104 (2025) 105542

Contents lists available at ScienceDirect

Poultry Science

journal homepage: www.elsevier.com/locate/psj

Review

Decoding chicken growth regulation through multi-omics insights and emerging genetic tools for growth optimization

Ali Hassan Nawaz[a], Jiqiang Ding[a], Munwar Ali[b], Dong Leng[a], Nasir Mukhtar[c], Ahtisham Ali[d], Chungang Feng[a,*]

[a] College of Animal Science and Technology, Nanjing Agricultural University, Nanjing 210095, China
[b] College of Veterinary Medicine, Nanjing Agricultural University, Nanjing 210095, China
[c] Department of Livestock Production and Management, Faculty of Veterinary and Animal Sciences, PMAS- Arid Agriculture University, Rawalpindi, Pakistan
[d] Department of Food Science, Auckland University of Technology, Auckland 1142, New Zealand

ARTICLE INFO

Keywords:
Chicken growth
GWAS
Genome editing
scRNA-seq
ChickenGTEx

ABSTRACT

Body weight and growth are crucial traits in chickens, regulated by an intricate genetic architecture that remains challenging to understand completely. Multiple quantitative trait loci (QTL) mapping and genome-wide association studies (GWAS) have revealed numerous genetic variations associated with these economically important traits, but the application of these findings for sustainable and efficient poultry production is limited. This review synthesizes existing knowledge on the genetic regulation of chicken growth, challenging the traditional approach and encouraging the development of integrated strategies to comprehend the regulatory mechanisms underlying complex growth phenotypes. This review highlights recent advances in omics studies (genomics, transcriptomics, proteomics, and metabolomics), emphasising the utility of single-cell RNA sequencing (scRNA-seq) in addressing cellular heterogeneity within growth-related tissues. The advancement of genome sequencing technologies, combined with progress in CRISPR/Cas9-mediated genome editing, has opened new avenues for the precision breeding of economically important traits in chickens. It also discusses how the newly developed Chicken Genotype-Tissue Expression (ChickenGTEx) project and other related data resources could potentially serve as crucial tools to reveal the regulatory mechanisms related to chicken growth, offering insights into tissue specific gene expression. By elucidating regulatory networks and identifying key knowledge gaps, this review intends to accelerate the development of precision breeding approaches for sustainable and efficient poultry production, ultimately enhancing global food security.

Introduction

As the population in the developing world continues to grow, the demand for affordable protein sources, including chicken meat, is on the rise. This increasing global demand for chicken meat necessitates advancements in chicken growth efficiency and meat quality traits, which are influenced by a complex interplay of environmental, epigenetic and genetic factors (Morris et al., 2024; Lu et al., 2024). Despite extensive quantitative trait loci (QTL) mapping and genome-wide association studies, the application of identified genetic variants associated with growth-related traits for achieving consistent improvements in commercial breeding programs still poses significant challenges (Tu et al., 2025). The primary factors contributing to this translational gap include the relatively modest effect sizes of individual QTLs, diverse population-specific genetic architectures influenced by natural and artificial selection, prevalent pleiotropy, epistasis, and limited functional studies on candidate genes. All of these mentioned factors, highlight the inherent complexity of chicken growth genetics (Ou et al., 2024; Li et al., 2025a).

Numerous genomics studies have identified this complex genetic architecture underlying growth-related traits in chickens. Studies show that most QTLs have small individual effects, contributing modestly to phenotypic variance but their cumulative influence become significant (Ou et al., 2024). The identification of specific genes within these QTL regions along with their functional roles in crucial biological pathways can provide a comprehensive view of the exact mechanisms influencing

Section: Genetics and Genomics
* Corresponding author.
E-mail addresses: ah93163@gmail.com (A.H. Nawaz), fengchungang@njau.edu.cn (C. Feng).

https://doi.org/10.1016/j.psj.2025.105542
Received 21 April 2025; Accepted 5 July 2025
Available online 5 July 2025
0032-5791/

chicken growth (Wang et al., 2020). While conventional approaches have identified certain chromosomal regions, genes, and pathways. A more comprehensive framework by integrating multi-omics technology is now essential to accurately explain the complexities of chicken development. Currently, rapid progress in sequencing technologies has advanced the transcriptomics and genomics research (Gheyas and Burt, 2013; Urgessa and Woldesemayat, 2023). On the other hand, mass-spectrometry-based proteomics technologies are regarded as cutting-edge innovations, offering unique insights into the content, structure, function, and regulation of the proteome, therefore elucidating intricate biological processes and phenotypes. Advancements in these technologies and bioinformatics use for the collection and analysis of extensive biological datasets have significantly enhanced our ability to comprehend the complex genetic mechanisms underpinning sophisticated polygenic traits such as body size and growth in chickens (Li et al., 2024; Di Luca et al., 2024). The synthesis of existing research regarding the regulatory mechanisms of chicken growth leads to an overarching question: how can we better interpret and utilize this complex genetic architecture of chicken growth to improve broiler production to ensure global food security?

The aim of this review is:1) to synthesize current research regarding the genetics of growth related traits in chickens from genomics to metabolomics. 2) To encourage multi-omics studies by merging genomic data with transcriptomics, metabolomics, and proteomics insights as this integrative approach will unveil the complex growth regulatory networks by highlighting every gene, protein and metabolite involved in growth regulation. 3) To explore, how recent genetic advancements such as single-cell RNA sequencing (scRNA-seq), are enhancing our understanding of cellular heterogeneity and regulatory dynamics in growth-related tissues (Li et al., 2025c). 4) To highlight the potential of public databases such as ChickenGTEx to accelerate chicken genetics research (Guan et al., 2025). Moreover, it also discusses the milestones regarding avian genome editing technology. Genome editing has tremendous significance in poultry production as it allows researchers to introduce desired genetic mutations by targeting certain genomic regions (such as *MSTN* and *IGF*). Genome editing technology is crucial for the application of omics findings into poultry breeding programs (Khwatenge and Nahashon, 2021). Therefore, a strategy that combines extensive integrative omics studies with the refinement of genome editing technology is essential for sustainable poultry production. Overall, this manuscript intends to accelerate the advancement of precision breeding techniques for sustainable and efficient chicken production by elucidating regulatory networks, evaluating tissue-specific expression patterns, and integrating multi-omics data.

Search strategy and selection criteria

We searched the online databases including Google Scholar, Science Direct, PubMed and Scopus for literature associated with chicken growth genomics and emerging genetic tools being employed in chicken research by using the search string: ("Chicken growth and genomics, QTLs, candidate genes"), ("Body weight traits in chickens"), ("Genetic architecture"), ("Genome-wide association studies and chicken growth"), ("Multi-omics in chicken and growth traits"), ("Chicken metabolomics and growth traits"), ("Single cell RNA sequencing and chicken growth"), ("Tissue specific gene expression in chicken specially Liver, skeletal muscle and hypothalamus"), ("Gene expression and pathways regulating chicken growth"), ("CRISPR/Cas9 genome editing in chickens"), ("ChickenGTEx project and atlas of regulatory variants"). These search terms yielded numerous review and research articles, which were subjected to intensive selection criteria by choosing only high quality and high impact research and review articles recently published in well-reputed and renowned SCI journals. We employed a rigorous search strategy across previously mentioned databases and then filtered high quality studies focusing on chicken growth genomics, multi-omics and emerging genetic tools as illustrated in Fig. 1.

Genomics approaches to understand chicken growth

Progress in sequencing technologies, especially whole-genome sequencing (WGS) and next-generation sequencing (NGS), has improved the accuracy and coverage for Quantitative Trait Loci (QTL) detection. Unlike microarrays that can only study specific genomic regions targeted by specific probes with limited coverage, thereby missing crucial regions (Liu et al., 2023; Tan et al., 2024; Ou et al., 2024).

For example, a recent whole-genome resequencing study on 209 chickens identified over 19 million single nucleotide polymorphisms (SNPs) and 1.98 million insertion-deletions (InDels) by covering 97.6 % of the chicken genome with a mapping rate of over 99 % (Tan et al., 2024). In contrast, pre-designed microarray probes have limited coverage and focus only on genomic regions in macrochromosomes, ignoring those in microchromosomes. While the latest sequencing technologies cover almost the whole genome with a higher density of SNPs and QTL regions, rarely missing crucial genomic areas (Ahsan

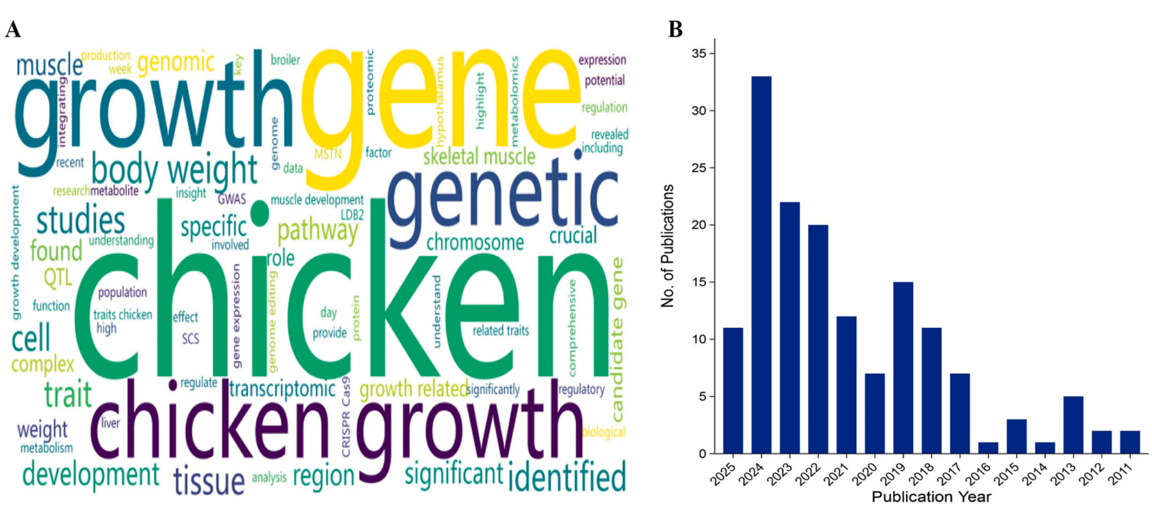

Fig. 1. Word cloud is used to visualize key terms in reviewed articles and trends of publications reviewed in this study. (A) Word cloud visualizes the key terms that are frequently used, such as "chicken", "growth", "gene", "genetic", "SCS", and "transcriptomic", reflecting the core idea of this review. (B) The graph highlights the distribution of reviewed studies based on the published year and most of the studies included are from January 2018 to April 2025. The highest number of studies published in 2024 shows an increasing trend of research activities regarding chicken growth and genetics in recent years.

et al., 2013; Smith et al., 2022). These rapid advancements in genome sequencing technologies have laid a solid foundation for GWAS and selection sweep studies to identify genetic variants associated with growth-related traits.

Genome-wide association studies, selection signature and QTL mapping

Genome-wide association studies (GWAS) help to identify genetic markers associated with growth, thereby improving genomic selection technology (Dou et al., 2022). In addition to GWAS, selection sweep studies using the fixation index (F_{ST}), nucleotide diversity (Pi), and other homozygosity approaches can detect genomic areas under selection (Bello et al., 2023). Selection sweep analysis effectively identifies candidate genes associated with traits such as body weight, growth, and heat tolerance (Nawaz et al., 2024; Wang et al., 2024b; Wu et al., 2024). Integrating findings from GWAS and selection sweep studies with functional studies provides valuable insights for marker-assisted selection and genomic prediction models in chicken growth.

A recent selection sweep study in Chinese indigenous chickens. Identified candidate divergent regions (CDRs) by suggesting strong candidate genes (*NELL1, XYLT1,* and *NCAPG/LCORL*) under selection for body weight trait (Wang et al., 2023). Similarly, another combined selection signature and GWAS study identified key genes (*DGKH, FOXO1, KPNA3,* and *CAB39L*) differing between high and low weight chickens. Furthermore, functional studies on these genes have suggested that they play a crucial role as regulators of muscle growth (Wang et al., 2020a). Likewise, another study found selection signatures linked to production traits in broilers, highlighting genes (*ACTC1, MYO* family, and *VCL*) involved in muscle development (Almeida et al., 2019).

These convergent results from several chicken populations imply that studies on selection signatures successfully find evolutionarily conserved genes connected to the regulation of muscle development and growth, therefore offering useful targets for marker-assisted selection initiatives meant to improve broiler production efficiency. These studies are prime example that how selection sweep analysis can provide crucial information about the genomic regions underwent intense selection pressure and subsequently help us to identify candidate genes associated to certain traits.

Shifting from genome-wide studies to QTL mapping, body weight and growth in chickens are complex polygenic traits controlled by several quantitative trait loci (QTLs) distributed across the genome. The chicken QTL database encompasses almost the whole genome, comprising 28,444 QTLs/associations for 245 different traits. Out of these 28,444 QTLs/associations, 9,863 are related to body weight while average daily gain has 354 and breast muscle weight has 163 known QTLs . Upon analyzing data from the Chicken QTL database (https://www.animalgenome.org/cgi-bin/QTLdb/GG/index), it was found that QTLs/associations are significantly prevalent on chromosomes 1, 4, and 27 for body weight-related traits, as shown in Fig. 2.

We reviewed studies focusing on these QTL-rich regions to identify functional candidate genes. A recent study detected 470 SNPs linked to 43 growth traits on chromosomes 1-6, 9, 10, 16, 18, 23, and 27. While, SNPs on chromosomes 1, 4, and 27 showed pleiotropy, affecting multiple traits (Zhang et al., 2021b). Further supporting these findings, additional studies have shown that the genetic determinants of body weight are influenced by various factors across multiple chromosomes. Collectively, these chromosomal hotspots serve as a roadmap for identifying specific candidate genes that underlie growth-related traits across diverse chicken populations, thereby bridging genomic associations with functional biological mechanisms.

Genomic regions and candidate genes related to body weight and growth

Beyond quantitative trait loci mapping, several population genomics studies have identified specific candidate genes strongly associated with growth and body weight regulation across diverse chicken breeds. For

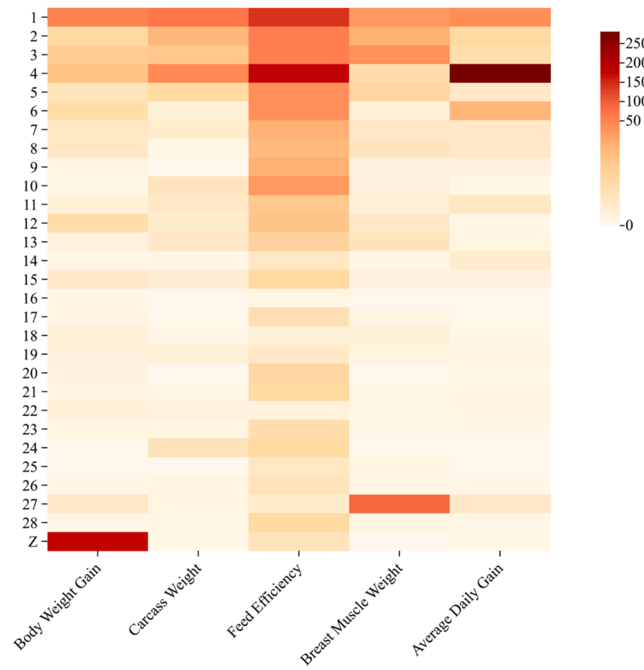

Fig. 2. Heat map representing the distribution of growth and production traits related to QTLs in different chromosomes. The x-axis denotes five traits, including Body Weight Gain, Carcass Weight, Feed Efficiency, Breast Muscle Weight, and Average Daily Gain and the y-axis represents chicken chromosomes (1–28 and Z). Color intensity indicates the number of QTLs on each chromosome for the respective trait, with darker red color showing dense QTL regions. From this heat map, it is visible that chromosomes 1, 4, 27 and Z host a significant number of QTLs, which signifies the role of these chromosomes in growth and production-related traits.

example, a study revealed a significant 1.5 Mb region (173.5–175 Mb) on chromosome 1, with five SNPs in the *KPNA3-FOXO1A* region, has the most pronounced effects on growth traits (Xie et al., 2012). The study also revealed presence of *gga-miR-15a* and *gga-miR-16-1* in 1.5 Mb *KPNA3-FOXO1A* region that could bind to mRNA of *IGF1, FOXO1A*, and *KPNA3* and might have regulatory role in chicken growth. It was further validated that the 1.5 Mb region at chromosome 1 had the strongest effects on chicken growth during 22-42 d (Xie et al., 2012).

Another study investigated 27 chicken tissues and found some genetic variants on chromosome 1 regulating overall growth. Additionally, it identified several candidate genes including *FOXO1, SPERT, CAB39L, POSTN, NCAPG* and *IGF2BP1*. Various functional studies have shown that candidate genes identified in this study are mainly linked to chicken muscle, visceral, and bone weight, potentially regulating the growth and development of chickens (Guo et al., 2017; Moreira et al., 2019; Li et al., 2021; Zhong et al., 2024). Out of all these genes, *IGF2BP1* is significantly associated with body, head, gizzard, leg, and wing weight in chickens (Tan et al., 2021; Wang et al., 2021). A previous study also suggested that *IGF2BP1* is crucial for cell proliferation, differentiation and metabolism, hence confirming *IGF2BP1* as strong candidate gene associated with chicken growth (Luo et al., 2024). Likewise, a study on the chicken pan-genome found that deletion of the *IGF2BP1* promoter region led to a significant increase in the chicken muscle growth (Wang et al., 2021).

In addition, another study has reported a genomic region at chromosome 1 (170.46-171.53 Mb), associated with body weight from 4 to 18 weeks and body size traits (Wang et al., 2024b). Furthermore, the annotation of this genomic region suggested the *CAB39L* and *WDFY2* as strong candidate genes might be involved in growth. Functional Studies have reported that *WDFY2* is an endosomal protein involved in the *PI-3K/AKT* signaling pathway. As *PI-3K/AKT* pathway is mainly involved in skeletal muscle growth and proliferation, which suggests

WDFY2 could be a potential candidate gene for growth and body weight regulation (Monti et al., 2019; Wang et al., 2022a). Another study identified QTL at the distal end of chromosome 1, having 14.4 % of the genetic variance related to growth in chickens. Further, this study fine mapped the locus using genome sequencing, narrowed the QTL region down to 1.2 Mb, and identified multiple regulatory mutations and one of these mutations was found to influence *CAB39L* expression, which is involved in energy balance and nutrient metabolism (Wang et al., 2020a). These studies highlight that fine mapping of candidate QTL regions can provide more precise idea about specific genes related to certain traits like in this case *CAB39L* and *LDB2* were observed to be associated with chicken growth traits. Although chromosome 1 has multiple significant regions affecting growth traits, studies have also shown chromosome 4 to be another important genomic site for growth-regulating genes significantly controlling body weight and muscle growth.

Multiple studies have confirmed the presence of key regulatory genes on chromosome 4, significantly influencing body weight, skeletal muscle development, and overall body size. Recent study by refining certain chromosomal locations identified a region of 7.41–7.64 Mb on chromosome 4 harboring *LCORL, LDB2*, and *PPARGC1A* genes, found to be highly associated with body weight and body size (Wang et al., 2024b). Similarly, another study identified a correlation between the *LDB2* gene and body weight at 7 to 12 weeks, as well as average daily gain during the 6 to 12-week period (Gu et al., 2011). Functional studies have shown these genes (*LCORL, LDB2*, and *PPARGC1A*) to be associated with the mitochondrial system, further influencing chicken skeletal muscle mass (Ma et al., 2022). A recent weighted single-step genome-wide association study (wssGWAS) identified multiple candidate regions and 14 candidate genes associated with body weight, explaining up to 19.05 % of the genetic variance in the body weight trait. Out of those 14 genes, *LDB2* is considered a high confidence candidate gene due to its strong functional role, as mentioned in published literature (Zhu et al., 2025b). Thus, consistent reporting of *LDB2* gene in multiple studies suggest that this specific genomic region on chromosome 4 is crucial for chicken growth.

In another study, a genomic region on chromosome 4 (17.3–21.3 Mb) was found to be strongly associated with keel bone length and body weight by harboring potential candidate genes including *myotubularin 1 (MTM1)* and *secreted frizzled-related protein 2 (SFRP2)*, which are mainly involved in muscle and bone growth (Lin et al., 2007; Lyu et al., 2023). However, functional validation of these genes is needed for further confirmation. Similarly, a GWAS study on Korean native chickens identified significant SNPs near genes such as *LCORL* (associated with body size and growth)*, LAP3* (involved in protein metabolism), and *LDB2* (transcriptional regulator involved in development), all of which have been previously implicated in growth and development regulation (Cha et al., 2021). One of the recent studies performing QTL mapping and selection sweep identified 16 loci for growth traits in chickens, highlighting *TRAK1, OSBPL8, YEATS4, CEP55, and PIP4K2B* as strong candidate genes, with a significant trans-regulatory hotspot (a genomic region where variation affects the expression of multiple genes) coinciding with a major growth locus (Johnsson et al., 2018). Functional studies on these candidate genes have revealed that these genes are mostly involved in processes including mitochondrial dynamics (*TRAK1*), lipid metabolism (*OSBPL8*), cell proliferation (*PIP4K2B, YEATS4*), and embryonic development (*CEP55*) (Zhou et al., 2011; Ogawa et al., 2014; Jeffery et al., 2015; Johnsson et al., 2018).

These studies, which identify both specific genes and broad chromosomal regions, enhance our understanding of the genetic architecture of body weight and growth across many chicken populations. Furthermore, identifying population-specific genetic elements highlights the distinct adaptations of indigenous chicken breeds to local conditions and selective pressures. Overall, the findings provide insights into the genetic basis of body weight variation and offer potential targets for genomic selection strategies to improve meat production in various chicken populations.

Although genomic research identifies genetic variations and candidate genes, understanding their tissue-specific expression is crucial for elucidating their functional roles and regulatory mechanisms.

Tissue-specific expression in chicken growth regulation

Regulating chicken development involves complex interactions across many organs, including the hypothalamus, skeletal muscle, and liver, each exhibiting distinct gene expression patterns that influence growth and development.

Through complex gene networks, the hypothalamus in chickens is a major regulatory region that significantly influences growth, metabolism, and energy balance. The hypothalamus controls the production of growth hormone (GH) through growth hormone-releasing hormone (GHRH) and somatostatin, via the somatotropic axis, directly affecting body composition, fat utilization, and development. The somatotropic axis is comprised of growth hormone (GH), insulin-like growth factors (IGFs), and associated regulatory molecules that work together to regulate growth, metabolism, and development (Piórkowska et al., 2018; Saneyasu, 2024). Hypothalamic gene expression is also responsible for the physiological requirements of chicken growth by regulating genes such as *POMC* and *GHRH* during early developmental stages (Fig. 3). Through its regulatory function, the hypothalamus guarantees metabolic homeostasis and coordinated development required to achieve ideal growth rates in fast-growing chickens (Piórkowska et al., 2018; Mo et al., 2022).

Furthermore, in chicken, the hypothalamus gene expression related to growth and body size mostly includes genes like *POMC, NPY* and *AgRP*, which are main regulators of appetite and energy balance. Increased mRNA expression levels of these genes lead to higher growth rates and larger body size in chickens Wang et al., 2017. *NPY* and *AgRP* both function to increase feed intake by producing anabolic effects. Whereas, *POMC* act as anorexigenic by decreasing feed intake and inducing a catabolic state. This suggests that a certain harmony between the activities of *AgRP* and *POMC* helps drive the homeostatic response to replenish depleted energy in chickens (Mishra et al., 2020; De Solis et al., 2024). This delicate synchronization between anabolic and catabolic genes is intelligently regulated by the hypothalamus, which highlights that understanding the role of the hypothalamus is crucial to gaining insights into the chicken's growth regulatory mechanisms.

Since the liver regulates metabolic and endocrine activities, hepatic gene expression is vital for the growth and development of chickens. The liver produces insulin-like growth factor 1 *(IGF-1)* in response to growth hormone (*GH*); hepatic *IGF-1* mRNA levels in chickens correlate significantly with body weight and growth rates (Vaccaro et al., 2022; Chen et al., 2022). The (*GHR/IGF-1/IGF-1R*) pathway of the somatotropic axis is essential for muscle growth and body size. Numerous studies have reported that *GH* and *IGF-1* act as the primary regulators of physiological development, since both hormones participate in glucose, protein, and lipid metabolism. The mRNA expression levels of somatotropic genes (*GHR, IGF-1,* and *IGF-1R*) may influence growth rate and weight gain in chickens by modulating growth hormones. A deletion mutation in *the GHR* gene causes dwarfism in some chicken breeds, indicating the role of *GHR* and the somatotropic axis in determining chicken body size and growth. Moreover, studies have reported higher mRNA expression of *IGF* in commercial broiler chickens having higher body weight and faster growth rates (Chen et al., 2009; Vaccaro et al., 2022).

Additionally, some studies have also reported the involvement of liver in fat metabolism and meat quality. A study reported that genes associated with lipid metabolism, such as *SREBF1* and *CPT1A*, are dynamically expressed in the liver and contribute to the regulation of energy intake and fat deposition throughout different developmental stages (Desert et al., 2018). These are some major genes and pathways crucial to chicken growth while some other genes have been summarized in Table 1.

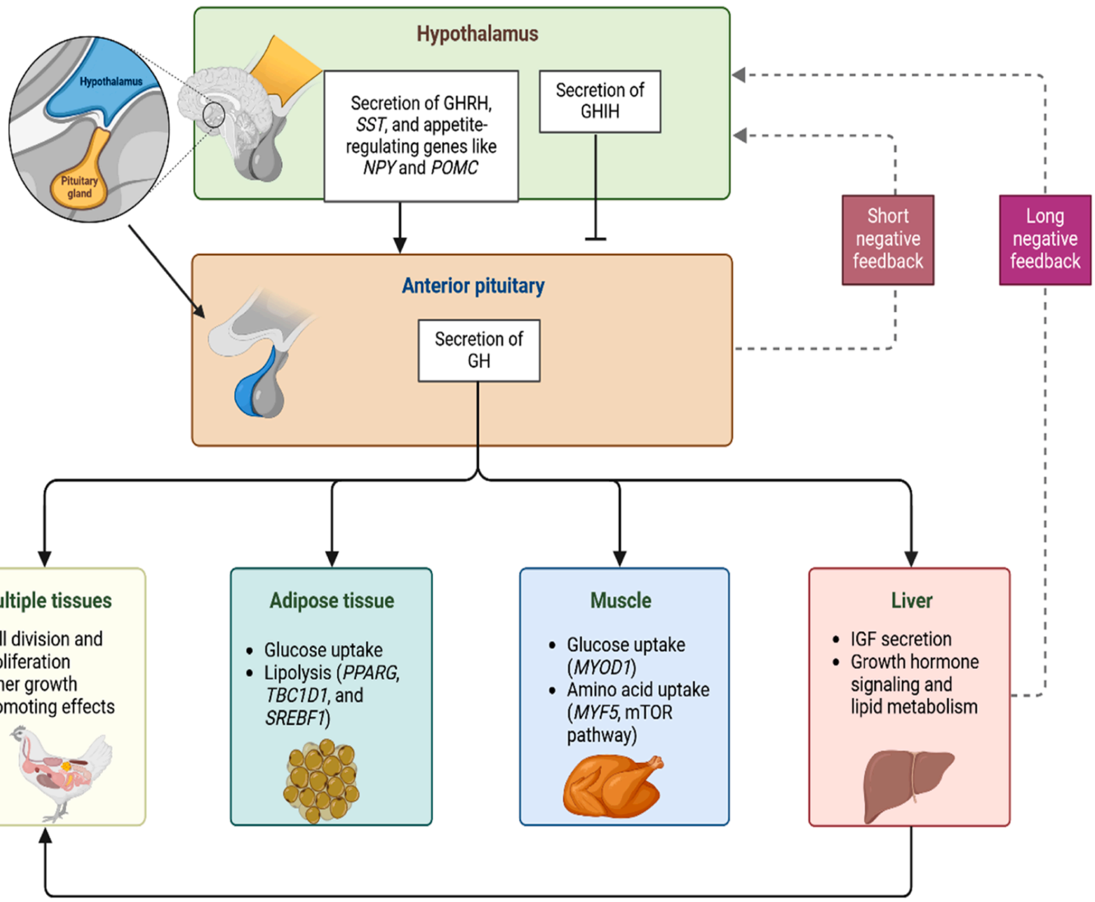

Fig. 3. The regulatory mechanism and systemic effect of growth hormone (GH) secretion are governed by the hypothalamus, indicating its role in growth and metabolism in different tissues. This figure shows that the hypothalamus, liver and skeletal muscle play a central role in chicken growth and developmental pathways. This figure is designed in Biorender (https://app.biorender.com).

Skeletal muscles comprised 40 % of chicken body weight, which play significant part in meat production and overall chicken growth. Skeletal muscle is a highly complex and heterogeneous tissue, and serves several important metabolic functions (Ouyang et al., 2017). Whereas, myoblasts are mainly responsible for skeletal muscle formation and growth. Precise understanding of myoblast properties and gene expression in muscle tissues is thus vital for skeletal muscle growth as it regulates the muscle fiber formation, differentiation and maturation (Nihashi et al., 2019; Lin et al., 2022; Kanakachari et al., 2022). Myogenic factors, including *MYF6, MYOD1, MR4, MYOG, MYF5*, and *MSTN* are key players in skeletal muscle development and growth (Li et al., 2022b). Particularly early in muscle development, *MYOD1* and *MYF5* are important as they initiate the myogenic pathway by stimulating the proliferation of myoblasts. As development progresses, both *MYOG* and *MRF4* become vital because these two are responsible for the differentiation of myoblasts into adult muscle fibers (Yin et al., 2021; Nawaz et al., 2021; Li et al., 2022b).

Mammalian target of rapamycin (mTOR) is a critical signaling pathway which promotes protein synthesis and muscle hypertrophy by phosphorylation of ribosomal protein S6 kinase 1 (S6K1) and eIF4E-binding protein 1 (4EBP1) (Rion et al., 2019; Xu and Velleman, 2023). From published literature, it is evident that mTOR pathway is essential for chicken skeletal muscle development and physiology, since it promotes myofiber protein accumulation and regulates satellite cell myogenesis and adipogenesis. Some studies also suggest that functions of mTOR may directly influence the quality of chicken meat (Lu et al., 2022).

Myostatin (*MSTN*), another crucial gene related to growth, is negative regulator of skeletal muscle growth. Deletion or inhibition of *MSTN* has been shown to increase muscle mass while significantly reducing fat deposition (Dou et al., 2018; Lee et al., 2024; Elashry et al., 2025). A study in broilers revealed that knockout of *MSTN* increased body weight by 26.9 % and reduced abdominal fat (Bhattacharya et al., 2017). The *MSTN* gene has been considered a potential genetic marker to improve meat production in industry (Ren et al., 2020; Lee et al., 2024). All of these studies and those summarized in Table 1 regarding the gene expression in skeletal muscle tissues emphasize the vital role of skeletal muscle in chicken growth regulation.

These tissue-specific expression patterns collectively form an integrated network controlling chicken growth and development, with cross talk between the hypothalamic-pituitary axis, liver metabolism, and muscle development pathways as shown in Fig. 3.

Multi-omics approach to understand chicken growth

Genomics, transcriptomics, proteomics, and metabolomics are crucial approaches that collectively provide a better understanding of chicken growth. Genomic research identifies candidate genes, transcriptomics helps with gene expression patterns, proteomics can provide insight into the proteins involved while metabolomics can help to decipher metabolic pathways vital for growth (Fig. 4).

Transcriptomics insights into chicken growth

Transcriptomics is a powerful tool to study the genetic mechanisms and pathways behind growth-related traits in chickens, as it reveals the crucial genes and regulatory networks involved in growth and development. Transcriptomics mainly involves microarray analysis and RNA-

Table 1
Key genes, pathways, and functions in skeletal muscle, hypothalamus and liver tissues influencing chicken growth.

Tissue	Key genes	Pathways	Function	References
Skeletal muscle	*MYOD1, MYF5, MYOG, MYF6, MSTN,CFL2*	Myogenesis, muscle fiber formation	Regulates muscle growth and carcass traits. *RPL3L* promotes proliferation and inhibits differentiation of myoblasts. MSTN negatively regulates muscle growth. MYF6 regulates myotube differentiation and maintenance of muscle fibers. CFL2 mediates myoblast proliferation.	(Yin et al., 2021; Lin et al., 2022; Guo et al., 2024)
	ACTC1, FDPS	Muscle Structure Development	Upregulated at D21, mainly linked to muscle structure development	(Gu et al., 2024)
	mTOR, S6K1, 4EBP1	Protein synthesis, muscle hypertrophy	*mTOR* signaling stimulates protein synthesis via phosphorylation of *S6K1* and *4EBP1*.	(Nakashima et al., 2020; Xu and Velleman, 2023)
	IGF1R, MYH9, YBX3	Adrenergic signaling	Regulates skeletal muscle development and differentiation.	(Wu et al., 2022)
	MYLK2, MYL4, ACTA1, FGF9	Striated muscle tissue development	Regulates actomyosin structure organization and myofibril assembly.	(Yin et al., 2021)
	FOXO3	FoxO signaling pathway	*FOXO3* regulates myoblast proliferation and differentiation through *AKT/FOXO/PTEN* signaling.	(Li et al., 2019)
	MUSTN1, FOS, TGFB3	Cell Differentiation, Muscle Regeneration	Upregulated at D42, mainly regulate cell differentiation and muscle regeneration after injury.	(Gu et al., 2024)
Hypothalamus	*POMC, NMU, PMCH, GHRH, CGA, LECT2, ALDH6, IGF2, IGFBP4, IGFBP7*	Anorexigenic and orexigenic pathways, growth regulation	Regulate feed intake and body weight; *CGA* interacts with *POMC* and *GHRH* to influence growth; *IGF2* and *IGFBPs* modulate growth at different developmental stages.	(Piórkowska et al., 2018)
	AGRP, NPY	Appetite regulation	Increased expression in fast-growing chicken genotypes, stimulating feed intake and promoting growth.	(Dunn et al., 2013)
	SIX1, RPS15, IGFBP7, ESR2	lipid metabolism, canonical Wnt signaling pathway, estrogen signaling	Synthesis and secretion of egg white proteins in laying hens.	(Wang and Ma, 2019; Mishra et al., 2020)
	AMPK and related genes	Energy homeostasis, appetite regulation	Upregulated during fasting, suggesting involvement in *AMPK*-mediated appetite regulation in the hypothalamus of chicks.	(Liu and Zhu, 2012)
	ACC, CPT-1, FAS, SREBP-1	Metabolic Flux and Anabolic Pathways	Regulate malonyl-CoA and long chain fatty acyl-CoA levels, which modulate expression of orexigenic and anorexigenic neuropeptides in melanocortin system neurons, crucial in *AMPK* Regulation.	(Liu and Zhu, 2012)
Liver	*IGF-1*	PI3K/Akt signaling pathway	Promotes growth and development, influences protein synthesis.	(Yu et al., 2015; Nawaz et al., 2023)
	GHR, SREBF1, CPT1A	Lipid metabolism	Regulates fatty acid synthesis, transport, and oxidation.	(Li et al., 2022a)
	PPARα, FAS, ACC, PGC-1α, SREBP-1c, PLIN1	Fatty acid synthesis/oxidation	Regulates lipid metabolism and energy balance; involved in fatty acid synthesis and oxidation pathways.	(Kang et al., 2022)
	MFGE8, HHLA1, CKAP2, ACSBG2	Lipid metabolism	Identified as hub genes in abdominal fat weight positively correlated modules.	(Xing et al., 2021)
	FoxO pathway genes	Cell cycle regulation, glucose metabolism	Implicated as active drivers of growth variations in chicken.	(Willson et al., 2018)
	GPAT, AGPAT, LPIN	Lipid metabolism	Expression levels change with age, particularly during peak laying period.	(Yang et al., 2019)
	IGFBP, IGF1, and FASN	Glucose metabolism and lipid metabolism	Show distinct expression patterns across developmental stages.	(Gao et al., 2024)

seq technology. Microarray is traditional approach for transcriptome profiling, while RNA-seq technology has emerged as an attractive option. RNA-seq is preferred over microarray due to its ability to detect new transcripts, wider dynamic range and higher specificity (Lowe et al., 2017; Chakraborty et al., 2022). Especially in livestock industry, RNA-seq technology can provide discrete and higher percentage of DEGs and can quantify expression data across wider dynamic ranges (Dong and Chen, 2013; Guo et al., 2021).

Transcriptomics enables to identify the differential expressed genes during crucial events such as cell proliferation, differentiation, muscle growth, cell division and lipid metabolism by comparing different populations (Shao et al., 2022; Chakraborty et al., 2022; Kanakachari et al., 2022; Shashank et al., 2024). For instance, a study identified differentially expressed genes (*KLF15, NRXN1, LOC107050638, MHCY11, HAO1*, and *BORCS6)* in tall vs short chickens by combining whole genome resequencing and transcriptomics. Further the enrichment analysis revealed that most of the DEGs were involved in glyoxylate and dicarboxylate metabolism pathway, peroxisome pathway, carbon metabolism and cell adhesion molecules pathways (Li et al., 2025a). This study provides valuable insights into different aspect of chicken growth as tall and short traits in chickens are strong indicators to evaluate growth.

Moreover, application of transcriptomics during different developmental phases (from embryo to post hatch) can identify specific genes, and molecular pathways activated during different developmental phases, which can help to compare gene expression patterns among various developmental and growth stages (Chen et al., 2019; Yin et al., 2021; Alsoufi et al., 2023). Similarly, a recent transcriptomics study examined three developmental phases of early chicken growth in muscle tissues. Pairwise comparison of three developmental phases revealed 978 differentially expressed genes (DEGs). Most of these DEGs were related to cell growth, muscular development, and cellular activity. Among these genes, those associated with chicken growth includes *MYOD1, GH, IGF2BP2, IGFBP3, SMYD1, CEBPB, FGF2,* and *IGFBP5* (Xue et al., 2017). Further KEGG enrichment analysis of identified DEGs found that these genes were involved in growth-related pathways, including extracellular matrix-receptor interaction, focal adhesion, tight junction, insulin signaling pathway, and regulation of the actin cytoskeleton (Xue et al., 2017).

Additionally, transcriptomic studies among indigenous chicken breeds identified various DEGs in the hypothalamus, pituitary, breast muscle, thigh muscle, and liver. Furthermore, they identified key genes (*FST, THSB, PTPRJ, CD36, PITX1, PITX2, AMPD1, PRKAB1, PRKAB2*) from hypothalamus-pituitary-muscle axis having high probability to be involved in muscle development through interacting with cytokine–cytokine receptor interaction signaling pathway, the PPAR signaling

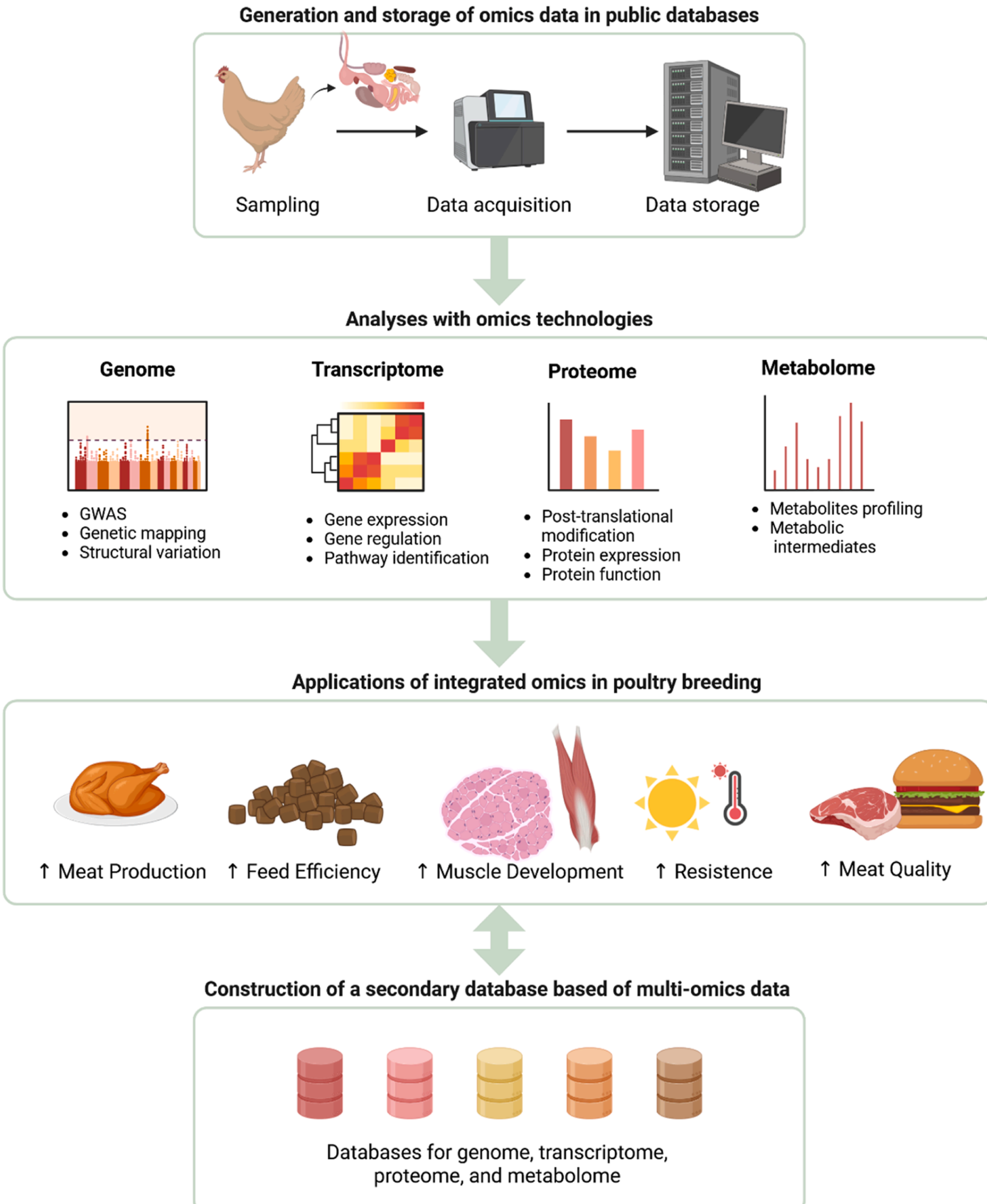

Fig. 4. Application of integrated omics for enhancing chicken growth and productivity. The integration of omics data and combined analysis can improve our understanding of growth regulators in chickens, ultimately leading to an enhancement of poultry breeding strategies. This figure is designed in Biorender (https://app.biorender.com).

pathway, and lipid metabolism (Shao et al., 2022). In another transcriptomic study conducted on fast and slow growing Jinghai yellow chickens, identified genes including *ANXA1, COL1A1, MYH15, TGFB3* and *ACTC1* showed differential expression in breast muscle tissues, indicating their involvement in muscle growth and development (Zhang et al., 2019; Shao et al., 2022). Similarly, a transcriptomic study on Jinghai Yellow chicken identified differentially expressed genes (*SNCG, MCL1, ARNTL, PLPPR4, VAMP1)* mainly associated with cell proliferation, cell differentiation and muscle growth (Chen et al., 2019), hence providing crucial information regarding genes and genetic pathways driving muscle development in chickens.

Comparative transcriptomic study between modern and legacy broiler lines has provided further insights regarding skeletal muscle gene expression. Based on the findings, analysis of breast muscle at days 6 and 21 post-hatch showed that modern broilers had higher expression of muscle development genes (*IGF1, IGF1R, WFIKKN2*). While legacy broilers exhibited greater activity of the growth inhibitor *MSTN* (Davis et al., 2015). So, conducting more studies like this by diving deep into the functioning of key genes regarding growth traits in chicken will further the advancement in chicken growth research. Transcriptomics studies by mimicking heat stress or applying different dietary protocols suggested that using RNA-seq assist to uncover the precise molecular pathways, genes and biological processes triggered by different environmental and dietary factors. Two studies published in 2025 used RNA seq data and found that some genes including *HSPA5, SSR1, SDF2L1,* and *SEC23B* were significantly differentiated under heat stress (Zhang et al., 2023b; Zhu et al., 2025a).

Research in chicken transcriptomics has found significant genes and pathways associated with muscle development, lipid metabolism, and growth-related traits. Fatty acid metabolism is a crucial factor in chicken growth, as a study on Huashang black chicken investigated the polyunsaturated fatty acids (PUFA) in chicken muscles and identified genes, including *FADS2* and *PRKAG3,* strongly associated with lipid metabolism by promoting growth in chickens (Yang et al., 2018). Similarly, another transcriptome profiling study in Chahua and Digao chickens identified significant DEGs related to meat quality in breast muscle tissues and these genes were mainly involved in oxidative phosphorylation, carbon metabolism and fatty acid degradation (Alsoufi et al., 2023). Feed efficiency is one of the major factors that plays a vital role in chicken growth. A recent transcriptomics study on feed efficiency in chickens identified several candidate genes that were enriched in nutrient metabolism, insulin signaling, MAPK signaling, and energy homeostasis pathways (Xiao et al., 2021).

All of these transcriptomics studies regarding growth, fatty acid metabolism, meat quality, and feed efficiency suggest that skeletal muscle growth is a multidimensional trait, and applying tools like transcriptomics can help us understand different aspects of chicken growth.

Potential of proteomics to elucidate mechanisms underlying chicken growth

Proteomic technology bridges the gap between genomic potential and phenotypic outcomes by directly identifying proteins that play a major role in the mechanisms regulating growth-related traits. Unlike transcriptomics and genomics, proteomics reveals the actual functional molecules in tissues that drive biological processes. The proteomics approach has been successful in identifying protein markers associated with meat quality and growth-related traits in several livestock species (López-Pedrouso et al., 2020). Gas chromatography–mass spectrometry (GC–MS) is widely employed in proteomics studies owing to its adaptability, high sensitivity, and capacity to provide a comprehensive overview of a diverse array of metabolites. Apart from this, mass spectrometry (MS), liquid chromatography tandem mass spectrometry (LC-MS/MS), two-dimensional gel electrophoresis (2DE), and isobaric tags for relative and absolute quantification (iTRAQ) are also used in proteomics (Alessandroni et al., 2024; Wadood and Xiquan, 2024).

Embryonic development of skeletal muscle plays a crucial role in determining the final muscle mass and, consequently, meat production in chickens. The total number of muscle fibers is established before birth and cannot be increased afterwards (Ouyang et al., 2017). Thus, embryonic myogenesis is crucial for enhancing muscle mass. Proteomic approaches, such as iTRAQ-based proteomics, are powerful tools for profiling protein expression during key stages of embryonic development. For instance, one study applied iTRAQ proteomics to analyze leg muscle samples from chickens at embryonic days 11 and 16, as well as on day 1 post-hatch. The study identified differentially expressed proteins during embryonic growth phases that were mainly involved in protein synthesis, muscle contraction, and oxidative phosphorylation pathways (Ouyang et al., 2017). Comparative proteomics research on fast- and slow-growing broilers identified 172 proteins that were differentially expressed, linked to muscle growth and metabolism. Many of these differentially expressed proteins were linked to the proteasome and glycolysis/gluconeogenesis-pathways (Di Luca et al., 2024). This study also identified potential biomarkers (*POSTN, HSPB1, TUBB4B, C3, ANXA2, ANXA6, PGM1,* and *TNNT*) that could indicate production potential, such as breast muscle growth in chickens.

Proteomic analysis of thigh muscle identified key proteins involved in muscle contraction, antioxidant defense and regulation of muscle growth. The identified proteins are primarily associated with muscle contraction, calcium signaling, glutathione metabolism, lipid transport, and signaling pathways such as PPAR and MAPK (Zhang et al., 2023a). These studies highlight the significance of proteomics that how it can help to elucidate the complex molecular mechanisms underlying growth traits in chickens, providing valuable information for improving breeding strategies and production efficiency in chickens.

These proteomics studies reveal that chicken growth depends on precisely coordinated protein networks involving energy metabolism, structural proteins, and regulatory pathways that change dynamically across developmental stages and differ between genetic lines and muscle types.

Potential of metabolomics to elucidate mechanisms underlying chicken growth

Metabolomics represents the downstream terminal point of the omics tools. It focuses on qualitative and quantitative analysis of small molecular metabolites ($\leq$1,000 Da) in cells, tissues, or organs. These small metabolites help to elucidate metabolic pathways of endogenous compounds during various growth and developmental stages (Zhang et al., 2024). Unlike transcriptomics and proteomics, metabolomics provides useful knowledge of the metabolic pathways, biochemical processes, and physiological functions that support different biological activities (Tian et al., 2023; Zhang et al., 2025). In metabolomics studies, gas chromatography–mass spectrometry (GC–MS) is extensively used for its reliability, high sensitivity, and ability to provide a comprehensive overview of several metabolites (Wadood and Zhang, 2024; Wang et al., 2024a).

In chicken research, metabolomics has proven vital for understanding growth-related traits. It provides tremendous opportunity for a comprehensive examination of metabolic changes throughout various embryonic and post-hatch developmental stages. The egg yolk, which is abundant with lipids, proteins, and minerals, is the major nutrient resource for embryonic development. The amount and type of yolk nutrients are dynamically changed during chicken embryogenesis to meet the requirements at different developmental stages. A metabolomics study on yolk metabolic changes in chicken found that the egg yolk metabolites at E09, E11, E15, E17, and E19 were different from each other, suggesting the developmental and metabolic changes of the egg yolk. Most of these metabolites were involved in amino acid metabolism pathways during embryonic development of broiler chickens (Liu et al., 2021).

Extending beyond yolk studies, Peng et al. (2018) employed LC/MS-QTOF to identify changes in major serum metabolites during embryonic development. They found that 39 metabolites changed from day 14 to 19 of incubation, and 68 metabolites changed significantly from day 19 to hatch (day 1). Among these differentially expressed metabolites, glutamine, threonine, and oestrone were identified as potential candidate indicators of early embryonic growth in chicken (Peng et al., 2018). Regarding production traits, a study using LC-MS/MS investigated the effects of selective breeding on chicken meat quality. The results revealed that selective breeding altered the metabolite profile in skeletal muscles and highlighted the significant role of glycerophospholipid metabolism in influencing muscle flavor and development (Shi et al., 2022). Similarly, a metabolomics study conducted in chickens at different ages revealed that the overall aroma intensity and aroma contributing metabolites increased with age (Wang et al., 2024c). Thus, such metabolomics studies can also help to determine the suitable marketing age of birds based on meat quality to enhance consumer acceptance and market value.

Collectively, these metabolomic studies reveal the dynamic metabolic changes underlying chicken growth and development, from embryogenesis to post-hatch development by identifying stage-specific metabolic signatures and pathways critical for growth.

Emerging genetic tools to understand growth related traits in chickens

Single-cell RNA sequencing

Single-cell RNA sequencing (SCS) technology is a powerful genomic tool that resolves cellular heterogeneity by profiling RNA transcripts at the individual cell level. It allows identification of target cells, tracks dynamic cellular changes, and uncovers intercellular communication pathways as shown in Fig. 5 (Cao et al., 2019; Liu et al., 2022). However, all cells, tissues, and organs within an organism have identical DNA, but have unique RNA expression patterns. These distinct expression profiles enable cells to produce specific proteins and perform specialised functions, contributing to biological diversity and tissue complexity. While, traditional RNA-seq methods evaluate whole transcriptome data by extracting total RNA from tissue samples. But traditional approaches are unable to distinguish the diverse expression patterns of various cell types (Stark et al., 2019; Yan et al., 2024). This limitation of traditional RNA-seq method hinders its use in diverse tissues. To address this problem, SCS was first introduced by Tang et al. in 2009 on a four-cell-stage mouse embryo, revealing the transcriptome profiles of individual cells (Tang et al., 2009).

SCS offers insights into biological heterogeneity and aids in the examination of low-quantity biological components often masked in bulk data, which are crucial for biological development (Liu et al., 2022). Due to advancements in the stability and sequencing throughput of SCS technology, together with decreased sequencing prices, this technique is now extensively used in reproductive development, immunology, tumor research, disease progression monitoring, mental health research, and several other domains (Papalexi and Satija, 2018; Cao et al., 2020; Peng and Qiao, 2021; Li et al., 2023; Yao et al., 2025 Liu et al., 2023). Studies utilising SCS technology have provided more profound knowledge regarding various organs, including the retina, hypothalamus, brain, stomach, blood, heart and lungs (Yan et al., 2024; Hawsawi et al., 2024).

Emphasising SCS relevance and implications for future chicken research, Table 2 offers a summary of current scRNA-seq studies in chickens. Although in its early stages in avian research, initial scRNA-seq studies have demonstrated its potential to uncover key developmental processes. For example, a recent study on Daheng broilers and Tibetan chickens used SCS to explain different pathways in skeletal muscle development during the embryonic stage, together with the identification of important genes involved in myogenesis and adipogenesis (Li et al., 2025c). Myogenesis and adipogenesis are two fundamental processes involved in chicken growth and they usually occur in the form of hypertrophy and hyperplasia. In this case, SCS can help to quantify the gene expression of individual cells in the tissue and can provide novel insights regarding myogenesis and adipogenesis (Li et al., 2020).

Improving meat production and meat quality in chickens is mainly dependent on understanding of different cell populations and their role in muscular growth and development; hence, SCS is crucial and can be transformative tool for growth optimization in poultry. Extending beyond chicken growth, a study mapped chicken leukocytes using SCS, therefore enabling the identification of several immune cell types and their roles independent of species-specific reagents (Maxwell et al., 2024). Recently, a study explored reproductive biology using SCS and found phenotypic differences between PGCs of chicken and zebra finch. These differences were mainly identified in various signaling pathways between gonadal PGCs and somatic cells. Based on findings, it revealed that FGF signaling pathway (usually involved in proliferation of chicken PGCs) was upregulated in chickens as compared to Zebra finch (Jung et al., 2023). Together, these studies illustrate how scRNA-seq can elucidate cellular mechanisms underlying economically important traits in poultry.

Despite its tremendous potential, there are few challenges in the complete adoption of this technology in chicken research. SCS requires

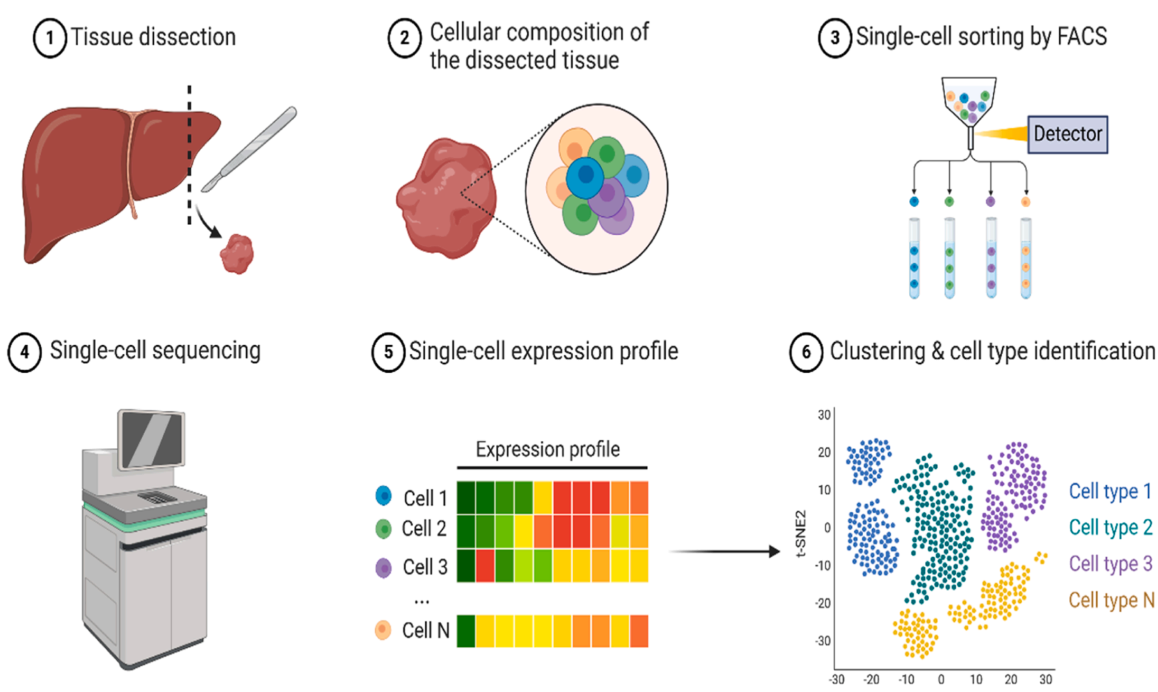

Fig. 5. Single-cell RNA sequencing workflow: 1. Tissue sampling from respective organs; 2. To check the cellular diversity of sampled tissue; 3. Isolation of individual cells using FACS; 4. Single-cell sequencing to obtain transcriptome files; 5. The gene expression profile for individual cells; 6. To make clusters using t-SNE based on expression profiles. This figure is designed in Biorender (https://app.biorender.com).

Table 2
Recent scRNA-seq studies in chicken and their implications for future research.

Purpose of study	Species	Tissue/cell type	Key findings	Potential applications to chicken research	References
Investigate skeletal muscle development	Chicken	Skeletal muscle cells	Identified distinct pathways in skeletal muscle development and key genes involved in myogenesis and adipogenesis	Understanding of muscle development and growth factors in chickens	(Li et al., 2025c)
Analyze Skeletal muscle development	Chicken	Breast muscle cells	Identified 10 cell clusters at day 5 post-hatching and 7 clusters at day 100; *APOA1* and *COL1A1* identified as biomarkers for intramuscular fat cells	Provides insights into muscle cell populations and intramuscular fat development at different growth stages	(Li et al., 2020)
Map avian embryo tailbud	Chicken	Embryonic trunk and tailbud	Generated molecular map of emerging trunk and tailbud; identified spatially restricted genes in somites and early myoblasts	Insights into body axis development in birds	(Mok et al., 2024)
Identify PGC-specific markers	Chicken, Zebra finch	Gonadal cells	Identified *NEGR1* and *SLC34A2* as novel PGC-specific markers in chickens, *ESYT3* in zebra finches	Potential for improving isolation and utilization of PGCs in various bird species	(Kim et al., 2024)
Map chicken leukocytes	Chicken	Blood cells	Identified putative cell types including T-cells, B-cells, monocytes, thrombocytes, and red blood cells	Provides a basis for further research into avian immunology and medicine	(Maxwell et al., 2024)
Characterize NDV target cells	Chicken	Lung tissue, DF-1 cell line	Identified five known and two unknown cell types as NDV targets in lungs; revealed different infection paths between in vivo and in vitro	Insights into NDV pathogenesis and potential interventions	(Liu et al., 2023b)
Investigate Marek's disease resistance	Chicken	Spleen cells	Identified allele-specific expression signatures enriched in transcription modulators	Provides insights into genetic factors influencing disease resistance, which can indirectly affect growth and productivity	(Velez-Irizarry et al., 2025)
Analyze social hierarchy response	Chicken	Amygdala cells	Created a cell atlas of chicken amygdala; identified diverse cell populations responding to social hierarchy	Offers understanding of neurobiological basis of social behavior, which can impact flock dynamics and overall growth	(Chen et al., 2024)
Characterize pituitary cell populations	Chicken	Anterior pituitary cells	Identified four endocrine cell clusters and four non-endocrine cell types; revealed novel marker genes for each cell type	Provides comprehensive understanding of pituitary cell types, crucial for growth hormone regulation	(Zhang et al., 2021a)
Map skin cell diversity	Chicken	Skin cells	Created a transcriptome atlas of black-bone chicken skin; identified various cell types and their gene expression profiles	Insights into skin development and pigmentation, relevant for breed-specific traits	(Wang et al., 2024d)
Investigate neural plate border cell fates	Chicken	Embryonic ectoderm cells	Characterized transcriptional changes during neural, neural crest, and placodal fate segregation	Insights into early embryonic development and cell fate decisions, foundational for overall growth	(Thiery et al., 2023)

advanced bioinformatics tools and expertise as current bioinformatics tools and algorithms are still suboptimal, which makes it challenging to extract some valuable insights from huge amount of data, which creates hurdle for its widespread use in chicken research. Another major limitation of SCS is the loss of spatial information data caused by tissue dissociation and this challenge can be addressed by performing an integrative study with spatial transcriptomics that can provide comprehensive view of cellular architecture and function (Desta et al., 2013; Potts et al., 2022; Wan et al., 2023). Overcoming these challenges will allow researchers to completely reap the benefits of SCS to improve molecular breeding accuracy and maximize chicken production traits.

CRISPR/Cas9 mediated genome editing

By targeting certain traits like growth and skeletal muscle development, CRISPR/Cas9 technology can be utilized to have desired genomic variations in chicken DNA. Traditional genome editing methods rely on multiple step process involving in vitro culturing and genome editing of primordial germ cells (PGCs), followed by transplantation of the genome-edited PGCs into host embryos to generate germline chimeric chickens, which then produce genome-edited progeny (Sid and Schusser, 2018; Pu et al., 2023). The traditional method of genome editing is heavily dependent on PGCs handling procedures (PGCs isolation, culturing, editing, screening, and transfer of PGCs into recipient embryos), which makes this process technically demanding (Xie et al., 2019; Qin et al., 2024).

A recent breakthrough came as a study generated genome edited chicken and duck by injecting an adenovirus comprising the CRISPR/Cas9 system into the blastoderms. The study further reported that offspring produced through this had desired insertion and deletion mutations without having any off-target mutations. Adenovirus mediated genome editing is easy, simple and not technically demanding like conventional avian genome editing (Lee et al., 2022). Moreover, recent innovations such as introduction of base and prime editing have further refined the precision in avian genome-editing technology, reducing off-target mutations while enabling single nucleotide mutations. These methods have been validated in creating disease-resistant chickens such as *ANP32A*-edited birds resistant to avian influenza (Idoko-Akoh et al., 2023).

Regarding chicken growth, a study utilized D10A/Cas9 nickase mediated genome-editing method in chicken by knocking out *MSTN* gene. Findings revealed an increase in skeletal muscle mass with high breast muscle growth in *MSTN* knocked out chickens. In addition, higher degree of skeletal muscle hypertrophy was induced in *MSTN* deleted chickens. Moreover, there was significant decrease in abdominal fat deposition in genome-edited chickens. This study suggests that genome editing can facilitate precise and efficient targeted genome engineering in chickens (Khwatenge and Nahashon, 2021). Another study generated *G0/G1 switch gene 2* (*G0S2*) knockout chickens through CRISPR/Cas9, these genome-edited chickens have shown significant reduction in abdominal fat deposition Li et al., 2025b. Further investigation revealed that *G0S2* knockout chickens had altered fatty acid compositions in their blood and abdominal fat compared with normal chickens (Park et al., 2019).

Avian genome editing is still in its early phases due to few constraints including homology directed pair efficiency and embryo viability issues. These limitations can be solved through the application of high fidelity Cas9 and enhanced sgRNA design (Idoko-Akoh et al., 2018). Despite of all these challenges, genome editing has high prospects in the future of chicken growth research. As the success of adenovirus mediated genome editing in chicken and duck has opened the avenues for smooth application of this technology on large scale by targeting specific genes related to economic traits in chickens, such as *IGF* and *MSTN* in case of muscle growth (Lee et al., 2022).

Chicken Genotype-Tissue Expression (ChickenGTEx) project

The ChickenGTEx project cataloged regulatory variants across 28 tissues using over 7,000 RNA-seq datasets and nearly 3,000 whole-genome sequences, offering a valuable resource for functional genomics in chickens. It includes millions of regulatory effects on primary expression (including protein-coding genes, lncRNA and exon) and post-transcriptional modifications. It further presents the tissue sharing and context-specificity of these regulatory variants, their underlying molecular mechanisms of action, and their utility in interpreting adaptation and genome-wide associations of 108 complex traits in chickens (Guan et al., 2025).

Availability of these datasets like ChickenGTEx project encourages studies based on statistical approaches aiming at identifying associations between transcripts and complex traits such as growth. Following analytical studies can be conducted in future using this platform:

a. Using ChickenGTEx platform, studies can be conducted to map tissue specific eQTLs for growth-related genes. These mapping studies will provide a comprehensive landscape of specific genetic variants that influence the gene expression of *IGF1, MSTN, and GH,* especially in growth related tissues including hypothalamus, liver, skeletal muscle and adipose tissues (Kineman et al., 2018).
b. Studies can be designed to construct growth stage specific regulatory networks by providing transcriptional atlas of muscle growth and reveal genetic links between myocyte differentiation, maturation, and proliferation (Dos Santos et al., 2023).
c. Integrating eQTLs data from ChickenGTEx with metabolomics data will help to unravel transcript-to-phenotype associations. These studies will highlight genetic variants, gene expression and metabolites responsible for growth related traits in chickens. Similarly, a recent study in humans has developed and applied a similar approach to investigate how metabolites mediate effect of gene expression on complex traits (Auwerx et al., 2023).
d. Through combining ChickenGTEx, data with Chicken chromatin accessibility atlas (50,796 open chromatin regions) can help to reveal transcription factor binding sites affected by genetic variants that possibly regulate growth related gene expression (Zhu et al., 2023).
e. Additionally, integrating eQTL data from ChickenGTEx with regulatory elements data (377 epigenomic, transcriptomic, and chromatin conformation datasets from 23 adult tissues by annotating 1.57 million regulatory elements) from Pan et al. (2023) would create a powerful framework to elucidate the genetic architecture of chicken growth. This integration may reveal growth-associated genetic variants influencing specific regulatory elements in growth-relevant tissues like muscle, bone, and liver. For instance, Pan et al. (2023) identified *CAB39L* and *RCBTB1* genes having potential role in body weight and growth, and integrating this with ChickenGTEx can reveal the associated regulatory networks and pathways.

Conclusions and future perspectives

Decades of QTL and GWAS studies have provided a strong foundation for understanding genetic basis of economically important traits. However, small effect sizes, population specific genetic architecture and limited studies to functionally validate candidate genes have hampered the application of these findings in poultry breeding. To further this progress, chicken research must divert its focus towards integrated multi-omics strategies to fully understand the dynamic interplay between specific genetic variants and their effects on particular phenotypes. Apart from association studies, more research should focus on validating the functional roles of candidate genes identified through QTL and GWAS by using CRISPR/Cas9 gene editing, overexpression or knockdown in cell culture, or targeted gene manipulation. Integrated omics studies should be conducted using transcriptomics, proteomics, and metabolomics to gain a comprehensive view of growth-related phenotypes. By integrating omics data with bioinformatics, researchers can analyze and interpret large datasets to identify key genes, pathways, and biological processes involved in chicken growth and development.

This article, through reviewing all these studies, including genomics to gene editing, has found various key lessons that can be helpful to organize and manage future research regarding the genetics behind chicken growth.

1. Future studies should focus on an integrative approach by combining genomics, transcriptomics, and metabolomics to better understand the complex genetic architecture in an organized way and pave the way for precision breeding.
2. The application of scRNA-seq technology in chicken research can be useful for understanding cellular heterogeneity in growth-related tissues, such as the liver, hypothalamus, and skeletal muscle, which can reveal the cellular dynamics of these tissues. SCS technology can help us to understand the origin, formation mechanisms and physiology underlying skeletal muscle tissues.
3. Developing and utilising the public databases, such as ChickenGTEx, can revolutionize our ability to understand the chicken genome more comprehensively and profoundly. Such databases can help to create a comprehensive atlas of regulatory variants among different chicken breeds and tissues.
4. It is crucial to conduct more functional studies to validate the candidate genes identified through genomics studies, as genomics can provide specific regions and genes whose roles must be clarified by investigating their functional significance.
5. Implementing advanced genetic tools, such as CRISPR/Cas9 genome editing, by targeting growth-related genes like *MSTN, IGF-1*, and *IGFBP2* can transform the growth efficiency and sustainability of growth production.
6. Developing efficient bioinformatics tools and establishing more databases can facilitate the analysis of large-scale genomic data in a short time, which can ultimately lead to data-driven precision breeding in the poultry industry.

Funding

This work was supported by the National Key R&D Program of China (Grant No. 2021YFD1300100), Guangxi Key R&D Program (No. AB241484013), and Jiangsu Agricultural Science and Technology Innovation Fund (JASTIF) (CX(23)1022).

Disclosures

All authors declare that they have no known competing interests.

References

Ahsan, M., Li, X., Lundberg, A.E., Kierczak, M., Siegel, P.B., Carlborg, Ö., Marklund, S., 2013. Identification of candidate genes and mutations in QTL regions for chicken growth using bioinformatic analysis of NGS and SNP-chip data. Front. Genet. 4, 226.
Alessandroni, L., Sagratini, G., Gagaoua, M., 2024. Proteomics and bioinformatics analyses based on two-dimensional electrophoresis and LC-MS/MS for the primary characterization of protein changes in chicken breast meat from divergent farming systems: organic versus antibiotic-free. Food Chem. Mol. Sci. 8, 100194.
Almeida, O.A.C., Moreira, G.C.M., Rezende, F.M., Boschiero, C., de Oliveira Peixoto, J., Ibelli, A.M.G., Ledur, M.C., de Novais, F.J., Coutinho, L.L., 2019. Identification of selection signatures involved in performance traits in a paternal broiler line. BMC Genomics 20, 449.
Alsoufi, M.A., Liu, Y., Cao, C., Zhao, J., Kang, J., Li, M., Wang, K., He, Y., Ge, C., 2023. Integrated transcriptomics profiling in chahua and digao chickens' breast for assessment molecular mechanism of meat quality traits. Genes 14 (1), 95.
Auwerx, C., Sadler, M.C., Woh, T., Reymond, A., Kutalik, Z., Porcu, E., 2023. Exploiting the mediating role of the metabolome to unravel transcript-to-phenotype associations. Elife 12, e81097.

Bello, S.F., Lawal, R..A., Adeola, A.C., Nie, Q., 2023. The study of selection signature and its applications on identification of candidate genes using whole genome sequencing data in chicken—a review. Poult. Sci. 102, 102657.
Bhattacharya, T.K., Shukla, R.., Chatterjee, R.N., Dushyanth, K., 2017. Knock down of the myostatin gene by RNA interference increased body weight in chicken. J. Biotechnol. 241, 61–68.
Cao, Y., Qiu, Y., Tu, G., Yang, C., 2020. Single-cell RNA sequencing in immunology. Curr. Genomics 21, 564–575.
Cao, J., Spielmann, M., Qiu, X., Huang, X., Ibrahim, D.M., Hill, A.J., Zhang, F., Mundlos, S., Christiansen, L., Steemers, F.J., Trapnell, C., Shendure, J., 2019. The single-cell transcriptional landscape of mammalian organogenesis. Nature 566, 496–502.
Cha, J., Choo, H., Srikanth, K., Lee, S.-H., Son, J.-W., Park, M.-R., Kim, N., Jang, G.W., Park, J.-E., 2021. Genome-wide association study identifies 12 loci associated with body weight at age 8 weeks in Korean native chickens. Genes 12, 1170.
Chakraborty, D., Sharma, N., Kour, S., Sodhi, S.S., Gupta, M.K., Lee, S.J., Son, Y.O., 2022. Applications of omics technology for livestock selection and improvement. Front. Genet. 13, 774113.
Chen, C.F., Chen, Y..H., Tixier-Boichard, M., Cheng, P.Y., Chang, C.S., Tang, P.C., Lee, Y. P., 2009. Effects of the chicken sex-linked dwarf gene on growth and muscle development. Asian-Australasian J. Anim. Sci. 22, 937–942.
Chen, P., Li, S., Zhou, Z., Wang, X., Shi, D., Li, Z., Li, X., Xiao, Y., 2022. Liver fat metabolism of broilers regulated by Bacillus amyloliquefaciens TL via stimulating IGF-1 secretion and regulating the IGF signaling pathway. Front. Microbiol. 13, 958112.
Chen, F., Wu, P., Shen, M., He, M., Chen, L., Qiu, C., Shi, H., Zhang, T., Wang, J., Xie, K., Dai, G., Wang, J., Zhang, G.X., 2019. Transcriptome analysis of differentially expressed genes related to the growth and development of the Jinghai yellow chicken. Genes 10 (7), 539.
Chen, S., Xing, L., Xie, Z., Zhao, M., Yu, H., Gan, J., Zhao, H., Ma, Z., Li, H., 2024. Single-cell transcriptomic reveals a cell atlas and diversity of chicken amygdala responded to social hierarchy. iScience 27, 109880.
Davis, R.V.N., Lamont, S.J., Rothschild, M.F., Persia, M.E., Ashwell, C.M., Schmidt, C.J., 2015. Transcriptome analysis of post-hatch breast muscle in legacy and modern broiler chickens reveals enrichment of several regulators of myogenic growth. PLoS One 10, 1–17.
De Solis, A.J., Del Río-Martín, A.., Radermacher, J., Chen, W., Steuernagel, L., Bauder, C. A., Eggersmann, F.R., Morgan, D.A., Cremer, A.-L., Sué, M., Germer, M., Kukat, C., Vollmar, S., Backes, H., Rahmouni, K., Kloppenburg, P., Brüning, J.C., 2024. Reciprocal activity of AgRP and POMC neurons governs coordinated control of feeding and metabolism. Nat. Metab. 6, 473–493.
Desert, C., Baéza, E., Aite, M., Boutin, M., Le Cam, A., Montfort, J., Houee-Bigot, M., Blum, Y., Roux, P.F., Hennequet-Antier, C., Berri, C., Metayer-Coustard, S., Collin, A., Allais, S., Le Bihan, E., Causeur, D., Gondret, F., Duclos, M.J., Lagarrigue, S., 2018. Multi-tissue transcriptomic study reveals the main role of liver in the chicken adaptive response to a switch in dietary energy source through the transcriptional regulation of lipogenesis. BMC Genomics 19, 187.
Desta, T.T., Dessie, T.., Bettridge, J., Lynch, S.E., Melese, K., Collins, M., Christley, R.M., Wigley, P., Kaiser, P., Terfa, Z., Mwacharo, J.M., Hanotte, O., 2013. Signature of artificial selection and ecological landscape on morphological structures of Ethiopian village chickens. Anim. Genet. 52, 17–29.
Di Luca, A., Bennato, F., Ianni, A., Martino, C., Henry, M., Meleady, P., Martino, G., 2024. Label-free liquid chromatography–mass spectrometry comparison of the breast muscle proteome profiles in two fast-growing broilers. Sci. Rep. 14, 16886.
Dong, Z., Chen, Y., 2013. Transcriptomics: advances and approaches. Sci. China Life Sci. 56, 960–967.
Dos Santos, M., Shah, A.M., Zhang, Y., Bezprozvannaya, S., Chen, K., Xu, L., Lin, W., McAnally, J.R., Bassel-Duby, R., Liu, N., Olson, E.N., 2023. Opposing gene regulatory programs governing myofiber development and maturation revealed at single nucleus resolution. Nat. Commun. 14, 4333.
Dou, T., Li, Z., Wang, K., Liu, L., Rong, H., Xu, Z., Huang, Y., Gu, D., Chen, X., Hu, W., Zhang, J., Zhao, S., Jois, M., Li, Q., Ge, C., te Pas, M.F.W., Jia, J., 2018. Regulation of myostatin expression is associated with growth and muscle development in commercial broiler and DMC muscle. Mol. Biol. Rep. 45, 511–522.
Dou, D., Shen, L., Zhou, J., Cao, Z., Luan, P., Li, Y., Xiao, F., Guo, H., Li, H., 2022. Genome-wide association studies for growth traits in broilers. BMC Genomic Data 23, 1–9.
Dunn, I.C., Wilson, P..W., Smulders, T.V., Sandilands, V., D'Eath, R.B., Boswell, T., 2013. Hypothalamic agouti-related protein expression is affected by both acute and chronic experience of food restriction and re-feeding in chickens. J. Neuroendocrinol. 25, 920–928.
Elashry, M.I., Schneider, V..C., Heimann, M., Wenisch, S., Arnhold, S., 2025. CRISPR/Cas9-targeted myostatin deletion improves the myogenic differentiation parameters for muscle-derived stem cells in mice. J. Dev. Biol. 13 (1), 5.
Gao, M., Chen, Y., Fan, H., Chen, S., Wang, H., Nie, W., Guo, Y., Lv, Z., 2024. Transgenerational effects on the gene transcriptome of chicken liver. Anim. Adv. 1, e003.
Gheyas, A.A., Burt, D.W., 2013. Microarray resources for genetic and genomic studies in chicken: a review. Genesis 51, 337–356.
Gu, X., Feng, C., Ma, L., Song, C., Wang, Y., Da, Y., Li, H., Chen, K., Ye, S., Ge, C., Hu, X., Li, N., 2011. Genome-wide association study of body weight in chicken F2 resource population. PLoS One 6, 1–5.
Gu, S., Huang, Q., Jie, Y., Sun, C., Wen, C., Yang, N., 2024. Transcriptomic and epigenomic landscapes of muscle growth during the postnatal period of broilers. J. Anim. Sci. Biotechnol. 15, 1–15.
Guan, D., Bai, Z., Zhu, X., Zhong, C., Hou, Y., Zhu, D., Li, H., Lan, F., Diao, S., Yao, Y., Zhao, B., Li, X., Pan, Z., Gao, Y., Wang, Y., Zou, D., Wang, R., Xu, T., Sun, C., Yin, H., Teng, J., Xu, Z., Lin, Q., Shi, S., Shao, D., Degalez, F., Lagarrigue, S., Wang, Y., Wang, M., Peng, M., Rocha, D., Charles, M., Smith, J., Watson, K., Buitenhuis, A.J., Sahana, G., Lund, M.S., Warren, W., Frantz, L., Larson, G., Lamont, S.J., Si, W., Zhao, X., Li, B., Zhang, H., Luo, C., Shu, D., Qu, H., Luo, W., Li, Z., Nie, Q., Zhang, X., Xiang, R., Liu, S., Zhang, Z., Zhang, Z., Liu, G.E., Cheng, H., Yang, N., Hu, X., Zhou, H., Fang, L., 2025. Genetic regulation of gene expression across multiple tissues in chickens. Nat. Genet. 57, 1298–1308.
Guo, J., Sun, C., Qu, L., Shen, M., Dou, T., Ma, M., Wang, K., Yang, N., 2017. Genetic architecture of bone quality variation in layer chickens revealed by a genome-wide association study. Sci. Rep. 7, 45317.
Guo, W., Tzioutziou, N.A., Stephen, G., Milne, I., Calixto, C.P., Waugh, R., Brown, J.W.S., Zhang, R., 2021. 3D RNA-seq: a powerful and flexible tool for rapid and accurate differential expression and alternative splicing analysis of RNA-seq data for biologists. RNA Biol. 18, 1574–1587.
Guo, X., Wang, H., Liu, M., Xu, J.M., Liu, Y.N., Zhang, H., He, X.X., Wang, J.X., Wei, W., Ren, D.L., Jiang, R.S., 2024. Weighted gene co-expression network analysis identifies important modules and hub genes involved in the regulation of breast muscle yield in broilers. Anim. Biosci. 37, 1673–1682.
Hawsawi, Y.M., Khoja, B.., Aljaylani, A.O., Jaha, R., AlDerbi, R.M., Alnuman, H., Khan, M.I., 2024. Recent progress and applications of single-cell sequencing technology in breast cancer. Front. Genet. 15, 1417415.
Idoko-Akoh, A., Goldhill, D.H., Sheppard, C.M., Bialy, D., Quantrill, J.L., Sukhova, K., Brown, J.C., Richardson, S., Campbell, C., Taylor, L., Sherman, A., Nazki, S., Long, J. S., Skinner, M.A., Shelton, H., Sang, H.M., Barclay, W.S., McGrew, M.J., 2023. Creating resistance to avian influenza infection through genome editing of the ANP32 gene family. Nat. Commun. 14, 6136.
Idoko-Akoh, A., Taylor, L., Sang, H.M., McGrew, M.J., 2018. High fidelity CRISPR/Cas9 increases precise monoallelic and biallelic editing events in primordial germ cells. Sci. Rep. 8, 15126.
Jeffery, J., Neyt, C., Moore, W., Paterson, S., Bower, N.I., Chenevix-Trench, G., Verkade, H., Hogan, B.M., Khanna, K.K., 2015. Cep55 regulates embryonic growth and development by promoting Akt stability in zebrafish. FASEB J. 29, 1999–2009.
Johnsson, M., Henriksen, R., Höglund, A., Fogelholm, J., Jensen, P., Wright, D., 2018. Genetical genomics of growth in a chicken model. BMC Genomics 19, 72.
Jung, K.M., Seo, M.., Han, J.Y., 2023. Comparative single-cell transcriptomic analysis reveals differences in signaling pathways in gonadal primordial germ cells between chicken (Gallus gallus) and zebra finch (Taeniopygia guttata). FASEB J. 37 (1), e22706.
Kanakachari, M., Ashwini, R., Chatterjee, R.N., Bhattacharya, T.K., 2022. Embryonic transcriptome unravels mechanisms and pathways underlying embryonic development with respect to muscle growth, egg production, and plumage formation in native and broiler chickens. Front. Genet. 13, 990849.
Kang, X., Amevor, F., Zhang, L., Shah, A., Zhu, Q., Tian, Y., Shu, G., Wang, Y., Zhao, X., 2022. Study on the major genes related with fat deposition in liver and abdominal fat of different breeds of chicken. Brazilian J. Poult. Sci. 24 (01).
Khwatenge, C.N., Nahashon, S.N., 2021. Recent advances in the application of CRISPR/Cas9 gene editing system in poultry species. Front. Genet. 12, 627714.
Kim, J.L., Jung, K..M., Han, J.Y., 2024. Single-cell RNA sequencing reveals surface markers of primordial germ cells in chicken and zebra finch. Mol. Genet. Genomics 299, 90.
Kineman, R.D., del Rio-Moreno, M., Sarmento-Cabral, A., 2018. 40 YEARS of IGF1: understanding the tissue-specific roles of IGF1/IGF1R in regulating metabolism using the Cre/loxP system. J. Mol. Endocrinol. 61, T187–T198.
Lee, J., Kim, D.-H., Karolak, M.C., Shin, S., Lee, K., 2022. Generation of genome-edited chicken and duck lines by adenovirus-mediated in vivo genome editing. Proc. Natl. Acad. Sci. 119 (45), e2214344119.
Lee, J., Kim, D.-H., Lee, K., 2024. Myostatin gene role in regulating traits of poultry species for potential industrial applications. J. Anim. Sci. Biotechnol. 15, 82.
Li, Y., Chen, Y., Jin, W., Fu, S., Li, D., Zhang, Y., Sun, G., Jiang, R., Han, R., Li, Z., Kang, X., Li, G., 2019. Analyses of microRNA and mRNA expression profiles reveal the crucial interaction networks and pathways for regulation of chicken breast muscle development. Front. Genet. 10, 197.
Li, X., Chen, X., Wang, Q., Yang, N., Sun, C., 2024. Integrating bioinformatics and machine learning for genomic prediction in chickens. Genes 15, 690.
Li, J., Chen, K., Zhu, M., Bi, J., Tang, H., Gao, W., 2025a. Integration of whole genome resequencing and transcriptome sequencing to identify candidate genes for tall and short traits in Baicheng Fatty chickens. Front. Vet. Sci. 12, 1534742.
Li, C., Guan, R., Li, W., Wei, D., Cao, S., Xu, C., Chang, F., Wang, P., Chen, L., Lei, D., 2023. Single-cell RNA sequencing reveals tumor immune microenvironment in human hypopharygeal squamous cell carcinoma and lymphatic metastasis. Front. Immunol. 14, 1168191.
Li, Z., Li, J., Lin, Z., Zhang, D., Zhang, G., Ran, J., Wang, Y., Yin, H., Liu, Y., 2022a. Knockdown of CPT1A induce chicken adipocyte differentiation to form lipid droplets. Brazilian J. Poult. Sci. 24 (04).
Li, C., Tian, D., Tang, B., Liu, X., Teng, X., Zhao, W., Zhang, Z., Song, S., 2021. Genome variation map: a worldwide collection of genome variations across multiple species. Nucleic Acids Res. 49, D1186–D1191.
Li, Y., Wang, B., Wang, Z., Wen, J., Zhou, T., Tang, J., Li, Z., 2025b. The effect of G0S2 gene knockout on the proliferation, apoptosis, and differentiation of chicken preadipocytes. Animals 15, 951.
Li, J., Xing, S., Zhao, G., Zheng, M., Yang, X., Sun, J., Wen, J., Liu, R., 2020. Identification of diverse cell populations in skeletal muscles and biomarkers for intramuscular fat of chicken by single-cell RNA sequencing. BMC Genomics 21, 752.

Li, J., Yang, D., Chen, C., Wang, J., Wang, Z., Yang, C., Yu, C., Li, Z., 2025d. Single-cell RNA transcriptome uncovers distinct developmental trajectories in the embryonic skeletal muscle of Daheng broiler and Tibetan chicken. BMC Genomics 26, 187.
Li, F., Yang, C., Xie, Y., Gao, X., Zhang, Y., Ning, H., Liu, G., Chen, Z., Shan, A., 2022b. Maternal nutrition altered embryonic MYOD1, MYF5, and MYF6 gene expression in genetically fat and lean lines of chickens. Anim. Biosci. 35, 1223–1234.
Lin, C.-T., Lin, Y.-T., Kuo, T.-F., 2007. Investigation of mrna expression for secreted frizzled-related protein 2 (sFRP2) in chick embryos. J. Reprod. Dev. 53, 801–810.
Lin, S., Xian, M., Ren, T., Mo, G., Zhang, L., Zhang, X., 2022. Mining of chicken muscle growth genes and the function of important candidate gene RPL3L in muscle development. Front. Physiol. 13, 1–16.
Liu, H., Ding, P., Tong, Y., He, X., Yin, Y., Zhang, H., Song, Z., 2021. Metabolomic analysis of the egg yolk during the embryonic development of broilers. Poult. Sci. 100, 101014.
Liu, Y., Shan, Y., Tu, Y., Zhang, M., Ji, G., Ju, X., Shi, S., Fan, C., Li, Y., Shu, J., 2023. Designing and evaluating a cost-effective single nucleotide polymorphism liquid array for Chinese native chickens. Anim. Res. One Heal. 1, 168–179.
Liu, Y., Liang, S., Wang, B., Zhao, J., Zi, X., Yan, S., Dou, T., Jia, J., Wang, K., Ge, C., 2022. Advances in single-cell sequencing technology and its application in poultry science. Genes 13 (12), 2211.
Liu, W., Xu, Z., Qiu, Y., Qiu, X., Tan, L., Song, C., Sun, Y., Liao, Y., Liu, X., Ding, C., 2023. Single-cell transcriptome atlas of newcastle disease virus in chickens both in vitro and in vivo. Microbiol. Spectr. 11, 3.
Liu, L., Zhu, L., 2012. Effect of 24 h fasting on gene expression of ampk, appetite regulation peptides and lipometabolism related factors in the hypothalamus of broiler chicks. Asian-Australasian J. Anim. Sci. 25, 1300–1308.
López-Pedrouso, M., Lorenzo, J., Gagaoua, M., Franco, D., 2020. Application of proteomic technologies to assess the quality of raw pork and pork products: an overview from farm-to-fork. Biology 9, 393.
Lowe, R., Shirley, N., Bleackley, M., Dolan, S., Shafee, T., 2017. Transcriptomics technologies. PLoS Comput. Biol. 13, e1005457.
Lu, T., Abdalla Gibril, B.A., Xu, J., Xiong, X., 2024. Unraveling the genetic foundations of broiler meat quality: advancements in research and their impact. Genes 15, 746.
Lu, P., Morawong, T., Molee, A., Molee, W., 2022. L-arginine alters myogenic genes expression but does not affect breast muscle characteristics by in ovo feeding technique in slow-growing chickens. Front. Vet. Sci. 9, 1030873.
Luo, J., Yang, Z., Li, X., Xiao, C., Yuan, H., Yang, X., Zhou, B., Zheng, Y., Zhang, J., 2024. High muscle expression of IGF2BP1 gene promotes proliferation and differentiation of chicken primary myoblasts: results of transcriptome analysis. Animals 14, 2024.
Lyu, S., Arends, D., Nassar, M.K., Weigend, A., Weigend, S., Wang, E., Brockmann, G.A., 2023. High-density genotyping reveals candidate genomic regions for chicken body size in breeds of Asian origin. Poult. Sci. 102, 102303.
Ma, M., Cai, B., Kong, S., Zhou, Z., Zhang, J., Zhang, X., Nie, Q., 2022. PPARGC1A Is a moderator of skeletal muscle development regulated by miR-193b-3p. Int. J. Mol. Sci. 23, 9575.
Maxwell, M., Söderlund, R., Härtle, S., Wattrang, E., 2024. Single-cell RNA-seq mapping of chicken peripheral blood leukocytes. BMC Genomics 25, 124.
Mishra, S.K., Chen, B., Zhu, Q., Xu, Z., Ning, C., Yin, H., Wang, Y., Zhao, X., Fan, X., Yang, M., Yang, D., Ni, Q., Li, Y., Zhang, M., Li, D., 2020. Transcriptome analysis reveals differentially expressed genes associated with high rates of egg production in chicken hypothalamic-pituitary-ovarian axis. Sci. Rep. 10, 5976.
Mo, G., Hu, B., Wei, P., Luo, Q., Zhang, X., 2022. The role of Chicken prolactin, growth hormone and their receptors in the immune system. Front. Microbiol. 13, 900041.
Mok, G., S. Turner, E. Smith, L. Mincarelli, A. Lister, J. Lipscombe, V. Uzun, W. Haerty, I. Macaulay, and A. Münsterberg. 2024. Single-cell and spatial transcriptomics of the avian embryo tailbud. Available at http://biorxiv.org/lookup/doi/10.1101/2024.02.05.578917.
Monti, P., Ciribilli, Y., Foggetti, G., Menichini, P., Bisio, A., Cappato, S., Inga, A., Divizia, M.T., Lerone, M., Bocciardi, R., Fronza, G., 2019. P63 modulates the expression of the WDFY2 gene which is implicated in cancer regulation and limb development. Biosci. Rep. 39 (12), BSR20192114.
Moreira, G.C.M., Salvian, M., Boschiero, C., Cesar, A.S.M., Reecy, J.M., Godoy, T.F., Ledur, M.C., Garrick, D., Mourão, G.B., Coutinho, L.L., 2019. Genome-wide association scan for QTL and their positional candidate genes associated with internal organ traits in chickens. BMC Genomics 20, 669.
Morris, K.M., Sutton, K., Girma, M., Sánchez-Molano, E., Solomon, B., Esatu, W., Dessie, T., Vervelde, L., Psifidi, A., Hanotte, O., Banos, G., 2024. Phenotypic and genomic characterisation of performance of tropically adapted chickens raised in smallholder farm conditions in Ethiopia. Front. Genet. 15, 1383609.
Nakashima, K., Ishida, A., Shimamoto, S., Ijiri, D., Ohtsuka, A., 2020. Insulin stimulation of protein synthesis and mTOR signaling in Chick myotube cultures. J. Poult. Sci. 57, 205–209.
Nawaz, A.H., Amoah, K., Leng, Q.Y., Zheng, J.H., Zhang, W.L., Zhang, L., 2021. Poultry response to heat stress: its physiological, metabolic, and genetic implications on meat production and quality including strategies to improve broiler production in a warming world. Front. Vet. Sci. 8, 699081.
Nawaz, A.H., Lin, S., Wang, F., Zheng, J., Sun, J., Zhang, W., Jiao, Z., Zhu, Z., An, L., Zhang, L., 2023. Investigating the heat tolerance and production performance in local chicken breed having normal and dwarf size. Animal 17, 100707.
Nawaz, A.H., Setthaya, P., Feng, C., 2024. Exploring evolutionary adaptations and genomic advancements to improve heat tolerance in chickens. Animals 14, 2215.
Nihashi, Y., Umezawa, K., Shinji, S., Hamaguchi, Y., Kobayashi, H., Kono, T., Ono, T., Kagami, H., Takaya, T., 2019. Distinct cell proliferation, myogenic differentiation, and gene expression in skeletal muscle myoblasts of layer and broiler chickens. Sci. Rep. 9, 16527.
Ogawa, F., Malavasi, E.L.V., Crummie, D.K., Eykelenboom, J.E., Soares, D.C., Mackie, S., Porteous, D.J., Millar, J.K., 2014. DISC1 complexes with TRAK1 and Miro1 to modulate anterograde axonal mitochondrial trafficking. Hum. Mol. Genet. 23, 906–919.
Ou, J.H., Rönneburg, T., Carlborg, Ö., Honaker, C.F., Siegel, P.B., Rubin, C.J., 2024. Complex genetic architecture of the chicken Growth1 QTL region. PLoS One 19, e0295109.
Ouyang, H., Wang, Z., Chen, X., Yu, J., Li, Z., Nie, Q., 2017. Proteomic analysis of chicken skeletal muscle during embryonic development. Front. Physiol. 8, 281.
Pan, Z., Wang, Y., Wang, M., Wang, Y., Zhu, X., Gu, S., Zhong, C., An, L., Shan, M., Damas, J., Halstead, M.M., Guan, D., Trakooljul, N., Wimmers, K., Bi, Y., Wu, S., Delany, M.E., Bai, X., Cheng, H.H., Sun, C., Yang, N., Hu, X., Lewin, H.A., Fang, L., Zhou, H., 2023. An atlas of regulatory elements in chicken: a resource for chicken genetics and genomics. Sci. Adv. 9, 18.
Park, T.S., W, M.F., Park, W., Srikanth, K., Kemp, S., Kim, J.-M., Lim, D., Park, J.-E., 2019. Transcriptomic profiles of muscle, heart, and spleen in reaction to circadian heat stress in Ethiopian highland and lowland male chicken. Cell Stress Chaperones 24, 175–194.
Papalexi, E., Satija, R., 2018. Single-cell RNA sequencing to explore immune cell heterogeneity. Nat. Rev. Immunol. 18, 35–45.
Peng, M.L., Li, S.N., He, Q.Q., Zhao, J.L., Li, L.L., Ma, H.T., 2018. Based serum metabolomics analysis reveals simultaneous interconnecting changes during chicken embryonic development. J. Anim. Physiol. Anim. Nutr. 102, 1210–1219.
Peng, Y., Qiao, H., 2021. The application of single-cell RNA sequencing in mammalian meiosis studies. Front. Cell Dev. Biol. 9, 673642.
Piórkowska, K., Zukowski, K., Poltowicz, K., Nowak, J., Wojtysiak, D., Derebecka, N., Wesoly, J., Ropka-Molik, K., 2018. Transcriptomic changes in broiler chicken hypothalamus during growth and development. Int. J. Genomics 14, 6049469.
Potts, H.G., Lemieux, M.E., Rice, E.S., Warren, W., Choudhury, R.P., Mommersteeg, M.T.M., 2022. Discordant genome assemblies drastically alter the interpretation of single-cell RNA sequencing data which can be mitigated by a novel integration method. Cells 11, 608.
Pu, L., Xie, L., Chen, J., Sun, H., Huang, Z., Xu, T., Tian, K., Zhong, J., Xu, H., Liu, X., Lu, Y., 2023. Tracking the dynamics of female germ cell development during peri-hatch periods using a gene-edited chicken model. Poult. Sci. 102, 102377.
Qin, H., Jia, X., Huang, Z., Zhi, Y., Ji, N., Lan, M., Zhang, L., Liu, X., Xu, H., Lu, Y., 2024. Establishing an induced infertile chicken line for efficient germline transmission of exogenous PGCs. J. Integr. Agric. https://doi.org/10.1016/j.jia.2024.08.009.
Ren, H., Xiao, W., Qin, X., Cai, G., Chen, H., Hua, Z., Cheng, C., Li, X., Hua, W., Xiao, H., Zhang, L., Dai, J., Zheng, X., Zhu, Z., Qian, C., Yao, J., Bi, Y., 2020. Myostatin regulates fatty acid desaturation and fat deposition through MEF2C/miR222/SCD5 cascade in pigs. Commun. Biol. 3, 612.
Rion, N., Castets, P., Lin, S., Enderle, L., Reinhard, J.R., Eickhorst, C., Rüegg, M.A., 2019. mTOR controls embryonic and adult myogenesis via mTORC1. Development 146 (7), dev172460.
Saneyasu, T., 2024. Recent research on mechanisms of feeding regulation in chicks. J. Poult. Sci. 61, 2024012.
Shao, M., Shi, K., Zhao, Q., Duan, Y., Shen, Y., Tian, J., He, K., Li, D., Yu, M., Lu, Y., Tang, Y., Feng, C., 2022. Transcriptome analysis reveals the differentially expressed genes associated with growth in Guangxi partridge chickens. Genes 13 (5), 798.
Shashank, C.G., Sejian, V., Silpa, M.V., Devaraj, C., Madhusoodan, A.P., Rebez, E.B., Kalaignazhal, G., Sahoo, A., Dunshea, F.R., 2024. Climate resilience in farm animals: transcriptomics-based alterations in differentially expressed genes and stress pathways. BioTech 13, 49.
Shi, K., Zhao, Q., Shao, M., Duan, Y., Li, D., Lu, Y., Tang, Y., Feng, C., 2022. Untargeted metabolomics reveals the effect of selective breeding on the quality of chicken meat. Metabolites 12, 367.
Sid, H., Schusser, B., 2018. Applications of gene editing in chickens: a new era is on the horizon. Front. Genet. 9, 456.
Smith, J., Alfieri, J.M., Anthony, N., Arensburger, P., Athrey, G.N., Balacco, J., Balic, A., Bardou, P., Barela, P., Bigot, Y., Blackmon, H., Borodin, P.M., Carroll, R., Casono, M.C., Charles, M., Cheng, H., Chiodi, M., Cigan, L., Coghill, L.M., Crooijmans, R., Das, N., Davey, S., Davidian, A., Degalez, F., Dekkers, J.M., Derks, M., Diack, A.B., Djikeng, A., Drechsler, Y., Dyomin, A., Fedrigo, O., Fiddaman, S.R., Formenti, G., Frantz, L.A.F., Fulton, J.E., Gaginskaya, E., Galkina, S., Gallardo, R.A., Geibel, J., Gheyas, A.A., Godinez, C.J.P., Goodell, A., Graves, J.A.M., Griffin, D.K., Haase, B., Han, J.-L., Hanotte, O., Henderson, L.J., Hou, Z.-C., Howe, K., Huynh, L., Ilatsia, E., Jarvis, E.D., Johnson, S.M., Kaufman, J., Kelly, T., Kemp, S., Kern, C., Keroack, J.H., Klopp, C., Lagarrigue, S., Lamont, S.J., Lange, M., Lanke, A., Larkin, D.M., Larson, G., Layos, J.K.N., Lebrasseur, O., Malinovskaya, L.P., Martin, R.J., Martin Cerezo, M.L., Mason, A.S., McCarthy, F.M., McGrew, M.J., Mountcastle, J., Muhonja, C.K., Muir, W., Muret, K., Murphy, T.D., Ng'ang'a, I., Nishibori, M., O'Connor, R.E., Ogugo, M., Okimoto, R., Ouko, O., Patel, H.R., Perini, F., Pigozzi, M.I., Potter, K.C., Price, P.D., Reimer, C., Rice, E.S., Rocos, N., Rogers, T.F., Saelao, P., Schauer, J., Schnabel, R.D., Schneider, V.A., Simianer, H., Smith, A., Stevens, M.P., Stiers, K., Tiambo, C.K., Tixier-Boichard, M., Torgasheva, A.A., Tracey, A., Tregaskes, C.A., Vervelde, L., Wang, Y., Warren, W.C., Waters, P.D., Webb, D., Weigend, S., Wolc, A., Wright, A.E., Wright, D., Wu, Z., Yamagata, M., Yang, C., Yin, Z.-T., Young, M.C., Zhang, G., Zhao, B., Zhou, H., 2022. Fourth report on chicken genes and chromosomes. Cytogenet. Genome Res. 162, 405–528.
Stark, R., Grzelak, M., Hadfield, J., 2019. RNA sequencing: the teenage years. Nat. Rev. Genet. 20, 631–656.
Tan, X., Liu, L., Liu, X., Cui, H., Liu, R., Zhao, G., 2021. Large-scale Whole Genome sequencing study reveals genetic architecture and key variants for breast muscle weight in native chickens. Genes (Basel) 13, 3.

Tan, X., Zhang, J., Dong, J., Huang, M., Li, Q., Wang, H., Bai, L., Cui, M., Zhou, Z., Yang, S., Wang, D., 2024. Whole-genome variants dataset of 209 local chickens from China. Sci. Data 11, 1–9.

Tang, F., Barbacioru, C., Wang, Y., Nordman, E., Lee, C., Xu, N., Wang, X., Bodeau, J., Tuch, B.B., Siddiqui, A., Lao, K., Surani, M.A., 2009. mRNA-Seq whole-transcriptome analysis of a single cell. Nat. Methods 6, 377–382.

Thiery, A.P., Buzzi, A..L., Hamrud, E., Cheshire, C., Luscombe, N.M., Briscoe, J., Streit, A., 2023. scRNA-sequencing in chick suggests a probabilistic model for cell fate allocation at the neural plate border. Elife 12, e82717.

Tian, J., Zhu, X., Wu, H., Wang, Y., Hu, X., 2023. Serum metabolic profile and metabolome genome-wide association study in chicken. J. Anim. Sci. Biotechnol. 14, 1–15.

Tu, T.-C., Lin, C.-J., Liu, M.-C., Hsu, Z.-T., Chen, C.-F., 2025. Genomic prediction and genome-wide association study for growth-related traits in Taiwan country chicken. Animals 15, 376.

Urgessa, O.E., Woldesemayat, A.A., 2023. OMICs approaches and technologies for understanding low-high feed efficiency traits in chicken: implication to breeding. Anim. Biotechnol. 34, 4147–4166.

Vaccaro, L.A., Porter, T..E., Ellestad, L.E., 2022. The effect of commercial genetic selection on somatotropic gene expression in broilers: a potential role for insulin-like growth factor binding proteins in regulating broiler growth and body composition. Front. Physiol. 13, 935311.

Velez-Irizarry, D., Cheng, H., Hearn, C., 2025. scRNA seq of an F1 cross of Marek's disease resistant and susceptible chickens identifies allele specific expression signatures enriched in transcription modulators. Sci. Rep. 15, 3689.

Wadood, A.A., Xiquan, Z., 2024. Unraveling the mysteries of chicken proteomics: insights into follicle development and reproduction. J. Proteomics. 308, 105281.

Wadood, A.A., Zhang, X., 2024. The omics revolution in understanding chicken reproduction: a comprehensive review. Curr. Issues Mol. Biol. 46, 6248–6266.

Wan, X., Xiao, J., Tam, S.S.T., Cai, M., Sugimura, R., Wang, Y., Wan, X., Lin, Z., Wu, A.R., Yang, C., 2023. Integrating spatial and single-cell transcriptomics data using deep generative models with SpatialScope. Nat. Commun. 14, 7848.

Wang, Y., Bu, L., Cao, X., Qu, H., Zhang, C., Ren, J., Huang, Z., Zhao, Y., Luo, C., Hu, X., Shu, D., 2020. Genetic dissection of growth traits in a unique chicken advanced intercross line. Front. Genet. 11, 2020.

Wang, Y., Cao, X., Luo, C., Sheng, Z., Zhang, C., Bian, C., Feng, C., Li, J., Gao, F., Zhao, Y., Jiang, Z., Qu, H., Shu, D., Carlborg, Ö., Hu, X., 2020a. Multiple ancestral haplotypes harboring regulatory mutations cumulatively contribute to a QTL affecting chicken growth traits. Commun. Biol. 3, 1–13.

Wang, K., Hu, H., Tian, Y., Li, J., Scheben, A., Zhang, C., Li, Y., Wu, J., Yang, L., Fan, X., Sun, G., Li, D., Zhang, Y., Han, R., Jiang, R., Huang, H., Yan, F., Wang, Y., Li, Z., Li, G., Liu, X., Li, W., Edwards, D., 2021. The Chicken Pan-Genome reveals gene content variation and a promoter region deletion in IGF2BP1 affecting body size. Mol. Biol. Evol. 38, 5066–5081.

Wang, L., Li, G., Gao, J., Cheng, J., Yuan, Z., Lu, H., Zeng, W., Zhang, T., 2024a. Untargeted metabolomics reveals the alteration of metabolites during the stewing process of Lueyang black-bone chicken meat. Front. Nutr. 11, 1479607.

Wang, J., Liu, J., Lei, Q., Liu, Z., Han, H., Zhang, S., Qi, C., Liu, W., Li, D., Li, F., Cao, D., Zhou, Y., 2024b. Elucidation of the genetic determination of body weight and size in Chinese local chicken breeds by large-scale genomic analyses. BMC Genomics 25, 1–15.

Wang, C., Ma, W., 2019. Hypothalamic and pituitary transcriptome profiling using RNA-sequencing in high-yielding and low-yielding laying hens. Sci. Rep. 9, 10285.

Wang, S., Wang, Y., Li, Y., Xiao, F., Guo, H., Gao, H., Wang, N., Zhang, H., Li, H., 2022a. Genome-wide association study and selective sweep analysis reveal the genetic architecture of body weights in a chicken f2 resource population. Front. Vet. Sci. 9, 1–9.

Wang, X.J., Xu, S..H., Liu, L., Song, Z.G., Jiao, H.C., Lin, H., 2017. Dietary fat alters the response of hypothalamic neuropeptide Y to subsequent energy intake in broiler chickens. J. Exp. Biol. 15 (220), 607–614.

Wang, L., Xue, Z., Tian, Y., Zeng, W., Zhang, T., Lu, H., 2024c. A single-cell transcriptome atlas of Lueyang black-bone chicken skin. Poult. Sci. 103, 103513.

Wang, Y., Liu, X., Wang, Y., He, Z., Zhao, G., Wen, J., Cui, H., 2024d. Characterization of the pattern of development of key compounds contributing to aroma quality of chicken meat and their metabolic markers. Anim. Res. One Heal. https://doi.org/10.1002/aro2.83.

Wang, H., Zhao, X., Wen, J., Wang, C., Zhang, X., Ren, X., Zhang, J., Li, H., Muhatai, G., Qu, L., 2023. Comparative population genomics analysis uncovers genomic footprints and genes influencing body weight trait in Chinese indigenous chicken. Poult. Sci. 102, 103031.

Willson, N.-L., Forder, R.E.A., Tearle, R., Williams, J.L., Hughes, R.J., Nattrass, G.S., Hynd, P.I., 2018. Transcriptional analysis of liver from chickens with fast (meat bird), moderate (F1 layer x meat bird cross) and low (layer bird) growth potential. BMC Genomics 19, 309.

Wu, S., Dou, T., Wang, K., Yuan, S., Yan, S., Xu, Z., Liu, Y., Jian, Z., Zhao, J., Zhao, R., Wu, H., Gu, D., Liu, L., Li, Q., Wu, D.-D., Ge, C., Su, Z., Jia, J., 2024. Artificial selection footprints in indigenous and commercial chicken genomes. BMC Genomics 25, 428.

Wu, P., Zhou, K., Zhang, J., Ling, X., Zhang, X., Zhang, L., Li, P., Wei, Q., Zhang, T., Wang, X., Zhang, G., 2022. Identification of crucial circRNAs in skeletal muscle during chicken embryonic development. BMC Genomics 23, 330.

Xiao, C., Deng, J., Zeng, L., Sun, T., Yang, Z., Yang, X., 2021. Transcriptome analysis identifies candidate genes and signaling pathways associated with feed efficiency in Xiayan chicken. Front. Genet. 12, 607719.

Xie, L., Luo, C., Zhang, C., Zhang, R., Tang, J., Nie, Q., Ma, L., Hu, X., Li, N., Da, Y., Zhang, X., 2012. Genome-wide association study identified a narrow chromosome 1 region associated with chicken growth traits. PLoS One 7, e30910.

Xie, L., Sun, J., Mo, L., Xu, T., Shahzad, Q., Chen, D., Yang, W., Liao, Y., Lu, Y., 2019. HMEJ-mediated efficient site-specific gene integration in chicken cells. J. Biol. Eng. 13, 90.

Xing, S., Liu, R., Zhao, G., Groenen, M.A.M., Madsen, O., Liu, L., Zheng, M., Wang, Q., Wu, Z., Crooijmans, R.P.M.A., Wen, J., 2021. Time course transcriptomic study reveals the gene regulation during liver development and the correlation with abdominal fat weight in chicken. Front. Genet. 12, 723519.

Xu, J., Velleman, S.G., 2023. Critical role of the mTOR pathway in poultry skeletal muscle physiology and meat quality: an opinion paper. Front. Physiol. 14, 1228318.

Xue, Q., Zhang, G., Li, T., Ling, J., Zhang, X., Wang, J., 2017. Transcriptomic profile of leg muscle during early growth in chicken. PLoS One 12, e0173824.

Yan, Y., Zhu, S., Jia, M., Chen, X., Qi, W., Gu, F., Valencak, T.G., Liu, J.-X., Sun, H.-Z., 2024. Advances in single-cell transcriptomics in animal research. J. Anim. Sci. Biotechnol. 15, 102.

Yang, L., Liu, Z., Ou, K., Wang, T., Li, Z., Tian, Y., Wang, Y., Kang, X., Li, H., Liu, X., 2019. Evolution, dynamic expression changes and regulatory characteristics of gene families involved in the glycerophosphate pathway of triglyceride synthesis in chicken (Gallus gallus). Sci. Rep. 9, 12735.

Yang, S., Wang, Y., Wang, L., Shi, Z., Ou, X., Wu, D., Zhang, X., Hu, H., Yuan, J., Wang, W., Cao, F., Liu, G., 2018. RNA-seq reveals differentially expressed genes affecting polyunsaturated fatty acids percentage in the Huangshan Black chicken population. PLoS One 13, e0195132.

Yao, S., Harder, A., Darki, F., Chang, Y.-W., Li, A., Nikouei, K., Volpe, G., Lundström, J. N., Zeng, J., Wray, N.R., Lu, Y., Sullivan, P.F., Hjerling-Leffler, J., 2025. Connecting genomic results for psychiatric disorders to human brain cell types and regions reveals convergence with functional connectivity. Nat. Commun. 16, 395.

Yin, X., Wu, Y., Zhang, S., Zhang, T., Zhang, G., Wang, J., 2021. Transcriptomic profile of leg muscle during early growth and development in Haiyang yellow chicken. Arch. Anim. Breed. 64, 405–416.

Yu, M., Wang, H., Xu, Y., Yu, D., Li, D., Liu, X., Du, W., 2015. Insulin-like growth factor-1 (IGF-1) promotes myoblast proliferation and skeletal muscle growth of embryonic chickens via the PI3K/Akt signalling pathway. Cell Biol. Int. 39, 910–922.

Zhang, R., Chang, L., Shen, X., Tang, Q., Mu, C., Fu, S., Bu, Z., 2025. Metabolomics analysis reveals characteristic functional components in pigeon eggs. Metabolites 15, 122.

Zhang, J., Chen, X., Cao, J., Chang, C., Geng, A., Wang, H., Chu, Q., Yan, Z., Zhang, Y., Liu, H., 2023a. Proteomic profiling of thigh meat at different ages of chicken for meat quality and development. Foods 12, 2901.

Zhang, Z., Du, H., Yang, C., Li, Q., Qiu, M., Song, X., Yu, C., Jiang, X., Liu, L., Hu, C., Xia, B., Xiong, X., Yang, L., Peng, H., Jiang, X., 2019. Comparative transcriptome analysis reveals regulators mediating breast muscle growth and development in three chicken breeds. Anim. Biotechnol. 30, 233–241.

Zhang, J., Lv, C., Mo, C., Liu, M., Wan, Y., Li, J., Wang, Y., 2021a. Single-cell RNA sequencing analysis of chicken anterior pituitary: a bird's-eye view on vertebrate pituitary. Front. Physiol. 12, 562817.

Zhang, Y., Wang, Y., Li, Y., Wu, J., Wang, X., Bian, C., Tian, Y., Sun, G., Han, R., Liu, X., Jiang, R., Wang, Y., Li, G., Li, W., Hu, X., Kang, X., 2021b. Genome-wide association study reveals the genetic determinism of growth traits in a Gushi-Anka F2 chicken population. Heredity 126, 293–307.

Zhang, M., You, M., Ma, N., Lv, J., 2024. Advance in the application of metabolomics technology in poultry. Front. Vet. Sci. 11, 1501630.

Zhang, T., Zhu, T., Wen, J., Chen, Y., Wang, L., Lv, X., Yang, W., Jia, Y., Qu, C., Li, H., Wang, H., Qu, L., Ning, Z., 2023b. Gut microbiota and transcriptome analysis reveals a genetic component to dropping moisture in chickens. Poult. Sci. 102, 102242.

Zhong, C., Li, X., Guan, D., Zhang, B., Wang, X., Qu, L., Zhou, H., Fang, L., Sun, C., Yang, N., 2024. Age-dependent genetic architectures of chicken body weight explored by multidimensional GWAS and molQTL analyses. J. Genet. Genomics 51, 1423–1434.

Zhou, T., Li, S., Zhong, W., Vihervaara, T., Béaslas, O., Perttilä, J., Luo, W., Jiang, Y., Lehto, M., Olkkonen, V.M., Yan, D., 2011. OSBP-Related Protein 8 (ORP8) regulates plasma and liver tissue lipid levels and interacts with the nucleoporin nup62. PLoS One 6, e21078.

Zhu, Y., Kubota, S., Pasri, P., Rakngam, S., Okrathok, S., Pukkung, C., Yang, S., Khempaka, S., 2025a. Transcriptome analysis of jejunal mucosal tissue in breeder hens exposed to acute heat stress. Poult. Sci. 104, 104532.

Zhu, X.-N., Wang, Y.-Z., Li, C., Wu, H.-Y., Zhang, R., Hu, X.-X., 2023. Chicken chromatin accessibility atlas accelerates epigenetic annotation of birds and gene fine-mapping associated with growth traits. Zool. Res. 44, 53–62.

Zhu, R., Zhang, Y., Jiang, Y., Xu, Z., Tai, Y., Lian, Z., Li, Z., Wang, X., Luo, N., Zhao, G., Deng, X., 2025b. Weighted single-step genome-wide association study identified genomic regions and candidate genes for growth and reproductive traits in Wenchang chicken. Poult. Sci. 104, 104733.