Black Sea Journal of Agriculture
doi: 10.47115/bsagriculture.1480033

Open Access Journal
e-ISSN: 2618 – 6578

Review
Volume 7 - Issue 4: 418-428 / July 2024

MYOGENIC REGULATOR GENES RESPONSIBLE FOR MUSCLE DEVELOPMENT IN FARM ANIMALS

Godswill Arinzechukwu IWUCHUKWU[1]*, Dilek GÖKCEK[1], Zeynep ÖZDEMİR[1]

[1]Ondokuz Mayıs University, Faculty of Agriculture, Department of Agricultural Biotechnology, 55139, Samsun, Türkiye

Abstract: Breeding farm animals, especially poultry, helps meet global meat demand and boosts meat production efficiency. To meet high-quality meat demand, muscle growth and development must improve. Fetal skeletal muscle formation involves myogenesis, fibrogenesis, and adipogenesis. Kinase-encoding genes and myogenic regulatory factor genes regulate a complex network of intrinsic and extrinsic components in two or three stages. MYF5, MYOD, myogenin, and MRF4 are helix-loop-helix transcription factors that govern skeletal muscle cell specification and differentiation throughout embryogenesis and postnatal myogenesis. The transcription factors MYF5, MYOD, Myogenin, and MRF4 have been discovered to determine the skeletal muscle lineage and regulate myogenic differentiation during development. These factors also determine the muscle satellite cell lineage that becomes the adult skeletal muscle stem cell compartment. MYF5, MYOD, Myogenin, and MRF4 serve small functions in adult muscle, but they again direct satellite cell activity to regenerate skeletal muscle, linking genetic regulation of development and regeneration myogenesis. Understanding and identifying these genes helps increase meat yield and quality. This detailed review examines myogenic regulatory variables in satellite cell specification, maturation, and skeletal muscle regeneration.

Keywords: Meat, Myogenesis, Satellite cell, Myogenic differentiation, Regeneration, Skeletal muscle

***Corresponding author:** Ondokuz Mayıs University, Faculty of Agriculture, Department of Agricultural Biotechnology, 55139, Samsun, Türkiye
E mail: godswill2014.gi@gmail.com (G. A. IWUCHUKWU)
Godswill Arinzechukwu IWUCHUKWU https://orcid.org/0009-0001-3621-7055
Dilek GÖKCEK https://orcid.org/0000-0001-8721-3380
Zeynep ÖZDEMİR https://orcid.org/0009-0003-2726-4743

Received: May 07, 2024
Accepted: July 02, 2024
Published: July 15, 2024

Cite as: Iwuchukwu GA, Gökcek D, Özdemir Z. 2024. Myogenic regulator genes responsible for muscle development in farm animals. BSJ Agri, 7(4): 418-428.

1. Introduction

The aim of every livestock breeder is to produce animals of sufficient body weight with optimum nutritional requirements at the least cost. More importantly, with the increase in global population and the need to meet the increasing human protein requirement for different age groups, the rapid growth rate and muscle development of livestock breeds have become essential characteristics for meat farmers and producers. According to some studies, myogenic regulatory factors (MRFs) and growth promoters are essential and crucial for muscle differentiation, growth and development in farm animals. It is also widely accepted that muscle development in both embryonic and postnatal stages of farm animals is affected by these factors. Therefore, it demonstrates the importance of examining and understanding muscle regulatory factors.

MRFs consist of *MRF4*, Myogenic Determination Factor 1 (*MYOD*), Myogenic Factor 5 (*MYF5*), Myogenin, also known as Herculin or Myf6. These regulatory factors direct myogenesis, that is, the formation of skeletal muscles, and as early as embryogenesis, these myogenic regulatory factors control different stages of developmental skeletal muscle formation. Two of the four MRFs, Myogenic Determination Factor 1 (*MYOD*) and Myogenic Factor 5 (*MYF5*), are regulators of myogenesis progenitor specification. While *MRF4* and Myogenin (MYOG) are expressed much later in embryonic development, they play a crucial role in determining and differentiating embryonic stem cells to become committed myogenic cells. MYOG is the primary determinant of myoblast differentiation, while *MRF4* is expressed in mature myocytes (Nabeshima et al., 1993).

Apart from these, a growth factor worth mentioning is Myostatin (MSTN). It is the most potent negative regulator of myogenesis, but is also expressed in adult muscles, indicating that it also inhibits postnatal muscle growth (McPherron et al., 1997; Lee and McPherron, 2001; Amthor et al., 2004).

On the other hand, understanding the impact of these regulatory factors on skeletal muscle gene expression and its impact on meat quality and yield, as well as considering future perspectives such as regenerative myogenesis, is essential to successfully modify these genes.

To manipulate the myogenetic potentials of farm animals, we need to have complete information about MRFs, hence the purpose of this paper.

2. Muscles

Skeletal system, with more than 600 separate muscles, is the body's most important tissue mass and is crucial for

movement and support. Skeletal and cardiac muscles constitute the two main forms of striated muscle. Skeletal muscle represents innervated, voluntary muscle cells that exhibit fatigue and have high energy requirements, whereas cardiac muscle functionally represents a set of self-exciting, non-fatiguing muscle cells with moderate energy requirements. The organism's ability to actively control skeletal muscles distinguishes them from cardiac and smooth muscles. Skeletal muscle is considered a very important organ for the muscular system because it is a complex and heterogeneous tissue (Bentzinger et al. 2012) (Figure 1). In vertebrates, this tissue is extremely abundant and performs a variety of vital metabolic functions. The amount of lean skeletal muscle controls how quickly the body burns calories (Mifflin et al. 1990; Nelson et al. 1992; Taguchi et al. 2011). According to theory, obesity can be prevented by increasing muscle mass and energy expenditure from muscle protein oxidation (Wolfe 2006). Skeletal muscle also has the highest insulin-stimulated glucose absorption, which helps keep the body's overall insulin sensitivity high (DeFronzo et al. 1981). High skeletal muscle development is very important in farm animals as it produces tissue that meets human requirements for meat consumption. Myogenesis (including myoblast proliferation, differentiation and fusion), fibrogenesis and adipogenesis (Du et al. 2010) are involved in the formation of fetal skeletal muscle produced from mesenchymal stem cells (MSCs). Myogenesis is controlled by a complex network of intrinsic and extrinsic factors, typically divided into two or three phases, and is regulated by genes encoding kinases. Meat quality may also be improved by shifting MSC commitment from muscle to adipocyte formation with the addition of overlaying intramuscular fat. Proliferation and differentiation of myoblasts, the progenitors of muscle cells, play an important role in the formation of skeletal muscle. Growth promoters and myogenic regulatory factors (MRFs) are required for muscle development in agricultural animals. (Parakati and DiMario, 2013).

In general, fiber type position can influence muscle growth, which is considered an inherited trait, especially in terms of metabolism, contraction rate, temperature and food availability (Leatherland, 1994; Rehfeldt et al. 2011). In response to growth and injury, skeletal muscle has a remarkable capacity to renew and rebuild itself by activating muscle stem cells or satellite cells (Shi et al., 2006; Meadows et al. 2008).

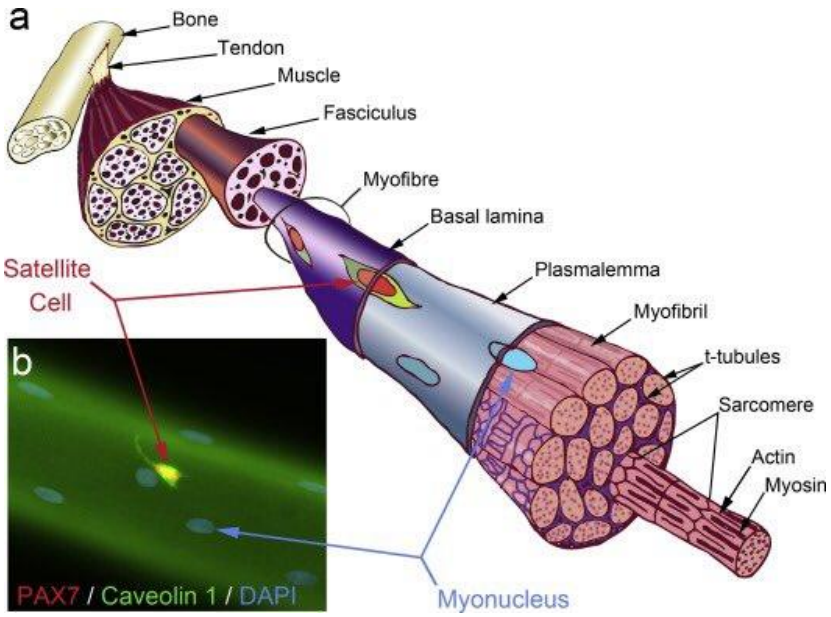

Figure 1. Skeletal muscle structure (a) and satellite cell (b). (Relaix et al., 2012) (Adapted with permission from The Company of Biologist, Ltd).

2.1. Myogenesis

Myogenesis is the complex process by which skeletal muscles are built in various species, including farm animals. Myogenesis is generally aimed at producing multinucleated myofibers with contractile activity. Different species require different periods of time for each stage of development (Knight and Kothary 2011). During embryogenesis, the basic components and structure of skeletal muscle are modeled (Buckingham et al. 2014; Bentzinger et al. 2012; Tapscott 2005). During early pregnancy, the locations and characteristics of the cells that will form the three germ layers (ectoderm, mesoderm and endoderm) are determined (Arnold SJ and Robertson, 2009). Depending on the distance from the midline/neural tube, the mesoderm is morphologically divided into paraxial, middle and lateral mesoderm. Paraxial mesoderm, a tissue that develops in the tail bud of embryonic axis elongation and subsequently in the primitive streak/blastopore during gastrulation, is the source of skeletal muscles. The

presomitic mesoderm at the posterior end of the embryo consists of the developing paraxial mesoderm. Presomitic mesoderm is a temporary tissue that can be divided into an immature posterior region and a specialized anterior region, the latter which divides to form somites. Skeletal myogenesis begins with the determination of premyogenic progenitors and skeletal myoblasts in the somites. Mononuclear myocytes fuse to form multinucleated myofibers after going through many stages of proliferation and differentiation. Myogenesis is typically controlled by a complex network of internal and external stimuli (Bentzinger et al. 2012) and is regulated at various stages by MRF genes and genes producing protein kinases (Knight and Kothary, 2011). The control of myogenesis is also significantly affected by nutrition. Both undernutrition and overnutrition during pregnancy inhibited fetal myogenesis, but only overnutrition promoted intermuscular fat accumulation (Zhao et al., 2019; Berri et al., 2006). Activation of the myogenic factor *MYF5* in cells in the dorsomedial part of the newly formed somite is the earliest indicator of myogenesis in mouse and chicken embryos (Ott et al., 1991; Pownall & Emerson, 1992).

According to studies carried out by Biressi et al. (2007) and Stockdale (1992), myogenesis can be divided into two stages throughout development: the early embryonic or primary stage (E10.5–E12.5 in mice; E3–7 in chicken) and the later fetal or secondary stage (E14.5 –17.5 in mice; E8+ in chicken). The first myofibers are initially generated from *PAX3*+/*PAX7*+ (in chickens) or *PAX3*+/*PAX3*+ (in mice) dermomyotomal progenitors (Horst et al., 2006 ; Hutcheson et al., 2009 ; Otto et al., 2006). These early myotomes and limb muscles are made from these early myofibers, which serve as building blocks for adult muscles (Murphy and Kardon, 2011). Muscle development is mostly maintained during secondary myogenesis by cell fusion and addition of myonuclei from dividing *PAX7*+ progenitors (White et al., 2010). Muscle satellite cells gradually function to support muscle growth after birth, while myogenic factors support and differentiate muscle throughout pregnancy. Farm animals undergo a series of biochemical processes, including protein deposition and muscle cell growth, to produce muscle (Du et al., 2010). Only a small fraction of the myotome's progenitor cells proliferate before differentiating into myoblasts. These myoblasts stop participating in the cell cycle and begin to differentiate and fuse with each other to form primary myofibers and myotubes (Buckingham et al. 2014).

Secondary muscle fibers are formed by proliferation and fusion of myoblasts in close proximity to primary muscle fibers (Beermann et al. 1978). The muscles of adult animals develop predominantly through secondary myogenesis. Satellite cells arise when some myogenic cells enter quiescence in the late fetal period. Therefore, in addition to influencing the number of muscle fibers, the number of myoblasts also influences the number of satellite cells present throughout postnatal development (Zhao et al., 2019). Fetal myogenesis is required for effective muscle growth in farm animals because, in the majority of cases, the number of muscle fibers does not change after birth (Du et al., 2010). Postnatal hypertrophy, or size expansion, results from the differentiation and fusion of satellite cells with pre-existing muscle fibers after initial proliferation of satellite cells. Without exogenous cues (such as injury and activity), satellite cells in mature animal muscles are dormant. Injured muscle fibers are repaired or replaced with activated satellite cells. Some age-related diseases cause a decrease in satellite cells, which impairs regeneration and causes muscle deterioration (Fukada, 2018).

2.2. Myogenic Regulatory Factors

2.2.1. Discovery of the bHLH myogenic regulatory factor.

Myogenic regulatory factors MRFs (*MYF5*, *MYOD*, myogenin, and *MRF4*), *PAX7*, and *PAX3* are among the unique muscle-related transcription factors that primarily regulate myogenesis. These elements function as regulators of the final signaling process and help produce appropriate transcripts for each step. *MYOD*, a basic helix-loop-helix factor (bHLH), was first discovered in 1987 by state-of-the-art subtractive hybridization research using myoblast cDNA libraries. These studies have shown that *MYOD* can convert various cell types, including fibroblasts, into cells that can fuse into myotubes. An important advance in understanding the molecular mechanisms underlying the selection and differentiation of muscle progenitors was the identification of *MYOD* and associated proteins. Subsequently, three additional myogenic basic helix-loop-helix factors, *MYF5*, Myogenin, and *MRF4* (also known as Myf6) has also been found to be able to induce myoblast properties in non-muscle cell lines (Braun et al. 1989; Edmondson and Olson 1989; Rhodes and Konieczny 1989; Braun et al. 1990; Miner and Wold 1990). When *MYOD*, *MYF5*, Myogenin, and *MRF4* are ectopically expressed, they can transform various cell types into myogenic lineages, which is one of their most remarkable features (Edmonson and Olson 1993). Thus, myogenic regulatory factors (MRFs) are the highly conserved genes *MYOD*, *MYF5*, myogenin, and *MRF4* that are collectively expressed in the skeletal muscle lineage (Weintraub et al. 1991; Rudnicki and Jaenisch 1995). The four MRF genes are expressed early during development, when myogenic lineage commitment is established in somites and developing limbs, as expected by several studies. The basic helix loop helix (bHLH) domain is a highly conserved core region found in *MYOD*, *MYF5*, myogenin, and *MRF4* proteins. The helix-loop-helix motif, found in the promoters of many muscle-specific genes, is required for heterodimerization with E proteins that mediate recognition of genomic E-boxes. In contrast, the basic domain of MRFs facilitates DNA binding. The resulting heterodimer has a strong affinity for the *CANNTG* DNA motif known as the E-box. According to

Edmonson and Olson (1993), such binding is required for transcriptional activation of E-box-containing genes. This motif can be found in the promoters of many, but not all, skeletal muscle-specific genes. The first MRF to be produced during embryonic development is *MYF5*, which is briefly upregulated in the paraxial mesoderm before working with other MRFs to help establish the myotome (Ott et al. 1991; Buckingham 1992).

2.2.2. Paired Homeobox Transcription (PAX) Factors

The next rung of the genetic ladder controlling myogenesis is dominated by the paired homeobox transcription factors *PAX3* and *PAX7*. Transcription factor paired box 7 (*PAX7*) is upregulated during myoblast differentiation but downregulated in proliferating myoblasts (Seale et al., 2000). In adult muscles, *PAX7* is expressed in both quiescent and proliferating satellite cells. (Zammit et al., 2004). Since all vertebrates appear to share at least one of these genes, it has been suggested that duplication of a particular gene from a common ancestor gave rise to these genes. (Noll, 1993).

Paired box transcription factors *PAX3* and *PAX7* are expressed by embryonic myogenic progenitors derived from the nuclear region of the somitic dermomyotome. (Seale et al., 2000, Relaix et al.). *MYF5* and *MYOD* are fully hierarchically induced at this stage of embryogenesis, followed by myogenin and *MRF4* and *MYOD*. Myogenesis is regulated by these three myogenic factors. Prior to the production of *MYF5* and *MYOD*, the paired box transcription factors are initially expressed in mesoderm cells (Buckingham, 2001). *PAX3* production during skeletal myogenesis upregulates *MYOD* expression, which is essential for skeletal muscle formation. In addition to regulating *MYF5* expression, *PAX7* maintains satellite cells in a quiescent state and is required for the growth of activated myoblasts (Knight et al.; Ridgeway et al.) Precursors of adult satellite cells that do not exhibit MRFs but still express *PAX3* and *PAX7* are thought to be a subset of myogenic precursor cells.

2.3. Function of MRFs in Muscle Development and Differentiation

2.3.1. *MYF5*, *MYOD*, and *MRF4* overlap in directing myogenic specification, whereas Myogenin is indispensable for myogenic differentiation.

Myogenic differentiation is hierarchically controlled by many transcriptional gene regulatory networks, each of which is precisely regulated by a master regulator located at specific temporal and geographical developmental stages (Buckingham et al. 2014) (Figure 2). The natural gene regulatory program for a non-muscle cell to become a myogenic-like cell can be overridden by ectopic expression of any of the MRFs that serve as master regulators of myogenesis. However, during development, the location, timing, and expression levels of MRFs are precisely modulated to ensure the correct progression of the developmental process. In cultured myogenic cells, sequential activation of bHLH myogenic regulators suggests that these elements have distinct functions in the regulation of myogenesis. Quiescent satellite cells do not express MRF at all. Myogenin and *MRF4* transcript increases are only seen when cells begin to differentiate, whereas *MYOD* and/or *MYF5* are the first MRFs produced in active muscle satellite cells (Smith et al., 1994; Yablonka-Reuveni and Rivera, 1994; Cornelison and Wold, 1997). The four MRFs express in a specific spatiotemporal pattern during mouse embryogenesis. (Currie and Ingham, 1998). *MYF5* is initially expressed in the dorsomedial cells of the dermomyotome that give rise to myogenic progenitors that develop into epaxial muscles. The ventrolateral dermomyotome cells, which form the progenitors of the hypaxial muscles, then begin to express the *MYOD* gene. According to Rehfeldt et al., myogenin and *MRF4* are required to support the differentiation and development of muscle fibers. *MYOD* and *MYF5* are very important for the emergence of different types of muscle cells. *MYF5* and *MYOD* are found earlier than myogenin-expressing cells during myotome development. Genes required for muscle stem cell proliferation are typically stimulated and activated by *MYF5*, *MYOD*, and *MRF4* (Knight and Kothary 2011). In addition, differentiation and fusion of myoblasts into myotubes depend on these elements.

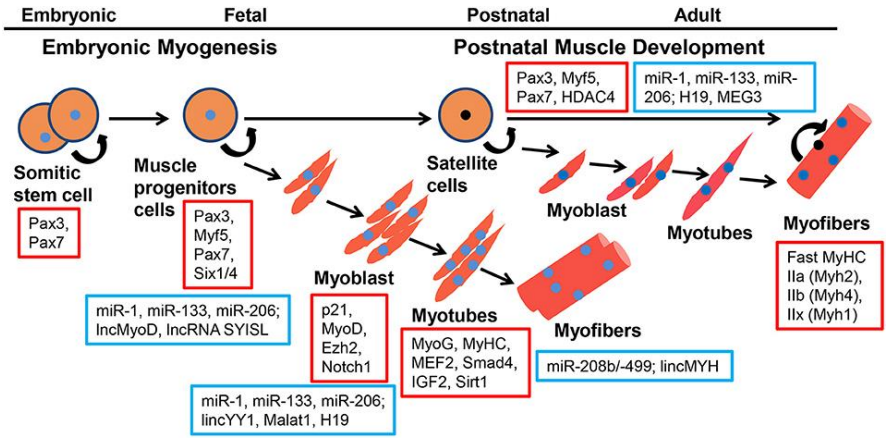

Figure 2. The process of embryonic and postnatal myogenesis is regulated by coding genes and noncoding RNAs. Red squares represent coding genes, while blue squares represent non-coding RNAs (Luo H. et al., 2021).

Myogenin and Myocyte Enhancer Factor 2 (*MEF2*), which work together to promote differentiation, are required for the differentiation of active myoblasts (Shi et al., 2006). According to Pownall and Emerson, *MYOD* has the power to activate additional MRFs, resulting in the production of muscle-specific proteins in avian species.

Expression of *MYF5* was significantly downregulated in Wagyu × Angus relative to Angus cattle, and samples from 6-month-old Angus cattle compared to Hereford and age-matched cattle. There was a higher myoblast proliferation rate at 5–20 h in in vitro cultures than samples from Wagyu × Angus cattle (Coles et al., 2015). On the day of hatching, the pectoralis major muscle of low-weight selected (LWS) chickens expressed more *PAX3*, *MYOD*, and *MRF4* than the pectoralis major muscle of high-weight selected (HWS) chickens, and on day 28, *PAX3*, *PAX7*, *MYF5*, *MYOD*1, *MYOG*, and *MRF4* expression was higher in HWS animals than in LWS animals (Yin et al., 2014). On the day of hatching, *PAX3*, *MYF5*, *MYOD* and *MYOG* expressions were higher in LWS chickens than in HWS chickens, and on the 28th day, *PAX7*, *MYF5*, *MYOD*1 and *MRF4* expressions were higher in LWS than HWS chickens (Yin et al., 2014). According to a quantitative real-time reverse transcription polymerase chain reaction (qRT-PCR) study on samples from Dzhalginsky Merino sheep, *MYOD*1 was one of 17 of the 48 genes studied and had the greatest expression in the loin muscle (Trukhachev et al., 2016). In pigs and cattle, *MYF5*, another important myogenesis regulator, has been associated with traits affecting meat quality (Ujan et al., 2011; Liu et al., 2008). Various regulatory transcription factors, such as *MYOD*1, have been discovered in the biceps femoris and longissimus dorsi muscles (LDMs) of purebred (IB) and Duroc-hybrid (IB DU) pigs (Ayuso et al. 2016). *MYOD*1 was expressed during two developmental periods (birth and growth) and may consequently have a significant impact on phenotypes. This makes pigs' gene an important candidate gene for the ability to build muscles.

Gene disruption in mice has also been used to clarify the function of bHLH myogenic regulators (Arnold and Winter, 1998). *MRF4* can initiate only a limited amount of myogenesis during embryonic development in the absence of both *MYF5* and *MYOD* (Kassar-Duchossoy et al., 2004). In the absence of *MYF5*, *MYOD*, and *MRF4*, a complete failure of myoblast differentiation and muscle formation occurs (Rudnicki et al., 1993). Consequently, these elements work together in transcriptional networks that are only partially redundant to control the fate of myoblast cells during embryonic and fetal development. However, while *MRF4* and *MYOD* can support some differentiation during embryogenesis, fetal myogenesis largely fails in Myogenin-null animals, with only a few differentiated myofibers present (Hasty et al., 1993; Nabeshima et al., 1993; Venuti et al., 1993). , 1995). This is where myogenin plays a unique function in fetal myocardial development. In cases where *MYOD* or *MYF5* null mutations are present, muscle growth is approximately normal. Careful examination revealed that early limb and branchial arch muscle development was delayed in *MYOD* null embryos, whereas trunk muscle development was slowed in *MYF5* null embryos. The total lack of skeletal myocytes or myofibers in mice with null mutations in both *MYOD* and *MYF5* genes suggests that *MYF5* or *MYOD* is required for the development and/or survival of myoblasts. Due to the already identified interference with the development of myogenic cells, the myogenin null mutation significantly reduces the amount of skeletal muscle tissue. Targeted silencing of the *MRF4* gene leads to largely normal muscle development, demonstrating that *MRF4* is not required to develop or maintain differentiated, functional skeletal muscle. *MRF4*/*MYOD* double mutants exhibit severe muscle deficiency equivalent to that conferred by myogenin gene deletion, although *MRF4* and *MYOD* single mutations have no effect on myogenesis. This suggests that when the *MYOD* gene is inactivated, myogenin alone cannot maintain proper muscle development. Based on the findings of null mutation studies, MRFs have unique but overlapping roles.

Muscle-related transcription factors play a role in the complex signaling cascades that trigger myogenesis, but they do not specifically control it. A crucial step in myogenesis is the essential and reversible phosphorylation process performed by the family of enzymes known as protein kinases. Numerous protein kinases have been shown to participate in various stages of myogenesis; therefore, activating or inhibiting them can directly alter the activity of muscle cells (Knight and Kothary 2011). Protein kinase A (PKA) is required for the formation of myogenic precursors in the dermomyotome at various stages of muscle development. In the case of PKA, myogenic factors such as *PAX3*, *MYOD*, and *MYF5* can form myotomes in dermomyotome cells (Chen et al., 2005). Wnt1 and Wnt7a, both produced by dorsal neural tubes outside the ectoderm, are involved in the initial phase of this activity. Myogenesis and adipogenesis are controlled by up- and down-regulation of (Wnt)/-catenin cascade signaling, respectively (Du et al. 2010). In addition to promoting the production of myogenic factors such as *MYF5*, *MYOD* and *PAX3*, PKA increases proliferation by phosphorylating MEF2 and inhibiting its effect (Knight and Kothary 2011). Retinoblastoma protein (Rb) is phosphorylated by cyclin-dependent kinases 2 and 4 (CDK2, 4) to prevent its binding to E2 factor (E2F), which maintains the expression of genes involved in the cell cycle and allows for its continued expression. Cell cycle progression is governed by this mechanism. In addition, phosphorylated Rb is unable to bind *MYOD*, which initiates S phase entry and allows CDK2 and CDK4 to suppress differentiation (Skapek et al, 1996; Gu et al, 1993). The presence of growth factors (GFs), such as fibroblast growth factor (FGF) and insulin-like growth factor (IGF), is required for extracellular signal-regulated kinase (ERK) activation. ERK1/2 activation is necessary for the prevention of myoblast

proliferation and myoblast differentiation in the early stages of myogenesis and for correct myocyte fusion in the late stages (Knight and Kothary, 2011). In addition to promoting proliferation, Akt1 also inhibits the expression of genes linked to cell cycle exit by phosphorylating FOXO1 (Nagata et al., 1998 ; Morooka et al., 1998 ; Bhat et al., 2007). Phosphorylation of MEF2 and E47 in myogenesis results in cell cycle exit of myogenic precursor cells. All of these elements work in concert to induce differentiation along with phosphorylated RNA polymerase II triggered by *MYOD* and CDK9.

2.3.2. Function of myogenic regulatory factors in mature muscle: In mature, healthy muscle, *MRF4* is the most expressed MRF.

Muscle progenitors at the postnatal satellite cell stage are identified by *PAX3* and *PAX7* proteins located beneath the basal lamina of adult myofibers (Kassar-Duchossoy et al., 2005). In the postnatal myofiber, all satellite cells express *PAX7*, but not all satellite cells express *PAX3*. Gene expression studies in primary myoblasts in conjunction with ChIP-seq research on *PAX7* and *PAX3* revealed that *PAX7* has a greater affinity for homeodomain binding motifs than *PAX3*, even though both transcription factors recognize the same DNA patterns. While *PAX7* specifically activates genes involved in the maintenance of the phenotype of adult satellite cells, from regulation of proliferation to inhibition of differentiation, *PAX3* binds a subset of *PAX7* target genes that are mainly involved in the regulation of embryonic functions and the maintenance of an undifferentiated phenotype (Soleimani et al., 2012). Research has predominantly focused on understanding how *MYF5* and *MYOD* expression is regulated in satellite cells and how this affects the cells' commitment to the myogenic lineage. Recent studies have shown that adult satellite cells do not express *MYOD* at rest, but use of a *MYOD*-iCre mouse strain with a lineage-tracing reporter allele shows that all progenitors derived from satellite cells express *MYOD* prenatally, regardless of their anatomical location and embryological origin (Kanisicak et al., 2009). To induce expression of *MYF5*, the histone methyltransferase complex Wdr5-Ash2l-Mll2 (Kmt2) must be recruited to the *MYF5* locus. This promotes transcriptional activation of *MYF5* through asymmetric muscle stem cell divisions (McKinnell et al., 2008). In addition, it was shown that satellite cells actually produce the *MYF5* gene, but the transcript is retained in mRNP granules by a process mediated by miR31, maintaining these cells in a quiescent state. Release of trapped transcripts and rapid translation of *MYF5* mRNAs occurs as a result of mRNP granule separation during satellite cell activation (Crist et al., 2012). The transcription factors FoxO3, Six1/4, *PAX3*, and *PAX7* stimulate *MYOD* expression in proliferating myoblasts (Grifone et al., 2005; Hu et al., 2008). As differentiation progresses towards the formation of myotubes, the *MYOD* locus migrates to the lumen of the nucleus, where the transcription factors TAF3/TRF3 promote *MYOD* expression (Yao et al., 2011). *MYOD* stimulates Myogenin production and inhibits *MYF5* expression in these conditions (Deato et al., 2008). The switch from *MYF5* to myogenin occurs simultaneously with cell cycle exit and the differentiation decision (Liu et al., 2012). Expression of the MRF-4 gene and other late muscle differentiation genes results from the combined activities of *MYOD* and Myogenin and drives the development of multinucleated fibers. . *MYOD* and Myogenin expression is then downregulated in mature muscle fibers, but *MRF4* is still produced at high levels to serve as the major MRF in adult differentiated muscle (Hinterberger et al., 1991). In adult rodent muscle, *MRF4* transcript levels are the highest among MRFs, and mice do not show a clear preference for any particular muscle or fiber type (Hughes et al., 1993; Voytik et al., 1993). *MRF4* mRNA is transiently produced in fetal mice and exhibits a biphasic expression pattern during muscle development, in contrast to previous reports in mice that *MRF4* expression is restricted to adult skeletal muscle (Rhodes and Konieczny, 1989; Hinterberger et al., 1991). *MRF4* mRNA was consistently expressed in growing chicken breast muscle, and subsequent studies using Northern blot hybridization found comparable results (Fujisawa-Sehara et al., 1992). *MRF4* mRNA expression has been found in adult pectoral muscle. There was no significant change in expression levels between ALD, PLD, and both. However, the *MYF5* expression level in these mature skeletal muscles was quite low.

2.4 Regulation of MRFs by signaling molecules

Direct expression of MRFs is synergistically induced by a combination of signaling molecules secreted from the neural tube and surrounding structures, which tightly control vertebrate myogenesis during embryonic development to identify myogenic progenitors in somites and drive their differentiation (Bryson-Richardson et al., 2008). Wnts, Sonic hedgehog (Shh), Notch receptor, and bone morphogenetic proteins (BMPs) are among the chemicals that can trigger myogenic specification (Bentzinger et al., 2012; Marcelle et al., 1997). A large family of glycoproteins known as Wnt proteins has been revealed to have multiple members that are essential for early myogenesis in somites (Rudnicki et al., 2015). In addition to Wnt proteins, Sonic hedgehog (Shh) produced from the notochord and dorsal neural tube functions in somitic tissue to promote myogenesis in vitro (Münsterberg, 1995). Shh signaling maintains *MYF5* and *MYOD* expression in mouse limb buds during the development of hypaxial muscles, and there is a significant deficiency in hypaxial limb muscles in Shh −/− animals (Krüger et al., 2001). Shh is an important protein found in the *MYF5* enhancer to identify myogenic progenitor cells. Gli- directly stimulates the expression of *MYF5* through its binding sites (Anderson et al., 2012). These findings suggest that Wnts and Shh may affect the myogenic potential of unknown cells.

It shows that they are working collaboratively to determine BMPs and the Notch receptor suppress the production of MRFs, while Wnt and Shh proteins

positively control the properties of myogenic progenitors (Hirsinger et al., 1997; Hirsinger et al., 2001; Schuster-Gossler et al., 2007). They prevent cells from differentiating, which promotes progenitor cell growth instead of differentiation. BMPs, members of the Transforming growth factor (TGF) superfamily, work through serine-threonine kinase receptors to activate SMAD proteins and their translocation to the nucleus, resulting in activation or repression of target genes (Hinck, 2012).

2.5. Myogenic Regulatory Factor Functions in Satellite Cells during Regenerative Myogenesis

To test satellite cell functionality in vivo, acute or chronic regeneration can be initiated. Acute regeneration models involve intramuscular injections of myotoxins, such as cardiotoxin or notexin, by freezing or crushing, which are more synchronous and traumatic (Hardy et al., 2016). Chronic regeneration is often evaluated using muscle disease models that experience repeated regenerative/degenerative episodes, such as the mdx mouse (Bulfield et al., 1984). Hepatocyte growth factor, sphingolipids, nitric oxide, and other signals are just a few of the signals that can activate satellite cells (Comai et al., 2014; Dumont et al., 2015a; Dumont et al., 2015b). In addition to *MYF5* protein, *MYF5* mRNA is released from mRNP granules in quiescent satellite cells to promote rapid translation (Crist et al., 2012). *MYOD* and Myogenin expression can be detected in mononuclear cells before DNA synthesis begins, which occurs 4–8 h after acute crush injury in a mouse. Expression levels in myotubes then begin to decrease after 8 days and return to pre-injury values (Grounds et al., 1992; Rantanen et al., 1995). When damage is combined with denervation, in which case *MYOD* is expressed more strongly and over a longer period of time, *MYOD* is detectable after only 12 h in vivo in mice and is only present momentarily in some nuclei of the least developed myotubes (Koishi et al., 1995; Rantanen et al., 1995). Therefore, if an acute injury is caused by muscle excision, marcaine HCl immersion, and regrafting (Fuchtbauer et al., 1992), denervation is likely to cause *MYOD* to express in both mononuclear cells and explains the subsequent discovery of entire nuclei of newly formed myotubes. Approximately 12 hours after injury, myogenin appears in mononuclear cells and later also in myotubes (Fuchtbauer et al., 1992; Rantanen et al., 1995). Adult muscle contains myonuclei where *MRF4* is located and is increased when muscle injury occurs (Zhou et al., 2001). Although *MRF4* has a limited role in establishing the myogenic lineage during embryogenesis, it is expressed in adults only after myoblasts have fused into myotubes and undergo maturation (Kassar-Duchossoy et al., 2004). Neither *MRF4* transcript nor *MRF4* protein is present during satellite cell activation and proliferation or even during early myogenic differentiation and fusion (Hinterberger et al., 1991; Zhou et al., 2001; Pavlath et al., 2003). Serum growth factors such as transforming growth factor-f (Vaidya et al., 1989; Heino et al., 1990), fibroblast growth factor (Vaidya et al., 1989; Brunetti et al., 1990) and insulin-like growth factor (Florini et al., 1991) has been shown to be involved in myogenic determination and differentiation by controlling the expression of myogenic factors in in vitro myogenesis systems. The mechanisms by which myogenic factors regulate muscle growth are currently not fully understood. However, previous research suggests that innervation regulates the development of chicken breast muscle. According to previous studies, isoform transition of myofibrillar proteins from the neonate to the adult state is prevented by denervation of neonatal chicken breast muscle (Obinata et al., 1984). In addition, these studies show that denervated adult muscle reexpresses neonatal isoforms such as slow C-protein, muscle-type f-tropomyosin and neonatal versions of troponin T (Obinata et al., 1984; Obinata et al., 1986). Therefore, it can be speculated that the different pattern of expression of myogenic factors may be vital in supporting muscle development from embryonic to adult fast or slow muscle, and innervation may play a crucial role in controlling this process.

2.6. Role of Growth Factors (GFs) in Skeletal Muscle Growth

Various types of GFs affect the differentiation and proliferation of skeletal muscle growth. Hepatocyte growth factor (HGF) has been shown to improve the surface elasticity of bovine satellite cells in vitro (Lapin et al., 2013) and to stimulate the proliferation and migration of myogenic cells (Bandow et al., 2004). In chickens, Fibroblast growth factor FGF2 has been discovered to inhibit cell differentiation and stimulate the proliferation of satellite cells and myoblasts, the two types of muscle precursor cells (Velleman, 2007). Therefore, FGF2 expression is essential for the normal development of muscle fibers throughout the embryonic stage. However, this substance also prevents the proper development of myotubes by inhibiting myogenin transcription (Brunetti et al., 1990). IGFs (insulin-like growth factor) control and promote cell proliferation, differentiation, hypertrophy, and protein synthesis associated with myogenesis (Kamanga-Sollo et al., 2003; Knight and Kothary 2011). Transforming growth factor (TGF) and myostatin (GDF-8) have opposing effects on differentiation (Shahjahan, 2015); consequently, their expression in agricultural animals for meat purposes should be restricted. IGF-1 mRNA expression in chicken muscle decreased during development, increased after hatching, and decreased once again after day 7 post-hatching (Wu et al., 2011). It was also significantly higher in embryonic muscle than in embryonic liver. IGF-I and IGF-II increased during differentiation in porcine satellite cells (Theil et al., 2006). IGF-II mRNA is most increased at gestational day 85 in fetal sheep, highlighting its importance for leg myogenic fiber development during this period (Fahey et al., 2005), while double-muscled Gerrard (DM) cattle show a delay in IGF-II expression and it developed more muscle fibers as a result of a mutation in the MSTN gene (Gerrard et al., 1994).

Another key element is growth hormone (GH), which plays an important role in the GH-IGF axis and influences skeletal muscle development in farm animals both genetically and environmentally (Rehfeldt et al. 2011).

3. Conclusion

The next phase of research should focus on finding the reasons why adult skeletal muscle stem cells as well as the many muscle lineages throughout embryonic development are present. There are still unanswered questions about the roles of myogenin and *MRF4* in adult skeletal muscle and regeneration myogenesis. In the field of developmental biology, single-cell approaches and lineage tracing experiments are currently being used to uncover new mechanistic insights into upstream regulatory networks in the embryo and link these to our current biochemical understanding of muscle differentiation. This will provide a satisfactory and comprehensive understanding to create new therapeutic techniques to treat skeletal muscle disorders such as muscular dystrophies and age-related regeneration difficulties. In farm animals, selection can significantly improve the complex but continuous process of muscle growth, and the discovery of associated candidate genes can improve it further. Understanding the processes underlying muscle growth and development has advanced significantly over the past few years. In addition, important regulators, including transcription factors and GFs, have been identified and their functions related to many aspects of muscle development have been examined. Identification of such important regulators and genes provides a great help for marker-assisted selection, is crucial for the goal of increasing meat yield and helps breeders in maximizing meat quantity and quality. Moreover, gene sets typically associated with muscle growth and development may be helpful in applied investigation of mammalian muscle growth. However, the principles underlying muscle growth and development in agricultural animals, particularly sheep and cattle, require further research.

Author Contributions

The percentage of the author(s) contributions is presented below. All authors reviewed and approved the final version of the manuscript.

	G.A.I.	D.G.	Z.Ö.
C	40	30	30
D	40	30	30
L	40	30	30
W	40	30	30
CR	40	30	30
SR	40	30	30

C=Concept, D= design, L= literature search, W= writing, CR= critical review, SR= submission and revision.

Conflict of Interest

The authors declare that there is no conflict of interest.

References

Amthor H, Nicholas G, McKinnell I, Kemp CF, Sharma M, Kambadur R, Patel K 2004. Follistatin complexes myostatin and antagonises myostatin-mediated inhibition of myogenesis. Devel Biol, 270: 19-30.

Anderson C, Williams VC, Moyon B, Daubas P, Tajbakhsh S, Buckingham ME, 2012. Sonic hedgehog acts cell-autonomously on muscle precursor cells to generate limb muscle diversity, Genes Dev, 26(18): 2103–2117.

Arnold HH, Winter B, 1998. Muscle differentiation: More complexity to the network of myogenic regulators. Curr. Opin. Genet. Giant, 8: 539-544.

Arnold SJ, Robertson EJ, 2009. Making a commitment: Cell lineage allocation and axis patterning in the early mouse embryo. Nature Reviews Molecular Cell Biology, 10(2): 91–103.

Ayuso M, Fernández A, Núñez Y, Benítez R, Isabel B, Fernández AI, Rey AI, González-Bulnes A, Medrano JF, Cánovas A, et al. 2016. Developmental stage, muscle and genetic type modify muscle transcriptome in pigs: Effects on gene expression and regulatory factors involved in growth and metabolism. PLoS ONE 11: e0167858.

Bandow K, Ohnishi T, Tamura M, Semba I, Daikuhara Y 2004. Hepatocyte growth factor/scatter factor stimulates migration of muscle precursors in developing mouse tongue. J. Cell Physiol. 201:236–243.

Beermann DH, Cassens RG, Hausman GJ 1978. A second look at fiber type differentiation in porcine skeletal muscle. J.Anim. Sci., 46: 125–132.

Bentzinger CF, Wang YX, Rudnicki MA. Building muscle: Molecular regulation of myogenesis cold spring war. Perspect. Biol. February 2 2012, 4: a008342.

Berri C, Godet E, Haj Hattab N, Duclos MJ 2006. Growth and differentiation of the chicken Pectoralis major muscle: Effect of genotype and early nutrition. Arch. Anim. Breed, 49:31–32.

Bhat NR, Zhang P, Mohanty SB 2007, p38 MAP kinase regulation of oligodendrocyte differentiation with CREB as a potential target. Neurochem. Pic., 32: 293– 302.

Biressi S, Molinaro M, Cossu G, 2007. Cellular heterogeneity during vertebrate skeletal muscle development. Giant. Biol. 308: 281-293.

Braun T, Bober E, Winter B, Rosenthal N, Arnold HH 1990. Myf-6, a new member of the human gene family of myogenic factors determination: Evidence for a gene cluster on chromosome 12. EMBO J 9: 821–831

Braun T, Buschhausen-Denker G, Bober E, Tannich E, Arnold HH 1989. A novel human muscle factor related to but distinct from MYOD1 induces myogenic conversion in 10T1/2 fibroblasts. EMBO J 8: 701– 709.

Brunetti A, Goldfine ID, 1990. Role of myogenin in myoblast differentiation and its regulation by fibroblast growth factor. J. Biol. Chem, 265: 5960–5963.

Bryson-Richardson RJ, Currie PD, The genetics of vertebrate myogenesis, Nat. Rev. Genet. 9 August 8 2008: 632–646.

Buckingham M, Rigby PWJ, Gene regulatory networks and transcriptional mechanisms that control myogenesis, Dev. Cell 28 February 3 2014: 225–238.

Buckingham M 1992. Making muscles in mammals. Trends Genet 8: 144–148.

Buckingham M 2001. Skeletal muscle formation in vertebrates. Curr. Opin. Genet. Giant, 11: 440–448.

Bulfield G, Siller WG, Wight PA, et al. 1984. X chromosome-linked muscular dystrophy (mdx) in the mouse, Proc. Natl. Acad. Sci. USA 81: 1189–1192.

Chen AE, Ginty DD 2005, Fan CM. Protein kinase A signaling via

CREB controls myogenesis induced by Wnt proteins. Nature, 433: 317–322.

Coles CA, Wadeson J, Leyton CP, Siddell JP, Greenwood PL, White JD, McDonagh MB 2015. Proliferation rates of bovine primary muscle cells relate to live weight and carcase weight in cattle. PLoS ONE, 10: e0124468.

Comai G, Tajbakhsh S 2014. Molecular and cellular regulation of skeletal myogenesis, Curr. Ball. Giant. Biol. 110:1–73.

Cornelison DDW, Wold BJ, 1997. Single-cell analysis of regulatory gene expression in quiescent and activated mouse skeletal muscle satellite cells. Giant. Biol. 191: 270-283.

Crist CG, Montarras D, Buckingham M 2012. Muscle satellite cells are primed for myogenesis but maintain quiescence with sequestration of MYF5 mrna targeted by microrna-31 in mrnp granules, Cell Stem Cell 11 July 1: 118–126.

Currie PD, Ingham PW, 1998. The generation and interpretation of positional information within the vertebrate myotome. Mech. Giant. 73, 321.

Deato MDE, Marr MT, Sottero T, Inouye C, Hu P, Tjian R, 2008. MYOD targets TAF3/TRF3 to activate myogenin transcription, Mol. Cell 32 October 1: 96– 105.

DeFronzo RA, Jacot E, Jequier E, Maeder E, Wahren J, Felber JP 1981. The effect of insulin on the disposal of intravenous glucose. Results from indirect calorimetry and hepatic and femoral venous catheterization. Diabetes, 30: 1000–1007.

Du M, Tong J, Zhao J, Underwood KR, Zhu M, Ford SP, Nathanielsz PW 2010. Fetal programming of skeletal muscle development in ruminant animals. J.Anim. Sci, 88: E51–E60.

Dumont NA, Bentzinger CF, Sincennes MC, et al., 2015. Satellite cells and skeletal muscle regeneration, Compr. Physiol. 5 2015b:1027–1059.

Dumont NA, Wang YX, Rudnicki MA 2015. Intrinsic and extrinsic mechanisms regulating satellite cell function, Development 142 2015a: 1572–1581.

Edmondson DG, Olson EN 1989. A gene with homology to the myc similarity region of MYOD1 is expressed during myogenesis and is sufficient to activate the muscle differentiation program. Genes Dev 3: 628–640.

Edmonson DG, Olson EN, 1993. Helixloophelix proteins as regulators of muscle-specific transcription J. Biol. Chem. 268, 755758

Fahey AJ, Brameld JM, Parr T, Buttery PJ 2005. Ontogeny of factors associated with proliferation and differentiation of muscle in the ovine fetus. J.Anim. Sci., 83: 2330–2338.

Florini JR, Ewton DZ, Roof SL 1991. Mol. Endo. 5: 718-724.

Fuchtbauer EM, Westphal H, 1992. MYOD and myogenin are coexpressed in regenerating skeletal muscle of the mouse, Dev. Dyn,193: 34–39.

Fujisawa-Sehara A, Nabeshima Y, Komiya T, Uetsuki T, Asakura, A, Nabeshima Y 1992. J. Biol. Chem. 267: 10031-10038.

Fukada S 2018. The roles of muscle stem cells in muscle injury, atrophy and hypertrophy. J. Biochem, 163: 353–358.

Gerrard DE, Grant AL, 1994. Insulin-like growth factor-II expression in developing skeletal Muscle of double muscled and normal cattle. home Anim. Endocrinol, 11: 339–347.

Grifone R, Demignon J, Houbron C, Souil E, Niro C, Seller MJ, et al. 2005. Six1 and six4 homeoproteins are required for PAX3 and mrf expression during myogenesis in the mouse embryo, Development 132, May 9 2005:2235–2249.

Grounds MD, Garrett KL, Lai MC, et al., 1992. Identification of skeletal muscle precursor cells in vivo by use of MYOD1 and myogenin probes, Cell Tissue Res. 267: 99– 104.

Gu W, Schneider JW, Condorelli G, Kaushal S, Mahdavi V, Nadal-Ginard B 1993. Interaction of myogenic factors and the retinoblastoma protein mediates muscle cell commitment and differentiation. Cell 1993, 72: 309–324.

Hardy D, Besnard A, Latil M, et al., 2016. Comparative study of injury models for studying muscle regeneration in mice, PLoS One 11: e0147198.

Hasty P, Bradley A, Morris JH, et al., 1993. Muscle deficiency and neonatal death in mice with a targeted mutation in the myogenin gene. Nature 364: 501–506.

Heino J, Massague J 1990. J. Biol. Chem. 265: 10181-10184.

Hinck AP 2012. Structural studies of the tgfs and their receptors–insights into evolution of the tgf-superfamily, FEBS Lett. 586 July 14 2012: 1860–1870.

Hinterberger TJ, Sassoon DA, Rhodes SJ, Konieczny SF, 1991. Expression of the muscle regulatory factor MRF4 during somite and skeletal myofiber development. Dev. Biol, 147 September 1 1991: 144–156.

Hirsinger E, Duprez D, Jouve C, Malapert P, Cooke J, Pourquié O, 1997. Noggin acts downstream of wnt and sonic hedgehog to antagonize BMP4 in avian somite patterning. Development 124, November 22 1997: 4605–4614.

Hirsinger E, Malapert P, Dubrulle J, Delfini MC, Duprez D, Henrique D, et al., 2001. Notch signaling acts in postmitotic avian myogenic cells to control MYOD activation, Development 128, January 1 2001: 107–116.

Horst D, Ustanina S, Sergi C, Mikuz G, Juergens H, Braun T, Vorobyov E, 2006. Comparative expression analysis of PAX3 and PAX7 during mouse myogenesis. Int. J. Dev. Biol. 50, 47-54.

Hu P, Geles KG, Paik JH, DePinho RA, Tjian R 2008. Codependent activators direct myoblast-specific MYOD transcription, Dev. Cell 15 October 4 2008: 534–546.

Hughes SM, Taylor JM, Tapscott SJ, et al., 1993. Selective accumulation of MYOD and myogenin mRNAs in fast and slow adult skeletal muscle is controlled by innervation and hormones, Development 118:1137–1147.

Hutcheson DA, Zhao J, Merrell A, Haldar M, Kardon G 2009. Embryonic and fetal limb myogenic cells are derived from developmentally distinct progenitors and have different requirements for beta-catenin. Genes Dev. 23: 997-1013.

Kamanga-Sollo E, Pampusch MS, White ME, Dayton WR 2003. Role of insulin-like growth factor binding protein (IGFBP)-3 in TGF β-and GDF 8 (myostatin)-induced suppression of proliferation in porcine embryonic myogenic cell cultures. J. Cell Physiol, 197: 225–231.

Kanisicak O, Mendez JJ, Yamamoto S, Yamamoto M, Goldhamer DJ 2009. Progenitors of skeletal muscle satellite cells express the muscle determination gene, MYOD, Dev. Biol. August 1 2009, 332:131–141.

Kassar-Duchossoy L, Gayraud-Morel B, Gomes D, et al. 2004. MRF4 determines skeletal muscle identity in MYF5: MYOD double-mutant mice, Nature 431:466–471.

Kassar-Duchossoy L, Giacone E, Gayraud-Morel B, Jory A, Gomès D, Tajbakhsh S 2005. PAX3/PAX7 mark a novel population of primitive myogenic cells during development, Genes Dev. June 12 2005, 19:1426–1431.

Knight JDR, Kothary R 2011. The myogenic kinome: Protein kinases critical to mammalian skeletal myogenesis. Skeletal Muscle, 1: 29.

Koishi K, Zhang M, McLennan IS, et al. 1995. MYOD protein accumulates in satellite cells and is neurally regulated in regenerating myotubes and skeletal muscle fibers, Dev. Dyn. 202: 244–254.

Krüger M, Mennerich D, Fees S, Schäfer R, Mundlos S, Braun T 2001. Sonic hedgehog is a survival factor for hypaxial muscles during mouse development, Development March 5 2001 128: 743–752.

Lapin MR, Gonzalez JM, Johnson SE 2013. Substrate elasticity affects bovine satellite cell activation kinetics in vitro. J.Anim. Sci. 91: 2083–2090.

Leatherland JF 1994. Reflections on the thyroidology of fishes: From molecules to human kind Guelph. Ichthyol. Rev, 2:1–67.

Lee SJ, McPherron AC 2001. Regulation of myostatin activity and muscle growth. Proceedings of the National Academy of Sciences of the United States of America 98: 9306–9311.

Liu QC, Zha XH, Faralli H, Yin H, Louis-Jeune C, Perdiguero E, et al., 2012. Comparative expression profiling identifies differential roles for myogenin and p38 MAPK signaling in myogenesis, J. Mol. Cell Biol. 4 December 6 2012 :386– 397.

Liu M, Peng J, Xu D, Zheng R, Li F, Li J, Zuo B, Lei M, Xiong Y, Deng C, et al. 2008. Association of MYF5 and MYOD1 gene polymorphisms and meat quality traits in Large White × Meishan F2 pig populations. Biochem. Genet, 46: 720–732.

Luo H, Lv W, Tong Q, Jin J, Xu Z, Zuo B 2021. Functional non-coding rna during embryonic myogenesis and postnatal muscle development and disease. Front. Cell Dev. Biol. 9:628339. doi: 10.3389/fcell.2021.628339

Marcelle C, Stark MR, Bronner-Fraser M 1997. Coordinate actions of bmps, wnts, shh and noggin mediate patterning of the dorsal somite, Development October 20 1997, 124: 3955–3963.

McKinnell IW, Ishibashi J, Le Grand F, Punch VGJ, Addicks GC, Greenblatt JF, et al., 2008. PAX7 activates myogenic genes by recruitment of a histone methyltransferase complex, Nat. Cell Biol. January 1 2008, 10: 77–84.

McPherron AC, Lee SJ 1997. Double muscling in cattle due to mutations in the myostatin gene. Proceedings of the National Academy of Sciences of the United States of America 94: 12457–12461.

Meadows E, Cho JH, Flynn JM, Klein WH 2008. Myogenin regulates a distinct genetic program in adult muscle stem cells. Giant. Biol, 322: 406–414.

Mifflin MD, St Jeor ST, Hill LA, Scott BJ, Daugherty SA, Koh YO 1990. A new predictive equation for resting energy expenditure in healthy individuals. Am. J. Clin. Nutr., 51:241–247.

Miner JH, Wold B 1990. Herculin, a fourth member of the MYOD family of myogenic regulatory genes Proc Natl Acad Sci 87: 1089–1093.

Morooka T, Nishida E, 1998. Requirement of p38 mitogen-activated protein kinase for neuronal differentiation in PC12 cells. J. Biol. Chem. 273: 24285–24288.

Münsterberg AE, Kitajewski J, Bumcrot DA, McMahon AP, Lassar AB 1995. Combinatorial signaling by sonic hedgehog and wnt family members induces myogenic bhlh gene expression in the somite, Genes Dev. December 23 1995, 9:2911–2922.

Murphy M, Kardon G 2011. Origin of vertebrate limb muscle: the role of progenitor and myoblast populations. Curr. Ball. Giant. Biol. 96: 1-32.

Nabeshima Y, Hanaoka K, Hayasaka M, Esumi E, Li S, Nonaka I, Nabeshima YI 1993. Myogenin gene disruption results in perinatal lethality because of severe muscle defect. Nature 364: 532–535.

Nagata Y, Takahashi N, Davis RJ, Todokoro K 1998. Activation of p38 MAP kinase and JNK but not ERK is required for erythropoietin-induced erythroid differentiation. Blood, 92: 1859–1869.

Nelson KM, Weinsier RL, Long CL, Schutz Y 1992. Prediction of resting energy expenditure from fat-free mass and fat mass. Am. J. Clin. Nutr, 56: 848– 856.

Noll M 1993. Evolution and role of Pax genesis. Curr Opin Genet Dev 3: 595–605.

Obinata T, Kawashima M, Kinani S, Saitoh O, Masaki T, Bader DM, Fischman, DA 1986. Molecular Biology of Muscle Development. Emerson C, Fischman DA, Nadal-Ginard B, Siddiquis AQ, eds. p293 -307.

Obinata T, Saitoh O, Takano-Ohmuro H 1984. J. Biochem. 95: 585 -588.

Ott MO, Bober E, Lyons G, Arnold H, Buckingham 1991. Early expression of the myogenic regulatory gene, myf-5, in precursor cells of skeletal muscle in the mouse embryo. Development 111: 1097-1107.

Otto A, Schmidt C, Patel K 2006. PAX3 and PAX7 expression and regulation in the avian embryo. Anat. Embryol. 211: 293-310.

Parakati R, DiMario JX 2013. Repression of myoblast proliferation and fibroblast growth factor receptor 1 promoter activity by KLF10 protein. J. Biol. Chem, 288: 13876–13884.

Pavlath GK, Dominov JA, Kegley KM, et al., 2003. Regeneration of transgenic skeletal muscles with altered timing of expression of the basic helix-loop-helix muscle regulatory factor MRF4, Am. J. Pathol. 162:1685–1691.

Pownall ME, Emerson CP 1992. Sequential activation of three myogenic regulatory genes during somite morphogenesis in quail embryos. Giant. Biol, 151: 67–79.

Rantanen J, Hurme T, Lukka R, et al., 1995. Satellite cell proliferation and the expression of myogenin and desmin in regenerating skeletal muscle: evidence for two different populations of satellite cells, Lab. Invest. 72:341–347.

Rehfeldt C, Te Pas MFW, Wimmers K, Brameld JM, Nissen PM, Berri C, Valente LMP, Power DM, Picard B, Stickland NC, et al. 2011. Advances in research on the prenatal development of skeletal muscle in animals in relation to the quality of muscle-based food. Animal 2011, 5:703–717.

Relaix F, Zammit PS 2012. Satellite cells are essential for skeletal muscle regeneration: the cell on the edge returns centre stage. Development, 139: 3845-56

Relaix F, Rocancourt D, Mansouri A, Buckingham M 2004. Divergent functions of murine PAX3 and PAX7 in limb muscle development, Genes Dev. May 9 2004, 18: 1088–1105.

Rhodes SJ, Konieczny SF 1989. Identification of MRF4: A new member of the muscle regulatory factor gene family. Genes Dev, 3: 2050–2061.

Ridgeway AG, Skerjanc IS 2001. PAX3 is essential for skeletal myogenesis and the expression of Six1 and Eya2. J. Biol. Chem, 276: 19033–19039.

Rudnicki MA, Jaenisch R 1995. The MYOD family of transcription factors and skeletal myogenesis Bioessays, 17:203–209

Rudnicki MA, Schnegelsberg PN, Stead RH, et al., 1993. MYOD or Myf-5 is required for the formation of skeletal muscle, Cell 75: 1351–1359.

Rudnicki MA, Williams BO, Wnt signaling in bone and muscle, Bone November 2015, 80: 60–66.

Schuster-Gossler K, Cordes R, Gossler A 2007. Premature myogenic differentiation and depletion of progenitor cells causes severe muscle hypotrophy in delta1 mutants, Proc. Natl. Acad. Sci. USA January 2 2007, 104: 537–542.

Seale P, Sabourin LA, Girgis-Gabardo A, Mansouri A, Gruss P, Rudnicki MA 2000. PAX7 is required for the specification of myogenic satellite cells. Cell 102:777–786.

Shahjahan MD 2015. Skeletal muscle development in vertebrate animals. Asian J. Med. Biol. Pic, 1: 139–148.

Shi X, Garry DJ 2006. Muscle stem cells in development, regeneration, and disease. Genes Giant, 20: 1692–1708.

Skapek SX, Rhee J, Kim PS, Novitch BG, Lassar AB 1996. Cyclin-

mediated inhibition of muscle gene expression via a mechanism that is independent of pRB hyperphosphorylation. Mole. Cell. Biol., 16: 7043–7053.

Smith CK, Janney MJ, Allen RE 1994. Temporal expression of myogenic regulation genesis during activation, proliferation, and differentiation of rat skeletal muscle satellite cells. J. Cell Physiol. 159: 379-385.

Soleimani VD, Punch VG, Kawabe YI, Jones AE, Palidwor GA, Porter CJ, et al., 2012. Transcriptional dominance of PAX7 in adult myogenesis is due to high-affinity recognition of homeodomain motifs, Dev. Cell, June 6 2012, 22: 1208–1220.

Stockdale FE 1992. Myogenic cell lineages. Giant. Biol. 154: 284-298.

Taguchi M, Ishikawa-Takata K, Tatsuta W, Katsuragi C, Usui C, Sakamoto S, Higuchi M 2011. Resting energy expenditure can be assessed by fat-free mass in female athletes regardless of body size. J. Nutr. Sci. Vitaminol, 57: 22–29.

Tapscott SJ 2005. The circuitry of a master switch: MYOD and the regulation of skeletal muscle gene transcription, Development, June 12 2005 132:2685–2695.

Theil PK, Sørensen IL, Nissen PM, Oksbjerg N 2006. Temporal expression of growth factor genesis of primary porcine satellite cells during myogenesis. Anim. Sci. J., 77: 330–337.

Trukhachev V, Stavropol State Agrarian University, Skripkin V, Kvochko A, Kulichenko A, Kovalev D, Pisarenko S, Volynkina A, Selionova M, Aybazov M, et al., 2016. Correlation between gene expression profiles in muscle and live weight in Dzhalginsky Merino sheep. RCCP, 29: 188–198.

Ujan JA, Zan LS, Ujan SA, Adoligbe C, Wang HB 2011. Back fat thickness and meat tenderness are associated with a 526 T →Amutation in the exon 1 promoter region of the MyF-5 gene in Chinese Bos taurus. Genet. Mole. Pic, 10: 3070–3079.

Vaidya TB, Rhodes SJ, Taparowsky EJ, Konieczny SF 1989. Mol. Cell. Biol. 9: 3576-3579.

Velleman SG 2007. Muscle development in the embryo and hatchling. Poult. Sci, 86: 1050–1054.

Venuti JM, Morris JH, Vivian JL, et al. 1995. Myogenin is required for late but not early aspects of myogenesis during mouse development, J. Cell Biol. 128: 563- 576

Voytik SL, Przyborski M, Badylak SF, et al. 1993. Differential expression of muscle regulatory factor genes in normal and denervated adult rat hindlimb muscles, Dev. Dyn. 198: 214–224.

Weintraub H, Davis R, Tapscott S, Thayer M, Krause M, Benezra R, Blackwell TK, Turner D, Rupp R, Hollenberg S, et al. 1991. The MYOD gene family: Nodal point during specification of the muscle cell lineage. Science 251: 761–766.

White RB, Biérinx AS, Gnocchi VF, Zammit PS 2010. Dynamics of muscle fiber growth during postnatal mouse development. BMC Dev. Biol. 10: 21.

Wolfe RR 2006. The underappreciated role of muscle in health and disease. Am. J. Clin. Nutr, 84: 475–482.

Wu G, Siegel PB, Gilbert ER, Yang N, Wong EA 2011. Expression profiles of somatotropic axis genes in lines of chickens divergently selected for 56-day body weight. Anim. Biotechnol, 22: 100–110.

Yablonka-Reuveni Z, Rivera A, 1994. Temporal expression of regulatory and structural muscle proteins during myogenesis of satellite cells on isolated adult rat fibers. Giant. Biol. 164: 588-603.

Yao J, Fetter RD, Hu P, Betzig E, Tjian R 2011. Subnuclear segregation of genes and core promoter factors in myogenesis, Genes Dev, March 6 2011, 25: 569–580.

Yin H, Zhang S, Gilbert ER, Siegel PB, Zhu Q, Wong EA 2014. Expression profiles of muscle genesis in postnatal skeletal muscle in lines of chickens divergently selected for high and low body weight. Poult. Sci, 93: 147–154.

Zammit PS, Golding JP, Nagata Y, Hudon V, Partridge TA, Beauchamp JR 2004. Muscle satellite cells adopt divergent fates: a mechanism for self-renewal? The Journal of Cell Biology 166: 347–357.

Zhao L, Huang Y, Du M 2019. Farm animals for studying muscle development and metabolism: Dual purposes for animal production and human health. Anim. Front, 9: 21–27.

Zhou Z, Bornemann A 2001. MRF4 protein expression in regenerating rat muscle, J. Muscle Pic. Cell Motil. 22: 311–316.