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Mini Review

Effects of CircRNAs on Sheep Muscle Development

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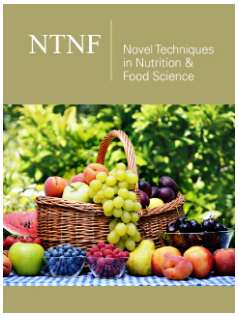

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Abstract

As one of the earliest domesticated mammals, sheep have played a pivotal role in the survival and development of human beings for a long time. In recent years, with the advancement of RNA-Seq technology, the regulation of ovine gene expression by circRNAs at the epigenetic level, transcriptional level, and post-transcriptional level has gradually become a research hotspot.

Keywords: Sheep muscle; CircRNAs; Ovine skeletal muscle; Domesticated mammals

Introduction

A large number of recent studies have shown that circRNAs are closely related to biological growth and development, stress response, disease occurrence and development, etc., and predict their application prospects in disease diagnostic markers [1]. At the same time, numerous reports have confirmed that circRNAs play an important role in proliferation, differentiation, autophagy, apoptosis, and immunity during cell development [2]. However, there are few related studies on the effect of circRNAs on sheep muscle development. This review focuses on the regulatory effects of circRNAs on sheep muscle development, aiming to provide a theoretical basis for related research.

Research Progress

With the development of high-throughput technologies, circRNAs have been found to play important regulatory roles in a variety of biological processes [3]. Studies have shown that circRNAs may have unique and important functions during muscle development in sheep [4]. Yang et al. [3] identified 886 circRNAs from an ovine skeletal muscle RNA library, of which many circRNAs were found to interact with muscle-specific miRNAs involved in muscle growth and development, especially circ776. GO and KEGG enrichment analysis revealed that host genes of circRNAs are involved in muscle cell development and signaling pathways [5]. The longissimus dorsi muscle of sheep fetus was collected at D85, D105 and D135 of Merino sheep embryos to construct a full transcriptome Library of sheep skeletal muscle development stage. 126 circRNAs that may participate in the regulation of RNA expression at the transcriptional level were screened out by RNA-seq sequencing and information analysis. GO analysis showed that circRNAs and their interacting miRNAs and mRNAs have important functions in the growth and development of skeletal muscle. KEGG enrichment analysis indicated that most DE circRNAs were enriched in physiological processes related to the developmental cycle and differentiation of myocytes, mediating the cellular response to the outside world.

In addition, circRNA7527 was predicted to specifically bind to bta-miR-135a, bta-miR-615, chi-mi R-133a-5p and mmu-mir-6240-p5_5, thereby inhibiting the expression of MEF2C and affecting sheep muscle differentiation [6]. Similarly, previous studies showed that circUSP13

sponge miR-29c promoted the differentiation of goat primary myoblasts and inhibited apoptosis by regulating the expression of IGF1[5]. Li [7] found that circ_0000385 possesses multiple binding sites with miR-143, miR-133, and miR-23 related to muscle development in the embryonic and adult Kazakh sheep. In addition, circRNAs are also different in the longissimus dorsi muscle of sheep before and after delivery. Li [8] detected 6113 circRNAs from RNA-seq data. Go and KEGG enrichment analysis showed that these circrnas not only participate in the growth and development of muscle related signaling pathways, but also may regulate the proliferation and differentiation of sheep muscle through circrnas-miRNAs-mRNA networks. CircRNAs can also adjust intramuscular fat content and improve meat quality by regulating the development of animal skeletal muscle [9]. In conclusion, circRNAs play an important regulatory role in sheep muscle development.

Outlook

The discovery of more and more circRNAs has provided new ideas for explaining the molecular regulation mechanism of mammalian reproduction, especially the regulation mechanism of sheep muscle development. Studying the role of circRNAs in sheep muscle development will help to clarify the regulatory mechanism of sheep muscle development and individual growth, provide an important theoretical basis for improving meat yield and quality, and provide valuable resources for circRNAs biology.

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