function in mice with advancing age, suggests that muscle cross-sectional area and grip/paw strength were unaffected by a 16-month treatment of rapamycin vs. aged-matched controls (Neff et al., 2013).

Similar to rapamycin-induced mTOR inhibition, global deletion of the ribosomal protein S6K1 in mice, a downstream effector of mTOR, also increases lifespan and improves healthspan in mice (Selman et al., 2009). In contrast to rapamycin treatment having no impact on muscle size (Neff et al., 2013), S6K1(−/−) myotubes are smaller, despite having a normal number of nuclei, and their response to a hypertrophic stimuli of IGF-I or nutrients is blunted (Ohanna et al., 2005). Further, deletion of S6K1 in mice induces SkM atrophy even in the presence of high nutrient availability via AMPK activation, where AMPK inhibition in S6K1-deficient myotubes restores SkM growth via increases in myotube diameter and sensitivity to nutrient signals (Aguilar et al., 2007). In aged human SkM, S6K1 is downregulated in response to amino acid feeding (Cuthbertson et al., 2005) and attenuated in old vs. young rodents during recovery from immobilization-induced atrophy (Morris et al., 2004). S6K1 is also reduced in contracting aged SkM in comparison with young muscle, suggesting it plays an important role in SkM protein synthesis, which is hampered with age (Parkington et al., 2004; Kumar et al., 2009). However, surprisingly little is currently known about whether basal muscle maintenance and function is altered in the context of aging in long-lived mTOR mutant or, as discussed, rapamycin-treated mice. Studies examining protein synthesis, protein degradation and SkM function in long-lived mouse models are urgently required if we are to increase our understanding of the potential trade-off between longevity and muscle function. Depicted in Figure 1 (Fig. 1).

Sirtuins: divergent roles in the modulation of lifespan vs. skeletal muscle mass

Sirtuins and their roles in aging and longevity

Significant recent research effort has focused on elucidating the various roles of sirtuins (silent information regulator 1–7; Sir1–7) in aging. Sirtuins are a group of seven highly conserved protein deacetylases involved in the process of chromatin remodelling and gene regulation (see Morris, 2013). They have also been shown to have pathophysiological
Sirtuins and their impact on IGF signalling and skeletal muscle

In terms of SkM growth and protein synthesis, evidence exists, implicating SIRT1 and SIRT6 as negative regulators of IGF-I and downstream Akt/mTOR signalling (Ghosh et al., 2010). For example, in mouse neural cells, SIRT1 silencing and overexpression increased and decreased IGF-I and associated Akt signalling, respectively (Sansone et al., 2013). Similarly, SIRT6 overexpression in mice has been associated with a reduction in circulating IGF-I (Kanfi et al., 2012a). An exciting recent link between SIRT1 and IGF-I has been established in a range of nonskeletal muscle human cell types. When stimulated with exogenous IGF-I for prolonged periods, cells exhibited reduced SIRT1 deacetylase activity, increased p53 acetylation and increased senescence, when compared with cells exposed to acute administration of IGF-I exhibiting increased proliferation (Tran et al., 2014). Although speculative, reductions in IGF-I with age could be an attempt to alleviate senescence and maintain SIRT1 activity (Tran et al., 2014). In SkM, our group has shown that the induction of apoptosis, by low-dose tumour necrosis factor-alpha (TNF-α) with the addition of IGF-I, is elevated compared with TNF-α administration alone. Death was associated with increased SIRT1 mRNA levels, which when suppressed using SRT1 siRNA, culminated in exacerbated, not reduced, apoptosis (Saini et al., 2008, 2012). Overall suggesting that under conditions of both anabolic and catabolic conflicts, SIRT1 was important to the maintenance of survival in skeletal muscle cells. Therefore, SIRT1 appeared fundamental in negatively regulating IGF-I basally, yet in the presence of inflammatory catabolic stress (Saini et al., 2008, 2012), or where IGF-I exposure was prolonged enough to induce cell death (Tran et al., 2014), SIRT1 was important in maintaining survival. It is also worth noting that SIRT2104, a synthetic small molecular activator of SIRT1, reduced circulating TNF-α in mice (Merck et al., 2014). Suggesting a potential regulatory loop between SIRT1 and TNF-α, yet this link in SkM is yet to be directly established. This concept is particularly relevant in aging muscle where chronic low-level TNF-α exposure and changing IGF-I concentrations are strongly associated with muscle wasting in vivo and the pathologies of sarcopenia and cachexia (Li & Reid, 2000; Meadows et al., 2000; Foulstone et al., 2001; Grewee et al., 2001; Bruunsgaard et al., 2003a,b; Bruunsgaard & Pedersen, 2003; Stewart et al., 2004; Grohmann et al., 2005; Li et al., 2005; Saini et al., 2006, 2008, 2010, 2012).

![Fig. 1 Depicts the extracellular and intracellular signaling molecules involved in the cross-talk between skeletal muscle mass regulation and life/health-span modulation. Genetic or pharmacological suppression of IIS, TOR and Sirtuin pathways increase organism life/health-spans. However, these pathways are fundamental in protein synthesis, growth, differentiation and survival in skeletal muscle into old age. This figure therefore provides the potential molecular and cross-talk modulators for this paradigm of lifespan versus muscle mass maintenance with age.](image-url)
In addition to its role in regulating IGF-I and survival in the presence of aberrant IGF-I, SIRT1 may also play a role in negatively regulating mTOR. SIRT1 (−/−) mouse embryonic fibroblasts (MEFs) and human HELA cells depleted of SIRT1 using shRNAi resulted in elevated mTOR signalling, which was not abolished by leucine deprivation (Ghosh et al., 2010). In the same study, SIRT1 activators and inhibitors (resveratrol/nicotinamide) reduced and increased mTOR activity, respectively (Ghosh et al., 2010).

SIRT1 activation following resveratrol administration in myoblasts inhibited IGF-I-associated signalling (Akt) and abolished leucine-stimulated increases in mTOR (Liu et al., 2010). These studies suggest that any changes in SIRT1 when age in response to catabolic stress or nutrient restriction could potentially impact on mTOR function and result in altered regeneration. Overall, these data present negative regulation by SIRT1 on pathways such as Akt/mTOR linked to SkM tissue or cells through overexpression on mTOR-dependent phosphorylation site Thr-389. In this case, acetylation blocked S6K activity and thus, deacetylation by the sirtuins may actually be involved in the phosphorylation of S6K (Hong et al., 2014). Furthermore, in cardiac muscle, SIRT1 can also deacetylate Akt and PDK, enabling binding to phosphatidylinositol 3,4,5-trisphosphate [PIP(3)], and thus its localization to the membrane where PDK can subsequently facilitate Akt phosphorylation (Sundaresan et al., 2011). Sirtuin activation, however, specifically in SKM tissue or cells through overexpression in rodent models or supplementation of resveratrol/its analogues in humans, requires further investigation to decipher its role in negatively regulate mTOR activity.

Therefore, as well as an important role in myoblast survival, SIRT1 may also be involved in maintaining adequate differentiation, hypertrophy and apoptosis respectively (Brunet et al., 2004; Greer & Brunet, 2005; Wang et al., 2007). This is important in maintaining the aging muscle tissue and to the promotion of longevity via FOXO3a and FOXO1, thereby activating FOXO DNA binding and elevating the expression of target genes such as p27(Kip1), manganese superoxide dismutase and Bim, proteins associated with cell cycle arrest, oxidative stress and apoptosis respectively (Brunet et al., 2004; Wang et al., 2007; Jacobs et al., 2008). The activation of FOXO transcription factors by the SIRT family appears to, however, impair the ability of FOXO to promote cell apoptosis, instead shifting its function towards oxidative stress resistance and DNA repair (Brunet et al., 2004; Greer & Brunet, 2005; Wang et al., 2007). It is also well established that overexpression of FOXO can extend lifespan in drosophila (Giannakou et al., 2004; Min et al., 2008; Alic et al., 2014). Interestingly, in TNF-α-stimulated SkM cells the activation of SIRT1 via resveratrol restored Akt/mTOR/S6K and 4E-BP1 signalling and reduced FOXO1 but not FOXO3a protein levels, all of which were unchanged basally (Wang et al., 2014). Therefore, the role for SIRT1 activation on FOXO3a in SkM tissue with age requires further investigation. FOXO1 and its role in oxidative stress resistance in aging SkM also requires attention, especially following catabolic stress or dietary restriction where SIRT1 elevation is associated with survival. It is worth mentioning here that class I histone deacetylases (HDACs) (sirtuins are class III HDACs) have also been linked with activating FOXO3a and the SkM-atrophy programme (via MAFFbx/atrogin-1) during nutrient deprivation and disuse-induced atrophy (Beharry et al., 2004; Edstrom et al., 2008; Alic et al., 2014). SIRT1 activation following resveratrol administration in myoblasts inhibited IGF-I-associated signalling (Akt) and abolished leucine-stimulated increases in mTOR (Liu et al., 2010). Therefore, despite its proposed negative regulation of IGF-I/Akt/mTOR, SIRT1 seems to be fundamental to SkM cell growth, enabling proliferation and impairing differentiation under control conditions, yet protecting differentiation under means of stress. Importantly, the impact of activating SIRT1 in aged SkM cells/tissue basally or under stress remains to be fully determined especially, we hypothesise, in situations of dietary restriction that directly regulate the NAD/NADH ratio and impact on SIRT expression.

Sirtuins: regulators of longevity and survival vs. activators of protein degradation in SkM via FOXO transcription factors

In addition to its role in SkM proliferation, SIRT1 has also been implicated in controlling protein degradative pathways, specifically via forkhead box protein O (FoxO) transcription factors. These transcription factors are involved in targeting and activating members of the ubiquitin proteasome, such as muscle atrophy F-box (MAFbx/atrogin1), muscle RING finger 2 (MuRF1), and autophagy-lysosome pathways involved in protein degradation (Sandri et al., 2004; Edstrom et al., 2006; Sandri, 2008). SIRTs have been shown to activate both FOXO3a gene expression and deacetylate FOXO3a, thereby activating FOXO DNA binding and elevating the expression of target genes such as p27(Kip1), manganese superoxide dismutase and Bim, proteins associated with cell cycle arrest, oxidative stress and apoptosis respectively (Brunet et al., 2004; Wang et al., 2007; Jacobs et al., 2008). The activation of FOXO transcription factors by the SIRT family appears to, however, impair the ability of FOXO to promote cell apoptosis, instead shifting its function towards oxidative stress resistance and DNA repair (Brunet et al., 2004; Greer & Brunet, 2005; Wang et al., 2007). It is also well established that overexpression of FOXO can extend lifespan in drosophila (Giannakou et al., 2004; Min et al., 2008; Alic et al., 2014). Interestingly, in TNF-α-stimulated SkM cells the activation of SIRT1 via resveratrol restored Akt/mTOR/S6K and 4E-BP1 signalling and reduced FOXO1 but not FOXO3a protein levels, all of which were unchanged basally (Wang et al., 2014). Therefore, the role for SIRT1 activation on FOXO3a in SkM tissue with age requires further investigation. FOXO1 and its role in oxidative stress resistance in aging SkM also requires attention, especially following catabolic stress or dietary restriction where SIRT1 elevation is associated with survival. It is worth mentioning here that class I histone deacetylases (HDACs) (sirtuins are class III HDACs) have also been linked with activating FOXO3a and the SkM-atrophy programme (via MAFFbx/atrogin-1) during nutrient deprivation and disuse-induced atrophy (Beharry et al., 2004; Edstrom et al., 2008; Alic et al., 2014). SIRT1 activation following resveratrol administration in myoblasts inhibited IGF-I-associated signalling (Akt) and abolished leucine-stimulated increases in mTOR (Liu et al., 2010). Therefore, despite its proposed negative regulation of IGF-I/Akt/mTOR, SIRT1 seems to be fundamental to SkM cell growth, enabling proliferation and impairing differentiation under control conditions, yet protecting differentiation under means of stress. Importantly, the impact of activating SIRT1 in aged SkM cells/tissue basally or under stress remains to be fully determined especially, we hypothesise, in situations of dietary restriction that directly regulate the NAD/NADH ratio and impact on SIRT expression.

Sirtuins and NF-κB and their roles in longevity and skeletal muscle mass loss with age

While discussing protein degradation above, it is worth noting that SIRT6 has been associated with modulating lifespan via nuclear factor κB...
Effect of Dietary Restriction (DR) on longevity and skeletal muscle mass

Calorie restriction is defined as a reduction in energy intake, while maintaining nutrient intake, relative to that consumed normally by individuals with free (ad libitum) access to food (Selman, 2014). For the purposes of this review, dietary restriction (DR) will incorporate both calorie restriction and those interventions in which macro/micronutrients are altered without any overall change in energy intake. DR is the most reproducible intervention, to date, to extend medium and maximum lifespan in various model species (Mair & Dillin, 2008; Speakman & Selman, 2011; Selman, 2014). In mice, there seems to be a strain-specific association with DR and longevity, and in primates, the link between lifespan extension and DR may also be confounded by genetic heterogeneity (reviewed by Selman, 2014). Nevertheless, DR reduces incidence and severity of various pathological conditions in rodents and primates, which are leaner, and display reductions in insulin resistance, glucose intolerance, cognitive decline and immune dysfunction (Masoro et al., 1982; Barger et al., 2003; Selman et al., 2005; Mattison et al., 2012), indicating DR per se is beneficial for health.

Trade-off between cellular energy metabolism and growth in skeletal muscle with dietary restriction

The intuitive impact of chronic DR on SkM mass is that over time, absolute muscle mass decreases. This is not surprising if you consider that in the presence of nutrient restriction, the cell shifts away from growth in an attempt to survive. Further, protein from SkM can provide energy during severe nutrient restriction. One of the first studies to demonstrate this and to establish the molecular link between AMPK energy sensing and cellular growth through mTOR/S6K signalling was that of Inoki and colleagues (Inoki et al., 2003). Using various cell types (HEK293, MEF, EEF, LEFs) under starvation conditions, they reported increased AMPK activity and phosphorylated tuberous sclerosis 2 (TSC2). The TSC2 inhibited mTOR and other substrates, including S6K, 4EBP-1 and EIF2, which resulted in reduced cell size and growth rates. The role of TSC2 in this process was confirmed in TSC2 KO cells, which grew and maintained normal size in the presence of starvation. The AMPK activation of TSC2 and inhibition of mTOR therefore appears central in responses to energy deprivation. Fascinating but perhaps unintuitively, given the data thus far, DR appears to delays or prevent age-related loss of SkM mass in rats and rhesus monkeys via attenuation of DNA damage, proteosomal machinery, autophagy, inflammatory signalling and mitochondrial abnormalities (Aspnes et al., 1997; Phillips & Leeuwenburgh, 2005; Hepple et al., 2008; McKiernan et al., 2011). Indeed, short-term DR can potentially increase SkM stem cell availability and subsequent SkM repair following cryo-injury in young and old mice (Cerletti et al., 2012). In a recent in vivo study, chronic DR (by 30% of recommended daily intake) for a period ranging from 4 to 20 years (mean 9.6 years), resulted in reduced IGF-I levels, and a threefold reduction in Akt mRNA 30–50% reduction in Akt activity, together with increased FOXO3a and FOXO4 expression (Mercken et al., 2013). These changes in FOXO were reported to modify several genes linked to longevity including genes associated with stress resistance, antioxidants, DNA repair, protein turnover and cell death (Mercken et al., 2013). In SkM however, this shift away from growth towards stress resistance, would potentially reduce protein synthesis and increase degradation over time (Sandri et al., 2004; Edstrom et al., 2006). Furthermore, superoxide dismutase 2 (SOD2) expression, a transcriptional target of FOXOs, was increased under DR, as was DNA damage-binding protein 1 (DBB1), both key regulators of DNA repair. Further, cyclin D2 was significantly downregulated during moderate DR, as a fundamental orchestrator of cell cycle progression for proliferation or growth (Mercken et al., 2013). Interestingly, DR in rats also reduced levels of the inflammatory cytokine TNF-α and associated signalling (Phillips & Leeuwenburgh, 2005). These studies therefore suggest that chronic moderate (~30%) DR results in transcriptional reprogramming, which shift cellular regulation from growth to maintenance/repair and lifespan activities, while potentially reducing local inflammation. Perhaps most importantly, humans and mice on DR diets had higher lean SkM mass-to-fat mass ratios (Mercken et al., 2013). Therefore, there is potentially an optimal level of DR which has the beneficial effect of longevity, while perhaps preventing growth but not inducing muscle loss. Although overall SkM mass is likely to be reduced by long-term DR, the ratio of lean mass to fat mass may be greater and total body weight maybe reduced, a signature conducive of reduced metabolic disease risk. It remains to be determined, however, whether chronic DR changes SkM strength or the proportions of extracellular matrix to muscle tissue, or alters contractile properties and force per cross-sectional area/muscle quality. Indeed, the influence on force production following DR could be affected by fibre type, as type I fibres were ~62% larger after DR (30% DR for 12 years) in rhesus monkeys vs. control. Furthermore, in this study it was observed that there was delay in type II fibre atrophy with age (McKiernan et al., 2011). So while data of long-term studies are limited, they do suggest potential for both longevity and muscle health.

Despite this body of work, several other studies oppose these findings. For example, although different to sustained DR, Lee and Goldberg investigated the impact of acute fasting in mice and showed that this resulted in a reduction in SIRT1 activity and an increase in the atrogenes MuRF-1 and atrogin-1, which ultimately led to a significant decrease in SkM mass (Lee & Goldberg, 2013). Dietary restriction (~30%) for 6 weeks, in combination with exercise, also reduced gastrocnemius SkM weight and cross-sectional area in comparison with similarly exercised mice under ad libitum feeding (Park et al., 2013). However, it should be noted that this study did not include a DR or ad libitum alone group. This does, however, highlight the temporal role
of short-duration fasting vs. longer duration DR and the modulation of SIRT1 (McKiernan et al., 2012; Mercken et al., 2013). DR in combination with physical activity and its impact on SkM phenotypes therefore requires further investigation. Finally, it is unlikely that DR is a pragmatic intervention for humans, given that there is a considerable level of motivation and restraint required, where DR mimetics maybe more practical as reviewed previously by Selman et al. (Selman, 2014).

Roles of amino acid feeding or high-protein diets in association with calorie restriction: potential impact on skeletal muscle mass vs. disease and longevity

One of the issues with DR is the contribution of total calories from carbohydrates vs. proteins. Most studies do not differentiate between the two. It is well established that protein intake can enhance muscle protein synthesis in a dose-responsive manner in young and old adults (Cuthbertson et al., 2005; Moore et al., 2009). Furthermore, increasing dietary protein can help maintain SkM mass during periods of disuse (reviewed in Wall & van Loon, 2013) and induce greater increases in skeletal muscle hypertrophy following chronic supplementation when combined with exercise (resistance) vs. exercise alone (meta-analysis Cermak et al., 2012). Indeed, there is substantial support to suggest that with DR, overall weight loss is no different with higher protein intakes vs. DR alone (Sacks et al., 2009; de Souza et al., 2012). With some acute trials showing that fat mass decreases while SkM is spared (Krieger et al., 2006), importantly, exercise in combination with higher protein content in DR diets seems to have a SkM maintaining effect (Garthe et al., 2011; Josse et al., 2011; Mojtahedi et al., 2011), without negative impact on markers of mitochondrial biogenesis, albeit after acute fasting in humans (Taylor et al., 2013). Interestingly, undertaking DR that is protein rich reduces both body mass and percentage body fat, with associated reductions in circulating insulin and IGF-I levels (Maestu et al., 2010), alluding to potential benefits for lifespan while potentially maintaining SkM mass. Supplementation with branched-chain amino acids (BCAAs) such as leucine, isoleucine, valine or metabolites of leucine such as β-hydroxy-β-methylbutyrate (HMB) have become a favoured intervention as they have been shown to activate mTOR and protein synthesis in SkM to a greater extent compared with other essential/nonessential amino acids (Atherton et al., 2010; Pimentel et al., 2011; Churchward-Venne et al., 2012; Salles et al., 2013). Leucine alone can activate protein synthesis in humans to the same extent as whey protein and mixed essential amino acids plus leucine when administered 1–3 h postresistance exercise (Churchward-Venne et al., 2012). However, the requirement for whey protein for optimal protein synthesis 3–5 h postexercise is acknowledged (Churchward-Venne et al., 2012; Phillips, 2014). Previously, Mourier and colleagues observed that DR in human males (wrestlers) when combined with supplementation of mixed BCAAs led to a reduction in total body mass and fat mass (~17.3%), although SkM mass was unchanged (Mourier et al., 1997). This suggests a potential role for BCAAs in maintaining SkM mass under DR conditions. Furthermore, a recent study highlighted that HMB attenuated the loss of SkM mass observed following DR in murine exercise models (Park et al., 2013). Mice underwent exercise at 6 m.min⁻¹ run for 1 h, three times a week alone or combined with HMB and/or DR. The HMB animals had higher lean mass than the training alone group. Grip strength decreased under DR, but was maintained in DR mice supplemented with HMB. Interestingly, gastrocnemius mass and myofibre cross-sectional area were greater with HMB in the presence of a DR diet compared to DR alone, albeit there were no data reported for either ad libitum or HMB alone supplemented mice (Park et al., 2013). This latter finding was also associated with the reduced ubiquitin ligase, MAFbx, alluding to reduced protein degradation. Surprisingly however, Akt and mTOR mRNA were elevated under DR conditions in SkM. Speculation based on evidence presented in above sections suggests this may be due to increased SIRT1, yet this hypothesis requires further investigation. Therefore, in the light of the above discussion it would be prudent to investigate, on a background of DR, how AMPK and SIRT1 (energy sensing) change in the presence of BCAAs and the way in which they impact on Akt/mTOR (growth) via the molecular modulators of TSC1/TSC2 (discussed above and seen in Fig. 1).

Finally, it is important to note that increased protein intake, especially BCAAs, stimulates targets such as mTOR and 56K, which are downstream of IIS, the precise signalling which is reportedly suppressed to enable longevity and to reduce age-related disease. This therefore contributes to the recently debated paradigm whereby downstream IIS signalling is still activated, yet independently of IGF binding to its receptor, and thus protein synthesis in SkM mass may be maintained with increased protein intake during aging. However, it has been conversely suggested that increased protein intake may increase incidence of diseases, such as cancer, and thus impact negatively on longevity (Renehan et al., 2004). Indeed, it is known that cancer patients who do not respond to chemotherapy or are end-stage patients have reduced protein diets that, while potentially adding to the chronically inflamed milieu that causes SkM loss (cachexia), can slow tumour progression. Examples include animal models where DR can attenuate tumorigenesis via inhibition of mTOR, whereas leucine feeding can increase pancreatic tumour growth in both lean and overweight mice (Vellai et al., 2003; Bjornsti & Houghton, 2004; Hursting et al., 2010; Lashinger et al., 2011; Liu et al., 2014). Restricting the amino acid methionine can also limit tumour growth, and both methionine and essential amino acid restriction increase lifespan in rodents (Richie et al., 1994; Miller et al., 2005; Emran et al., 2014; Sinha et al., 2014). Overall, these studies suggest caution for cancer patients and amino acid supplementation, even those who suffer with muscle loss (Liu et al., 2014). The role of higher protein diets with age and the impact on disease risk and early mortality have recently received a high level of attention. Cohorts of 6381 adults aged 50 and over were studied for their habitual dietary intake and macronutrient composition with corresponding disease and mortality incidence (Levine et al., 2014). Between the ages of 60 and 65, those who reported high animal-derived protein intake had a 75% increased risk in overall mortality and a fourfold increase in cancer risk during the subsequent 18 years. If aged over 65 years of age, however, higher protein intake was associated with reduced cancer risk, but a fivefold increased risk of diabetes. These results therefore suggested that a low-protein diet is potentially beneficial in midlife; however, the benefits reduce with age. In an attempt to compliment these studies with mechanisms, high-protein diets were implemented in middle-aged mice, where the increase in GH/IGF signalling observed was associated with increased progression of tumours. The authors did, however, suggest that low protein impacted negatively on SkM mass in aged mice (Levine et al., 2014). In agreement with this study, an investigation published in the same issue as that by Levine et al. using a Geometric Framework approach to investigate the contributions of protein-to-carbohydrate ratios and their association with increased longevity in mice, suggested that healthy aging is not as a consequence of high-protein low calorie diets, but low-protein (especially BCAAs) diets, with the remaining macronutrients being made up of carbohydrate rather than fat (Solon-Biet et al., 2014). Also, data by Levine et al. have been scrutinized in terms of the methodological design. For example, 24-h dietary recalls
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suggesting up to 18 years of habitual diet are potentially not appropriate to account for lifelong habitual dietary intake. Furthermore, the grouping of the low- to high-protein categories [based on Institute of Medicines’ (IOM) Acceptable Macronutrient Distribution Range] has also received attention, where the low-protein group would probably be classed as protein deficient. It is also worth stating that in the total cohort (50 years and over), the level of protein intake was not associated with differences in all-cause, cancer or CVD mortality. Importantly, however the study did find a significant association between the subjects aged 50–55, higher protein consumption and cancer/mortality. Amongst 2253 subjects, the risk of cancer and mortality was increased in the high-protein subjects who also had higher IGF-I serum levels. It is indeed, established that people in the highest circulating IGF-I quintiles are at the highest risk of developing cancer (Hankinson et al., 1998; Kaaks et al., 2000; Giovannucci et al., 2003) and the role of IGF-I and associated signalling in cancer cells and tumour development is fairly robust (Pollak et al., 2004; Guevara-Aguirre et al., 2011). It is important to note that these are similar pathways to growth/amino acid stimuli required for SkM maintenance with age. The future paradigm we should be addressing would therefore be the trade-off between maintenance of SkM mass vs. longevity, potentially at the expense of age-related diseases.

Conclusion

The understanding of aging and the development of interventions to increase healthy lifespan has been greatly aided by the development of genetic mutants for IIS, TOR and sirtuin pathways as well as the use of pharmacological agents known to act on these pathways. However, all of these pathways are fundamental in regulating the trade-off between survival and maintenance vs. growth, particularly in skeletal muscle where age-associated losses in SkM mass and function are observed with advancing age. This provides a paradigm in which there is potentially reduced regenerative capacity within SkM tissue with age in an attempt to promote longevity of the organism and survival within the tissue. Optimizing dietary restriction (DR) or using DR mimetics in combination with amino acid administration may be critical interventions to help attenuate SkM loss with advancing age, while enabling healthy aging.

Author contributions

Sharples, AP is the corresponding author who instigated/conceptualized the review and wrote the first draft of the manuscript, amended all drafts and worked extensively on the final draft as well as in creating the final figure to complete the manuscript. Hughes, DC and Deane, CS wrote sections of the review with Sharples, AP and significantly inputted additions throughout. Stewart, CE contributed extensively to editing the manuscript while writing sections of the review with Sharples, AP and significantly inputted the final figure to complete the manuscript. Hughes, DC and Deane, CS wrote substantial portions of the review.

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exercise-induced AMPK signalling when in a glycogen-depleted state: implications for train-low compete-high.


