




HIF-hypoxia signaling in skeletal muscle physiology and fibrosis

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Abstract

Hypoxia refers to the decrease in oxygen tension in the tissues, and the central effector of the hypoxic response is the transcription factor Hypoxia-Inducible Factor α (HIF- α). Transient hypoxia in acute events, such as exercising or regeneration after damage, play an important role in skeletal muscle physiology and homeostasis. However, sustained activation of hypoxic signaling is a feature of skeletal muscle injury and disease, which can be a consequence of chronic damage but can also increase the severity of the pathology and worsen its outcome. Here, we review evidence that supports the idea that hypoxia and HIF-1 α can contribute to the establishment of fibrosis in skeletal muscle through its crosstalk with other profibrotic factors, such as Transforming growth factor β (TGF- β), the induction of profibrotic cytokines expression, as is the case of Connective Tissue Growth Factor (CTGF/CCN2), or being the target of the Renin-angiotensin system (RAS).

Keywords Muscle fibrosis · Hypoxia · Vasculature · CCN2/CTGF · Renin-angiotensin system

Abbreviations

AP-1	Activator Protein 1	DMD	Duchenne muscular dystrophy
ALS	Amyotrophic lateral sclerosis	ECM	Extracellular matrix
ACE	Angiotensin Converting Enzyme	FOG	Fast-twitch oxidative glycolytic
Ang-II	Angiotensin II	PHD	HIF-prolyl hydroxylases domain-containing enzymes
Ang-1-7	Angiotensin-(1–7)	HIF- α	Hypoxia-Inducible Factor α
AT1	Angiotensin Type I receptor	HRE	Hypoxia Response Elements
ARBs	Angiotensin Type I receptor antagonists	NO	Nitric oxide
CTGF/CCN2	Connective Tissue Growth Factor	nNOS μ	Nitric oxide synthase
CTX	Cardiotoxin	NTX	Notexin
DMOG	Dimethyloxalylglycine	RAS	Renin-angiotensin system
		SO	Slow-twitch oxidative
		TGF- β	Transforming growth factor β
		VEGF	Vascular Endothelial Growth Factor
		VSMC	Vascular smooth muscle cells

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Hypoxic signaling

Hypoxia refers to the decrease in oxygen tension in the tissue. The central effector of the hypoxic response is the transcription factor Hypoxia-Inducible Factor α (HIF- α) (Koh et al. 2009). Under normoxic conditions, HIF- α is constitutively expressed and continuously degraded via the ubiquitin-proteasome pathway following its hydroxylation by HIF-prolyl hydroxylases domain-containing enzymes (PHD) (Ivan et al. 2001). The Von Hippel-Lindau E3 ubiquitin-ligase recognizes the hydroxylated form of HIF- α for

ubiquitination and degradation. By contrast, during hypoxia, low oxygen pressure inhibits PHD, allowing HIF- α stabilization and translocation to the nucleus where it promotes the expression of target genes that are necessary for cell survival and adaptation under hypoxic conditions. Among the target genes, we found: the glucose transporter 1, which favors glycolic anaerobic metabolism to allow cell survival; Vascular Endothelial Growth Factor (VEGF), which promotes angiogenesis to reestablish the vascular network; and Erythropoietin, which promotes production of erythrocytes to increase oxygen transport through the bloodstream (Ameln et al. 2005; Ke and Costa 2006). The discovery of this oxygen sensing and response pathway (Nobel Prize in Physiology or Medicine 2019), has helped to understand many physiopathological processes in several types of tissues and organs (Leu et al. 2019; Zhang et al. 2019). Moreover, due to the hypoxic environment present in some tumors, hypoxic signaling has been widely studied in the context of different types of cancer and used as a target for reducing tumor vascularization and growth (Akanji et al. 2019).

The role of HIF-1 α in skeletal muscle

The physiological role of HIF-1 α in skeletal muscle is related to transient hypoxia, which might occur when oxygen pressure drops in response to acute dynamic exercise (Richardson et al. 1995). In this scenario, metabolic oxygen consumption by muscle cells during contraction could exceed oxygen availability from capillaries. As a response to transient hypoxia, HIF-1 α stabilizes and in response, VEGF expression is induced (Ameln et al. 2005). HIF-1 α has a pro-angiogenic function in skeletal muscle since the overexpression of HIF-1 α and HIF-2 α induces VEGF expression and the development of capillaries that express CD-31 *in vivo* (Niemi et al. 2014). Consequently, VEGF triggers angiogenesis in muscle subjected to exercise but is also essential for angiogenesis in sedentary muscle (Olfert et al. 2010; Tang et al. 2004). Moreover, skeletal muscle contraction by itself also induces vasodilation in microvasculature through nitric oxide (NO)-dependent and independent mechanisms in order to try to recover oxygen supply for its metabolic demands (Hong and Kim 2017).

Hypoxic signaling does not seem to be involved in muscle formation since neither HIF-1 α nor HIF-2 α are necessary for skeletal muscle development. Double knockout experiments for HIF-1 α and HIF-2 α show that they are dispensable for skeletal muscle development (Yang et al. 2017). Similar results have been reported using myogenic progenitors that do not express HIF-1 α (Majmundar et al. 2015). Thus, HIF-mediated hypoxic signaling seems to be more associated with muscle homeostasis than muscle formation.

After an injury, the skeletal muscle niche becomes hypoxic. It has been reported that acute damage induced by eccentric contraction, cardiotoxin (CTX), notexin (NTX) or barium chloride

injection trigger a marked disruption in the muscle's microvasculature (Hardy et al. 2016; Hotta et al. 2018). In fact, HIF-1 α signaling has been detected in injured skeletal muscle, increasing from day 1 to day 7 after CTX injection (Drouin et al. 2019). In parallel, after eccentric contraction injury the expression of HIF target genes, such as VEGF, are increased during regeneration. This increment in gene expression occurs in a temporal window that correlates with microvasculature permeability (Hotta et al. 2018). Functional experiments demonstrated that VEGF expression stimulates muscle regeneration, supporting that HIF downstream signaling through VEGF plays a pro-angiogenic role during regeneration (Arsic et al. 2004; Borselli et al. 2010; Mason et al. 2004; Messina et al. 2007). Moreover, VEGF and angiogenesis can improve the outcome and increase regeneration in chronic skeletal muscle diseases (Ennen et al. 2013; Shimizu-Motohashi and Asakura 2014).

Another axis of HIF-mediated hypoxic signaling is related to skeletal muscle adult stem cells (satellite cells). However, HIF function in muscle progenitors is very complex. *In vitro* experiments in myoblasts have shown that myogenesis is impaired under hypoxic conditions concomitantly with HIF-1 α activation (Gustafsson et al. 2005; Majmundar et al. 2012). On the other hand, myogenesis is also inhibited in the absence of HIF-1 α (Ono et al. 2006). Therefore, HIF-1 α signaling in myogenesis is complex and reports seem to be contradictory however, the data unveils that its function might be restricted to a very bounded threshold.

In vivo, satellite cells reside in a hypoxic niche and they express HIF-2 α at basal levels (Xie et al. 2018). *In vivo* experiments have shown that muscle regeneration is delayed under environmental hypoxic conditions, resulting in decreased expression of myogenic markers, such as myogenin or MyoD, and loss of muscle mass (Chaillou et al. 2014). However, the role of HIF-mediated hypoxic signaling on satellite cells can be very specific. Some reports show that HIF-1 α deletion in satellite cells accelerates regeneration and myogenesis in ischemia experiments, suggesting that HIF-1 α negatively regulates regeneration through satellite cell proliferation (Majmundar et al. 2015). On the other hand, HIF-1 α and HIF-2 α double knockout experiments in satellite cells show delayed regeneration after injury and self-renewal inhibition of satellite cells under hypoxic conditions, evidencing the active role of HIF-2 α (Yang et al. 2017). Interestingly, transient inhibition of HIF-2 α in satellite cells contributed to a better understanding of the mechanism, showing accelerated muscle regeneration and myoblast proliferation in the short term. Nevertheless, long term HIF-2 α ablation produces depletion of satellite cells and regenerative failure, indicating that HIF-2 α is responsible for stemness maintenance and self-renewal of satellite cells (Xie et al. 2018). Therefore, HIF-mediated signaling seems to be implicated in muscle stem cell quiescence and activation, having an impact on skeletal muscle regeneration.

Myeloid hypoxic signaling also plays an important role in skeletal muscle homeostasis. Experiments in knockout mice for HIF-1 α in myeloid cells demonstrate that hypoxic signaling in these cells is essential for skeletal muscle regeneration after injury. In these knockout mice, macrophage invasion is delayed and there are fewer myogenic MyoD positive cells recruited to damaged muscles (Scheerer et al. 2013). Accordingly, activation of HIF-mediated signaling through PHD inhibition protects muscle from eccentric injury through myeloid HIF-1 α -mediated iNOS activity (Billin et al. 2018). Besides, NO has been related to satellite cell activation (Anderson 2000; Buono et al. 2012; Rigamonti et al. 2013). Therefore, the physiological role of HIF-1 α in myeloid cells affects skeletal muscle homeostasis through macrophage activation and NO signaling during regeneration.

Recently, we showed that different models of skeletal muscle damage and fibrosis (hindlimb denervation, Amyotrophic lateral sclerosis (ALS) murine model, and *mdx* dystrophic skeletal muscle) have decreased capillary density and activated hypoxia signaling (Valle-Tenney et al. 2019). This evidence supports the idea that HIF-mediated hypoxic signaling activation occurs and has a role during acute and chronic events of damage in skeletal muscle.

Skeletal muscle fiber type-specific hypoxic response

It has been hypothesized that regulation of the oxygen homeostasis system in skeletal muscle depends on fiber type. The basal expression level of HIF-1 α is different in each type of fiber and is tightly related to the metabolic profile of each one: fast-twitch oxidative glycolytic (FOG) fibers express higher basal levels of HIF-1 α than slow-twitch oxidative (SO) fibers (Mounier et al. 2010; Pisani and Dechesne 2005).

In agreement with this hypothesis, the reports describe the effect of hypoxia signaling activation as a slow-to-fast fiber type switch. HIF-1 α overexpression in C2C12 myoblasts that are then differentiated to myotubes, induces the expression of fast MyHC isoforms. Moreover, HIF-1 α overexpression in EDL and soleus muscles in vivo displays a slow-to-fast fiber type switch (Lunde et al. 2011). Similarly, in hypoxic muscle, the proportion of fiber types changes to adapt to oxygen deprivation in several physiological and pathological conditions, tending to increase FOG fibers over SO fibers (Chaillou 2018).

On the other hand, reports using different genetic approaches do not support this hypothesis. PHD1^{-/-} mice show more tolerance to hypoxia, partly through metabolic reprogramming leading to a shift from oxidative toward anaerobic/glycolytic metabolism in skeletal muscle without causing a switch in myofiber type (Aragones et al. 2008). Genetic ablation of HIF-2 α showed a reduction in slow-twitch fibers and an up-regulation of fast-twitch fibers (Rasbach et al. 2010). Besides, HIF-1 α deletion in the skeletal

muscle caused an endurance training-like adaptation in resting mice without significant changes in fiber type composition. Nevertheless, following six-weeks of endurance training, knockout mice for HIF-1 α do not improve toward an oxidative metabolic profile and there is no fast-to-slow fiber-type shift as shown in *wt* mice (Mason and Johnson 2007). A similar effect has been reported in high-altitude trekkers. Mountaineers show an increase in slow fibers accompanied by a decrease in fast muscle fibers after an expedition to the Himalaya where they spend 23 days over 5000 m a.s.l. (Doria et al. 2011).

Thus, the contribution of hypoxia-mediated signaling to muscle fiber type composition seems to be more related to the overall effect of hypoxia and is highly influenced by training conditions as recapitulated in Chaillou 2018. Furthermore, the involvement of HIF-1 α or HIF-2 α signaling pathways on fiber type switch needs to be fully understood. Despite this, the contribution of the hypoxic response in pathological states such as muscle fibrosis could be differentially regulated according to fiber type. Specifically, FOG fibers that express more HIF-1 α could be more prone to exert hypoxic HIF-1 α -dependent signaling over pro-fibrotic effectors eliciting the fibrotic response.

Skeletal muscle fibrosis

Skeletal muscle fibrosis, in which functional and contractile fibers are replaced by rigid scar-like tissue, underlies several pathological conditions. Many muscle pathologies including dystrophies, motor-neuron diseases and pathological states associated with chronic myotrauma cause the development of fibrosis in the skeletal muscle tissue (Gonzalez et al. 2017; Pessina et al. 2014; Smith and Barton 2018).

The fibrotic environment in skeletal muscle is characterized by the elevated deposition of extracellular matrix (ECM) proteins, overexpression of pro-fibrotic factors, myofibroblast over-activation and persistent inflammation (Mahdy 2018; Mann et al. 2011; Wynn and Ramalingam 2012). Among the ECM proteins that show increased levels in muscle fibrosis, we found fibronectin, collagens, and proteoglycans (Alvarez et al. 2002; Caceres et al. 2000; Pessina et al. 2014; Serrano and Munoz-Canoves 2017).

The mononuclear cells that infiltrate fibrotic skeletal muscle include fibroblasts, immune, myogenic, and vascular cells. These different cell populations proliferate transiently during acute damage and regeneration in a synchronized and coordinated fashion (Bentzinger et al. 2013). However, the overlapping degeneration and regeneration cycles that occur in muscular dystrophies and chronic damage from other pathologies lead to the asynchronous remodeling of the microenvironment that finally progresses to fibrosis (Dadgar et al. 2014).

Vasculature in skeletal muscle fibrosis

The vascular hypothesis of muscular dystrophy has been studied for several years but little is known for other skeletal muscle pathologies. This hypothesis explains part of the pathological state of the disease through muscle fiber apoptosis via functional ischemia due to reduced vasculature and mislocalization of the muscle-specific isoform of neuronal nitric oxide synthase (nNOS μ) (Gargioli et al. 2008; Thomas 2013; Thomas et al. 2003). Nitric oxide (NO) produced by sarcolemmal nNOS μ acts as a local paracrine signal that inhibits vasoconstriction in active muscles (Chavoshan et al. 2002; Jendzjowsky and DeLorey 2013). Further research has shown that the deteriorated vascular component is part of the fibrotic disease and can be manipulated to improve muscle condition. Vascular therapies including vaso-relaxation drugs and pro-angiogenic treatments have been successful in improving the dystrophic phenotype in Duchenne muscular dystrophy (DMD) patients or *mdx* mice (Ennen et al. 2013; Matsakas et al. 2013; Podkalicka et al. 2019; Shimizu-Motohashi and Asakura 2014). Nevertheless, even when there is considerable evidence that links vascular damage to skeletal muscle pathologies associated with fibrosis, such as muscular dystrophies (DMD, *mdx* and *Sgcd*^{-/-}) and denervation (Borisov et al. 2000; Gargioli et al. 2008; Hudlicka 1967; Matsakas et al. 2013), the role of the damage induced by decreased oxygen availability and consequent hypoxic signaling in skeletal muscle fibrosis is not fully understood.

Relationship between hypoxia and skeletal muscle fibrosis

Experimental data obtained in tissues other than skeletal muscle pointed to a relationship between hypoxia and fibrosis (Darby and Hewitson 2016; Norman et al. 2000). It has been described that hypoxia by itself is able to exacerbate the expression of ECM proteins in epidermal fibroblasts from systemic sclerosis patients (Distler et al. 2007), human renal fibroblasts (Norman et al. 2000), proximal tube cells (Orphanides et al. 1997), tubular epithelial cells (Kimura et al. 2008) and epithelial kidney cells (Rana et al. 2015). Nevertheless, the relationship between hypoxia and fibrosis has not been fully addressed in skeletal muscle. In vivo experiments have shown that muscle regeneration is delayed under ambient hypoxic conditions (Chaillou et al. 2014). In this line, there is evidence showing that altered skeletal muscle regeneration results in muscle fibrosis: the overlapping degeneration and regeneration cycles that occur in muscular dystrophies lead to an asynchronous remodeling of the microenvironment that finally develops fibrosis (Dadgar et al. 2014; Serrano et al. 2011). Chronic damage induced by six consecutive rounds of intramuscular injections of barium chloride has the same fibrotic effect (Contreras et al. 2016; Pessina

et al. 2014; Riquelme et al. 2014). The histological analysis made by Chaillou et al. 2014 shows that muscles damaged with an intramuscular injection of NTX under hypoxic conditions for 28 days presented delayed regeneration. Moreover, although not the focus of the same work, the published images suggest an increment of the interstitial area at the end of the treatment that could be related to exacerbated connective tissue deposition. Furthermore, HIF-1 α activated signaling has been found in different models of skeletal muscle damage, all of them associated with fibrosis (Valle-Tenney et al. 2019).

Furthermore, although VEGF plays a pro-angiogenic role as a downstream effector of the HIF-mediated hypoxic signaling, it could have pro-fibrotic effects. VEGF induces stress fiber formation in fibroblasts isolated from dystrophic muscle, a marker of differentiation to myofibroblasts, which are the main producers of ECM (Gutpell and Hoffman 2015). Therefore, sustained/chronic hypoxic signaling activation in dystrophic muscle due to vasculature damage could be one of the mechanisms contributing to fibroblast-overactivation, as a result of VEGF overexpression, which finally elicits fibrosis.

Interestingly, data we obtained using a prolyl-hydroxylase inhibitor, dimethylxalylglycine (DMOG), administered daily in a chronic type approach to sustainably activate HIF-hypoxic signaling shows induction of ECM proteins in skeletal muscle that are characteristic of a fibrotic phenotype. Administration of DMOG leads to a transient increase of HIF-1 α , with a peak around 4 h post-dose, inducing the expression of the HIF-1 α target gene VEGF in skeletal muscle (Fig. 1a). To obtain sustained pharmacological HIF-1 α stabilization, the drug was administered daily for a total of 17 days I.P. to 10-month-old *wt* C57BL10 mice (Fig. 1b). In homogenates obtained from the diaphragm, we observed that sustained HIF-1 α pharmacological stabilization induces the expression of collagen and fibronectin, and increases the expression of profibrotic factor Connective Tissue Growth Factor (CTGF/CCN2), see below), suggesting a potential relationship between the chronic hypoxia response and muscle fibrosis (Fig. 2c,d).

Acute, intermittent or short-term pharmacological inhibition of PHD, and subsequent HIF-1 α stabilization, has been shown to be protective in several conditions: cerebral ischemic damage (Reischl et al. 2014), cisplatin-induced kidney injury (Yang et al. 2018), and ischemic cardiac protection (Olenchok et al. 2016). PHD inhibition also accelerates blood recovery after severe irradiation (Forristal et al. 2013). Moreover, HIF controls the production of erythropoietin production by the kidney and the liver coordinating erythropoiesis with iron metabolism (Joharapurkar et al. 2018). Currently, several prolyl hydrolase inhibitors are now tested under different clinical trials. Of them, three oral inhibitors have now advanced to global phase III clinical trial for the treatment of anemia (Joharapurkar et al. 2018; Sanghani and Haase 2019). Nevertheless, to the light of our results (Valle-Tenney et al.

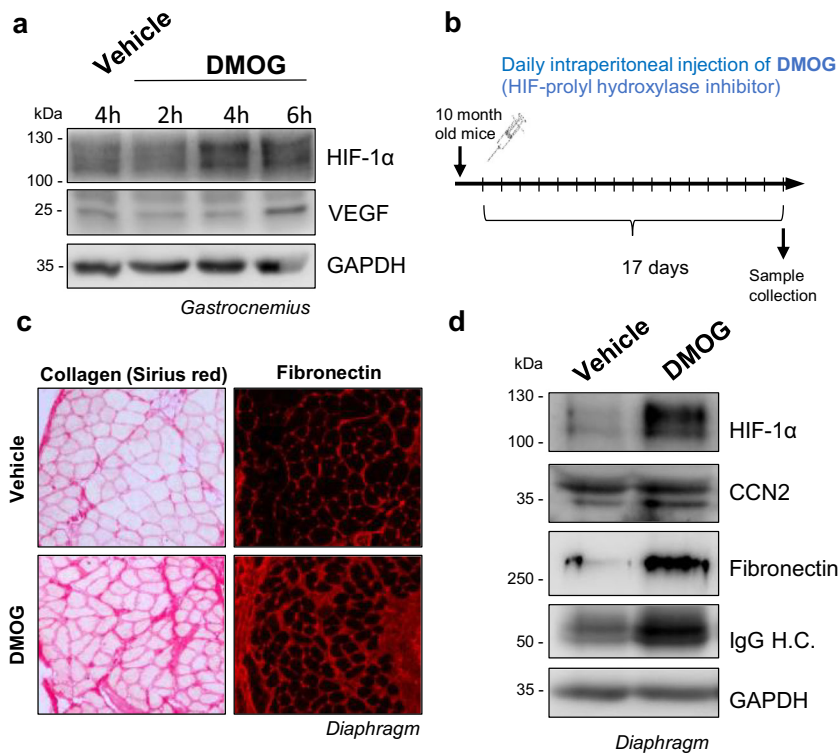


Fig. 1 Sustained pharmacological HIF activation leads to a fibrotic muscle phenotype. **a.** 10-month-old *wt* C57BL10 mice were treated with DMOG (I.P. 150 mg/Kg) and euthanized 2, 4 and 6 h after administration. Western blot of total homogenates from hindlimb gastrocnemius muscle of treated mice shows that DMOG treatment can induce transient HIF-1 α stabilization, which peaks 4 h post-administration, and also the expression of the HIF-1 α downstream target gene VEGF. **b.** Scheme of the sustained DMOG treatment protocol: 10-month-old *wt* C57BL10

mice were treated daily with DMOG (I.P. 150 mg/Kg/day) or vehicle for 17 days. 4 h after the last DMOG injection, mice were euthanized, and muscle samples were collected. **c.** Collagen (Sirius red) staining and fibronectin immunofluorescence in diaphragm cryosections of DMOG or vehicle-treated mice. **d.** Western blot from diaphragm homogenates. HIF pharmacological stabilization induces the overexpression of collagen, fibronectin, IgG, and CCN2

2019) and Fig. 2, caution should be taken evaluating the potential effect of these inhibitors in long-term sustained treatments in order to avoid undesired consequences such as a muscle fibrotic response.

Regulation of skeletal muscle CCN2/CTGF expression

Transforming growth factor β (TGF- β) signaling has been described as the master fibrotic driver in several organs and tissues including skeletal muscle, where is up-regulated in fibrosis-related pathologies of diverse etiology (Cabello-Verrugio et al. 2012b; Ismaeel et al. 2019; Leask and Abraham 2004). TGF- β signaling occurs through Smad-dependent or Smad-independent pathways driving the expression of target genes such as collagens, fibronectin, and CCN2, among others. CCN2, a member of the CCN family of matricellular proteins, has risen as a crucial pro-fibrotic factor in skeletal muscle, and it is considered one of the downstream effectors of fibrotic TGF- β signaling (Biernacka et al. 2011; Duncan et al. 1999; Vial et al. 2008). CCN2 is overexpressed in biopsies of fibrotic skeletal muscle from DMD (Sun et al. 2008), and in the *mdx* mouse model for DMD (Au et al. 2011;

Morales et al. 2013b), under conditions of repetitive damage (Pessina et al. 2014), the transgenic mouse model for ALS (tg hSOD1^{G93A}) (Gonzalez et al. 2017; Gonzalez et al. 2018), and after denervation by sciatic nerve transection (Rebolledo et al. 2019). Accordingly, CCN2 reduction or blockage attenuates skeletal muscle fibrosis in these pathological models (Gonzalez et al. 2018; Morales et al. 2013b; Rebolledo et al. 2019) evidencing its critical role in fibrosis progression. Therefore, the understanding of how CCN2 is regulated results particularly relevant in fibrotic diseases.

The CCN2 promoter region has several transcription factor response elements, including Smad Binding Elements, Activator Protein 1 (AP-1), Specific protein 1, Nuclear factor 'kappa-light-chain-enhancer' of activated B-cells, SOX9, and also Hypoxia Response Elements (HRE) (Cordova et al. 2015; Chaqour et al. 2006; Higgins et al. 2004; Leask et al. 2001; Oh et al. 2016). Therefore, CCN2 can be regulated by hypoxia even though the role of HIF-1 α on CCN2 expression is intriguing and appears to be highly cell-type specific. Several reports show that hypoxia induces CCN2 expression in skin fibroblasts (Hong et al. 2006; Mingyuan et al. 2018) and in mouse tubular cells (Higgins et al. 2004). On the other

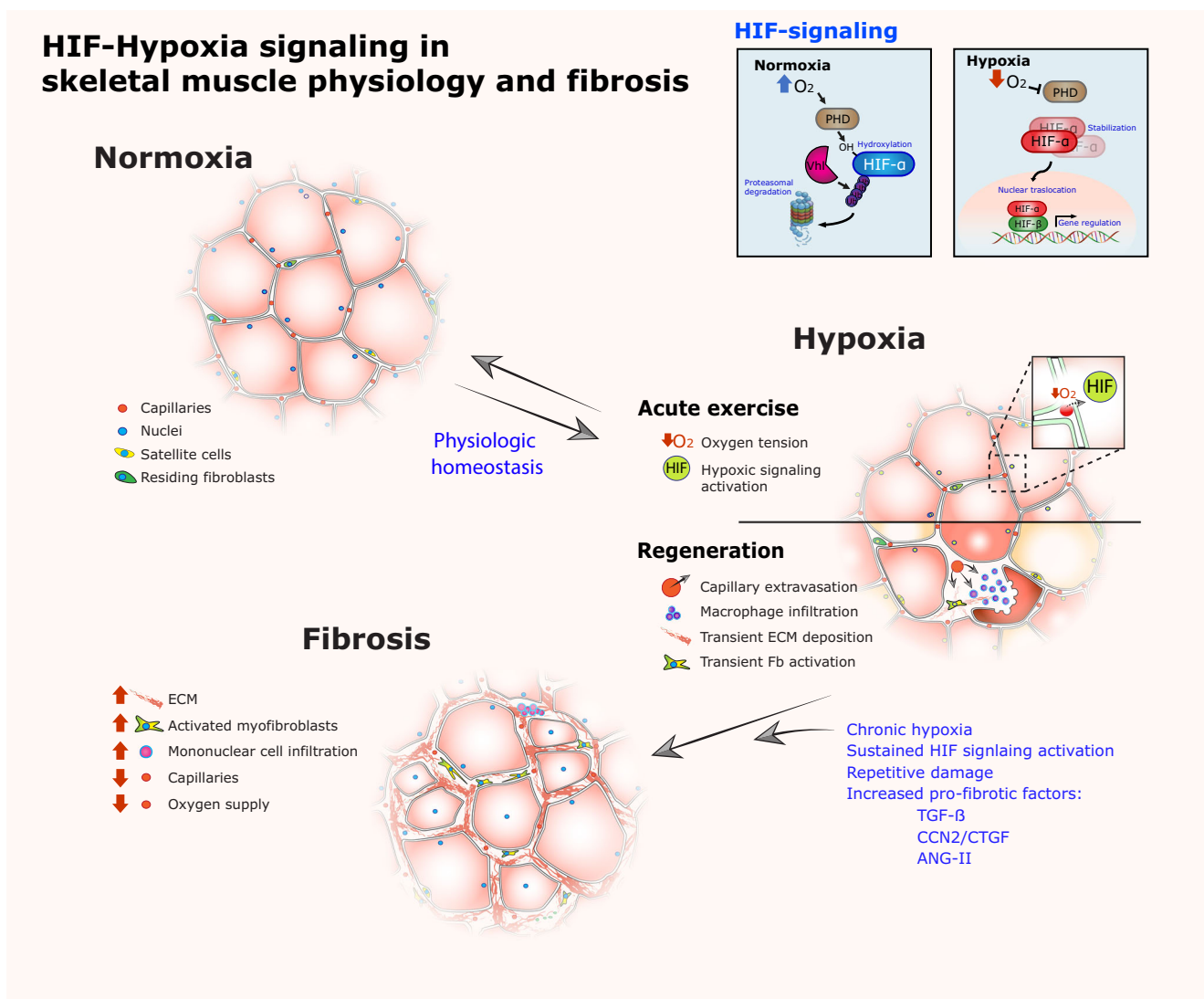


Fig. 2 HIF-Hypoxia signaling in skeletal muscle physiology and fibrosis. In normoxia, blood flows through vessels and capillaries (5 per muscle fiber on average) (Valle-Tenney, 2019) allowing oxygen to reach the cells in the muscle tissue. In this condition, the HIF- α transcription factor is continuously hydroxylated by HIF-prolyl hydroxylases domain-containing enzymes (PHD). This mark is recognized by Von Hippel-Lindau E3 ubiquitin-ligases and ubiquitinated for degradation via the ubiquitin-proteasome pathway. During exercise, oxygen consumption could exceed oxygen availability, in addition to vasoconstriction, decreased oxygen diffusion generates a hypoxic state where HIF-signaling is activated. In the hypoxic state, HIF- α is no longer hydroxylated and it accumulates and translocates to the nucleus where it binds to HIF- β to exert its function as a transcription

factor. The same effect has been described for muscle regeneration where the skeletal muscle cell niche becomes hypoxic after injury by extravasation of capillaries and impaired blood flow through the tissue. In this context, HIF-signaling plays multiple roles including angiogenesis, myeloid cell activation and myogenesis by satellite cell proliferation. In situations of exercise and regeneration, normoxia is reestablished after a transient period of hypoxia. However, in chronic skeletal muscle pathologies the hypoxic state, in addition to repetitive damage and pro-fibrotic factors overexpression, elicits the establishment of fibrosis. In this condition, sustained HIF-activation in crosstalk with other pro-fibrotic pathways (TGF- β or Renin-Angiotensin system) could promote the overexpression of key profibrotic cytokines such as CCN2

hand, the activation of HIF-1 α downregulates CCN2 expression in chondrocytes (Tran et al. 2010) and in human renal tubular cells (Preisser et al. 2016). We recently showed that hypoxia, through HIF-1 α , induces CCN2 expression in skeletal muscle fibers in vitro, and in vivo (Valle-Tenney et al. 2019).

In the context of fibrosis, CCN2 expression could be regulated by HIF-1 α in conjunction with other transcription

factors related to non-canonical TGF- β signaling pathways. For example, it has been described that the promoter region of the CCN2 gene has an AP-1 site that is responsive to GLI proteins, which are downstream of the MEK/ERK pathway (Cheng et al. 2016). Also, CCN1 gene expression (another member of the CCN protein family) is induced by hypoxia and HIF-1 interaction with c-Jun/AP-1 in melanoma cells (Kunz and Ibrahim 2003). Therefore, several transcription

factors, including TGF- β -activated transcription factors, could be involved in HIF-1 α -dependent regulation of CCN2 expression in skeletal muscle fibrosis. When hypoxia or HIF-1 α stabilization occurs in an environment enriched in TGF- β , a synergistic overexpression of CCN2 is observed, which is greater than the response for each separate factor. Interestingly, this effect is specific for skeletal muscle myotubes/fibers and not for other skeletal muscle resident cell types, supporting the idea that the regulation of CCN2 by HIF-1 α is highly cell-specific (Valle-Tenney et al. 2019). It has been reported that Smads can interact with several transcription factors in some cases serving as a scaffold for a large transcription complex that regulates a variety of genes (Euler-Taimor and Heger 2006). Among them, the SP1/SMAD3/HIF-1 α multiprotein complex regulates endoglin (Sanchez-Elsner et al. 2002), and the YAP-TEAD4-Smad3-p300 complex regulates CCN2 in cancer cells (Fujii et al. 2012). Thus, HIF-1 α signaling could exert a pro-fibrotic effect in skeletal muscle through the expression of the pro-fibrotic factor CCN2 in sustained hypoxic conditions. However, more research is needed in order to understand the transcriptional regulation of CCN2 by HIF and cofactors in skeletal muscle fibrosis.

Relationship between muscle fibrosis, hypoxia, and the renin-angiotensin system

The renin-angiotensin system (RAS) is involved in numerous physiological functions that regulate vasoconstriction, fluid volume regulation, cardiac output, cell growth, vascular wall integrity and fibrosis (Arendse et al. 2019; Santos et al. 2018). The RAS has two axes with opposite functions. The classical axis is composed of the octapeptide Angiotensin II (Ang-II), the enzyme that synthesizes it, Angiotensin Converting Enzyme (ACE) and Angiotensin Type I receptor (AT1). Ang-II via the AT1 receptor produces vasoconstriction, sodium retention, water reabsorption, vascular remodeling, inflammation and fibrosis (Arendse et al. 2019). Since Ang-II induces vasoconstriction it suggests that it could contribute to a hypoxic niche and could be another way to induce damage. The alternative RAS axis is the non-classical, composed of Angiotensin-(1–7) (Ang-1–7), its receptor Mas and ACE2 (Santos et al. 2019; Santos et al. 2018). Ang-(1–7), through the activation of Mas, has the opposite functions of the classic RAS: induces vasodilation, reduces inflammation, reduces oxidative damage and fibrosis. In cardiac tissue, Ang-(1–7) counteracts the effects of Ang-II, and through Mas induces activation of eNOS that results in increased NO levels, which reduce oxidative damage and produce an increase in blood flow in the heart by vasodilating the coronary arteries and blood vessels (Costa et al. 2010; Dias-Peixoto et al. 2008; Ferreira et al. 2019; Sampaio et al. 2007), suggesting that one of the beneficial effects of Ang-(1–7) could be a reduction of the hypoxic state.

In skeletal muscle Ang-II is involved in inflammation and fibrosis progression associated with pathologies. It is also involved in the loss of muscle mass by increasing levels in oxidative stress and inflammatory mediators (Brink et al. 2001; Delafontaine and Yoshida 2016; Semprun-Prieto et al. 2011; Sukhanov et al. 2011). In models of muscular dystrophy, the treatment with AT1 antagonists (ARBs) or ACE inhibitors (ACEi) leads to a reduction of skeletal muscle fibrosis, reduced TGF- β signaling, reduction of CCN2 levels, inflammation and oxidative stress (Cabello-Verrugio et al. 2012a; Cohn et al. 2007; Cozzoli et al. 2011; Morales et al. 2013a). These results support a contribution of Ang-II to skeletal muscle damage in these pathologies. The inhibition of ACE activity has been used as a therapeutic treatment in *mdx* mice and in patients with Becker and DMD to improve the cardiomyopathy associated with dystrophy (Bauer et al. 2009; Russo et al. 2018; Silva et al. 2017).

On the other hand, the non-classical RAS pathway plays a protective role in skeletal muscle diseases. In *mdx* mice, Ang-(1–7) infusion or oral administration ameliorate skeletal muscle architecture, decrease local fibrosis, and improve muscle function by reducing TGF- β signaling (Acuña et al. 2014) and decreasing CCN2 levels (Acuña et al. 2019). Similar effects in improving the fibrotic phenotype were also observed in the sarcoglycan delta null mice, a different model of skeletal muscular dystrophy (Sabharwal and Chapleau 2014). Moreover, the overexpression of ACE2 reduces fibrosis in *mdx* mice and in a model of fibrosis caused by chronic injury (Riquelme et al. 2014).

Even though it seems that Ang-(1–7) effects are caused by the attenuation of fibrotic pathways, there is also evidence that in vascular tissue it can induce NOS activity, specifically eNOS in endothelial cells. This event suggests the induction of local vasodilation, which leads to reduced fibrosis, vascular remodeling and inflammation (Santos et al. 2018). Moreover, Ang-(1–7) effects are reduced by treatment with L-NAME or Guanylyl cyclase inhibitors that block NO signaling (Ferreira et al. 2019; Gomes et al. 2010; Ren et al. 2002). Taking this data together, we suggest that the beneficial effect of the Ang-(1–7) axis of the RAS system in muscle fibrosis is tightly linked to NO production and vasodilation, and also inhibition of pro-fibrotic cytokines, leaving open the question if such activity could contribute to decreasing the chronic activation of hypoxia signaling in skeletal muscle.

RAS and HIF-1 α in skeletal muscle dystrophies

There is evidence showing that Ang-II induces HIF-1 α in the kidney, vascular smooth muscle cells (VSMC), and cardiomyocytes (Huang et al. 2019; Qi et al. 2019; Richard et al. 2000; Yan et al. 2020; Zhu et al. 2011). Interestingly, selective HIF-1 α knock out in VSMC indicates that Ang-II-induced vascular remodeling is mediated by HIF-1 α . These

knockout mice show reduced inflammation and decreased blood pressure in an Ang-II-induced hypertension model (Qi et al. 2019). In another report, Ang-II induced fibrosis and inflammation in podocytes was reduced when HIF-1 α expression was knockdown by siRNA (Huang et al. 2019). Similarly, kidney injury caused by Ang-II infusion was reduced by HIF-1 α silencing in rats (Zhu et al. 2011). Even though there is no evidence of Ang-II induction of HIF-1 α in skeletal muscle, it remains a relevant question since Ang-II induces TGF- β and CCN2 in skeletal muscle and could be acting upstream of these profibrotic factors. Also, Ang-II in VSMC induces HIF-1 α by a mechanism independent of hypoxia (Richard et al. 2000). Therefore, it would be interesting to evaluate if ARBs or ACEi treated *mdx* muscles have reduced levels of HIF-1 α , and if HIF-1 α could also be a mediator of the Ang-II induced fibrotic response in this model or in other models of skeletal muscle fibrosis.

There is also evidence that links the other RAS axis to HIF-1 α . Ang-(1–7) treatment reduces inflammation and damage, by a mechanism involving the induction of NO and reduction of HIF-1 α , in a model of reflux esophagitis (Pawlik et al. 2014). In kidney damage by diabetic nephropathy, Ang-(1–7) reduced the induction of HIF-1 α (Giani et al. 2012). In vitro, Ang-(1–7) treatment also reduced Hif-1 α expression in vascular sarcoma cells (Petty et al. 2012) and attenuated long-term hypoxia-stimulated apoptosis by inhibiting HIF-1 α nuclear translocation, via Mas receptor, in cardiomyocytes (Chang et al. 2016). Therefore, the non-classical arm of RAS is a novel target regarding hypoxia and HIF-1 α signaling.

In skeletal muscle, RAS plays a role in the progression of fibrosis, whether Ang-II induces HIF-1 α and Ang-(1–7) can reduce HIF-1 α signaling in skeletal muscle pathologies is still an open question and needs further investigation.

Conclusion and future perspectives

Considering all the evidence presented above, transient hypoxia and HIF signaling in acute events such as exercising or regeneration after muscle damage, play an important role in homeostasis promoting angiogenesis by vascular remodeling, the metabolic adaptation of muscle fibers, maintenance of stem cell stemness and immune response modulation. However, the role of sustained activation of hypoxic signaling in pro-fibrotic diseases has not been studied. Here, we propose that the chronic hypoxic state present in skeletal muscle pathologies is an important feature that contributes to the establishment of fibrosis. Moreover, based on the preliminary data presented here (Fig. 1), we hypothesize that HIF-mediated hypoxic signaling is determinant for the detrimental effects of chronic hypoxia resulting in CCN2 overexpression as we recently publish (Valle-Tenney et al. 2019)

Several reports have pointed to a relationship between capillary dysfunction and skeletal muscle damage and fibrosis. This evidence leads us to hypothesize that hypoxic signaling through HIF-1 α could be active in the muscle inducing the expression of several genes with HRE on their promoters that could be triggering a fibrotic response. Among these genes, CCN2 is a key pro-fibrotic factor that is regulated by hypoxia. We have recently shown that hypoxia through HIF-1 α leads to overexpression of CTGF. Furthermore, HIF-1 α synergizes with TGF- β on driving CCN2 overexpression (Valle-Tenney et al. 2019). In this way, HIF-1 α can be acting together with other transcription factors that are also increased in pathological conditions, contributing to the establishment of fibrosis. The knowledge of these crosstalks can help to develop new combinatory therapies for skeletal muscle diseases where fibrosis is involved.

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