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Expression Patterns and Regulatory Mechanisms of microRNAs Related to Animal Muscle Growth and Development: Postprint

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Abstract

MicroRNAs (miRNAs) are endogenous non-coding small RNAs that can target and regulate the expression of numerous genes, thereby participating in the regulation of various biological processes. The growth and development of animal muscle tissue is a complex process that is precisely controlled by numerous regulatory factors. This review summarizes the expression patterns and regulatory mechanisms of miRNAs, particularly muscle-specific miRNAs, during animal muscle growth and development.

Full Text

Expression Patterns and Regulatory Mechanisms of MicroRNAs in Animal Muscle Growth and Development

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Abstract

MicroRNAs (miRNAs) are endogenous non-coding small RNAs that regulate the expression of numerous target genes, thereby participating in the modulation of various life activities. The growth and development of animal muscle tissue is a complex process under precise control by multiple regulatory factors.

This review summarizes the expression patterns and regulatory mechanisms of miRNAs, particularly muscle-specific miRNAs, during animal muscle growth and development.

Keywords: microRNAs; muscle; muscle cell; muscle-specific miRNA

Muscle is an extremely important tissue and organ in animals, and its normal growth and development ensures proper functioning of the locomotor system and maintains energy metabolism balance. Additionally, the number, type, and status of muscle fibers profoundly influence meat quality. Muscle formation and development generally comprise three stages: myoblast differentiation and formation, myoblast migration and proliferation, and multinucleated myocyte/myotube formation [1]. Muscle cells are the basic units of muscle tissue; their number stabilizes during late embryonic development, while postnatal growth involves muscle cell hypertrophy and increased muscle fiber number [2]. Furthermore, extensive muscle cell proliferation also occurs during muscle trauma repair in animals.

Muscle tissue growth and development is a complex regulatory process in which muscle precursor cells differentiate into multinucleated myocytes (myotubes) under precise control by numerous factors. Sequential expression of myogenic regulatory factors such as myogenic factor 5 (Myf5), myogenic determination gene (MyoD), muscle regulatory factors-4 (Mrf4), and myogenin (MyoG), along with MADS homeobox proteins, zinc finger proteins, and Wnt family members, plays crucial roles in muscle cell formation, differentiation, and muscle tissue morphogenesis [2-6].

1. Generation and Regulation of MicroRNAs (miRNA)

miRNAs are a class of regulatory non-coding small RNAs widely present in animals and plants. In eukaryotic genomes, primary miRNA transcripts (pri-miRNAs) are typically located in intergenic or intronic regions. Under the action of Drosha (a member of the RNase III family) and its cofactor Pasha [a double-stranded RNA (dsRNA) binding protein], pri-miRNAs are processed into precursor miRNAs (pre-miRNAs) of approximately 70 nucleotides with a stem-loop structure. Subsequently, RNA-GTP and exportin 5 transport pre-miRNAs to the cytoplasm, where Dicer (another RNase III family member) cleaves them into functional mature miRNAs of about 22 nucleotides. Compared with other non-coding RNAs such as long non-coding RNAs, circular RNAs, and piRNAs, the regulatory mechanism of miRNAs is relatively straightforward. The 2-8 nucleotides at the 5' end of mature miRNAs constitute the "seed sequence," which can bind complementarily to the 3' untranslated region (3' UTR) of target genes, guiding the silencing complex to degrade target mRNAs or repress their translation [7-8]. The generation and regulatory mechanism of miRNAs is illustrated in Figure 1 [Figure 1: see original paper] [9].

The number of identified and confirmed miRNAs in animals continues to grow. The miRBase database (v21.0) has cataloged 1,920 mouse, 430 porcine, and 1,009 chicken mature miRNAs. These numerous miRNAs can function individually or form coordinated regulatory networks. Notably, many miRNA genes are clustered on chromosomes (forming miRNA clusters), often located within a single polycistron and co-expressed to exert synergistic regulatory functions in embryonic development, cell cycle, and cell differentiation [10]. Typically, one miRNA can regulate up to hundreds of target mRNAs, while a single gene may simultaneously be targeted by multiple miRNAs [11]. Through regulation of numerous target genes, miRNAs participate in various life activities, including cell proliferation, differentiation, apoptosis, stress response, intracellular metabolism, and signal transduction [11-12].

2. Expression Patterns of miRNA

miRNA expression exhibits tissue specificity. Babak et al. [13] used microarrays to detect miRNA expression in 17 different mouse tissues and found that at least half of the 78 detected miRNAs showed tissue-specific distribution. Liang et al. [14] examined 345 miRNAs across 40 human organs and, through cluster analysis, categorized them into eight tissue-specific expression groups: muscle, gastrointestinal tract/epithelial cells, brain, brain/peripheral blood mononuclear cells, heart, liver, placenta, and testis. miRNA expression patterns also display temporal specificity. In adult mice [15] and pigs [14], over 100 miRNAs are stably expressed in muscle tissue, with most showing low expression during embryonic and early growth stages that increases significantly with animal growth, while a minority exhibit the opposite trend. Additionally, some miRNAs demonstrate wave-like expression patterns over time [16].

Normal miRNA expression is essential for muscle formation and growth. Dicer is a necessary endonuclease for mature miRNA processing in mammals. Conditional knockout of Dicer in mice results in impaired skeletal muscle development with hypoplasia [17], demonstrating the critical importance of miRNAs for skeletal muscle development. Moreover, muscle-related diseases such as cardiac and skeletal muscle hypertrophy, muscle atrophy, and heart failure are all accompanied by significant abnormal miRNA expression [17-19].

Muscle cells specifically express or highly express certain miRNAs, which are considered muscle-specific miRNAs, such as skeletal muscle-specific miR-1, miR-133, and miR-206, and cardiac muscle-specific miR-208a/b. Most muscle-specific miRNAs can directly or indirectly act on myogenic genes like Myf5 and MyoD, thereby influencing muscle cell proliferation, differentiation, and apoptosis. Additionally, some non-muscle-specific miRNAs in muscle cells have been confirmed to participate in molecular regulatory networks affecting muscle cell growth. These miRNAs either directly target regulators of muscle cell proliferation and differentiation or indirectly participate in muscle cell activities through intracellular signal transduction and transcriptional regulation. Furthermore, normal miRNA expression not only plays important

roles in embryonic muscle cell formation but also significantly impacts muscle repair after injury in adults.

With rapid development of high-throughput sequencing and microarray technologies, increasing numbers of miRNAs involved in muscle growth regulation have been discovered and confirmed. Many miRNAs show not only tissue-specific expression but also distinct differences among different muscle types. Nie [20] used Solexa sequencing to identify 363 miRNAs expressed in both porcine longissimus dorsi and psoas major muscles, with 193 showing significant expression differences, possibly related to muscle fiber type differences. Ma et al. [21] constructed small RNA libraries from porcine red muscle, white muscle, and mixed muscle fibers, revealing differential miRNA expression among different muscle types (Figure 2 [Figure 2: see original paper]). These studies suggest that future research should more rigorously distinguish differential miRNA regulation of muscle fiber types and functions.

3. Regulation of Animal Skeletal Muscle by miRNA and Its Mechanisms

3.1 Muscle-Specific miRNAs

miR-1, miR-133a, and miR-206 are among the most extensively studied muscle-specific miRNAs. They are highly expressed only in animal heart and skeletal muscle, regulating muscle cell proliferation and differentiation and representing key factors in muscle formation. In the mouse genome, miR-1, miR-133, and miR-206 form three gene clusters: miR-1-2 and miR-133a-1 on chromosome 18, miR-1-1 and miR-133a-2 on chromosome 2, and miR-206 and miR-133b on chromosome 1. These can form bicistronic transcripts for simultaneous transcription, though their regulatory functions differ. Additionally, newly discovered miRNAs such as miR-208a/b, miR-486, and miR-499 are also considered muscle-specific.

Chen et al. [22] first reported that miR-1 could target histone deacetylase 4 (HDAC4) to promote muscle growth. In 2010, Chen et al. [23] further demonstrated that miR-1 and miR-206 promote skeletal muscle satellite cell differentiation while significantly inhibiting proliferation. Paired box gene 7 (Pax7), a member of the Pax gene family, can induce pluripotent stem cells to become myogenic cells, with muscle stem cell emergence depending on normal Pax3 and Pax7 expression. Chen et al. [23] confirmed Pax7 as a direct common target of miR-1 and miR-206, which influence muscle cell development by regulating Pax7 expression. Downregulating miR-1 and miR-206 increases Pax7 protein levels and promotes muscle cell proliferation, while their deficiency decreases Pax7 expression and inhibits differentiation. Subsequent studies confirmed the key regulatory roles of miR-1 and miR-206 in C2C12 cell differentiation [24]. Nakajima et al. [25] compared differential regulatory effects of miR-1 on myogenic, osteogenic, and adipogenic differentiation of C2C12 cells, finding that miR-1 overexpression significantly promoted myogenic differentiation and my-

otube formation without affecting osteogenic or adipogenic differentiation under induction conditions, indicating stable directional regulatory functions of muscle-specific miRNAs.

Studies based on knockout mice revealed that individual deletion of miR-133a-1 or miR-133a-2 did not significantly affect muscle growth and development, but combined deletion caused fast muscle fiber lesions accompanied by mitochondrial damage and fiber type switching between fast and slow fibers [26]. This directly reflects the important role of miR-133a in maintaining normal muscle growth and function. However, knockout mice did not show more severe muscle lesions, possibly because many miRNAs share common target genes, allowing functional compensation by other miRNAs when one is dysregulated. In cell studies, miR-133 promoted muscle cell proliferation by targeting serum response factor (SRF) [22] and inhibited skeletal muscle cell differentiation by suppressing neuronal polypyrimidine tract-binding protein (nPTB), altering nPTB-regulated alternative splicing patterns during muscle differentiation [27]. The effect of miR-133b on muscle growth remains unclear, though studies have found downregulated miR-133b expression in myocardium during myocardial infarction [28].

Numerous studies have confirmed the muscle growth-promoting effects of miR-206, which significantly promotes myogenic cell differentiation and myotube fusion in vitro. A series of negative regulators of myogenesis are its targets, including Notch3, Igfbp5, Meox2, retinoic acid receptor β (RARB), Fzd7, MAP4K3, CLCN3, NFAT5, and MMP3 [29]. Most studies suggest miR-206 functions together with miR-1. Additionally, during myogenesis, miR-206 and miR-29 jointly inhibit the transforming growth factor-β (TGF-β) signaling pathway, a negative regulator of muscle cell differentiation [30].

3.2 Non-Muscle-Specific miRNAs

Many non-muscle-specific miRNAs have also demonstrated regulatory effects on muscle growth and development. Although these miRNAs are widely expressed across different tissues, their abnormal expression in muscle tissue or muscle cells can positively or negatively affect muscle growth and development.

Some ubiquitously expressed miRNAs play positive regulatory roles. Overexpression of miR-148a promotes differentiation of C2C12 myoblasts and mouse primary skeletal muscle cells, enhancing myogenesis by degrading Rho-associated coiled-coil containing protein kinase 1 (ROCK1) [31]. Yun et al. [32] found miR-143-3p expression in both skeletal muscle and myoblasts, with overexpression promoting C2C12 differentiation. miR-29 also promotes muscle formation by downregulating serine/threonine protein kinase (Akt3) expression, inhibiting skeletal muscle cell proliferation while promoting differentiation [33]. miR-181 promotes myoblast differentiation by suppressing homeobox-A1 (Hox-A1) expression [34].

Other miRNAs negatively regulate muscle growth and development. Wang et

al. [35] predicted that miR-23a seed sequences could bind fast myosin heavy chain genes (MYH1, 2, and 4). They found miR-23a expression in mouse muscle tissue was highly negatively correlated with muscle growth, and functional studies in C2C12 cells confirmed miR-23a inhibits muscle cell differentiation. However, normal miR-23a expression is also essential for muscle growth. During muscle atrophy, increased expression of MAFbx/atrogin-1, MuRF1, and E3 ligases regulates mucosal atrophy changes. miR-23a can inhibit expression of MAFbx/atrogin-1 and MuRF1, thereby suppressing muscle atrophy [36]. These findings indicate miR-23a plays crucial roles in both muscle growth and injury repair. Seok et al. [37] showed miR-155 targets myogenic factor MEF2A, affecting skeletal muscle cell differentiation. Xiong et al. [38] found miR-155 inhibits C2C12 myoblast differentiation and reduces myotube formation, identifying T cell factor 4 (TCF4) as a miR-155 target gene. TCF4 is a key factor in the canonical Wnt pathway regulating myogenic differentiation, playing important roles in embryonic muscle formation and serving as a critical regulator of terminal muscle cell differentiation and satellite cell orientation.

Additionally, multiple miRNAs including miR-27a/b, miR-31, and miR-489 have demonstrated regulatory effects on myogenic cell activation, myogenic maintenance, and muscle cell proliferation and differentiation.

4. Regulation of Animal Cardiac Muscle by miRNA and Its Mechanisms

Cardiac muscle shares similar structure with skeletal muscle as a type of striated muscle, though cardiac muscle cells typically contain only one nucleus. Various cardiac diseases and functional impairments are associated with abnormal cardiac muscle growth, with aberrant miRNA expression considered an important marker of cardiac disease. miR-208a and miR-208b are considered cardiac muscle-specific miRNAs, with miR-208b expressed exclusively in cardiac tissue. Both miR-208a and miR-208b are closely associated with cardiac fiber formation, myocardial ischemia, cardiac hypertrophy, and heart failure, and can serve as serum markers for clinical diagnosis and treatment of myocardial injury [39-41]. Additionally, miR-1 and miR-133 also significantly impact cardiac muscle growth and development. Overexpression of miR-1 in cardiomyocytes significantly inhibits phenylephrine-induced cardiomyocyte hypertrophy, with further studies suggesting miR-1 may participate in cardiac hypertrophy by negatively regulating twinfilin-1 (TWF1) protein expression [42]. Upregulation or downregulation of miR-1 in mice or Drosophila consistently results in cardiac developmental malformations [43-44]. Ischemic heart disease in rats is accompanied by significantly elevated miR-1 levels in the myocardium [45]. Furthermore, during oxidative stress-induced cardiomyocyte apoptosis, miR-1 promotes apoptosis while miR-133 inhibits it [46]. Current research on miRNAs in heart development and myocardial injury primarily focuses on specific miRNAs, with expression and functions of more non-specific miRNAs awaiting further exploration.

5. Regulation of Animal Smooth Muscle by miRNA and Its Mechanisms

Smooth muscle, also called non-striated muscle, is widely distributed in invertebrate somatic muscle and constitutes the main muscle fiber type in most visceral organs of vertebrates, with distinct fiber types and metabolic characteristics compared to striated muscle (skeletal and cardiac muscle). Research on miRNA regulation of smooth muscle growth remains relatively limited compared to skeletal muscle. Current studies indicate that several miRNAs, including miR-29, miR-145, and miR-143, participate in smooth muscle development, particularly vascular smooth muscle. miR-145 can inhibit embryonic stem cell self-renewal while promoting their directional differentiation. Xu et al. [47] found miR-145 promotes pluripotent stem cell differentiation into vascular smooth muscle cells primarily by inhibiting transcription of pluripotency factors OCT4, SOX2, and KLF4, with OCT4 able to inhibit miRNA promoters, suggesting a potential bidirectional negative feedback mechanism. In miR-29-deficient distal lung vasculature, F-box protein 32 (FBXO32) expression is significantly increased in vascular smooth muscle cells, indicating miR-29 may play important roles in smooth muscle cells by regulating FBXO32 expression [48]. Additionally, miR-124 significantly regulates proliferation and differentiation of pulmonary artery smooth muscle cells [49].

6. miRNA and Livestock Muscle Growth

Current research on miRNAs in meat-producing livestock remains limited, though miRNAs are clearly closely related to animal muscle growth and meat quality traits. Due to their evolutionary conservation and functional stability, miRNA synthesis pathways are identical across different animals, and miRNA target sites are also highly conserved. For example, muscle-specific miR-1 exists in nearly all vertebrates and is closely associated with muscle generation and development, suggesting that mechanistic studies in model animals like mice have certain extrapolative value. However, animal science researchers must conduct more specific studies in livestock and poultry to better guide animal production.

Recent studies have begun examining miRNA expression and function related to muscle in pigs, chickens, and ruminants, though these primarily focus on detecting miRNA expression profiles and identifying key miRNAs affecting meat quality. Research teams led by McDaneld et al. [50], Nielsen et al. [51], and Hou et al. [52] used high-throughput sequencing to detect and analyze miRNA expression in porcine skeletal muscle across different growth stages and tissues, identifying novel miRNAs that provide a foundation for further research. Li [53] compared miRNA expression differences between pig breeds, finding 90% similarity between Lantang and Large White pigs, with 10 significantly differentially expressed miRNAs involved in muscle growth and development. Sequencing studies revealed 517 conserved miRNAs and 2 goat genome-specific

miRNAs in goat muscle tissue, with 306 stably expressed [54]. Han et al. [55] examined expression patterns of seven miRNAs including miR-1, miR-133, and miR-24 in cashmere goat muscle, finding similar expression patterns for miR-1 and miR-133 that were affected by age and sex. These findings collectively indicate significant differences in muscle miRNA expression among animals of different breeds, sexes, and growth stages. Additionally, castration affects muscle miRNA expression, with 32 significantly different miRNAs detected between bull and steer muscle tissues [56]. Nutritional level and specific nutrient intake also influence muscle growth and miRNA expression, including amino acids, unsaturated fatty acids, and chromium picolinate [19,57-58]. These studies in large animals enhance our understanding of meat quality formation mechanisms and enable genetic improvement and nutritional regulation strategies to enhance meat quality.

miRNAs are receiving increasing attention due to their broad involvement in regulating various life activities. As research technologies advance, more miRNAs and their regulatory targets involved in muscle growth and development will be discovered and confirmed. Investigating miRNA expression, function, and targets in muscle tissue, along with their regulatory roles in muscle growth and development, will deepen our understanding of molecular regulatory mechanisms underlying muscle formation. Such research will facilitate development of diagnostic markers and targeted therapeutic drugs for muscle-related diseases, while also enabling genetic improvement and nutritional strategies to enhance animal meat quality.

References

[1] CHARGÉ S B P, RUDNICKI M A. Cellular and molecular regulation of muscle regeneration[J]. Physiological Reviews, 2004, 84(1): 209–238.

[2] WIGMORE P M, STICKLAND N C. Muscle development in large and small pig fetuses[J]. Journal of Anatomy, 1983, 137(2): 235–245.

[3] SABOURIN L A, RUDNICKI M A. The molecular regulation of myogenesis[J]. Clinical Genetics, 2000, 57(1): 16–25.

[4] BASKIN K K, WINDERS B R, OLSON E N. Muscle as a "mediator" of systemic metabolism[J]. Cell Metabolism, 2015, 21(2): 237–248.

[5] RUDNICKI M A, SCHNEGELSBERG P N J, STEAD R H, et al. MyoD or Myf-5 is required for the formation of skeletal muscle[J]. Cell, 1993, 75(7): 1351–1359.

[6] OJIMA K, ICHIMURA E, YASUKAWA Y, et al. Dynamics of myosin replacement in skeletal muscle cells[J]. American Journal of Physiology: Cell Physiology, 2015, doi: 10.1152/ajpcell.00170.2015.

[7] AMBROS V. The functions of animal microRNAs[J]. Nature, 2004, 431(7006): 350–355.

[8] BARTEL P. MicroRNAs: genomics, biogenesis, mechanism, and function[J]. Cell, 2004, 116(2): 281-297.

[9] HUANG Y, ZOU Q, SONG H T, et al. A study of miRNAs targets prediction and experimental validation[J]. Protein & Cell, 2010, 1(11): 979-986.

[10] ZHANG Y F, ZHANG R, SU B. Diversity and evolution of microRNA gene clusters[J]. Science in China Series C: Life Sciences, 2009, 39(1): 114-120.

[11] ZENG Y, YI R, CULLEN B R. MicroRNAs and small interfering RNAs can inhibit mRNA expression by similar mechanisms[J]. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100(17): 9779-9784.

[12] FRIEDMAN R C, FARH K K H, BURGE C B, et al. Most mammalian mRNAs are conserved targets of microRNAs[J]. Genome Research, 2009, 19(1): 92-105.

[13] BABAK T, ZHANG W, MOEEIS Q, et al. Probing microRNAs with microarrays: tissue specificity and functional inference[J]. RNA, 2004, 10(11): 1813-1819.

[14] LIANG Y, RIDZON D, WONG L, et al. Characterization of microRNA expression profiles in normal human tissues[J]. BMC Genomics, 2007, 8: 166.

[15] LAGOS-QUINTANA M, RAUHUT R, YALCIN A, et al. Identification of tissue-specific microRNAs from mouse[J]. Current Biology, 2002, 12(9): 735-739.

[16] HUANG T H, ZHU M J, LI X Y, et al. Discovery of porcine microRNAs and profiling from skeletal muscle tissues during development[J]. PLoS One, 2008, 3(9): e3225.

[17] BERNSTEIN E, KIM S Y, CARMELL M A, et al. Dicer is essential for mouse development[J]. Nature Genetics, 2003, 35(3): 215-217.

[18] ZHU M J, ZHAO S H. miRNA and muscle development[J]. Swine Industry Science, 2007, 24(3): 78-80.

[19] HUANG Z Q, CHEN X L, YU B, et al. Functions of MicroRNA in skeletal muscle development and nutritional regulation of its expression[J]. Chinese Journal of Animal Nutrition, 2011, 23(10): 1647-1650.

[20] NIE J. Differential expression analysis of miRNA in different porcine muscle tissues[D]. Master' s thesis. Ya' an: Sichuan Agricultural University, 2012: 10-37.

[21] MA J D, WANG H M, LIU R, et al. The miRNA transcriptome directly reflects the physiological and biochemical differences between red, white, and intermediate muscle fiber types[J]. International Journal of Molecular Sciences, 2015, 16(5): 9635-9653.

[22] CHEN J F, MANDEL E M, THOMSON J M, et al. The role of microRNA-1 and microRNA-133 in skeletal muscle proliferation and differentiation[J]. Nature

Genetics, 2005, 38(2): 228–233.

[23] CHEN J F, TAO Y Z, LI J, et al. microRNA-1 and microRNA-206 regulate skeletal muscle satellite cell proliferation and differentiation by repressing Pax7[J]. The Journal of Cell Biology, 2010, 190(5): 867–879.

[24] GOLJANEK-WHYSALL K, PAIS H, RATHJEN T, et al. Regulation of multiple target genes by miR-1 and miR-206 is pivotal for C2C12 myoblast differentiation[J]. Journal of Cell Science, 2012, 125(15): 3590–3600.

[25] NAKAJIMA N, TAKAHASHI T, KITAMURA R, et al. MicroRNA-1 facilitates skeletal myogenic differentiation without affecting osteoblastic or adipogenic differentiation[J]. Biochemical and Biophysical Research Communications, 2006, 350(4): 1006–1012.

[26] LIU N, BEZPROZVANNAYA S, WILLIAMS A H, et al. MicroRNA-133a regulates cardiomyocyte proliferation and suppresses smooth muscle gene expression in the heart[J]. Genes & Development, 2008, 22(23): 3242–3254.

[27] BOUTZ P L, CHAWLA G, STOILOV P, et al. MicroRNAs regulate the expression of the alternative splicing factor during muscle development[J]. Genes & Development, 2007, 21(1): 71–84.

[28] BOŠTJANČIČ E, ZIDAR N, ŠTAJER D, et al. MicroRNAs miR-1, miR-133a, miR-133b and miR-208 are dysregulated in human myocardial infarction[J]. Cardiology, 2010, 115(3): 163–169.

[29] KIM H K, LEE Y S, SIVAPRASAD U, et al. Muscle-specific microRNA miR-206 promotes muscle differentiation[J]. The Journal of Cell Biology, 2006, 174(5): 677–687.

[30] WINBANKS C E, WANG B, BEYER C, et al. TGF-β regulates miR-206 and miR-29 to control myogenic differentiation through regulation of HDAC4[J]. Journal of Biological Chemistry, 2011, 286(16): 13805–13814.

[31] ZHANG J, YING Z Z, TANG Z L, et al. MicroRNA-148a promotes myogenic differentiation by targeting the ROCK1 gene[J]. Journal of Biological Chemistry, 2012, 287(25): 21093–21101.

[32] YUN Q, WU G F, WEI H, et al. miR-143-3p promotes C2C12 myoblast differentiation[J]. Chinese Journal of Biochemistry and Molecular Biology, 2013, 29(6): 569–577.

[33] WEI W, HE H B, ZHANG W Y, et al. MiR-29 targets Akt3 to reduce proliferation and facilitate differentiation of myoblasts in skeletal muscle development[J]. Cell Death & Disease, 2013, 4(6): e668.

[34] NAGUIBNEVA I, AMEYAR-ZAZOUA M, POLESSKAYA A, et al. The microRNA miR-181 targets the homeobox protein Hox-A11 during mammalian myoblast differentiation[J]. Nature Cell Biology, 2006, 8(3): 278–284.

[35] WANG L, CHEN X, ZHENG Y Y, et al. MiR-23a inhibits myogenic differentiation through regulating fast myosin heavy chain isoforms[J]. Experimental Cell Research, 2012, 318(18): 2324-2334.

[36] WADA S, KATO Y, OKUTSU M, et al. Translational suppression of atrophic regulators by microRNA-23a integrates resistance to skeletal muscle atrophy[J]. Journal of Biological Chemistry, 2011, 286(44): 38456-38465.

[37] SEOK H Y, TATSUGUCHI M, CALLIS T E, et al. MiR-155 inhibits expression of the MEF2A protein to repress skeletal muscle differentiation[J]. Journal of Biological Chemistry, 2011, 286(41): 35339-35346.

[38] XIONG Y, WANG Y, WEI N, et al. Overexpression of miR-155 inhibits C2C12 myogenic differentiation[J]. Chinese Journal of Biotechnology, 2014, 30(2): 182-193.

[39] CAI B Z, PAN Z W, LU Y J. The roles of microRNAs in heart diseases: a novel important regulator[J]. Current Medicinal Chemistry, 2010, 17(5): 407-411.

[40] OLIVEIRA-CARVALHO V, CARVALHO V O, BOCCHI E A. The emerging role of miR-208a in the heart[J]. DNA and Cell Biology, 2013, 32(1): 8-12.

[41] HE F C, ZHAO X, GAO F, et al. Expression levels and clinical significance of plasma miR-208b and miR-145 in patients with acute coronary syndrome[J]. Journal of Second Military Medical University, 2013, 34(1): 109-111.

[42] SONG X W. Functions and mechanisms of MiR-1 and MiR-199 in cardiac hypertrophy[D]. Master's thesis. Shanghai: Second Military Medical University, 2009: 3-6.

[43] ZHAO Y, SAMAL E, SRIVASTAVA D. Serum response factor regulates a muscle-specific microRNA that targets Hand2 during cardiogenesis[J]. Nature, 2005, 436(7048): 214-220.

[44] KWON C, HAN Z, OLSON E N, et al. MicroRNA1 influences cardiac differentiation in Drosophila and regulates Notch signaling[J]. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102(52): 18986-18991.

[45] XU C Q, LU Y J, PAN Z W, et al. The muscle-specific microRNAs miR-1 and miR-133 produce opposing effects on apoptosis by targeting HSP60, HSP70 and caspase-9 in cardiomyocytes[J]. Journal of Cell Science, 2007, 120(17): 3045-3052.

[46] LUO X B, LIN H X, PAN Z W, et al. Down-regulation of miR-1/miR-133 contributes to re-expression of pacemaker channel genes HCN2 and HCN4 in hypertrophic heart[J]. Journal of Biological Chemistry, 2008, 283(29): 20045-20052.

[47] XU N, PAPAGIANNAKOPOULOS T, PAN G J, et al. MicroRNA-145 regulates OCT4, SOX2, and KLF4 and represses pluripotency in human embryonic cells[J]. Cell, 2009, 137(4): 647–658.

[48] CUSHING L, COSTINEAN S, XU W, et al. Disruption of mir-29 leads to aberrant differentiation of smooth muscle cells selectively associated with distal lung vasculature[J]. PLoS Genetics, 2015, 11(5): e1005238.

[49] KANG K, PENG X, ZHANG X Y, et al. MicroRNA-124 suppresses the transactivation of nuclear factor of activated T cells by targeting multiple genes and inhibits the proliferation of pulmonary artery smooth muscle cells[J]. Journal of Biological Chemistry, 2013, 288(35): 25414–25427.

[50] MCDANELD T G, SMITH T P L, DOUMIT M E, et al. MicroRNA transcriptome profiles during swine skeletal muscle development[J]. BMC Genomics, 2009, 10: 77.

[51] NIELSEN M, HANSEN J H, HEDEGAARD J, et al. MicroRNA identity and abundance in porcine skeletal muscles determined by deep sequencing[J]. Animal Genetics, 2010, 41(2): 159–168.

[52] HOU X H, TANG Z L, LIU H L, et al. Discovery of microRNAs associated with myogenesis by deep sequencing of serial developmental skeletal muscles in pigs[J]. PLoS One, 2012, 7(12): 52123.

[53] LI H Y. Mining of miRNA in porcine pituitary, muscle and adipose tissue and functional analysis of miRNA targeting TNF-α[D]. PhD thesis. Guangzhou: South China Agricultural University, 2012: 1–2.

[54] LING Y H, ZHANG X D, WANG L J, et al. Solexa sequencing and bioinformatics analysis of microRNAs in goat muscle tissue[J]. Journal of Animal Husbandry and Veterinary Medicine, 2013, 44(3): 481–487.

[55] HAN Z L, ZHAO D C, FU S Y, et al. Analysis of miRNA and target gene expression profiles in cashmere goat skeletal muscle[J]. Journal of Animal Husbandry and Veterinary Medicine, 2012, 43(10): 1539–1546.

[56] XIA G J. Combined analysis of miRNA and functional gene transcriptome to screen candidate genes for meat quality traits in Yanbian cattle[D]. PhD thesis. Yanji: Yanbian University, 2014: 3–8.

[57] PAN Y Z, LYU X H, HUANG C X, et al. Study on the effect of chromium picolinate on miRNA expression in broilers[J]. Animal Husbandry and Veterinary Medicine, 2012, 44(Supplement): 117–118.

[58] DRUMMOND M J, GLYNN E L, FRY C S, et al. Essential amino acids increase microRNA-499, -208b, and -23a and downregulate myostatin and myocyte enhancer factor 2C mRNA expression in human skeletal muscle[J]. The Journal of Nutrition, 2009, 139(12): 2279–2284.

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