Transcriptomic regulation of muscle growth in meat-type rabbits

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Abstract. Skeletal muscle development is a key determinant of meat production efficiency in rabbits, yet species-specific transcriptomic data remain limited. This mini-review synthesizes current knowledge on transcriptomic regulation of muscle growth in meat-type rabbits by integrating findings from rabbits and other livestock and model organisms. Central regulatory mechanisms include microRNAs (miRNAs), particularly myomiRs, which orchestrate myoblast proliferation, differentiation, and regeneration through post-transcriptional control and modulation of signaling pathways such as JNK/MAPK and mTOR. The insulin-like growth factor (IGF)/AKT/mTOR axis emerges as a pivotal driver of muscle accretion, with tissue-specific expression of IGF ligands, receptors, and binding proteins playing a more critical role than systemic levels. Advances in multi-omic approaches, including RNA-seq, ATAC-seq, and single-cell transcriptomics, reveal complex regulatory networks involving chromatin accessibility and transcription factor dynamics that govern muscle development across livestock species. In rabbits, genomic selection and genome-wide association studies have identified candidate genes and markers associated with growth and carcass traits, enabling improved breeding strategies. Collectively, these insights provide a framework for linking molecular regulation with phenotypic outcomes and highlight the potential for integrating transcriptomic data into selection programs to enhance meat production in rabbits.

Key Words: skeletal muscle development, rabbits, transcriptomics, microRNAs, IGF signaling, mTOR pathway, myogenesis, genomic selection, chromatin accessibility, livestock genetics.

Introduction. Skeletal muscle development is central to meat production efficiency in rabbits (Bud et al., 2011; Botha et al., 2013; Petrescu-Mag et al., 2014). Although direct rabbit transcriptomic data are limited, research in rabbits, pigs, cattle, poultry, fish and model systems outlines key regulatory layers: miRNAs controlling myogenesis, IGF/IGFBP signaling, and genomic selection for growth and carcass traits.

The aim of this mini-review is to synthesize current knowledge on the transcriptomic mechanisms regulating skeletal muscle growth in meat-type rabbits, with particular emphasis on miRNA-mediated control, IGF signaling pathways, and insights derived from multi-omic studies in livestock. Additionally, the review seeks to contextualize rabbit-specific genetic and genomic findings within broader comparative frameworks, in order to identify key regulatory networks and potential molecular targets that can be leveraged in breeding programs to improve growth performance, carcass traits, and meat quality.

miRNAs Involved in Myogenesis. Muscle-enriched miRNAs ("myomiRs" such as miR 1, miR 133, miR 206) are integral to coordinated phases of myoblast proliferation, differentiation and regeneration, acting through post transcriptional repression of target genes and modulation of major signaling pathways (Horák et al., 2016; Xu et al., 2020; Wang et al., 2018; Xie et al., 2018). Some miRNAs are upregulated in differentiated muscle and promote differentiation (e.g. miR 1, miR 24, miR 26a, miR 181, miR 206), whereas others are enriched in proliferating myoblasts and inhibit differentiation (miR 221, miR 222), or can promote both proliferation and differentiation (miR 214) (Wang et al., 2018). Myogenesis associated miRNAs collectively inhibit the JNK/MAPK cascade by targeting multiple upstream kinases, relieving repression of MyoD and reinforcing a double negative feedback loop that stabilizes the differentiated state (Xie et al., 2018). Additional miRNAs, such as miR 100 5p, regulate the balance between proliferation and differentiation via targets like Trib2 and downstream mTOR/S6K signaling, linking miRNA control directly to growth pathways relevant for muscle mass accretion (Wang et al., 2023; Cenan & Perșa 2026) (Table 1, Figure 1).

Table 1

Representative miRNA functions and pathways in myogenesis

miRNA / group	*Main functional effect in myogenesis*	*Key signaling / targets (examples)*	*References*
MyomiRs (miR-1/133/206 etc.)	Coordinate proliferation, differentiation, regeneration	Multiple myogenic TFs and structural genes	(Horák et al., 2016; Wang et al., 2018; Xie et al., 2018)
mamiRs inhibiting JNK/MAPK	Promote differentiation via JNK/MAPK repression	MEKK1, MEKK2, MKK7, c-Jun	(Xie et al., 2018)
miR-100-5p	Promotes proliferation, inhibits differentiation	Trib2, mTOR/S6K pathway	(Wang et al., 2023; Xu et al., 2020).

IGF Pathway and Transcriptomic Control of Muscle Growth. The IGF/AKT/mTOR axis is a central positive regulator of skeletal muscle mass. IGF regulated signaling and its integration with miRNAs and other pathways (e.g. TGF β, MAPK) are repeatedly identified as critical for myogenic programs (Xu et al., 2020). Developmental studies in poultry and fish show that local, tissue specific expression of IGF ligands, receptors and IGF binding proteins (IGFBPs) is more informative for muscle growth than circulating IGF levels, with dynamic shifts in IGF1/IGF2 and IGFBP transcripts across embryonic and early post hatch or post feeding stages (Chen et al., 2026; Vaccaro et al., 2024; Bower & Johnston, 2010). In ducks and broilers, coordinated expression of IGF1/IGF2, IGF1R, IGFBPs and myogenic regulators (MYOD1, MYF5, PAX7, MYF6) defines the transition from hyperplasia to hypertrophy and underscores the importance of local IGF signaling for muscle fiber hypertrophy relevant to meat yield (Chen et al., 2026; Vaccaro et al., 2024). In vitro, IGF1 and amino acids act synergistically to upregulate IGF1 and specific IGFBPs via positive feedback, demonstrating nutrient sensitive transcriptional regulation of the IGF axis during myotube maturation (Bower & Johnston, 2010). Experimental activation of IGF1 transcription using CRISPR based gene activation in human and mouse myoblasts increases multiple IGF1 isoforms, enhances AKT phosphorylation, promotes myotube differentiation and protects against atrophy, illustrating how IGF1 transcript regulation can be leveraged to enhance muscle growth (Roberston et al., 2020). Across livestock, mTOR signaling emerges as a common node integrating IGF input and miRNA control; miRNA mediated modulation of mTOR/S6K, as shown for miR 100 5p, mechanistically links transcriptomic regulation to muscle accretion (Xu et al., 2020; Wang et al., 2023).

Muscle Transcriptomics and Chromatin Accessibility in Livestock (Relevance to Rabbits). Multi omic studies in pigs and cattle show that skeletal muscle development is governed by complex, stage- and breed-specific transcriptional programs, controlled by chromatin accessibility and transcription factor networks (Cai et al., 2023; Miao et al., 2021; Wang et al., 2022; Xu et al., 2023; Feng et al., 2023). Single cell RNA seq and ATAC seq in bovine and porcine muscles identify distinct myogenic subpopulations, temporal gene expression clusters and accessible regulatory elements enriched for motifs of key myogenic transcription factors, including MYF5, MYOD1, MYOG, MEF2 family members and others (Cai et al., 2023; Miao et al., 2021; Wang et al., 2022; Feng et al., 2023). Integration of RNA seq and ATAC seq reveals hundreds of hub genes and muscle specific open chromatin regions associated with muscle structure development, cell differentiation and signaling pathways (WNT, IGF, mTOR, MAPK, BMP, MSTN, TGFB, VEGF, FGF), many of which influence fiber type, growth rate and intramuscular fat relevant to meat quality (Cai et al., 2023; Miao et al., 2021; Wang et al., 2022; Feng et al., 2023). Breed comparisons (e.g. obese vs. lean pigs) link differences in chromatin accessibility and transcription factor binding to divergent muscle fiber size and metabolic characteristics, implicating specific candidate genes whose differential regulation may underlie meat quality differences (Miao et al., 2021; Feng et al., 2023). Single cell atlases in pigs further demonstrate that artificial selection reshapes muscle resident cell composition and transcriptional states, particularly in fibro adipogenic progenitors, which act as interaction hubs and influence myogenic outcomes and muscle phenotype under selection for production traits (Xu et al., 2023).

Genomic Selection and Candidate Genes for Meat Rabbit Growth and Carcass Traits. In rabbits, genetic studies show substantial variation in growth, carcass composition and meat quality, and demonstrate that selection on growth traits is effective but can alter adult weight, carcass yield and intramuscular fat (Blasco et al., 2018; Estany et al., 1992). Classical selection experiments for post weaning to slaughter weight gain achieved annual realized responses of roughly 2–3% of the initial mean, though correlated responses included increased adult size and variable effects on carcass yield and sensory traits (Blasco et al., 2018; Estany et al., 1992). Candidate gene reviews in rabbits identify numerous growth, carcass and meat quality genes and mutations that can be incorporated into marker assisted selection schemes to accelerate improvement, provided they explain meaningful fractions of additive variance (Helal et al., 2021). More recently, genome wide approaches in meat rabbits have used low coverage whole genome sequencing and SNP based genomic selection models to optimize marker density and prediction accuracy for growth and slaughter traits; multi trait GBLUP models using around 50k markers improve prediction accuracy compared with single trait models by exploiting genetic correlations among traits (Li et al., 2024). Genome wide association studies in crossbred meat rabbits increasingly identify SNPs and candidate genes linked to body weight and other economic traits and characterize runs of homozygosity (ROH) patterns, offering molecular markers for assisted selection and tools to manage inbreeding in breeding programs (Xiao et al., 2024). Together with the broader livestock transcriptomic literature, these genetic and genomic tools in rabbits provide a framework to connect selection decisions with underlying regulatory networks controlling myogenesis, IGF signaling and muscle phenotype, even where rabbit specific transcriptomic maps are still emerging.

Conclusions. Transcriptomic regulation of skeletal muscle growth in meat-type rabbits is governed by a complex interplay of post-transcriptional, transcriptional, and epigenetic mechanisms. miRNAs, especially myomiRs, play a central role in fine-tuning myogenesis by coordinating proliferation and differentiation through key signaling pathways such as JNK/MAPK and mTOR. The IGF/AKT/mTOR axis represents a critical integrative hub linking nutrient availability, hormonal signaling, and gene expression to muscle hypertrophy and overall growth.

Although rabbit-specific transcriptomic datasets are still emerging, substantial insights can be extrapolated from studies in other livestock species, where multi-omic approaches have elucidated the importance of chromatin accessibility, transcription factor networks, and cell-type heterogeneity in muscle development. These findings underscore the relevance of regulatory elements and epigenomic landscapes in shaping phenotypic variation.

From an applied perspective, advances in genomic selection, SNP-based analyses, and identification of candidate genes offer promising tools for improving economically important traits in meat rabbits. The integration of transcriptomic data with genomic selection frameworks represents a key future direction, enabling more precise and biologically informed breeding strategies.

Overall, bridging the gap between molecular regulation and phenotypic outcomes will be essential for optimizing muscle growth and meat quality in rabbits, particularly through the incorporation of high-resolution transcriptomic and multi-omic data into selection programs.

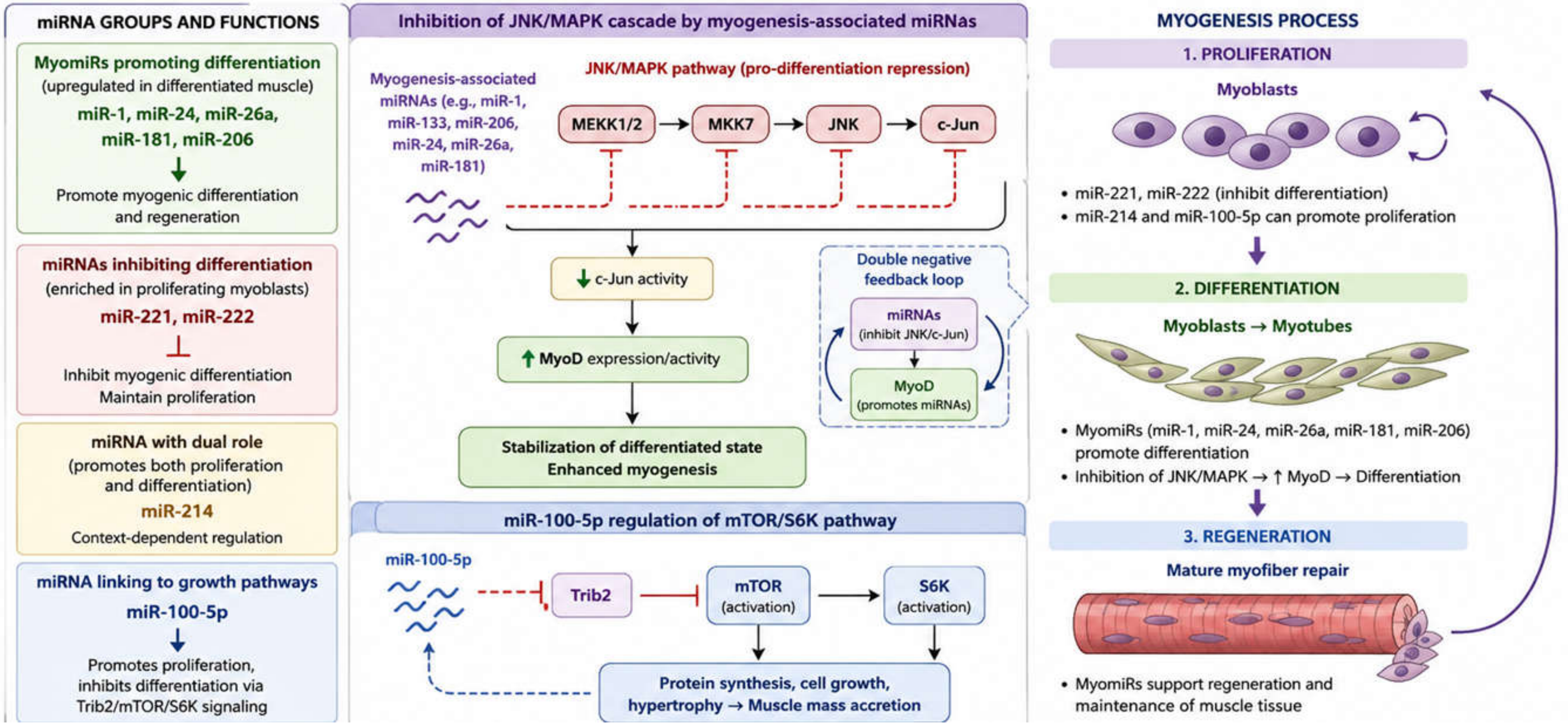

Figure 1. miRNAs in myogenesis: post-transcriptional regulation and signaling pathways.

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