frontiers | Frontiers in Genetics

TYPE Review
PUBLISHED 08 January 2026
DOI 10.3389/fgene.2025.1740301

Check for updates

OPEN ACCESS

EDITED BY
Albano Beja-Pereira,
University of Porto, Portugal

REVIEWED BY
Marcos Edgar Herkenhoff,
Santa Catarina State University, Brazil
Armughan Ahmed Wadood,
South China Agricultural University, China

*CORRESPONDENCE
Julia Metzger,
julia.metzger@tiho-hannover.de

RECEIVED 05 November 2025
REVISED 16 December 2025
ACCEPTED 17 December 2025
PUBLISHED 08 January 2026

CITATION
Sode A, Halder A and Metzger J (2026) Omics in mini-livestock: a genomic perspective on the future of sustainable food systems.
Front. Genet. 16:1740301.
doi: 10.3389/fgene.2025.1740301

COPYRIGHT
© 2026 Sode, Halder and Metzger. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.

Omics in mini-livestock: a genomic perspective on the future of sustainable food systems

Alexander Sode, Arindam Halder and Julia Metzger*

Veterinary Functional Genomics, Institute of Animal Genomics, University of Veterinary Medicine Hannover, Hannover, Germany

Mini-livestock refers to small vertebrates and invertebrates used as human food, animal feed, or for other beneficial purposes. They represent sustainable alternatives to conventional livestock, whose potential is now being revealed through advances in omics technologies. Omics approaches such as genomics, transcriptomics, proteomics, metabolomics, and epigenomics provide comprehensive insights into growth, reproduction, adaptation, and disease resistance of these species, enabling the identification of genetic markers to enhance breeding efficiency and to improve productivity. However, the application of omics technologies in mini-livestock remains limited due to challenges such as high costs, lack of reference genomes, and limited bioinformatics resources. Overcoming these barriers will be crucial for fully harnessing the potential of mini-livestock in improving global food security and environmental sustainability.

KEYWORDS

animal improvement, epigenomics, genomics, metabolomics, mini-livestock, omics, proteomics, sustainability

1 Introduction

"Mini-livestock," from edible insects to small vertebrates, appear as a sustainable alternative to traditional livestock with hidden potential ready to be unleashed by the latest omics technologies. The term mini-livestock includes all vertebrates and invertebrates, which are used as human food, animal feed, a source of income, or for other applications for human benefit, and are at the same time extremely small forms of conventional farm animals or naturally small-scale mammals, birds, reptiles, molluscs or insects (Vietmeyer, 1984; National Research Council, 1991; Hardouin, 1995; Hardouin et al., 2003; Titilola et al., 2015; Ingweye and Kalio, 2020). Mini-livestock have a versatile use and were proposed to be highly beneficial in terms of raising them in small areas and clusters, especially in rural, peri-urban and urban regions to provide human food, capital or manure (Ogunjimi et al., 2012; Klapwijk et al., 2020). It is anticipated that, in the future, these animals will play an increasing role in food security and economically responsible food production (Branckaert, 1995; Paoletti and Dreon, 2005). Among other livestock, mini-livestock have been co-evolving over decades in stressful environments and adapted to harsh conditions with limited feed resources and water availability (Assan, 2013). As an example, edible mealworm species have an unpretentious nature, low water footprint and offer at the same time a protein-rich food resource (Miglietta et al., 2015; van Broekhoven et al., 2015; Sellem et al., 2024). In order to gain detailed insights into the biology of mini-

livestock and to comprehensively understand the genetic basis of traits of interest for future breeding strategies, omics technologies such as genomics, epigenomics, transcriptomics, proteomics or metabolomics have been increasingly recognized as key tools for translating the genome into the phenome (Riggs et al., 2017; Rexroad et al., 2019; Yang X. et al., 2020; Chakraborty et al., 2022; Verardo et al., 2023). Particularly, DNA and RNA sequencing analyses have been frequently applied for conventional and mini-livestock, investigating specific characteristics such as body development and condition, feed conversion, meat quality, or growth (Hu et al., 2007; Lu et al., 2021; Posbergh and Huson, 2021; Manzanilla-Pech et al., 2022; Silva-Vignato et al., 2022; Zhang C. et al., 2022).

Therefore, the aim of this review is to give a comprehensive understanding of mini-livestock and their potential roles across various domains. It explores the application of different omics approaches in advancing mini-livestock research, particularly with regard to improving productivity, product quality, addressing biomedical questions and reducing greenhouse gas emissions and highlights existing limitations and challenges.

2 The concept of mini-livestock

The definition of mini-livestock has evolved over time, making the list of animals classified under this term broad, dynamic, and subject to change (Ingweye and Kalio, 2020). Prior to the current definition of mini-livestock, various earlier terms were employed to describe smaller farm animals (e.g., poultry, rabbits or guinea pigs), as well as breeds that are half of their original size, including micro-pigs or micro-cattle (National Research Council, 1991; Ingweye and Kalio, 2020). The term mini-livestock is not limited to endothermic animals, but also includes ectothermic species like snakes, snails, lizards, frogs, silkworms, honey bees and crickets (Cicogna, 1992; Defoliart, 1995; Hardouin, 1995; Imoru and Babadipe, 2019). Likewise, edible insects like the yellow mealworm, the common house fly or the black soldier fly were considered as mini-livestock and have the highest potential of being animal feed (Voulgari-Kokota et al., 2023).

In the mid-1980s in Latin America, researchers began to categorize livestock based on their different sizes, distinguishing between “main-frames” like cattle and “mini-frames” like sheep. Additionally, the term micro-livestock was introduced to describe small animals suited for household husbandry, especially in resource-poor urban or rural environments in the Global South (Vietmeyer, 1984; Titilola et al., 2015). Micro-livestock typically includes species that adapt to harsh environments, efficiently recycle nutrients, or utilize unconventional resources like rabbits, guinea pigs, or bees (Peters, 1987). However, the term “micro” has also been used more broadly to describe microorganisms, including yeast, fungi or bacteria that serve as a protein source (Hardouin, 1995).

Another early root of the term mini-livestock was the label “unconventional livestock”, referring to species that are not used in conventional agriculture or traditionally domesticated (Peters, 1987). To further differentiate such species, some authors proposed using a relative weight production index, which accounts for the live weight at purchase and meat yield of offspring in proportion to the annual availability of reproductive females (Cicogna, 2000). Based on this index, guinea pigs produced meat equivalent to 6–10 times their own live body weight per year, whereas cattle yielded only about 0.4 times their body weight annually (Cicogna, 2000).

Despite these different backgrounds, the use of the terms “unconventional livestock”, “micro-livestock” or “mini-livestock” remained inconsistent across scientific publications and other sources, which can lead to confusion regarding the species included by these concepts (Hardouin, 1995; Ingweye and Kalio, 2020). Mini-livestock were reported to reproduce quickly, in high numbers, and are economically efficient, resulting in a higher input-output ratio (Hardouin et al., 2003; Titilola et al., 2015). More recently, environmental sustainability has become a key criterion: mini-livestock often generate lower greenhouse gas emissions (CO2-equivalents) per unit of protein produced than conventional livestock (Schanes et al., 2016; Imoru and Babadipe, 2019; Ghosh et al., 2021; Bai et al., 2023). As livestock production is considered to be a large contributor to climate change, accounting for up to 14.5% of all anthropogenic greenhouse gas emissions, more and more efforts are made to study mini-livestock as a potential alternative protein resource (Gerber et al., 2013; Alexander et al., 2017). For example, a study on Global Warming Potential suggested that insect-based resources had a significant potential to reduce the carbon footprints of European consumers, especially when insects are directly consumed as food or used for feeding in broiler production systems (Van Alfen, 2014; Vauterin et al., 2021).

The emission intensity of greenhouse gas has been shown to vary widely across different countries, livestock species, breeds and production systems (Hyslop, 2008; Herrero et al., 2013). Among different strategies to mitigate emissions, breeding schemes that promote the selection of traits enhancing production efficiency, such as residual feed intake or longevity, were suggested to reduce overall emissions (Wall et al., 2010). Ruminants, in particular, served as a model species in this context, as they have been extensively studied for their potential to reduce enteric methane emissions through selective breeding (de Haas et al., 2021). Overall, these studies suggest that genetic selection, alongside improved management practices, offers substantial potential for reducing livestock emissions on a global scale. However, the growing impact of climate change highlights the limitations of mitigation-focused breeding approaches and the pressing need for breeding strategies towards climate-resilience to maintain system integrity (Mutale et al., 2025). Omics approaches present a critical resolution for the identification and selection of traits providing resilience to high temperatures, drought, and climate-driven diseases (Liu et al., 2015; Vitorino Carvalho et al., 2021; Reed et al., 2023; Shi et al., 2023; Feng X. et al., 2024; Karami et al., 2025). In addition to pure physiological tolerance, a variety of adaptive mechanisms have emerged from multi-omics analysis, such as microbially driven plasticity, nutritional stress-driven metabolic flexibility, and epigenetic control in response to varying environments (Wallberg et al., 2017; Guilliet et al., 2022; Sukmak et al., 2024). Furthermore, genomic understanding of photoperiodic and light responses opens a way to consolidate reproductive rhythms or ontogenetic trajectories affected by different climate regions (Morris et al., 2020; Yuyan et al., 2025; Zhao X. et al., 2025).

Building on this, the integration of multi-omics data into breeding programs is essential to unravel the complex biological

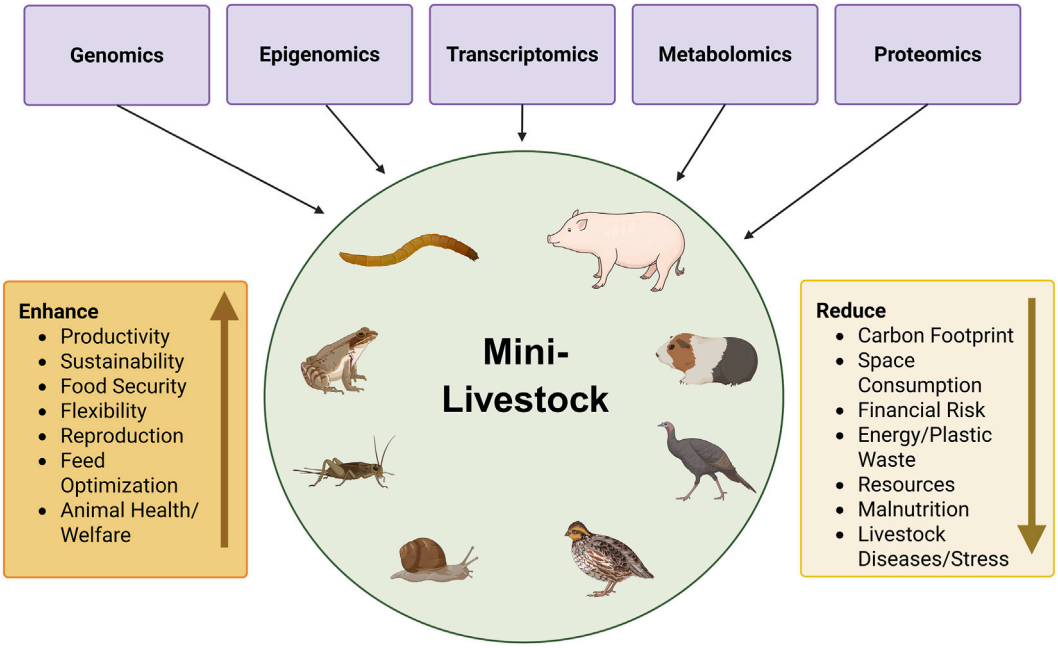

FIGURE 1
Integration of multi-omics approaches in mini-livestock research and their impacts. This figure illustrates how various omics technologies contribute to mini-livestock research. Created in BioRender, agreement no. PZ296612JU.

mechanisms underlying trait variation, enabling more precise and effective selection strategies, not only in conventional livestock but also in emerging mini-livestock species, which have so far received limited attention in this regard (Berry et al., 2011; Yang et al., 2017; Fonseca et al., 2018; Ahmad et al., 2022; Liu and Penagaricano, 2025). While the primary focus of mini-livestock research is on species that contribute to sustainable food and feed production, it is important to recognize that breeding strategies for certain miniature vertebrates, such as laboratory-bred miniature pigs, have followed a different trajectory. These animals are not typically part of food-oriented mini-livestock systems but have made significant contributions as biomedical models, addressing important clinical and translational research questions (Arora et al., 2022; Chakraborty et al., 2022; Jia Y. et al., 2024; Miao et al., 2024b; Zhang J. et al., 2025).

3 A multi-omics perspective on mini-livestock

To fully exploit the genetic potential of mini-livestock in sustainable production systems (Figure 1), comprehensive multi-omics approaches, encompassing genomics, transcriptomics, proteomics, epigenomics, and/or metabolomics, are needed to decode the molecular basis of key traits (Riggs et al., 2017; Yang et al., 2017; Poma et al., 2022). The advent of omics technologies has transformed biological research by shifting the focus from isolated molecular components to the comprehensive analysis of complex biological systems under varying conditions (Hasin et al., 2017; Karczewski and Snyder, 2018). These technologies offer powerful tools for advancing mini-livestock research, enabling deeper insights into the molecular mechanisms underlying key traits (Poma et al., 2022; Xiong et al., 2023; Jia X. et al., 2024). Traditional breeding approaches, initially based on phenotypic selection and later supported by marker-assisted selection (MAS) based on Quantitative Trait Loci (QTL), have contributed significantly to genetic improvement (Meuwissen et al., 2001; Ikeobi et al., 2002; de Koning, 2016). However, these approaches faced limitations, particularly in identifying the genetic basis of complex traits due to high costs and limited resolution (Lande and Thompson, 1990; Grisel, 2000). The integration of genome-wide approaches, such as genome-wide association studies (GWAS), has further advanced our understanding of trait architecture and genetic variation across species, though such studies may still fail to capture systematically gene-gene and gene-environment interactions (Andersson, 2009; Ober et al., 2012; Fang et al., 2019). Subsequently, whole genome sequencing (WGS) has significantly improved the prediction accuracy compared to standard SNP arrays and allowed a more comprehensive assessment of genetic diversity across populations (Moghaddar et al., 2019; Xia et al., 2021). Further insights into the gene expression regulation have been offered by transcriptomics, highlighting the underlying mechanisms and gene-regulatory pathways for traits of interest (Xue Q. et al., 2017; Li J. et al., 2022). Beyond these studies solely focusing on the genetic code itself, epigenomics has emerged as a more recent field, which targets DNA modifications that affect gene expression without altering the DNA sequence itself (Wang and Ibeagha-Awemu, 2020; Zhou et al., 2020). Epigenetic processes, including DNA methylation, chromatin remodelling, histone modifications and non-coding RNA-activity, can lead to heritable changes in gene expression and have been shown to play key roles in development, adaptation, and phenotype variability (Lyko et al., 2010; Felsenfeld, 2014; Herman et al., 2014; Sarg et al., 2015). To fully understand how

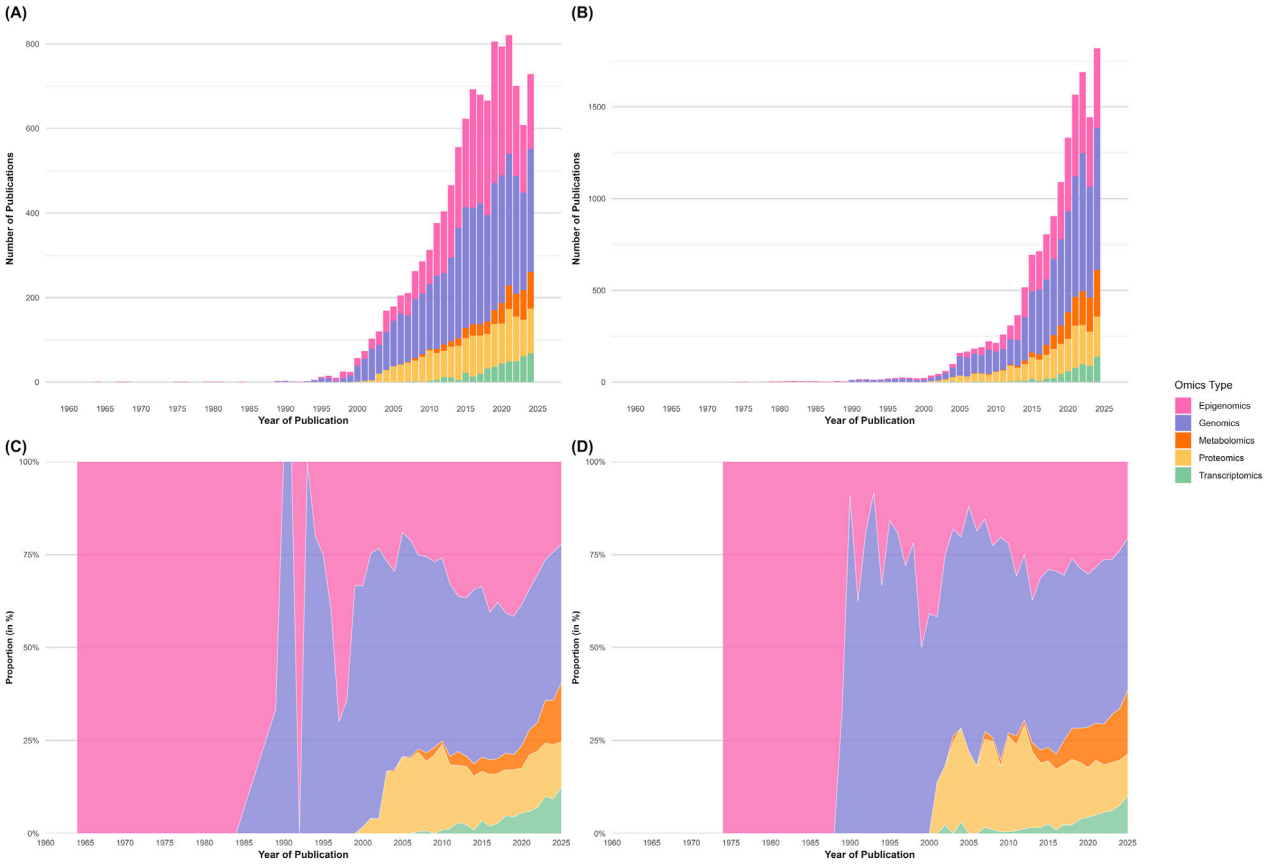

FIGURE 2
Trends and relative proportions of publications applying omics technologies in mini-livestock research. PubMed indexed publications were classified into five major omics categories: epigenomics, genomics, transcriptomics, proteomics and metabolomics. The absolute number of publications per year in invertebrates **(A)**, and in vertebrates **(B)** highlights the expansion of mini-livestock omics research, particularly driven by genomic studies. **(C,D)** Depict the relative proportion of each omics discipline over time for invertebrates and vertebrates, illustrating the diversification of research approaches and the increasing prominence of transcriptomic and proteomic methods. Data source: PubMed (accessed 4 December 2025; search queries utilized specific taxonomic terms and common names for all organisms referenced in this review (e.g., "*Hermetia illucens*", "Black Soldier Fly"), combined with Boolean operators across omics categories).

these regulatory mechanisms shape biological functions, proteomics adds another layer of information targeting the actual protein products and their roles in cellular processes (Haider and Pal, 2013; Aslam et al., 2017). Proteomic analyses enable the investigation of changes in protein levels, post-transcriptional modifications, and interactions in response to various stimuli (Franco et al., 2015; Sierra et al., 2021). Furthermore, metabolomics, as the downstream layer of omics, focuses on the comprehensive profiling of small-molecule metabolites. By examining the metabolome, researchers can gain insights into metabolic pathways and how they impact cellular processes and phenotypic variations (Poma et al., 2022; Du et al., 2025). Complementing these host-centric approaches, metagenomics analyses the collective genomes of microbiota, revealing how microbial communities influence digestion, immune competence, and environmental resilience as factors especially important to the productivity and sustainability of mini-livestock species (Yang et al., 2022; Hou et al., 2024).

To fully exploit the complementary nature of these omics' layers, integrative analytical frameworks are increasingly required. Multi-omics integration enables the joint analysis of diverse molecular layers to understand biological mechanisms that are not detectable when studied in isolation (Hasin et al., 2017; Baiao et al., 2025). Classical approaches rely on correlation-based techniques such as Canonical Correlation Analysis (CCA), which identifies shared patterns across datasets and has been widely applied to multi-omics applications (Jiang et al., 2023). Network-based strategies, including Weighted Gene Co-expression Network Analysis (WGCNA), enable the construction of cross-layer regulatory modules and facilitate the identification of key molecular drivers underlying complex traits (Langfelder and Horvath, 2008). Complementary knowledge-driven approaches, such as pathway and functional enrichment analysis, integrate multi-omics signatures into curated biological pathways through resources such as Kyoto Encyclopedia of Genes and Genomes (KEGG) and Reactome, providing mechanistic interpretability (Kanehisa, 2002; Jassal et al., 2020). More recent advances make use of machine learning, including random forests and deep learning, which can model non-linear relationships and high-dimensional feature interactions characteristic of multi-omics datasets (Libbrecht and Noble, 2015; Abbasi et al., 2024).

TABLE 1 Overview of mini-livestock studies in the field of omics focusing on insects. The table provides a comprehensive summary of omics studies identified for insects, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Black Soldier Fly *(Hermetia illucens)*	Gen-, Epigen-	WGS, Hi-C	High-quality chromosome-level genome assembly, inbreeding events, functional characterization of genes	Generalovic et al. (2021)
Black Soldier Fly *(Hermetia illucens)*	Gen-	WGS	Phylogenetic analysis, cryptic genetic and genomic diversity over five continents, adaptation to different lineages, mitochondrial genome	Guilliet et al. (2022)
Black Soldier Fly *(Hermetia illucens)*	Gen-	WGS	Differentiation of two captive populations, implementation of a breeding program, marker set, monitoring of inbreeding	Cai et al. (2024)
Black Soldier Fly *(Hermetia illucens)*	Gen-	WGS	Nutrients and energy, functions of protein-coding genes, metabolic capability and versatility, insights into transforming waste	Sukmak et al. (2024)
Black Soldier Fly *(Hermetia illucens)*	Gen-, Transcript-	WGS, RNA-seq	High-quality genome, CRISPR/Cas9-based gene editing approach for flightless and enhanced feeding capacity phenotypes, optimizing BSF lines for industrialization and better natural waste recycling, functional gene annotation and pathway-enrichment	Zhan et al. (2020)
Black Soldier Fly *(Hermetia illucens)*	Prote-, Lipid-	nanoLC-MS/MS, GC-MS	Mass spectrometry for proteomic and lipidomic analysis, non-food potential of oil and proteins from insects	Rabani et al. (2019)
Black Soldier Fly *(Hermetia illucens)*	Transcript-, Prote-	RNA-seq, LC-MS/MS	Analysis of cold- and heat-tolerant larvae, differential gene expression analysis, changes in bodyweight, survival rate and metabolism	Feng et al. (2024b)
Black Soldier Fly *(Hermetia illucens)*	Metabol-	LC-MS	Larvae feed utilization rate after UV treatment	Lu et al. (2022a)
Black Soldier Fly *(Hermetia illucens)*	Transcript-	RNA-seq	*De novo* transcriptome sequencing, crude fat accumulation mechanisms, usage for insectile biodiesel	Zhu et al. (2019)
Black Soldier Fly *(Hermetia illucens)*	Transcript-	RNA-seq	Investigation of lysozymes, antimicrobial activity	Zhang et al. (2022c)
Black Soldier Fly *(Hermetia illucens)*	Transcript-, Metabol-	RNA-seq, LC-MS/MS	Effect of pig manure and swill on the transcriptome and metabolome, GO and KEGG enrichment analysis, optimizing substrate selection	Zhang et al. (2024a)
Cricket *(Gryllus veletis and Gryllus lineaticeps)*	Transcript-	RNA-seq	Assembling of the complete mitochondrial genomes, phylogenetic analysis	Torson et al. (2022)
Cricket *(Gryllus spp.& Acheta domesticus)*	Transcript-	RNA-seq	Draft transcriptome, analysis of life stages in different species	Oppert et al. (2020)
Cricket *(Acheta domesticus)*	Transcript-	RNA-seq	Genes associated with flight muscle histolysis	Lu et al. (2022b)
Cricket – Asian *(Teleogryllus occipitalis)*	Gen-	WGS	Draft genome, mitochondrial genome assembly and annotation	Kataoka et al. (2020)
Cricket *(Acheta domesticus)*	Gen-	WGS	High-quality annotated genome assembly, gene groups related to immunity, CRISPR/Cas9-approaches, developing technologies for downstream commercial applications	Dossey et al. (2023)
Cricket *(Gryllus bimaculatus) and (Laupala kohalensis)*	Gen-, Transcript-	WGS, RNA-seq	Comparing two different species, genome assembly and annotation, methylation levels	Ylla et al. (2021)

(Continued on following page)

TABLE 1 (*Continued*) Overview of mini-livestock studies in the field of omics focusing on insects. The table provides a comprehensive summary of omics studies identified for insects, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Earthworm *(Eisenia andrei)*	Gen-, Transcript-	WGS, RNA-seq, scRNA-seq	*De novo* genome assembly, genome annotation, large-scale transcriptome and single-cell sequencing during regeneration	Shao et al. (2020)
Hazelnut weevil *(Curculio dieckmanni)*	Transcript-	RNA-seq	Upregulation of immune-related transcripts, antimicrobial peptides, stress-responsive proteins (e.g., Heat shock protein HSP70), metabolic reprogramming marked by the downregulation of carbohydrate metabolic pathways, energy conservation mechanisms	Wang et al. (2025)
Honey bee – Asian *(Apis cerana)*	Gen-	WGS	*De novo* assembly methods, draft genome, social insect communication, behaviour, evolutionary trajectory	Park et al. (2015)
Honey bee – Asian *(Apis dorsata and Apis mellifera)*	Gen-	WGS	*De novo* assembly, comparison of the two subspecies, and candidate genes for defensive aggression traits	Oppenheim et al. (2020)
Honey bee – Drones *(Apis mellifera)*	Gen-	WGS	Sequencing drones, genomic selection for royal jelly	Wragg et al. (2016)
Honey bee – Italian *(Apis mellifera ligustica)*	Gen-	WGS	Population structure on the Italian peninsula, pattern of genetic variation, morphometric analysis, limited genetic introgression from other breeds	Minozzi et al. (2021)
Honey bee – Swiss/Western *(Apis mellifera mellifera)*	Gen-	WGS	Sequencing individuals from natural history museum, genetic bottlenecks and diversity, selection signatures between modern and historic bees	Parejo et al. (2020)
Honey bee – Western *(Apis mellifera)*	Transcript-	RNA-seq	Meta-Analysis of public RNA-Seq data, construction of reference transcriptome	Yokoi et al. (2022)
Honey bee – Western *(Apis mellifera mellifera)*	Gen-	WGS	Variant detection and genetic variability, association between genomic variants and scouting behaviour, genes for neuronal function, exoskeleton, immune response, salivary gland development and enzymatic food processing	Southey et al. (2016)
Honey bee *(Apis mellifera ligustica)*	Gen-	WGS	Genetic diversity, population structure	Chen et al. (2022a)
Honey bee *(Apis mellifera lineaus)*	Transcript-	RNA-seq	Sublethal effects of insecticides (neonicotinoid thiamethoxam) on the transcriptome, pathway analysis	Shi et al. (2017)
Honey bee *(Apis mellifera)*	Gen-	WGS	Re-sequencing of highland and lowland bees, candidates for adaptation to highland habitats	Wallberg et al. (2017)
Honey bee *(Apis mellifera)*	Gen-, Transcript-	WGS, RNA-seq	Improved assembly, *de novo* annotation, improved gene prediction	Elsik et al. (2014)
Honey bee *(Apis mellifera)*	Transcript-	miRNA-seq	Social behaviour in nurse bees, miRNAs in the brain, differential miRNA expression	Greenberg et al. (2012)
Honey bee *(Apis mellifera)*	Transcript-	RNA-seq	Comparison between queen and worker destined larvae, differential gene expression analysis	Chen et al. (2012)
Honey bee *(Apis mellifera)*	Transcript-	RNA-seq	Brains of honey bee queens	Manfredini et al. (2015)
Honey bee *(Apis mellifera)*	Transcript-	RNA-seq	Molecular effects of cypermethrin, functional analysis of muscular development, structure and function, physiological consequences	Fent et al. (2020)

(Continued on following page)

TABLE 1 (*Continued*) Overview of mini-livestock studies in the field of omics focusing on insects. The table provides a comprehensive summary of omics studies identified for insects, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Honey bee *(Apis mellifera)*	Transcript-	RNA-seq	Sex determination of queen, worker and drone larvae, different pattern of gene expression regulation during the larval development	He et al. (2019b)
Honey bee *(Apis mellifera)*	Transcript-	RNA-seq	Nosema ceranae (parasite) infection, reduced immune function	Badaoui et al. (2017)
Honey bee *(Apis mellifera)*	Transcript-	RNA-seq	Investigation of p-coumaric acid, gene regulation in caste determination, diet of queen-destined larvae	Mao et al. (2015)
Honey bee *(Apis mellifera)*	Transcript-, Epigen-	RNA-seq, BS-seq	Bisulfite sequencing (BS-seq), Israeli Acute Paralysis Virus (IAPV) infection, fat bodies, two distinct molecular pathways, mediated by transcription and methylation	Galbraith et al. (2015)
Honey bee *(Apis mellifera)*	Transcript-	scRNA-seq	Mapping of cell types to different developmental stages of the worker honey bee	Patir et al. (2023)
Honey bee *(Apis mellifera)*	Transcript-	scRNA-seq	Distinct gene expression in the brains of queens and workers	Zhang et al. (2022e)
Honey bee *(Apis mellifera)*	Transcript-	RNA-seq, scRNA-seq	Single-cell transcriptomics and gene regulatory network analyses, bee aggression	Traniello et al. (2023)
Honey bee *(Apis mellifera)*	Transcript-	snRNA-seq, spatial transcriptomics	Expression patterns of brain cells associated with the behavioural maturation from nursing to foraging	Mu et al. (2025)
Honey bee *(Apis mellifera)*	Transcript-, Epigen-	RNA-seq, WGBS	Whole-genome bisulfite sequencing (WGBS), parent-of-origin effects manifested in both DNA methylation and gene expression	Wu et al. (2020b)
Palm Weevil (Rhynchophorus ferrugineus)	Transcript-	RNA-seq	*De novo* transcriptome, differential gene expression, peroxisome pathway associated with metabolic pathways, material transportation and organ tissue formation	Yang et al. (2020a)
Silkworm *(Bombyx mori)*	Gen-, Epigen-	WGS, Hi-C	*De novo* genome assembly, telomere-to-telomere reference genome, synteny	Zhang et al. (2022d)
Silkworm *(Bombyx mori)*	Epigen-	MethylC-Seq	Silkworm domestication, differential analysis of methylomes	Xiang et al. (2013)
Silkworm *(Bombyx mori)*	Gen-, Transcript-	WGS, RNA-seq	High-quality *de novo* genome assembly, prediction and identification of gene families and repetitive elements, gene prediction	Kawamoto et al. (2019)
Silkworm *(Bombyx mori)*	Gen-, Epigen-, Transcript-	WGS, RNA-seq, WGBS	Genome, transcriptome and WGBS sequencing analysis, multi-omics approach, silkworm heterosis	Xu et al. (2022a)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Transcriptome study at different developmental stages	Li et al. (2012)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Susceptibility and resistance to fungal infection of different strains	Xing et al. (2017)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Susceptibility and resistance to fungal infection of different strains	Luan et al. (2018)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Differential gene expression associated with lipopolysaccharide-induced immune priming	Yi and Wu (2024)

(Continued on following page)

TABLE 1 (*Continued*) Overview of mini-livestock studies in the field of omics focusing on insects. The table provides a comprehensive summary of omics studies identified for insects, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Expression changes of the fat body in response to selenium treatment, differentially expressed genes in lipid metabolism and antioxidant defense	Jiang et al. (2020)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Hydrogen sulfide exposure, genes involved in endocytosis, glycolysis/gluconeogenesis, citrate cycle, synthesis of fibroin	Zhang et al. (2021a)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Differentially expressed genes under different temperature conditions	Guo et al. (2018)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Differentially expressed genes in wild versus domestic individuals, immune response, antioxidant systems	Fang et al. (2015)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Differentially expressed genes associated with cocoon and silk yields	Li et al. (2016)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Lead-induced detoxification-related genes	Ye et al. (2024)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Transcriptomics of the anterior silk gland, ion transportation, energy metabolism, protease inhibitors and cuticle proteins involved in the process of silk formation and spinning	Chang et al. (2015)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Differential expression of genes between diapause-inducing and non-diapause-inducing groups	Chen et al. (2017)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Long-non-coding RNAs, hub lncRNAs as regulators of biosynthesis, translocation, and secretion of silk proteins	Wu et al. (2016)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Dosage compensation	Gopinath et al. (2017)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Dimethoate exposure on eggs, silkworm reproduction	Zheng et al. (2022)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Immune priming in haemocytes	Yi et al. (2019)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Immune response to bidensovirus infection, antioxidant genes	Sun et al. (2020)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	High temperature and humidity	Xiao et al. (2017)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Thermal parthenogenesis, differentially expressed genes related to reactive oxygen species removal, DNA repair and heat shock response	Liu et al. (2015)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Ovaries, differentially expressed genes involved in metabolism, genetic information processing, environmental information processing, cellular processes and organismal systems	Xue et al. (2015)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Time-course transcriptome expression data of parts of the silk gland	Masuoka et al. (2024)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Reference transcriptome, expression analysis and profiling, transcriptional factor genes	Yokoi et al. (2021)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Naked pupa mutant, cellular stress responses	Hu et al. (2019)

(Continued on following page)

TABLE 1 (*Continued*) Overview of mini-livestock studies in the field of omics focusing on insects. The table provides a comprehensive summary of omics studies identified for insects, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq	Treatment with titanium dioxide nanoparticle, effect on silk gland, enrichment of metabolic pathway-related genes	Xue et al. (2017a)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq (long reads)	Transcriptome atlas of silk glands using single-molecule long-read sequencing	Chen et al. (2020)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq (long reads)	Improved gene annotation, differentially expressed genes for midgut related to digestive enzyme production, transmembrane transport, chitin metabolism, and hormone regulation	Shen et al. (2022)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq, scRNA-seq	Classification of silkworm hemocytes under baculovirus-infection, infection suppresses the RNA interference and immune response	Feng et al. (2021a)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq, scRNA-seq	Single-cell transcriptomic atlas of the silk-producing organ	Ma et al. (2022)
Silkworm *(Bombyx mori)*	Transcript-	RNA-seq, snRNA-seq, spatial transcriptomics	Single-nucleus and spatial transcriptomics atlas of silk-secreting organs	Ma et al. (2024)
Silkworm *(Bombyx mori)*	Transcript-	scRNA-seq	Hemocyte clusters, broad division of hemocytes in granulocytes, plasmatocytes, oenocytoids	Feng et al. (2022)
Silkworm *(Bombyx mori)*	Transcript-	snRNA-seq	Single-nucleus sequencing of brain hemocytes, cell subsets with antiviral function	Feng et al. (2024a)
Silkworm *(Bombyx mori)*	Transcript-	snRNA-seq	Single-nucleus sequencing of fat body, response to nucleopolyhedrovirus infection	Feng et al. (2023)
Silkworm *(Bombyx mori)*	Transcript-	scRNA-seq	Brain cell repertoire, individual neuropeptide expression	Liu et al. (2024b)
Silkworm *(Bombyx mori)*	Prote-	Tandem-MS	Comparative analysis, diverse functions and dynamic changes, silk protein compositions	Dong and Chen (2013)
Silkworm *(Bombyx mori and Philosamia cynthia ricini)*	Prote-	MADLI-TOF MS	Silk gland proteins, phosphate residues	Zhang et al. (2006)
Silkworm *(Bombyx mori)*	Prote-	nanoLC-MS/MS	Comparative analysis of silk gland, ribosome biogenesis, protein identification and quantification, protein synthesis	Li et al. (2015)
Superworm *(Zophobas atratus)*	Gen-	WGS	Complete mitochondrial genome, phylogenetic analysis	Bai et al. (2019)
Superworm *(Zophobas atratus)*	Transcript-	RNA-seq	*De novo* transcriptome and functional genome annotation, prediction of antimicrobial peptides and haemolytic activity	Lee et al. (2021)
Superworm *(Zophobas atratus)* Yellow mealworm *(Tenebrio molitor)*	Gen-	WGS	High-quality genome assemblies, gene prediction, phylogenomic and synteny analysis	Kaur et al. (2023)
Yellow Mealworm *(Tenebrio molitor)*	Gen-, Transcript-	WGS, RNA-Seq	Genome assembly based on combination of long, short reads and Hi-C data	Eleftheriou et al. (2021)
Yellow Mealworm *(Tenebrio molitor)*	Gen-	WGS	*De novo* genome assembly, mitochondrial genome	Eriksson et al. (2020)

(Continued on following page)

TABLE 1 (*Continued*) Overview of mini-livestock studies in the field of omics focusing on insects. The table provides a comprehensive summary of omics studies identified for insects, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Yellow Mealworm *(Tenebrio molitor)*	Gen-, Epigen-, Transcript-	WGS, Hi-C, RNA-seq	Assembly, gene prediction, gene annotation, CRISPR-Cas gene editing, life stage-specific transcriptomes	Oppert et al. (2023)
Yellow Mealworm *(Tenebrio molitor)*	Transcript-	RNA-seq	Gene expression profiling, identify chitin coding genes, coding enzymes, polygenetic dividing, biological functions	Li et al. (2022b)
Yellow Mealworm *(Tenebrio molitor)*	Transcript-	RNA-seq	Sequencing with focus on immune response genes to parasitisation, molecular host-parasitoid interaction	Zhu et al. (2013)
Yellow Mealworm *(Tenebrio molitor)*	Transcript-	RNA-seq	Immune gene expression after infection, identifying defence mechanisms, pathway analysis	Johnston et al. (2013)
Yellow Mealworm *(Tenebrio molitor)*	Transcript-, Prote-	RNA-seq, MALDI-TOF MS	Comparison of neuropeptides and transcriptomic data, *de novo* sequencing, gene bank (neuropeptidomics)	Marciniak et al. (2022)

Together, this integration of omics layers provides a resource for dissecting complex traits and guiding precision breeding and management strategies (Yang et al., 2017).

The technological advances and integrative analytical capabilities have also contributed to the growing adoption of omics-based research in mini-livestock species, with publication numbers increasing steadily since 2010 (Figures 2A,B). In invertebrates, epigenomics was the first omics discipline to be reported, with studies dating back to 1964, whereas transcriptomics was introduced much later, with the first publications appearing in 2007. In vertebrates, the first record in the field was in epigenomics in 1974, and transcriptomics was introduced as the latest field in 2002. Beyond these initial milestones, the composition of the field has shifted considerably. The relative contribution of functional omics, most notably transcriptomics and proteomics, has increased markedly in recent years, as illustrated in Figures 2C,D. However, studies focused on mini-livestock still represent only a small fraction of the approximately 2.5 million omics-related publications currently indexed in PubMed (https://pubmed.ncbi.nlm.nih.gov/), with genomic studies making up the majority of this research. With this growing body of research on omics technologies and their potential applications, we can now examine how these approaches are being applied to different mini-livestock groups. Among them, insects have emerged as a particularly well-studied category, with numerous omics investigations providing deep insights into their physiology, genetics, and potential for sustainable production.

4 Omics in invertebrates

Invertebrates, particularly those considered as mini-livestock, have become a major focus of recent omics research due to their potential for sustainable protein production. Among them, edible insects have been studied extensively, revealing key adaptations and breeding opportunities (Table 1). In this review, species are presented according to the extent of available scientific literature and ongoing research activities, which is influenced by industrial relevance, and does not reflect any intended prioritization by the authors. For example, the black soldier fly (BSF, *Hermetia illucens*), has emerged as a model species due to its nutritional profile, rearing efficiency, and strong potential as a sustainable protein source (Rumpold and Schlüter, 2013; Huang et al., 2019; Zhan et al., 2020). Subsequently, a novel chromosome-level genome assembly was generated in BSF using long reads, linked short reads and chromatin conformation data (Hi-C) (Generalovic et al., 2021). In addition, another research group constructed a high-quality genome from BSF based on short-read sequencing data and highlighted its findings of 50 antimicrobial peptides, the largest antimicrobial peptide family identified in insects to date, as well as a set of core microbiota suggesting a targeted adaptation of BSF to a pathogen-rich environment and digestion of organic waste (Zhan et al., 2020). Using these reference genomes, multiple studies performed WGS to monitor inbreeding of populations and applied genomic information for commercial breeding programs (Cai et al., 2024). To construct mitochondrial assemblies, whole genome shotgun sequencing was performed, enabling the reconstruction of phylogenetic relationships among major lineages and revealing their long-term evolution with low genomic diversity (Guilliet et al., 2022). Furthermore, WGS-based annotations of gene and protein functions of different BSF strains highlighted major metabolic gene functions and pathways involved in nutrient and energy metabolism (Sukmak et al., 2024). Similarly, initial insights into the genomic potential of the house cricket (*Acheta domesticus)* as a food source and for broader applications were provided by sequencing and assembling a reference genome using both long-read sequencing, Chicago libraries, and Hi-C data (Dossey et al., 2023). Furthermore, sequencing, assembly and annotation of the Mediterranean field cricket (*Gryllus bimaculatus*) genome, and its comparison to the Hawaiian cricket (*Laupala kohalensis)* and other insects, revealed that hemimetabolous (incomplete metamorphosis) genomes have expanded largely through transposable element activity (Ylla et al., 2021). In the yellow mealworm (*Tenebrio molitor*), long and short

reads and long-range data obtained from a male pupa, transcripts from 12 different life stages/sexes, as well as an adult individual's head, highlighted the challenge posed by a comparatively large genome with mostly homogeneous satellite DNA sequences of high copy numbers, and provided a framework for future genomics studies (Eriksson et al., 2020; Eleftheriou et al., 2021; Oppert et al., 2023). A similar approach was used to build a reference genome for the superworm (*Zophobas morio* = *Zophobas atratus*) and a further independent reference for the yellow mealworm (Kaur et al., 2023). Subsequent comparison of both genomes revealed extensive macrosynteny across the family *Tenebrionidae*, as well as numerous within-chromosome rearrangements (Kaur et al., 2023). An even higher level of reference genome completeness was reached in the silkworm (*Bombyx mori)*, for which researchers produced a telomere-to-telomere assembly using long-read sequencing technologies as well as a reference transcriptome (Kawamoto et al., 2019; Yokoi et al., 2021; Zhang T. et al., 2022). In the earthworm (*Eisenia andrei*), researchers produced a chromosome-level reference genome, a large-scale transcriptome and single-cell RNA-sequencing data to investigate the cause for its strong regenerative ability (Shao et al., 2020). Furthermore, *de novo* assembly methods were applied in the honey bee (*Apis mellifera/dorsata/cerana*) to produce draft genomes, which were used to support research in the field of social communication, defensive aggression and scouting behaviour (Elsik et al., 2014; Park et al., 2015; Southey et al., 2016; Oppenheim et al., 2020). Functional genomic analysis revealed 60 genomic variants associated with scout and recruit behavioural castes, within 39 genes corresponding with neuronal function, exoskeleton, immune response, salivary gland development and enzymatic food processing (Southey et al., 2016). In addition, genomic sequences from modern and historic honey bee populations were studied for potential genetic bottlenecks, selection signatures and diversity (Wragg et al., 2016; Parejo et al., 2020; Minozzi et al., 2021; Chen C. et al., 2022).

As a result, genomic studies have provided a comprehensive understanding of the genetic code, whereas epigenetic research has elucidated the complex interplay between environmental factors and gene expression in insect mini-livestock. The utilization of insects as model organisms in epigenetic studies has yielded significant insights into the epigenetic mechanisms underlying disease susceptibility and transgenerational inheritance patterns (Mukherjee et al., 2015). For example, studies on silkworm revealed the role of DNA methylation in rapid phenotypic adaptation mediated by DNA methyltransferase 1 (DNMT1), which might have contributed to the domestication of this species (Xiang et al., 2013; Wang X. et al., 2021). However, on the level of gene expression, transcriptomics studies showed that modern breeding potentially had a stronger selection effect on silk yield traits and pathogen tolerance in the silkworm than its domestication (Fang et al., 2015; Li et al., 2016; Luan et al., 2018). Furthermore, RNA-seq data from larvae provided an insight into the resistance and susceptibility of different strains against fungal, virus or bacterial infection, thermo-tolerance, diapause preparation, detoxification mechanisms and antioxidant defence, highlighting the complexity of the silkworm transcriptome (Li et al., 2012; Chen et al., 2017; Xiao et al., 2017; Xing et al., 2017; Guo et al., 2018; Jiang et al., 2020; Sun et al., 2020; Zhang R. et al., 2021; Ye et al., 2024; Yi and Wu, 2024). In contrast to protein-coding mRNAs, long non-coding RNAs were postulated to be even more specific for different silkworm tissues and were found to be involved as regulators of the biosynthesis, translocation, and secretion of silk proteins (Wu et al., 2016). At even higher resolution, single cell sequencing of silkworm haemocytes revealed a high level of specialization of these cells and showed a significant effect of RNA interference (RNAi) suppression induced by a baculovirus infection (Feng M. et al., 2021; Feng et al., 2022). A similar strategy was used to build long-read-based transcriptome and single-cell transcriptome atlases of the silk gland, which offered a comprehensive and detailed understanding of its function and regulation (Chen et al., 2020; Ma et al., 2022). This was even enhanced by a spatiotemporal transcriptomic atlas of the silk glands, and multi-omics approaches, providing a valuable reference for elucidating the mechanism of efficient silk protein synthesis (Xu H. et al., 2022; Ma et al., 2024). On the protein level, silk gland development and silk protein protection and compositions further completed the picture (Zhang et al., 2006; Dong et al., 2013; Li et al., 2015).

Similar to the silkworm, functional omics studies in BSF were aimed at the non-food potential of this species. *De novo* transcriptome sequencing has identified genes involved in fat metabolism, thereby contributing to more economical BSF-based biodiesel production (Zhu et al., 2019). In contrast, transcriptome, metabolome and proteome analyses of BSF larvae have elucidated bioconversion performance under different temperature conditions and dependent on the type of organic waste, as well as highlighted an association of UV light treatment of larvae with the generation of functional proteins and bioactive compounds (Lu J. et al., 2022; Zhang S. et al., 2022; Feng X. et al., 2024). It was found that the active intestinal microbes and their functional genes in the BSF gut microbiome delineated the genetic variability in wild-collected and domesticated BSF populations from different continents and showed a response to high concentrations of antibiotics (Khamis et al., 2020; Pei et al., 2023).

In the yellow mealworm, gene expression profiling was particularly carried out to learn more about tissue- or developmental stage-specific genes and their potential function, identifying enzymes involved in chitin metabolism, parasitoid-induced immune-related genes, and factors underlying long-lasting immune response to bacterial challenge (Johnston et al., 2013; Zhu et al., 2013; Li L. et al., 2022). Similarly, a *de novo* transcriptome assembly and functional annotation in the superworm was used to predict antimicrobial peptides and haemolytic activity (Lee et al., 2021). Both yellow mealworm and superworm also underwent transcriptomic and mass spectrometry analyses of the central nervous system to identify neuropeptides and neuropeptide-like and protein hormones (Marciniak et al., 2022). In general, the brain has been a target of various insect species studies, due to the interest in socially regulated behaviour such as division of labour among honey bees. For example, mRNA or microRNA expression levels in the honey bee brain have been analyzed for their role in behavioural specialization of adult workers or queen (Greenberg et al., 2012; Manfredini et al., 2015). Single-nucleus RNA sequencing and spatial transcriptomics of the honey bees brain revealed expression patterns of brain cells associated with the behavioural maturation from nursing to foraging (Mu et al., 2025). In addition, honey bee caste differentiation was investigated using high-throughput RNA-Seq of larvae (Chen

TABLE 2 Overview of mini-livestock studies in the field of omics focusing on molluscs. The table provides a comprehensive summary of omics studies identified for molluscs, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Apple Snail *(Pomacea canaliculata)*	Gen-	WGS	*De novo* genome assembly at chromosome level, transposable elements, cellular homeostasis system, invasiveness	Liu et al. (2018a)
Apple Snail *(Pomacea canaliculata)*	Gen-	WGS, RNA-seq, Hi-C	*De novo* genome assembly, gene annotation, genes associated with low temperature adaption	Lu et al. (2024)
Apple Snail *(Pomacea canaliculata)*	Transcript-, Metabol-	RNA-seq, LC-MS/MS	Arsenic pollution, stress response in freshwater snails	Bi et al. (2024)
Apple Snail *(Pomacea canaliculata)*	Transcript-	RNA-seq	*De novo* transcriptome assembly of different genera of *Ampullariidae*, development of AmpuBase database	Ip et al. (2018)
Apple Snail *(Pomacea canaliculata)*	Prote-	LC-MS/MS	Perivitelline fluid proteomes, aquatic and aerial egg-laying *Ampullariidae*, selection events, evolutionary transition	Ip et al. (2019)
Asian Tramp Snail *(Bradybaena similaris)*	Gen-, Transcript-, Epigen-	WGS, RNA-seq, Hi-C	*De novo* chromosome-level assembly, gene annotation, structural arrangement via Hi-C	Ishii et al. (2025)
Asian Tramp Snail *(Bradybaena similaris)*	Gen-, Transcript-	RNA-seq, sRNA-seq	Xenobiotic metabolism-related genes and potential regulatory miRNA	Yang et al. (2020b)
Chinese Mystery Snail *(Cipangopaludina cathayensis)*	Gen-, Transcript-, Epigen-	WGS, Hi-C, RNA-seq	First chromosome-level genome, anchoring pseudochromosomes with Hi-C, putative genes for evolutionary studies	Ma et al. (2023)
Giant African Land Snail *(Achatina fulica)*	Gen-, Transcript-, Epigen-	WGS, Hi-C, RNA-seq	First *de novo* chromosomal-level genome assembly, k-mer-based method, phylogenetic analysis	Guo et al. (2019)
Roman Snail *(Helix pomatia)*	Transcript-	RNA-seq	Complete mitogenome, phylogeny	Orabek et al. (2019)
Roman Snail (*Helix pomatia*)	Transcript-	RNA-seq	Reference transcriptome, adenosine deaminase-related growth factor	Tzertzinis et al. (2023)
Rough Periwinkle *(Littorina saxatilis)*	Gen-	WGS	Genomics of rapid parallel adaptation in response to two independent environmental axes, chromosomal inversions	Morales et al. (2019)
Rough Periwinkle *(Littorina saxatilis and arcana)*	Gen-	WGS	Whole genome data from 107 snails, chromosomal inversion polymorphisms	Reeve et al. (2024)
Rough Periwinkle *(Littorina saxatilis)*	Gen-, Epigen-, Transcript-	WGS, RNA-seq, Hi-C	Chromosome-scale reference genome	De Jode et al. (2024)
Thyme Snail *(Candidula unifasciata)*	Gen-, Transcript-	WGS, RNA-seq	*De novo* genome assembly, gene annotation	Chueca et al. (2021)

et al., 2012; Mao et al., 2015; He X. J. et al., 2019). More recently, single cell RNA sequencing (scRNA-seq) has been applied to identify caste differentiation-related factors in the queen and to map cell types across developmental stages (prepupa at day 11 and pupa at day 15) of worker honey bees (Zhang W. et al., 2022; Patir et al., 2023). Furthermore, the impact of numerous biotic stressors on honey bees has been extensively studied using functional omics methods; Researchers employed RNA-seq to characterize immune responses to parasite infection or insecticide exposure, and examined methylation patterns in the fat body linked to virus infection (Galbraith et al., 2015; Badaoui et al., 2017; Shi et al., 2017; Fent et al., 2020). Similarly, immune responses were studied in the red palm weevil (*Rhynchophorus ferrugineus*), with a primary focus on effective pest-management through potential gene knockdowns, although its possible application as a food source was also considered (Yang H. et al., 2020; Fernando et al., 2023).

Although most of these above-mentioned studies focused on individual research questions and species, efforts have also been made to analyse omics data across species; For example, High-Performance Liquid Chromatography–Tandem Mass Spectrometry (HPLC-MS/MS) technology was applied to construct a novel integrated metabolic database for nine insect species across three metamorphosis types identifying 1,442 metabolites (Li et al., 2023). The study by Li *et al.* revealed significantly enriched pathways, including ABC transporters and tyrosine metabolism, thereby creating a valuable reference that enhances our understanding of insect metabolic evolution and adaptation (Li et al., 2023). Genome assemblies of insects and further omics data have been collected in the InsectBase (http://www.insect-genome.com), which has made significant progress by storing more than 16 million sequences from 815 species to date (Yin et al., 2016; Mei et al., 2022). However, this represents only a small fraction of the 2,205 insects classified as edible (Omuse et al., 2024), highlighting the need for greater efforts to gather more comprehensive data on these species. Modern urban insect farming projects, such as small-scale cricket rearing initiatives in Kenya, BSF bioconversion facilities in Singapore, and a yellow mealworm pilot production in the Netherlands, demonstrated how insect breeding could be integrated into future city environments

TABLE 3 Overview of mini-livestock studies in the field of omics focusing on mammals. The table provides a comprehensive summary of omics studies identified for mammals, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Cane Rat *(Thryonomys swinderianus)* Guinea Pig *(Cavia porcellus)*	Metabol-, Transcript-	UHPLC-MS/MS, RNA-Seq	Ultra-High-Performance Liquid Chromatography –Tandem Mass Spectrometry (UHPLC-MS/MS), common molecular markers and pathways between rats and guinea pigs in response to liver toxicity	Schyman et al. (2021)
Capybara *(Hydrochoerus hydrochaeris)*	Gen-	WGS	Gigantism, phylogenetic pathways, adaptive protein evolution, postnatal bone growth	Herrera-Alvarez et al. (2021)
Capybara *(Hydrochoerus hydrochaeri)*	Gen-	WGS	Draft genome	Babarinde and Saitou (2020)
Capybara *(Hydrochoerus hydrochaeris)* Guinea Pig *(Cavia porcellus) (Cavia aperea)*	Gen-	WGS (from archive)	Mitochondrial analysis, phylogenetic inference, pattern identification, comparison with guinea pigs	da Silva et al. (2024)
Guinea Pig *(Cavia aperea)*	Gen-, Epigen-	WGS, MEBS	Methylated DNA Enrichment by Binding and Sequencing (MEBS), methylome analysis, DNA enrichment	Weyrich et al. (2014)
Guinea Pig *(Cavia porcellus)*	Gen-	WGS (from archive)	Phylogenetics, immunoglobulin heavy and light chain genes, antibody diversity	Guo et al. (2012)
Guinea Pig *(Cavia porcellus)* Rabbit *(Oryctolagus cuniculus)*	Transcript-	RNA-seq	Brain gene expression level of domesticated versus wild animals	Albert et al. (2012)
Miniature pig *(Sus Scrofa domesticus)*	Gen-	WGS	Comparison of the genomic sequence of microminipigs, small-scale SNPs and translational modifications, large-scale deletion and insertion polymorphisms	Miura et al. (2014)
Miniature pig *(Sus Scrofa domesticus)*	Gen-, Transcript-	WGS, RNA-seq	Population genomics in different minipigs (Bama, Göttingen, Mini-LEWE, Wuzhishan, Yucatan, Korean, Minnesota), *PLAG1*, *CHM*, and *ESR1* are candidate key genes for body size determination	Kwon et al. (2024)
Miniature pig *(Sus Scrofa domesticus)*	Metabol-	LC-MS	Liquid Chromatography–Tandem Mass Spectrometry (LC-MS/MS), postprandial metabolic responses, significant amino acids and phospholipids significant in metabolism after food intake	Polakof et al. (2015)
Miniature pig – Bama minipig *(Sus scrofa domesticus)*	Gen-, Epigen-, Transcript-	WGS, RNA-seq, Hi-C	3D genome organization and performed transcriptome characterization of two adipose depots	Zhang et al. (2022b)
Miniature pig – Bama minipig *(Sus scrofa domesticus)*	Gen-, Epigen-, Transcript-	WGS, RNA-seq, Hi-C	Full chromosome-scale reference genome, model for diabetic disease	Zhang et al. (2019)
Miniature pig – Bama minipig *(Sus scrofa domesticus)*	Prote-	LC-MS/MS	Cartilage post-traumatic osteoarthritis of anterior cruciate ligament reconstruction, osteoarthritis-related proteins	Li et al. (2020a)
Miniature pig – Bama minipig *(Sus scrofa domesticus)*	Metabol-	LC-MS/MS	Biomarkers for early diagnosis of atherosclerosis under high-cholesterol and high-fat diet	Jia et al. (2024b)
Miniature pig – Bama minipig *(Sus scrofa domesticus)*	Transcript-	scRNA-seq	Single-cell transcriptomic atlas, unique markers for various tissues and organs	Chen et al. (2025)
Miniature pig – Bama minipig *(Sus scrofa domesticus)*	Transcript-	snRNA-seq	Single-nucleus RNA sequencing (snRNA-seq), transcriptome profiling of Peyer's patches, mesenteric lymph node, and spleen of germ-free and specific pathogen-free piglet	Miao et al. (2024b)
Miniature pig – Bama minipig *(Sus scrofa domesticus)*	Transcript-	snRNA-seq	Single-cell sequencing of Bama pig testes from fetal stage through infancy, puberty to adulthood	Wang et al. (2024a)

(Continued on following page)

TABLE 3 (*Continued*) Overview of mini-livestock studies in the field of omics focusing on mammals. The table provides a comprehensive summary of omics studies identified for mammals, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Miniature pig – Bama minipig *(Sus scrofa domesticus)*	Transcript-	scRNA-seq	Single-nucleus RNA sequencing on myocardial samples from both wild-type and metabolic disease-susceptible transgenic pigs	Zhang et al. (2025a)
Miniature pig – Bama minipig, Tibetan pig *(Sus scrofa domesticus)*	Transcript-	RNA-seq	Transcriptome profiling in pituitary gland	Shan et al. (2014)
Miniature pig – Banna miniature pig *(Sus scrofa domesticus)*	Gen-, Epigen-, Transcript-	WGS, RNA-seq, Hi-C	High-quality chromosome-scale reference genome	Chen et al. (2024)
Miniature pig – Diannan small-ear minipig *(Sus scrofa domesticus)*	Gen-	WGS	Genomic characterization, selection signatures for genomics regions affecting meat quality, body size, adaptability, and appetite	Wu et al. (2020a)
Miniature pig – Diannan small-ear minipig *(Sus scrofa domesticus)*	Gen-	WGS	Re-sequencing, mutation for white-point coat colour	Lu et al. (2016)
Miniature pig – Diannan small-ear minipig *(Sus scrofa domesticus)*	Transcript-	RNA-seq, miRNA-seq	Differential gene expression of muscle tissue from Diannan Small-ear, Tibetan pig, Landrace and Yorkshire, key genes for lipid deposition and muscle growth	Wang et al. (2015)
Miniature pig – different types *(Sus Scrofa domesticus)*	Gen-	WGS	Multi-tool copy number detection, miniature pig breeds across different geographical regions	Berghofer et al. (2022)
Miniature pig – Goettingen minipig *(Sus scrofa domesticus)*	Transcript-	scRNA-seq	Pertussis vaccine, antigen-specific humoral and cellular responses, PBMCs	Vaure et al. (2021)
Miniature pig – Goettingen minipig *(Sus scrofa domesticus)*	Transcript-	RNA-seq	Analysis of human antibody transcripts in humanised animals, immunoglobulin gene rearrangements and expression, testing therapeutic approaches	Flisikowska et al. (2022)
Miniature pig – Goettingen minipig *(Sus scrofa domesticus)*	Epigen-	LHC-BS	Liquid Hybridization Capture Bisulfite Sequencing, diet-induced DNA methylation in liver, obesity-related effects	Feng et al. (2021b)
Miniature pig – Goettingen minipig *(Sus scrofa domesticus)*	Prote-	UHPLC/MS	Obesity-related metabolome and gut microbiota	Curtasu et al. (2020)
Miniature pig – Goettingen minipig *(Sus scrofa domesticus)* Tibetan wild boar *(Sus scrofa)*	Gen-, Transcript-	WGS, RNA-seq	Chromosome-level based genome of Göttingen minipig, transcriptomics for tissues with pharmaceutical relevance	Heckel et al. (2015)
Miniature pig – Goettingen minipig Mini-LEWE *(Sus scrofa domesticus)*	Gen-	WGS	Selective sweeps, body size, androgen receptor AR gene as candidate	Reimer et al. (2018)
Miniature pig – Korean minipig *(Sus scrofa domesticus)*	Gen-, Transcript-	WGS, RNA-seq	High-quality chromosome-level genome annotation and assembly	Wy et al. (2024)
Miniature pig – Korean minipig *(Sus scrofa domesticus)*	Gen-, Transcript-	WGS, RNA-seq	Immune response, gene expression patterns, genes as potential biomarkers	Arora et al. (2022)
Miniature pig – Micro-pig from Medi Kinetics *(Sus scrofa domesticus)*	Gen-	WGS	Genes of interest in Micro-pigs, runs of homozygosity analysis	Son et al. (2020)
Miniature pig – MiniLEWE *(Sus scrofa domesticus)*	Transcript-	RNA-seq	Identification of bone marrow-derived mesenchymal stem cell markers, key driver genes for differentiation, differential gene expression analysis	Khaveh et al. (2024)
Miniature pig – Ossabaw *(Sus scrofa domesticus)*	Gen-, Transcript-	WGS, RNA-seq (from database)	*De novo* genome assembly and annotation, leptin receptor has possible significant effects on obesity	Zhang et al. (2021b)
Miniature pig – Wisconsin Miniature Swine *(Sus scrofa domesticus)*	Gen-, Epigen-	WGS, Hi-C	Draft genome assembly	Veith et al. (2025)

(Continued on following page)

TABLE 3 (*Continued*) Overview of mini-livestock studies in the field of omics focusing on mammals. The table provides a comprehensive summary of omics studies identified for mammals, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Miniature pig – Wuzhishan pig *(Sus scrofa domesticus)*	Gen-	WGS	*De novo* Chinese pig genome, high level of homozygosity	Fang et al. (2012)
Miniature pig – Wuzhishan pig *(Sus scrofa domesticus)*	Epigen-	MeDIP-seq	DNA methylome of blood leukocytes, Chinese indigenous versus Western pig breeds	Yang et al. (2016)
Miniature pig – Yucatan minipig (*Sus scrofa domesticus*)	Gen-	WGS (from database)	Identification of non-synonymous single nucleotide polymorphisms (nsSNPs) in selective sweep regions	Kwon et al. (2019)
Miniature pig – Yucatan minipig *(Sus Scrofa domesticus*	Metabol-	UHPLC–MS/QTOF	Metabolome of serum, urine and liver, diet- and cloning-induced metabolic changes	Curtasu et al. (2019)
Miniature pig – Yucatan minipig *(Sus scrofa domesticus)*	Prote-	LC-MS/MS	Collagen subtypes and crosslinks in different cartilages	Bielajew et al. (2021)
Mole-Rat – African *(Cryptomys hottentotus)*	Transcript-	RNA-seq	Positive selection analysis for candidate genes associated with lifespan	Sahm et al. (2018)
Mole-Rat – African *(Cryptomys hottentotus)*	Epigen-	ChIP-seq, Hi-C (from archive)	Regulatory evolution in the heart and liver tissue, epigenomic profiles, Chromatin Immunoprecipitation Sequencing (ChIP-seq)	Parey et al. (2023)
Rabbit *(Oryctolagus spp.)*	Gen-, Transcript-, Metabol-	RNA-seq, LC-MS/MS	Microbiological regulation with antibiotic-free diet, microbial gene sequencing, differential gene expression and metabolome analysis	Chen et al. (2022b)
Rabbit *(Oryctolagus cuniculus)*	Gen-	SLAF-seq	Genetic variants associated with growth, carcass and meat quality, GWAS	Yang et al. (2020c)
Rabbit *(Oryctolagus cuniculus)*	Prote-	LC-MS/MS	Ageing model system, rabbit liver, liver proteins across age groups, alterations in metabolism affect protein expression	Amin et al. (2020)
Rabbit *(Oryctolagus spp.)*	Gen-	WGS	Resequencing and comparison of wild and domestic rabbits, loci for tame behaviour	Carneiro et al. (2014b)
Rabbit *(Oryctolagus spp.)*	Metagen-	Shotgun metagenome sequencing	Effects of probiotics on growth performance, immunity, intestinal flora and antioxidant capacity, effect of probiotics on health, genome sequencing of microbes	Hou et al. (2024)
Rabbit *(Oryctolagus spp.)*	Metagen-, Metabol-	WMS, LC-MS	WMS (shotgun metagenomic sequencing), longitudinal dynamics of rabbit gut microbiota and host adaptability, functional gene diversity, comparing lipid metabolism in newborns versus adults	Zhao et al. (2024)
Rabbit *(Oryctolagus spp.)*	Metagen-, Transcript-, Metabol	RNA-seq, UHPLC–MS/MS	Microbial metagenomics, transcriptome, and non-targeted metabolomics sequencing of the cecum microflora, differential gene expression analysis	Wang et al. (2022a)
Rabbit *(Oryctolagus spp.)*	Prote-	LC-MS/MS	Comparative and quantitative analysis of colostrum and mature milk, differentially abundant proteins related to immune response and fatty acid metabolism	Huang et al. (2024)
Rabbit *(Oryctolagus spp.)*	Prote-	nanoLC-MS/MS	Characterizing seminal plasma proteins, influence of genetic origin and seasonality	Casares-Crespo et al. (2018)
Rabbit *(Oryctolagus spp.)*	Transcript-, Prote-	RNA-seq, LC-MS/MS	Obese models with high fat diet, differential gene expression analysis	Li et al. (2021)
Rabbit *(Oryctolagus spp.)*	Metabol-	H-NMR metabolomics	Proton Nuclear Magnetic Resonance (H-NMR) metabolomics, influence of early plant saccharide ingestion on gene expression signatures and gut bacteriome and metabolome	Paes et al. (2024)

to supply sustainable protein and manage organic waste streams (Ayieko et al., 2016; Dalton and Al-Zubiedi, 2019; Ramzy et al., 2025).

Beyond insects, other invertebrate groups such as molluscs (Table 2) are also gaining attention, particularly because of their central role in aquaculture and their unique physiological adaptations revealed by omics studies (Klein et al., 2019). As with insects, several mollusc species were already characterized through *de novo* genome sequencing and chromosome-level assemblies (Liu C. et al., 2018; Guo et al., 2019; Chueca et al., 2021; Ma et al., 2023; Ishii et al., 2025). The combination of short reads and long reads with Hi-C sequences and a transcriptome for annotation substantially improved assembly quality, surpassing that of most other *Panpulmonata* proteomes (Guo et al., 2019; Ma et al., 2023; De Jode et al., 2024; Ishii et al., 2025). Thus, in the rough periwinkle (*Littorina saxatilis/arcana*), WGS and mapping to the annotated genome allowed to study inversion polymorphisms often widespread across the species and associated with rapid parallel adaptation to heterogeneous environments (Morales et al., 2019; Reeve et al., 2024). Similarly, the rapid adaptive capacity of the invasive apple snail (*Pomacea canaliculate*) to diverse environments was allocated to its high genetic diversity studied by different omics techniques (Lu et al., 2024). Furthermore, sequencing of the transcriptome and small RNA sequencing (sRNA-seq) in the Asian tramp snail (*Bradybaena similaris)* highlighted genes and regulatory elements involved in xenobiotic metabolism (Yang Q. et al., 2020). This complex system for metabolizing xenobiotics was also found to be affected by arsenic pollution in the apple snail, displaying a dose-dependent effect on growth (Bi et al., 2024). To learn more about the genetics of the family of apple snails, the *Ampullariidae*, a transcriptome database was generated for seven subspecies using WGS and previous RNA-seq data (Ip et al., 2018). Subsequently, taking full advantage of this database, a multi-omics approach was applied to study the perivitelline fluid proteome from apple snail eggs, highlighting the adaptive capacities of different subspecies (Ip et al., 2019).

5 Omics in vertebrates

Omics technologies have significantly advanced research not only in invertebrates but also in vertebrate species classified as mini-livestock, though with distinct applications and challenges. In particular, mammalian research (Table 3) has benefited substantially from progress in the genomic field (Georges et al., 2019). As noted above for the invertebrates, the emphasis on certain species reflects the current availability of scientific literature and research activity, rather than a prioritization by the authors.

In livestock species, such as the domestic pig, reference genome sequences have provided a foundation for genetics and genomics research, enabling the use of genetic variants to study breed-specific traits and signatures of selection (Warr et al., 2020; Berghofer et al., 2022). These findings in porcine genetics were not limited to large high-production pigs but could be readily applied to minipigs, offering new opportunities for basic research, medical applications and breeding programs (Wang et al., 2020; Arora et al., 2022; Jia Y. et al., 2024). Research in miniature pigs has led to the creation of further high-quality chromosome level genome assemblies for various breeds (Bama, Banna, Goettingen, Korean, Ossabaw, Wuzhishan, Wisconsin) that have provided a critical framework for genetic studies (Fang et al., 2012; Heckel et al., 2015; Zhang et al., 2019; Zhang Y. et al., 2021; Chen et al., 2024; Wy et al., 2024; Veith et al., 2025). Re-sequencing and mapping to these genomes have enabled the discovery of selection signatures, facilitating the detection of body-size associated genes such as *PLAG1, CHM,* and *ESR1* and further breed- or minipig-specific traits (Miura et al., 2014; Heckel et al., 2015; Lu et al., 2016; Reimer et al., 2018; Kwon et al., 2019; Son et al., 2020; Wu F. et al., 2020; Berghofer et al., 2022; Kwon et al., 2024). The availability of these genomic studies has also enhanced the value of the minipigs as donors for xenotransplantation (Wang Y. et al., 2024; Peng et al., 2025), for toxicological testing (Liu et al., 2008; Bode et al., 2010; Flisikowska et al., 2022), and use as disease models (Curtasu et al., 2019; Curtasu et al., 2020; Li P. et al., 2020; Vaure et al., 2021; Niu et al., 2023; Jia Y. et al., 2024). For example, in the Göttingen minipig, characteristic diet-epigenome interactions were studied for future treatment of obesity, whereas findings in the back muscle of Diannan small-ear pig highlighted the expression of key genes involved in lipid metabolic and fatty acid biosynthetic process, as well as miRNAs regulating lipid deposition and muscle growth (Wang et al., 2015; Feng Y. et al., 2021). Similarly, metabolomic profiling revealed rapid shifts in plasma metabolites after feeding and obesity-related biomarkers after long-term intake of fructose and resistant starch (Polakof et al., 2015; Curtasu et al., 2020). In Bama pigs, promoter-enhancer interactions were shown to be highly dynamic in adipose depots, whereas large-scale compartments of the chromatin and topologically associated domains (TADs) were mostly conserved (Zhang J. et al., 2022).

Building on these insights into tissue-specific growth processes, transcriptome profiling was applied in the pituitary gland to explore the dynamic gene expression patterns during postnatal development in Bama pigs, as well as to characterize mesenchymal stem cell populations in prepubertal Mini-LEWE, providing a broader perspective on growth regulation in minipigs (Shan et al., 2014; Khaveh et al., 2024). Moreover, the establishment of a single-cell transcriptomic profile of mini-pigs has provided a valuable resource for dissecting cell- or nuclei-specific gene expression patterns with applications ranging from postnatal testicular development to metabolic diseases and immune cell maturation (Miao et al., 2024b; Wang X. et al., 2024; Chen et al., 2025; Zhang J. et al., 2025). Subsequently, numerous studies have particularly focused on minipigs for various reasons, including their small size or biomedical relevance.

Nevertheless, there are other vertebrates traditionally raised as mini-livestock, such as members of the family of rodents, e.g., guinea pigs *(Cavia porcellus)*, capybaras (*Cavia aperea*), African mole-rat (*Cryptomys hottentotus*) or cane rat (*Thryonomys swinderianus*), which also underwent omics studies targeting growth, adaptive evolution or their potential as unconventional meat species (Guo et al., 2012; Weyrich et al., 2014; Sahm et al., 2018; Dalle Zotte and Cullere, 2019; Babarinde and Saitou, 2020; Herrera-Alvarez et al., 2021; Schyman et al., 2021; da Silva et al., 2024). Comparative epigenomic profiling suggested that evolutionary changes in regulatory elements underlie key metabolic and physiological adaptations in naked mole-rat and other African mole-rat species, providing insights into their unique traits and offering a

TABLE 4 Overview of mini-livestock studies in the field of omics focusing on poultry. The table provides a comprehensive summary of omics studies identified for poultry, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Chicken *(Gallus gallus)*	Gen-	WGS	Re-sequencing, selective sweeps, difference between wild and domestic animals	Qanbari et al. (2019)
Chicken *(Gallus gallus)*	Gen-	WGS	Re-sequencing for improving further future investigations	Pertille et al. (2016)
Chicken *(Gallus gallus)*	Gen-	WGS	Re-sequencing of Bangladeshi indigenous chicken, insights into new breeding schemes	Rabbani et al. (2024)
Chicken *(Gallus gallus)*	Gen-	WGS	Genomic footprints and genes influencing body weight in Chinese indigenous chicken, *NELL1, XYLT1*, and *NCAPG/LCORL* strongly selected	Wang et al. (2023a)
Chicken *(Gallus gallus)*	Gen-	WGS	Re-sequencing of chicken from national local poultry genetic resources conservation farm, selection signatures associated with adaptation to tropical and frigid environments	Shi et al. (2023)
Chicken *(Gallus gallus)*	Gen-	WGS	Patterns of variation in two breeds, economic traits, selective sweeps	Fan et al. (2013)
Chicken *(Gallus gallus)*	Gen-	WGS	Patterns of diversity, genome-wide variation, population structure studies, selection signatures	Li et al. (2019a)
Chicken *(Gallus gallus)*	Gen-, Transcript-	WGS, RNA-seq	Candidate genes in egg production of upright and pendulous-comb chicken	Cai et al. (2023)
Chicken *(Gallus gallus)*	Gen-, Transcript-	WGS, RNA-seq	Feed efficiency (residual feed intake), GWAS, reducing environmental impact	Ye et al. (2020)
Chicken (*Gallus gallus*)	Gen-, Transcript-	WGS, RNA-seq	Maternal heat stress, adaptive mechanisms concerning heat tolerance	Karami et al. (2025)
Chicken *(Gallus gallus)*	Transcript-	RNA-seq	Characterization of Wooden Breast phenotype, localized hypoxia, oxidative stress, increased intracellular calcium, and muscle fibre-type switching as key features	Mutryn et al. (2015)
Chicken *(Gallus gallus)*	Transcript-	RNA-seq	Evaluation of the coverage and depth of transcriptome from chicken lungs	Wang et al. (2011)
Chicken *(Gallus gallus)*	Transcript-	RNA-seq	Shear force breast muscles (tenderness), differential gene expression analysis suggests the involvement of the extracellular matrix in the determination of meat tenderness	Piorkowska et al. (2016)
Chicken *(Gallus gallus)*	Transcript-	RNA-seq	Signaling pathways associated with disease resistance to avian influence virus infection	Wang et al. (2014)
Chicken *(Gallus gallus)*	Transcript-	RNA-seq	Gene expression in abdominal fat of high- and low-feed-efficiency in broiler chickens	Zhuo et al. (2015)
Chicken *(Gallus gallus)*	Transcript-	scRNA-seq	Immune cell populations, peripheral blood leukocyte analysis, chicken health	Maxwell et al. (2024)
Chicken *(Gallus gallus)*	Transcript-	RNA-seq	Meat quality characteristics, differential expressed genes, fat metabolism in broiler and laye breeds	Liu et al. (2024c)
Chicken *(Gallus gallus)*	Transcript-	RNA-seq	Insights into feed efficiency, differences between low and high feed efficiency breeds, genes involved in muscle growth	Zhou et al. (2015)

(Continued on following page)

TABLE 4 (*Continued*) Overview of mini-livestock studies in the field of omics focusing on poultry. The table provides a comprehensive summary of omics studies identified for poultry, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Chicken (*Gallus gallus*)	Transcript-	RNA-seq	Heterosis effects on egg numbers and clutch size, KEGG and REACTOME pathways	Isa et al. (2022)
Chicken (*Gallus gallus*)	Transcript-	RNA-seq	Comparing mRNA and microRNA on oxidative muscle sartorius and glycolytic muscle, candidate genes for muscle fibre type determination	Liu et al. (2020)
Chicken *(Gallus gallus)*	Transcript-, Metabol-	RNA-seq, LC-MS/MS	Egg production mechanisms, analysis of ovaries in two breeds, signalling pathways, genes associated with reproduction	Huang et al. (2022)
Chicken *(Gallus gallus)*	Transcript-, Metbol-	RNA-seq, LC-MS/MS	Integrative analysis, meat quality, myofiber characteristics, different rearing systems	Cui et al. (2024)
Chicken (*Gallus gallus*)	Epigen-	Hi-C	Breast muscle growth and intramuscular fat between fast-growing broilers and slow-growing indigenous chickens, effects of chromatin loops	Wang et al. (2024c)
Chicken *(Gallus gallus)*	Prote-	LC-MS/MS	Protein biomarkers, protein changes in breast meat from divergent farming systems, muscle structure and energy metabolism, muscle proteome	Alessandroni et al. (2024)
Chicken *(Gallus gallus)*	Prote-	MALDI-MS, LC-MS/MS	Qualitative and quantitative approaches, semen peptidome/proteome and molecular phenotype related to sperm quality	Labas et al. (2015)
Duck *(Anas platyrhynchos)*	Gen-	WGS	Developmental wing deformity (angel wings), GWAS	Mohammadi (2024)
Duck *(Anas platyrhynchos)*	Transcript-	RNA-seq	Skeletal muscle growth in two duck breeds, differential gene expression analysis	Cao et al. (2023)
Duck *(Anas platyrhynchos)*	Transcript-	RNA-seq	Transcriptome analysis of Hanzhong Ma duck	Hu et al. (2021b)
Duck *(Anas platyrhynchos)*	Transcript-	RNA-seq	Transcriptome analysis of abdominal fat tissue, circRNAs involved in regulating duck abdominal fat production	Yang et al. (2024b)
Duck *(Anas platyrhynchos)*	Transcript-	RNA-seq	*De novo* assembly, insights into muscle yield and meat quality gene expressions	Liu et al. (2018b)
Duck *(Anas platyrhynchos)*	Transcript-	RNA-seq	Transcriptome analysis of Pekin duck	Hu et al. (2021a)
Duck *(Anas platyrhynchos)* Muscovy Duck *(Cairina moschata)*	Transcript-	RNA-seq	Analysis of hepatic gene expression, *ad libitum* feed options	Herault et al. (2019)
Duck *(Anas platyrhynchos)*	Transcript-, Metabol-	RNA-seq, LC-MS/MS	Skeletal muscle development during embryonic stage, correlation analysis, KEGG-pathway analysis	Hu and Liu (2023)
Duck *(Anas platyrhynchos)*	Prote-	MALDI-TOF MS	Matrix-Assisted Laser Desorption/ Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF MS), liver protein profile, functional enrichment analysis, differentially expressed proteins significantly related to lipid metabolic processes	Ge and Geng (2022)

(Continued on following page)

TABLE 4 (*Continued*) Overview of mini-livestock studies in the field of omics focusing on poultry. The table provides a comprehensive summary of omics studies identified for poultry, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Duck *(Anas platyrhynchos)*	Prote-	TMT, LC-MS/MS	Duck meat from birds exposed to heat stress, potential protective proteins involved in the defensive mechanisms against heat stress	He et al. (2019a)
Goose *(Anser cygnoides)*	Gen-, Transcript-, Epigen-	WGS, RNA-seq, Hi-C	Chromosome-level genome of a Chinese indigenous goose, diversity analysis of two different breeds, insertion in EDNRB2 determines the white plumage	Ouyang et al. (2022)
Goose *(Anser cygnoides)*	Gen-, Epigen-	WGS, Hi-C	Chromosome-level goose assembly generated by adopting a hybrid *de novo* assembly approach	Li et al. (2020b)
Goose *(Anser cygnoides)*	Gen-	WGS	Draft sequence by shotgun sequencing, molecular mechanism involved in the susceptibility of geese to fatty liver disease	Lu et al. (2015)
Goose *(Anser cygnoides)* *(Branta ruficollis)*	Gen-	WGS	Re-sequencing of geese, exon-based phylogenomic approach, evolutionary history, timing of divergence, phylogenetic incongruences	Ottenburghs et al. (2016)
Goose *(Anser cygnoides)* *(Anser anser)*	Gen-	WGS	Population structure analysis of re-sequencing data, introgression of Yili geese by Chinese domestic geese	Wen et al. (2023)
Goose *(Anser cygnoides)*	Transcript-	RNA-seq	Transcriptome of hypothalamus, pituitary, and ovaries, reference for light regulation of reproduction	Zhao et al. (2025a)
Goose *(Anser cygnoides)*	Transcript-	RNA-seq	Transcriptome of hypothalamus of geese under different photocycles	Yuyan et al. (2025)
Goose *(Anser cygnoides)*	Transcript-	RNA-seq	Differentially expressed genes of abdominal fat and breast muscle	Zhao et al. (2025b)
Goose *(Anser cygnoides)*	Transcript-, Prote-	RNA-seq, LC-MS/MS	Reproduction cycles in testicles, genes related to spermatogenesis and fertility	Liu et al. (2024a)
Goose *(Anser cygnoides)*	Transcript-	scRNA-seq	Multi-omics approach with genome sequencing data and single-cell transcriptome data from ovarian tissues from three female embryos, *LHX9* and *ARID5B* as potential regulators of degeneration of the right ovary	Ouyang et al. (2025)
Guinea Fowl – Helmeted *(Numida meleagris)*	Gen-	WGS	Draft assembly, wild and domestic populations, selection signatures related to domestication or importation to Europe, plumage colouration	Vignal et al. (2019)
Guinea Fowl – Helmeted *(Numida meleagris)*	Gen-	WGS	High-quality *de novo* genome assembly, wild and domestic birds, selective signatures in behaviour and locomotion changes	Shen et al. (2021)
Guinea Fowl *(Numida spp.)*	Prote-	nanoLC-MS/MS	Eggshell formation	Le Roy et al. (2019)
Jiaji Duck *(Cairina moschata)*	Transcript-, Metabol-	RNA-seq, LC-MS/MS	Integrated study of embryonic breast muscle, KEGG-pathway correlations and integration, differential gene expression and differential metabolomics analysis	Gu et al. (2024)
Muscovy Duck *(Cairina moschata)*	Prote-, Metabol-	LC-MS/MS	Differentially expressed proteins in ovary tissues during the broody and laying periods	Wu et al. (2019)

(Continued on following page)

TABLE 4 (*Continued*) Overview of mini-livestock studies in the field of omics focusing on poultry. The table provides a comprehensive summary of omics studies identified for poultry, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Muscovy Duck *(Cairina moschata)*	Gen-, Epigen-, Transcript-	WGS, RNA-seq, Hi-C, ATAC-seq	Multo-omics methods including Assay for Transposase-Accessible Chromatin using sequencing (ATAC-seq), fatty liver, chromosome-level assembly, differential gene expression analysis involved in hepatic lipid catabolism	Xu et al. (2022b)
Muscovy Duck *(Cairina moschata)*	Gen-	WGS	Domestication history, guidance for breeding programs and enhancing commercial traits, genes implicated in fatty acid metabolism, development and immunity pathways	Li et al. (2024a)
Muscovy Duck *(Cairina moschata)*	Transcript-	RNA-seq	Full-length transcriptome from ovaries	Lin et al. (2021)
Quail – Japanese *(Coturnix japonica)*	Gen-	WGS	High-quality reference genome, identification of quail-specific genes, GWAS for plumage colour	Wu et al. (2018)
Quail – Japanese *(Coturnix japonica)*	Gen-	WGS	Draft assembly	Kawahara-Miki et al. (2013)
Quail – Japanese *(Coturnix japonica)*	Transcript-	RNA-seq	Thermal manipulation on eggs impacting postnatal response and gene expression in the hypothalamus, genes related to mitochondrial and heat-response	Vitorino Carvalho et al. (2021)
Quail – Japanese *(Coturnix japonica)*	Transcript-	RNA-seq	Developmental patterns of leg muscles in quail embryos and regulatory networks reconstruction	Zhang et al. (2024b)
Quail – Japanese *(Coturnix japonica)*	Transcript-	RNA-seq	Sexual dimorphism, expression patterns of genes involved in sex-determination mechanisms	Park et al. (2024)
Quail – Japanese *(Coturnix japonica)*	Metabol-	LC-MS/MS	Characterization of the quail liver metabolome, effects on lipid metabolism	Legrand et al. (2021)
Quail – Japanese *(Coturnix japonica)*	Gen-, Transcript-	WGS, RNA-seq	High-quality quail genome sequence, candidate genes for social behaviour, effects and interaction of photoperiod and temperature	Morris et al. (2020)
Quail – Japanese *(Coturnix japonica)*	Gen-	WGS	Copy number variant detection, markers for stress responses	Khatri et al. (2019)
Quail – Japanese *(Coturnix japonica)*	Transcript-	RNA-seq	Skeletal muscle development, regulatory networks	Zhang et al. (2024b)
Quail – Japanese *(Coturnix japonica)*	Transcript-	RNA-seq	Exposure to glucocorticoids, differential gene expression, stressors with long-term effects on the brain	Marasco et al. (2016)
Quail *(Coturnix coturnix)* Duck *(Anas platyrhynchos)* Chicken *(Gallus gallus)*	Prote-	MALDI-TOF/TOF MS	Matrix-Assisted Laser Desorption/ Ionization Time-of-Flight/Time-of-Flight Mass Spectrometry (MALDI-TOF/TOF MS), comparison of the protein composition of egg white	Hu et al. (2016)
Turkey *(Meleagris gallopavo)*	Gen-	WGS	Draft assembly, comparative analysis of the turkey, chicken, and zebra finch genomes	Dalloul et al. (2010)
Turkey *(Meleagris gallopavo)*	Gen-, Epigen-	WGS, Hi-C	High-quality chromosome-level assemblies using long-read technologies and genome-wide chromatin interaction data	Barros et al. (2022)

(Continued on following page)

TABLE 4 (*Continued*) Overview of mini-livestock studies in the field of omics focusing on poultry. The table provides a comprehensive summary of omics studies identified for poultry, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Turkey *(Meleagris gallopavo)*	Gen-	WGS	Re-sequencing of 32 individual turkeys from different populations, genomic regions with low nucleotide variation in domestic turkey	Aslam et al. (2012)
Turkey *(Meleagris gallopavo)*	Gen-	WGS	Re-sequencing, selective sweeps regions, associated with growth	Aslam et al. (2014)
Turkey *(Meleagris gallopavo)*	Transcript-	RNA-seq	Transcriptome profiles of normal, pale and exudative meat	Malila et al. (2014)
Turkey *(Meleagris gallopavo)*	Transcript-	RNA-seq	Liver transcriptome, response to selenium status	Sunde and Taylor (2019)
Turkey *(Meleagris gallopavo)*	Transcript-	RNA-seq	lncRNA regulation associated with sperm motility	Jastrzebski et al. (2022)
Turkey (*Meleagris gallopavo*)	Transcript-	RNA-seq	Identifying and characterizing differential expression of satellite cells from muscles, prediction of miRNA and mRNA interactions, thermal challenge response	Reed et al. (2023)

new phylogenetic framework for studying regulatory evolution across species (Parey et al., 2023). Omics studies in rabbits *(Oryctolagus cuniculus)* investigated evolutionary dynamics, highlighting gene alleles associated with brain development and aggression related to the domestication process (Albert et al., 2012; Carneiro et al., 2014a; Carneiro et al., 2014b). Alongside tameness, growth and meat quality were highly important traits under selection since domestication of rabbits, which were considered to be an ideal food source with high protein, low fat, low cholesterol and low sodium contents (Yang X. et al., 2020). Thus, marker genes were studied for these desired traits using Specific-Locus Amplified Fragment sequencing (SLAF-seq) and subsequent genome-wide association analysis (Yang X. et al., 2020). Furthermore, various research studies explored the metagenome and metabolome of the rabbit gut, caecum and colon across different conditions, attributed to the impact on host health and adaptation (Chen Y. et al., 2022; Wang J. et al., 2022; Hou et al., 2024; Paes et al., 2024; Zhao et al., 2024).

In addition to mammals, poultry (Table 4) has also become a major focus of omics research aiming at an increased production efficiency, disease resistance and understanding phenomena like epigenetic inheritance (Urgessa and Woldesemayat, 2023; Wadood et al., 2025). Population genomics studies characterized genetic diversity across chicken breeds, detecting selection signatures and identifying candidate genes for economically important traits (Fan et al., 2013; Li D. et al., 2019; Qanbari et al., 2019; Shi et al., 2023; Wang H. et al., 2023; Rabbani et al., 2024). By integrating genomics data with transcriptome information or by detecting differential gene expression levels in chicken, researchers could highlight functional genetic effects affecting egg production performance, feeding efficiency and meat quality (Mutryn et al., 2015; Zhou et al., 2015; Zhuo et al., 2015; Piorkowska et al., 2016; Ye et al., 2020; Huang et al., 2022; Cai et al., 2023; Cui et al., 2024; Liu Y. et al., 2024). Additionally, breast muscle proteomes from chicken kept in antibiotic-free or organic farming systems revealed differentially abundant proteins as putative biomarkers for meat or farming system authenticity (Alessandroni et al., 2024). For future enhanced integration studies of multi-omics chicken data, an omics data repository (GalBase) was constructed to facilitate the identification of genetic variants and functional genes associated with common traits of interest (Fu et al., 2022). Similarly, researchers in the field of duck genomics initiated the Duck 1,000 genomes project, which integrates multi-omics data for studies on economically important traits in ducks (Fan et al., 2024). Particularly, growth, feed conversion efficiency, meat quality and meat yield were investigated intensively using genomics, transcriptomics or mass spectrometry (Liu Y. et al., 2018; He J. et al., 2019; Hu et al., 2021a; Hu et al., 2021b; Cai et al., 2023; Cao et al., 2023; Hu and Liu, 2023; Mohammadi, 2024; Yang Y. et al., 2024) (In contrast, in Muscovy ducks, the strong female behaviour of incubating eggs instead of laying was of major interest and therefore explored with different omics methods (Wu et al., 2019; Lin et al., 2021).

Similarly to the duck's reference genome, research benefited significantly from the availability of a chromosome-level assembly from Tianfu goose *(Anser cygnoides)* or a hybrid *de novo* assembly from Chinese indigenous goose, as well as the recent introduction of a "Goose Multi-omics Database" (Li Y. et al., 2020; Ouyang et al., 2022; Huang et al., 2025). Subsequent re-sequencing allowed studies on the evolutionary history of geese and gene flow in domestic populations (Ottenburghs et al., 2016; Wen et al., 2023). Furthermore, transcriptomic approaches using RNA-sequencing elucidated molecular mechanisms underlying economically important traits, including the identification of key genes for differential fat deposition, photoperiodic reproductive control and fertility (Liu Q. et al., 2024; Yuyan et al., 2025; Zhao X. et al., 2025). In a multi-omics joint analysis, the integration of genomic variants and single-cell transcriptomic information allowed the detection of two genes, *LHX9* and *ARID5B*, potentially associated with the rate of degeneration in the right ovary of avian species (Ouyang et al., 2025).

TABLE 5 Overview of mini-livestock studies in the field of omics focusing on amphibians and reptiles. The table provides a comprehensive summary of omics studies identified for amphibians and reptiles, detailing the omics category, sequencing methodology, targeted biological features, and overall study design.

Investigated mini-livestock species	Omics field ("-omics")	Sequencing-technique	Targets and study design	References
Bullfrog – American *(Lithobates catesbeianus)*	Transcript-	RNA-seq	Gene expression profiles in the liver, significant pathways in metabolism and immune response	Yang et al. (2024a)
Bullfrog – American *(Rana catesbeiana)*	Transcript-	RNA-seq	Functional investigation of the prestin (SLC26A5) gene and its evolution	Wang et al. (2021b)
Frog – Chinese Edible Frog *(Hoplobatrachus rugulosus)*	Gen-	WGS	Resistance to clinical antimicrobials, multidrug resistance, *Salmonella* as agent of gastrointestinal disease, high number of virulence determinants	Boss et al. (2023)
Frog – Giant Spiny Frog *(Quasipaa spinosa)*	Gen-	WGS	Genome re-sequencing, sex specific markers	Zhang et al. (2025b)
Frog – Heilongjiang Brown Frog *(Rana amurensis)*	Transcript-	RNA-seq	Comparative studies, samples from different organs, antimicrobial peptides in the skin	Li et al. (2022c)
Frog – Ornate Burrowing Frog *(Platyplectrum ornatum)*	Gen-, Transcript-	WGS, RNA-seq	Mechanisms of genome reduction in comparison to other frog species, sex-differentiation pathways	Lamichhaney et al. (2021)
Frog – Plateau Brown Frog *(Rana kukunoris)*	Gen-	WGS	Chromosome-level assembly, amphibian genome evolution and adaptation	Chen et al. (2023)
Frog – Tibetan *(Nanorana parkeri)*	Gen-, Transcript-	WGS, RNA-seq	Synteny analysis, transposable elements	Sun et al. (2015)
Lizard – Common *(Zootoca vivipara)*	Gen-	WGS	Chromosome-level assembly, high-density linkage map, novel analytic pipelines	Yurchenko et al. (2020)
Lizard – Easter Fence Lizard *(Sceloporus undulatus)*	Gen-, Transcript-	WGS, RNA-seq	Chromosome-level assembly, physiological and evolutionary ecology	Westfall et al. (2021)
Lizard – Oriental Garden Lizard *(Calotes versicolor)*	Gen-. Transcript-	WGS, RNA-seq	Draft genome, genome landscape, phylogenetic relationship	Wang et al. (2023b)
Salamander – Chinese Giant Salamander *(Andrias davidianus)*	Transcript-	RNA-seq	*De novo* transcriptome assembly	Geng et al. (2017)

Significant progress has also been made in the turkey *(Meleagris gallopavo)*, where an initial draft genome was improved to a high quality, chromosome-level assembly (Dalloul et al., 2010; Barros et al., 2022). Subsequent population analyses identified large genomic regions under intense selection in commercial lines enriched for economically relevant genes (Aslam et al., 2012; Aslam et al., 2014). Furthermore, transcriptome sequencing studies provided insights into sperm motility, meat quality parameters and adaptation to high dietary selenium (Malila et al., 2014; Sunde and Taylor, 2019; Jastrzebski et al., 2022).

Comparable advances have also been made in the Japanese quail (*Coturnix japonica*), for which recent genome, transcriptome and mass spectrometry data provided valuable insights into egg white protein functions, lipid metabolism, social behaviour, stress responses, effects of photoperiod and temperature on eggs and birds, muscle development and plumage colour (Hu et al., 2016; Marasco et al., 2016; Wu et al., 2018; Khatri et al., 2019; Morris et al., 2020; Legrand et al., 2021; Vitorino Carvalho et al., 2021; Zhang W. et al., 2024). Similar traits were also of interest in studies on helmeted guinea fowl *(Numida meleagris),* in which signatures of selection in the genome were investigated for behaviour and locomotion changes or plumage colouration (Vignal et al., 2019; Shen et al., 2021).

Another group of vertebrates, namely amphibians and reptiles (Table 5), are also utilized as edible animals, providing alternative sources of high-quality protein in various regions of the world, and has increasingly been studied using omics approaches. For example, frogs are a popular source of meat in aquaculture worldwide and, like conventional livestock, have implications for both human nutrition and health (Boss et al., 2023; Zhang L. et al., 2025). Genomic studies in different frog species highlighted multi-genome synteny blocks, mechanisms driving or constraining genome size and positively selected genes for adaptation to high altitude (Sun et al., 2015; Lamichhaney et al., 2021; Chen et al., 2023). Transcriptome analyses in the American bullfrog *(Lithobates catesbeianus)* and the Heilongjiang brown frog *(Rana amurensis)* revealed target pathways for metabolism and immune response, as well as antimicrobial peptides in the skin (Li W. et al., 2022; Yang P. et al., 2024). In addition, chromosome-level assemblies and *de novo* transcriptome datasets of reptiles, such as edible lizards and salamanders, have been generated, providing valuable resources for studying their physiology and adaptation (Geng et al., 2017; Yurchenko et al., 2020; Westfall et al., 2021; Wang Q. et al., 2023). In summary, the application of omics technologies in a wide range of vertebrate mini-livestock has provided comprehensive

insights into their genetic architecture, physiological regulation, and adaptive diversity.

6 Translating omics insights into mini-livestock improvement: challenges and future directions

The rapid advancement of omics technologies has generated extensive datasets describing the genetic, transcriptomic, proteomic, and metabolic architecture of mini-livestock. Harnessing these insights into practical breeding applications enables more accurate selection for desirable traits, such as growth, meat quality, fat metabolism, feed intake, tameness, and other key productive traits (Albert et al., 2012; Jegou et al., 2016; Southey et al., 2016; Zhong et al., 2022; Zhao Z. et al., 2025).

The global livestock sector faces the dual challenge of ensuring food security for a growing population while controlling its environmental footprint (Niu et al., 2024). In livestock science, omics technologies have become powerful tools for unravelling the molecular mechanisms underlying complex traits, thereby supporting more sustainable and efficient animal production (Chakraborty et al., 2022). Genomics accelerate the early selection of traits of interest, such as milk yield for dairy cows or the quantity of meat produced by beef cattle (Mesbah-Uddin et al., 2022; Nanaie et al., 2025). While these approaches have already advanced genetic improvement in major livestock species, their application in mini-livestock remains comparatively limited. However, the availability of high-quality reference genomes and transcriptomic datasets has recently enabled the first insights into the molecular backgrounds of important production and adaptation traits in these species (Chen et al., 2012; Generalovic et al., 2021; Ouyang et al., 2022; Wy et al., 2024; Chen et al., 2025). Sequencing or re-sequencing of mini-livestock species such as chicken, rabbit or honey bee resulted in millions of SNPs to identify genotype to phenotype correlations for complex traits (Carneiro et al., 2014b; Wallberg et al., 2017; Moreira et al., 2018).

While these omics applications yielded valuable insights into mini-livestock biology and production, several challenges and limitations remain to be addressed before their full potential can be realized in mini-livestock breeding and management. Omics technologies represent a paradigm shift in the optimization of mini-livestock systems by enhancing productivity, sustainability and biomedical relevance as already demonstrated in agricultural and conventional livestock species (Van Emon, 2016; Chakraborty et al., 2022; Rotimi, 2025). A primary limitation is the requirement for highly equipped laboratories and expensive instrumentation for omics data generation (Van Emon, 2016; Chakraborty et al., 2022). Protocols for sample collection and processing have to be optimized for each species and tissue type, as for example in insects, in which the pupal stage was suggested as the most suitable developmental stage for high-quality genomic DNA extraction (Oppert et al., 2019). Downstream of sequencing, the assembly of high-quality reference genomes for many species, particularly insects, remains challenging due to high polymorphism, limited DNA yield from small-bodied individuals, and difficulties in achieving homozygosity (Richards and Murali, 2015; Li F. et al., 2019). Data analysis on omics research requires substantial expertise in statistics, bioinformatics, and computational tools to ensure accurate interpretation (Yamada et al., 2021). Analytical frameworks such as statistical models and network-based approaches evolve rapidly, demanding continual updates to maintain performance (Jiang et al., 2019). Beyond the challenges of handling large and complex single-omics datasets, data integration remains a major obstacle for effective multi-omics analyses (Misra et al., 2019). Furthermore, the implementation of omics technologies in livestock faces practical challenges, as farmers' acceptance largely depends on the extent to which these tools align with their expertise and operational needs (Hostiou et al., 2017; Vazquez-Diosdado et al., 2019). Thus, handling omics data requires domain-specific knowledge and proper study design to harness the full potential, particularly considering the growing scale of datasets and the economic importance of traditional livestock species (Thornton, 2010).

These limitations discussed above underline the need for future strategies that scale from individual studies to coordinated, community-driven efforts. Experiences from large international consortia demonstrate that shared standards, common data models, and openly accessible workflows are crucial for reproducibility and for lowering the entry barrier into omics research: The initiative of the Functional Annotation of Animal Genomes (FAANG) project, whose aim is to produce comprehensive maps of functional elements in the genomes of domesticated animal species, has already shown significant progress in filling the genotype-to-phenotype gap and the establishment of data analysis standards for various species, including mini-livestock (Andersson et al., 2015; Tuggle et al., 2016). Similarly, the ENCODE Consortium provides clear examples of how community-curated benchmark datasets, guides and uniform data-processing methods can provide comprehensive views of the organization and variability of genes and regulatory information across species and individuals (ENCODE Project Consortium, 2012). Furthermore, the 5,000 arthropod genomes initiative (i5K) highlighted that such coordination was also feasible for less conventional livestock and agricultural species (i5K Consortium, 2013). The European Reference Genome Atlas (ERGA) model, which distributed sequencing across 26 facilities and established coordinated library preparation hubs, offers valuable lessons for scaling mini-livestock genomics programs while ensuring broader participation from researchers in resource-limited settings (Mc Cartney et al., 2024).

A further major development in this context is the implementation of pangenome frameworks representing the global genomic diversity of a species rather than a singular reference (Wang T. et al., 2022). Such approaches are now beginning to appear also in non-traditional model organisms, for example, in the Asian honeybee *(Apis cerana)*, in which the first pangenome recently demonstrated its feasibility in the analysis of genomic variations (Li Y. et al., 2024). This highlights the potential of transferring existing pangenome-related strategies from traditional livestock to mini-livestock to identify variants involved in phenotypic and genotypic diversity, environmental adaptation mechanisms and other desired phenotypes (Zhou et al., 2022; Miao et al., 2024a; Azam et al.,

2025; Dai et al., 2025). Beyond improving variant discovery, these resources also provide a foundation for developing cost-effective genotyping approaches. Established procedures in traditional livestock, such as low-density SNP panels combined with imputation (van Binsbergen et al., 2015), genotyping-by-sequencing (Elshire et al., 2011), and low-coverage whole-genome imputation (Zhang et al., 2023), demonstrated that accurate genomic information could be obtained to perform large-scale genome-wide association studies and genomic selection. As more comprehensive variant catalogues and pangenomes become available, these methods could also be tailored to species and breeds where no commercial genotyping tools currently exist (Crysnanto et al., 2019; Bian et al., 2024).

Addressing the remaining gaps in omics applications will additionally require integrating phenotype-level information and advancing multi-layer analytical strategies (Brito et al., 2020). Artificial intelligence-driven phenotyping tools offer a promising route toward generating standardized, high-throughput behavioural and performance data, which are essential for linking molecular variation to observable traits (Distante et al., 2025). Developing applications in insect farming already demonstrated that artificial intelligence can automate identification, counting, behaviour detection, and health monitoring, providing scalable solutions for mini-livestock systems where manual data collection is difficult (Bjerge et al., 2022; Roy et al., 2024). When combined with genomic and management strategies, these technologies have the potential to improve production efficiency and reduce costs (Neculai-Valeanu et al., 2025; Papadopoulos et al., 2025), which are the key factors for ensuring the long-term sustainability and competitiveness of mini-livestock production systems in the future.

7 Conclusion

Omics technologies have demonstrated transformative potential across diverse mini-livestock species, as outlined in this review. Integrating multi-omics approaches has greatly enhanced our understanding of genetic architecture, physiological regulation, and adaptive diversity. Future advances will rely on expanding reference genomes, standardizing phenotyping, and applying robust integration frameworks, such as CCA, WGCNA, pathway-based enrichment tools, and machine-learning approaches. Together, these strategies can accelerate trait mapping and support breeding programs targeting growth efficiency, food and feed utilization, product quality, and resilience to environmental stressors. From a policy perspective, embedding multi-omics integration into agricultural strategies can facilitate evidence-based breeding, emission-reduction goals, and internationally harmonized data-sharing standards.

Author contributions

AS: Conceptualization, Writing – review and editing, Writing – original draft. AH: Conceptualization, Writing – review and editing. JM: Conceptualization, Writing – review and editing.

Funding

The author(s) declared that financial support was not received for this work and/or its publication.

Acknowledgements

We acknowledge financial support by the Open Access Publication Fund of the University of Veterinary Medicine Hannover, Foundation.

Conflict of interest

The author(s) declared that this work was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Generative AI statement

The author(s) declared that generative AI was used in the creation of this manuscript. The authors used ChatGPT (GPT-5, OpenAI) to improve grammar and clarity and Perplexity for literature search. All content was checked for accuracy and approved by the authors, who retail full responsibility for the final manuscript.

Any alternative text (alt text) provided alongside figures in this article has been generated by Frontiers with the support of artificial intelligence and reasonable efforts have been made to ensure accuracy, including review by the authors wherever possible. If you identify any issues, please contact us.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

References

Abbasi, E. Y., Deng, Z., Ali, Q., Khan, A., Shaikh, A., Reshan, M. S. A., et al. (2024). A machine learning and deep learning-based integrated multi-omics technique for leukemia prediction. *Heliyon* 10 (3), e25369. doi:10.1016/j.heliyon.2024.e25369

Ahmad, S. M., De Donato, M., Bhat, B. A., Diallo, A. B., and Peters, S. O. (2022). Editorial: omics technologies in livestock improvement: from selection to breeding decisions. *Front. Genet.* 13, 1113417. doi:10.3389/fgene.2022.1113417

Albert, F. W., Somel, M., Carneiro, M., Aximu-Petri, A., Halbwax, M., Thalmann, O., et al. (2012). A comparison of brain gene expression levels in domesticated and wild animals. *PLoS Genet.* 8 (9), e1002962. doi:10.1371/journal.pgen.1002962

Alessandroni, L., Sagratini, G., and 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. (Oxf.)* 8, 100194. doi:10.1016/j.fochms.2024.100194

Alexander, P., Brown, C., Arneth, A., Dias, C., Finnigan, J., Moran, D., et al. (2017). Could consumption of insects, cultured meat or imitation meat reduce global agricultural land use? *Glob. Food Secur-Agr.* 15, 22–32. doi:10.1016/j.gfs.2017.04.001

Amin, B., Ford, K. I., and Robinson, R. A. S. (2020). Quantitative proteomics to study aging in rabbit liver. *Mech. Ageing Dev.* 187, 111227. doi:10.1016/j.mad.2020.111227

Andersson, L. (2009). Genome-wide association analysis in domestic animals: a powerful approach for genetic dissection of trait loci. *Genetica* 136 (2), 341–349. doi:10.1007/s10709-008-9312-4

Andersson, L., Archibald, A. L., Bottema, C. D., Brauning, R., Burgess, S. C., Burt, D. W., et al. (2015). Coordinated international action to accelerate genome-to-phenome with FAANG, the functional annotation of animal genomes project. *Genome. Biol.* 16 (1), 57. doi:10.1186/s13059-015-0622-4

Arora, D., Park, J. E., Lim, D., Cho, I. C., Kang, K. S., Kim, T. H., et al. (2022). Multi-omics approaches for comprehensive analysis and understanding of the immune response in the miniature pig breed. *PLoS One* 17 (5), e0263035. doi:10.1371/journal.pone.0263035

Aslam, M. L., Bastiaansen, J. W., Elferink, M. G., Megens, H. J., Crooijmans, R. P., Blomberg le, A., et al. (2012). Whole genome SNP discovery and analysis of genetic diversity in Turkey (meleagris gallopavo). *BMC Genomics* 13, 391. doi:10.1186/1471-2164-13-391

Aslam, M. L., Bastiaansen, J. W., Megens, H. J., Crooijmans, R. P., Nasreen, F., Blomberg le, A., et al. (2014). Genome-wide candidate regions for selective sweeps revealed through massive parallel sequencing of DNA across ten Turkey populations. *BMC Genet.* 15, 117. doi:10.1186/s12863-014-0117-4

Aslam, B., Basit, M., Nisar, M. A., Khurshid, M., and Rasool, M. H. (2017). Proteomics: technologies and their applications. *J. Chromatogr. Sci.* 55 (2), 182–196. doi:10.1093/chromsci/bmw167

Assan, N. (2013). Promoting micro livestock farming to enhance animal product supply in sub Saharan Africa.

Ayieko, M. A., Ogola, H. J., and Ayieko, I. A. (2016). Introducing rearing crickets (gryllids) at household levels: adoption, processing and nutritional values. *J. Insect Food Feed* 2 (3), 203–211. doi:10.3920/Jiff2015.0080

Azam, S., Sahu, A., Pandey, N. K., Neupane, M., Van Tassell, C. P., Rosen, B. D., et al. (2025). Constructing a draft Indian cattle pangenome using short-read sequencing. *Commun. Biol.* 8 (1), 605. doi:10.1038/s42003-025-07978-0

Babarinde, I. A., and Saitou, N. (2020). The dynamics, causes, and impacts of mammalian evolutionary rates revealed by the analyses of capybara draft genome sequences. *Genome Biol. Evol.* 12 (8), 1444–1458. doi:10.1093/gbe/evaa157

Badaoui, B., Fougeroux, A., Petit, F., Anselmo, A., Gorni, C., Cucurachi, M., et al. (2017). RNA-Sequence analysis of gene expression from honeybees (apis mellifera) infected with Nosema ceranae. *PLoS One* 12 (3), e0173438. doi:10.1371/journal.pone.0173438

Bai, Y., Wang, H., Li, G. Y., Luo, J. L., Liang, S., and Li, C. (2019). Complete mitochondrial genome of the super mealworm (Fab.) (insecta: coleoptera: tenebrionidae). *Mitochondrial DNA B Resour.* 4 (1), 1300–1301. doi:10.1080/23802359.2019.1591237

Bai, Z., Wu, X., Lassaletta, L., Haverkamp, A., Li, W., Yuan, Z., et al. (2023). Investing in mini-livestock production for food security and carbon neutrality in China. *Proc. Natl. Acad. Sci. U S A.* 120 (43), e2304826120. doi:10.1073/pnas.2304826120

Baiao, A. R., Cai, Z., Poulos, R. C., Robinson, P. J., Reddel, R. R., Zhong, Q., et al. (2025). A technical review of multi-omics data integration methods: from classical statistical to deep generative approaches. *Brief. Bioinform* 26 (4), bbaf355. doi:10.1093/bib/bbaf355

Barros, C. P., Derks, M. F. L., Mohr, J., Wood, B. J., Crooijmans, R., Megens, H. J., et al. (2022). A new haplotype-resolved Turkey genome to enable Turkey genetics and genomics research. *Gigascience* 12, giad051. doi:10.1093/gigascience/giad051

Berghofer, J., Khaveh, N., Mundlos, S., and Metzger, J. (2022). Simultaneous testing of rule- and model-based approaches for runs of homozygosity detection opens up a window into genomic footprints of selection in pigs. *BMC Genomics* 23 (1), 564. doi:10.1186/s12864-022-08801-4

Berry, D. P., Meade, K. G., Mullen, M. P., Butler, S., Diskin, M. G., Morris, D., et al. (2011). The integration of 'omic' disciplines and systems biology in cattle breeding. *Animal* 5 (4), 493–505. doi:10.1017/S1751731110002120

Bi, X., Qiu, M., Li, D., Zhang, Y., Zhan, W., Wang, Z., et al. (2024). Transcriptomic and metabolomic analysis of the mechanisms underlying stress responses of the freshwater snail, Pomacea canaliculata, exposed to different levels of arsenic. *Aquat. Toxicol.* 267, 106835. doi:10.1016/j.aquatox.2024.106835

Bian, P., Li, J., Zhou, S., Wang, X., Gong, M., Guo, X., et al. (2024). A graph-based goat Pangenome reveals structural variations involved in domestication and adaptation. *Mol. Biol. Evol.* 41 (12), msae251. doi:10.1093/molbev/msae251

Bielajew, B. J., Hu, J. C., and Athanasiou, K. A. (2021). Methodology to quantify collagen subtypes and crosslinks: application in minipig cartilages. *Cartilage* 13 (2_Suppl. l), 1742S–1754S. doi:10.1177/19476035211060508

Bjerge, K., Mann, H. M. R., and Høye, T. T. (2022). Real-time insect tracking and monitoring with computer vision and deep learning. *Remote. Sens. Ecol. Conserv.* 8 (3), 315–327. doi:10.1002/rse2.245

Bode, G., Clausing, P., Gervais, F., Loegsted, J., Luft, J., Nogues, V., et al. (2010). The utility of the minipig as an animal model in regulatory toxicology. *J. Pharmacol. Toxicol. Methods* 62 (3), 196–220. doi:10.1016/j.vascn.2010.05.009

Boss, S., Stephan, R., Horlbog, J. A., Magouras, I., Colon, V. A., Lugsomya, K., et al. (2023). Serotypes, antimicrobial resistance profiles, and virulence factors of salmonella isolates in Chinese edible frogs (Hoplobatrachus rugulosus) collected from wet markets in Hong Kong. *Foods* 12 (11), 2245. doi:10.3390/foods12112245

Branckaert, R. D. (1995). Minilivestock - sustainable animal resource for food security. *Biodivers. Conserv.* 4(3), 336–338. doi:10.1007/Bf00055978

Brito, L. F., Oliveira, H. R., McConn, B. R., Schinckel, A. P., Arrazola, A., Marchant-Forde, J. N., et al. (2020). Large-scale phenotyping of livestock welfare in commercial production systems: a new frontier in animal breeding. *Front. Genet.* 11, 793. doi:10.3389/fgene.2020.00793

Cai, D., Wang, Z., Zhou, Z., Lin, D., Ju, X., and Nie, Q. (2023). Integration of transcriptome sequencing and whole genome resequencing reveal candidate genes in egg production of upright and pendulous-comb chickens. *Poult. Sci.* 102 (4), 102504. doi:10.1016/j.psj.2023.102504

Cai, Z., Hansen, L. S., Laursen, S. F., Nielsen, H. M., Bahrndorff, S., Tomberlin, J. K., et al. (2024). Whole-genome sequencing of two captive black soldier fly populations: implications for commercial production. *Genomics* 116 (5), 110891. doi:10.1016/j.ygeno.2024.110891

Cao, C., Cai, Y., Li, Y., Li, T., Zhang, J., Hu, Z., et al. (2023). Characterization and comparative transcriptomic analysis of skeletal muscle in female pekin duck and hanzhong Ma duck during different growth stages using RNA-seq. *Poult. Sci.* 102 (12), 103122. doi:10.1016/j.psj.2023.103122

Carneiro, M., Albert, F. W., Afonso, S., Pereira, R. J., Burbano, H., Campos, R., et al. (2014a). The genomic architecture of population divergence between subspecies of the European rabbit. *PLoS Genet.* 10 (8), e1003519. doi:10.1371/journal.pgen.1003519

Carneiro, M., Rubin, C. J., Di Palma, F., Albert, F. W., Alfoldi, J., Martinez Barrio, A., et al. (2014b). Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. *Science* 345 (6200), 1074–1079. doi:10.1126/science.1253714

Casares-Crespo, L., Fernandez-Serrano, P., Vicente, J. S., Marco-Jimenez, F., and Viudes-de-Castro, M. P. (2018). Rabbit seminal plasma proteome: the importance of the genetic origin. *Anim. Reprod. Sci.* 189, 30–42. doi:10.1016/j.anireprosci.2017.12.004

Chakraborty, D., Sharma, N., Kour, S., Sodhi, S. S., Gupta, M. K., Lee, S. J., et al. (2022). Applications of omics technology for livestock selection and improvement. *Front. Genet.* 13, 774113. doi:10.3389/fgene.2022.774113

Chang, H., Cheng, T., Wu, Y., Hu, W., Long, R., Liu, C., et al. (2015). Transcriptomic analysis of the anterior silk gland in the domestic silkworm (*Bombyx mori*) - insight into the mechanism of silk formation and spinning. *PLoS One* 10 (9), e0139424. doi:10.1371/journal.pone.0139424

Chen, X., Hu, Y., Zheng, H., Cao, L., Niu, D., Yu, D., et al. (2012). Transcriptome comparison between honey bee queen- and worker-destined larvae. *Insect. Biochem. Mol. Biol.* 42 (9), 665–673. doi:10.1016/j.ibmb.2012.05.004

Chen, Y. R., Jiang, T., Zhu, J., Xie, Y. C., Tan, Z. C., Chen, Y. H., et al. (2017). Transcriptome sequencing reveals potential mechanisms of diapause preparation in bivoltine silkworm *Bombyx mori* (lepidoptera: bombycidae). *Comp. Biochem. Physiol. Part D. Genomics Proteomics* 24, 68–78. doi:10.1016/j.cbd.2017.07.003

Chen, T., Sun, Q., Ma, Y., Zeng, W., Liu, R., Qu, D., et al. (2020). A transcriptome atlas of silkworm silk glands revealed by PacBio single-molecule long-read sequencing. *Mol. Genet. Genomics* 295 (5), 1227–1237. doi:10.1007/s00438-020-01691-9

Chen, C., Parejo, M., Momeni, J., Langa, J., Nielsen, R. O., Shi, W., et al. (2022a). Population structure and diversity in european honey bees (apismellifera L.)-An empirical comparison of pool and individual whole-genome sequencing. *Genes (Basel)* 13 (2), 182. doi:10.3390/genes13020182

Chen, Y., Wang, J., Fan, H., Xia, S., Zhao, K., Chen, G., et al. (2022b). The multi-omics analysis revealed microbiological regulation of rabbit Colon with diarrhea fed an antibiotic-free diet. *Anim. (Basel)* 12 (12), 1497. doi:10.3390/ani12121497

Chen, W., Chen, H., Liao, J., Tang, M., Qin, H., Zhao, Z., et al. (2023). Chromosome-level genome assembly of a high-altitude-adapted frog (Rana kukunoris) from the Tibetan Plateau provides insight into amphibian genome evolution and adaptation. *Front. Zool.* 20 (1), 1. doi:10.1186/s12983-022-00482-9

Chen, H. M., Xu, K. X., Yan, C., Zhao, H., Jiao, D. L., Si, S., et al. (2024). A chromosome-scale reference genome of the banna miniature inbred pig. *Sci. Data* 11 (1), 1345. doi:10.1038/s41597-024-04201-3

Chen, L., Tong, X., Wu, Y., Liu, C., Tang, C., Qi, X., et al. (2025). A dataset of single-cell transcriptomic atlas of bama pig and potential marker genes across seven tissues. *BMC Genom. Data* 26 (1), 16. doi:10.1186/s12863-025-01308-3

Chueca, L. J., Schell, T., and Pfenninger, M. (2021). *De novo* genome assembly of the land snail Candidula unifasciata (Mollusca: gastropoda). *G3 (Bethesda)* 11 (8), jkab180. doi:10.1093/g3journal/jkab180

Cicogna, M. (1992). First international seminar on farming of invertebrates and other minilivestock. *Tropicultura* 10 (4), 155–159.

Cicogna, M. (2000). Les Cobayes. *B.E.D.I.M* 4.

Crysnanto, D., Wurmser, C., and Pausch, H. (2019). Accurate sequence variant genotyping in cattle using variation-aware genome graphs. *Genet. Sel. Evol.* 51 (1), 21. doi:10.1186/s12711-019-0462-x

Cui, Z., Amevor, F. K., Lan, X., Tang, B., Qin, S., Fu, P., et al. (2024). Integrative metabolomics and transcriptomics analysis revealed specific genes and metabolites affecting meat quality of chickens under different rearing systems. *Poult. Sci.* 103 (9), 103994. doi:10.1016/j.psj.2024.103994

Curtasu, M. V., Knudsen, K. E. B., Callesen, H., Purup, S., Stagsted, J., and Hedemann, M. S. (2019). Obesity development in a miniature Yucatan pig model: a multi-compartmental metabolomics study on cloned and normal pigs fed restricted or Ad libitum high-energy diets. *J. Proteome Res.* 18 (1), 30–47. doi:10.1021/acs.jproteome.8b00264

Curtasu, M. V., Tafintseva, V., Bendiks, Z. A., Marco, M. L., Kohler, A., Xu, Y., et al. (2020). Obesity-related metabolome and gut microbiota profiles of juvenile gottingen minipigs-long-term intake of fructose and resistant starch. *Metabolites* 10 (11), 456. doi:10.3390/metabo10110456

da Silva, I. B., Menegídio, F. B., Garcia, C., Kavalco, K. F., and Pasa, R. (2024). Genetic chronicle of the capybara: the complete mitochondrial genome of *Hydrochoerus hydrochaeris*. *Mamm. Biol.*, 1–7. doi:10.1007/s42991-024-00417-3

Dai, S., Zhao, P., Li, W., Peng, L., Jiang, E., Du, Y., et al. (2025). Global pangenome analysis highlights the critical role of structural variants in cattle improvement and identifies a unique event as a novel enhancer in IGFBP7+ cells. *Mol. Biol. Evol.* 42 (9), msaf205. doi:10.1093/molbev/msaf205

Dalle Zotte, A., and Cullere, M. (2019). "Carcass traits and meat quality of rabbit, hare, Guinea pig and capybara," in *More than beef, pork and chicken–the production, processing, and quality traits of other sources of meat for human diet* (Springer), 167–210.

Dalloul, R. A., Long, J. A., Zimin, A. V., Aslam, L., Beal, K., Blomberg Le, A., et al. (2010). Multi-platform next-generation sequencing of the domestic Turkey (meleagris gallopavo): genome assembly and analysis. *PLoS Biol.* 8 (9), e1000475. doi:10.1371/journal.pbio.1000475

Dalton, S., and Al-Zubiedi, H. (2019). The mealworm farm project: a low-cost household mealworm farm.

de Haas, Y., Veerkamp, R. F., de Jong, G., and Aldridge, M. N. (2021). Selective breeding as a mitigation tool for methane emissions from dairy cattle. *Animal* 15 (Suppl. 1), 100294. doi:10.1016/j.animal.2021.100294

De Jode, A., Faria, R., Formenti, G., Sims, Y., Smith, T. P., Tracey, A., et al. (2024). Chromosome-scale genome assembly of the rough periwinkle *Littorina saxatilis*. *Genome Biol. Evol.* 16 (4), evae076. doi:10.1093/gbe/evae076

de Koning, D. J. (2016). Meuwissen et al. on Genomic Selection. *Genetics* 203 (1), 5–7. doi:10.1534/genetics.116.189795

Defoliart, G. R. (1995). Edible insects as minilivestock. *Biodiversity and conservation* 4, 306–321.

Distante, D., Albanello, C., Zaffar, H., Faralli, S., and Amalfitano, D. (2025). Artificial intelligence applied to precision livestock farming: a tertiary study. *Smart. Agric. Technol.* 11, 100889. doi:10.1016/j.atech.2025.100889

Dong, Z., and Chen, Y. (2013). Transcriptomics: advances and approaches. *Sci. China Life Sci.* 56 (10), 960–967. doi:10.1007/s11427-013-4557-2

Dong, Z., Zhao, P., Wang, C., Zhang, Y., Chen, J., Wang, X., et al. (2013). Comparative proteomics reveal diverse functions and dynamic changes of *Bombyx mori* silk proteins spun from different development stages. *J. Proteome Res.* 12 (11), 5213–5222. doi:10.1021/pr4005772

Dossey, A. T., Oppert, B., Chu, F. C., Lorenzen, M. D., Scheffler, B., Simpson, S., et al. (2023). Genome and genetic engineering of the house cricket (acheta domesticus): a resource for sustainable agriculture. *Biomolecules* 13 (4), 589. doi:10.3390/biom13040589

Du, R., Yan, S., Yao, W., Zhang, H., Xue, Y., Zhao, Y., et al. (2025). Discrepancies in the rumen microbiome, metabolome, and serum metabolome among Hu sheep, East Friesian sheep, and East Friesian x Hu crossbred sheep. *Front. Microbiol.* 16, 1498050. doi:10.3389/fmicb.2025.1498050

Eleftheriou, E., Aury, J. M., Vacherie, B., Istace, B., Belser, C., Noel, B., et al. (2021). Chromosome-scale assembly of the yellow mealworm genome. *Open Res. Eur.* 1, 94. doi:10.12688/openreseurope.13987.3

Elshire, R. J., Glaubitz, J. C., Sun, Q., Poland, J. A., Kawamoto, K., Buckler, E. S., et al. (2011). A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. *PLoS One* 6 (5), e19379. doi:10.1371/journal.pone.0019379

Elsik, C. G., Worley, K. C., Bennett, A. K., Beye, M., Camara, F., Childers, C. P., et al. (2014). Finding the missing honey bee genes: lessons learned from a genome upgrade. *BMC Genomics* 15, 86. doi:10.1186/1471-2164-15-86

ENCODE Project Consortium (2012). An integrated encyclopedia of DNA elements in the human genome. *Nature* 489 (7414), 57–74. doi:10.1038/nature11247

Eriksson, T., Andere, A. A., Kelstrup, H., Emery, V. J., and Picard, C. J. (2020). The yellow mealworm (*Tenebrio molitor*) genome: a resource for the emerging insects as food and feed industry. *J. Insect Food Feed* 6 (5), 445–455. doi:10.3920/Jiff2019.0057

Fan, W. L., Ng, C. S., Chen, C. F., Lu, M. Y., Chen, Y. H., Liu, C. J., et al. (2013). Genome-wide patterns of genetic variation in two domestic chickens. *Genome Biol. Evol.* 5 (7), 1376–1392. doi:10.1093/gbe/evt097

Fan, W., Hou, S., and Zhou, Z. (2024). The duck 1000 genomes project: achievements and perspectives. *Animal Res. One Health* 2 (4), 366–376. doi:10.1002/aro2.89

Fang, X., Mou, Y., Huang, Z., Li, Y., Han, L., Zhang, Y., et al. (2012). The sequence and analysis of a Chinese pig genome. *Gigascience* 1 (1), 16. doi:10.1186/2047-217X-1-16

Fang, S. M., Hu, B. L., Zhou, Q. Z., Yu, Q. Y., and Zhang, Z. (2015). Comparative analysis of the silk gland transcriptomes between the domestic and wild silkworms. *BMC Genomics* 16 (1), 60. doi:10.1186/s12864-015-1287-9

Fang, G., Wang, W., Paunic, V., Heydari, H., Costanzo, M., Liu, X., et al. (2019). Discovering genetic interactions bridging pathways in genome-wide association studies. *Nat. Commun.* 10 (1), 4274. doi:10.1038/s41467-019-12131-7

Felsenfeld, G. (2014). A brief history of epigenetics. *Cold Spring Harb. Perspect. Biol.* 6 (1), a018200. doi:10.1101/cshperspect.a018200

Feng, M., Xia, J., Fei, S., Peng, R., Wang, X., Zhou, Y., et al. (2021a). Identification of silkworm hemocyte subsets and analysis of their response to baculovirus infection based on single-cell RNA sequencing. *Front. Immunol.* 12, 645359. doi:10.3389/fimmu.2021.645359

Feng, Y., Cirera, S., Tasoz, E., Liu, Y., Olsen, L. H., Christoffersen, B. O., et al. (2021b). Diet-dependent changes of the DNA methylome using a gottingen minipig model for obesity. *Front. Genet.* 12, 632859. doi:10.3389/fgene.2021.632859

Feng, M., Swevers, L., and Sun, J. (2022). Hemocyte clusters defined by scRNA-Seq in bombyx mori: *in silico* analysis of predicted marker genes and implications for potential functional roles. *Front. Immunol.* 13, 852702. doi:10.3389/fimmu.2022.852702

Feng, M., Xia, J., Fei, S., Huang, Y., Lai, W., Swevers, L., et al. (2023). Single-nucleus sequencing of fat body reveals distinct metabolic and immune response landscapes in silkworm larvae after *Bombyx mori* nucleopolyhedrovirus infection. *J. Immunol.* 211 (1), 140–153. doi:10.4049/jimmunol.2300007

Feng, M., Fei, S., Zou, J., Xia, J., Lai, W., Huang, Y., et al. (2024a). Single-nucleus sequencing of silkworm larval brain reveals the key role of lysozyme in the antiviral immune response in brain hemocytes. *J. Innate Immun.* 16 (1), 173–187. doi:10.1159/000537815

Feng, X., Memon, F., Ma, C., Zhu, J., Huang, Z., Tettamanti, G., et al. (2024b). Proteomic and transcriptomic analysis of cold-and heat-tolerant Black soldier fly (Hermetia illucens) larvae. *J. Insect Food Feed* 1 (aop), 1–19. doi:10.1163/23524588-00001215

Fent, K., Schmid, M., and Christen, V. (2020). Global transcriptome analysis reveals relevant effects at environmental concentrations of cypermethrin in honey bees (apis mellifera). *Environ. Pollut.* 259, 113715. doi:10.1016/j.envpol.2019.113715

Fernando, I., Siddiqui, S. A., Nugraha, W. S., Yudhistira, B., Adli, D. N., Nagdalian, A. A., et al. (2023). Overview of larvae of red palm weevil, (olivier) (coleoptera: curculionidae), as human food. *J. Insect Food Feed* 9 (10), 1265–1283. doi:10.3920/Jiff2022.0095

Flisikowska, T., Egli, J., Flisikowski, K., Stumbaum, M., Kung, E., Ebeling, M., et al. (2022). A humanized minipig model for the toxicological testing of therapeutic recombinant antibodies. *Nat. Biomed. Eng.* 6 (11), 1248–1256. doi:10.1038/s41551-022-00921-2

Fonseca, P. A. S., Id-Lahoucine, S., Reverter, A., Medrano, J. F., Fortes, M. S., Casellas, J., et al. (2018). Combining multi-OMICs information to identify key-regulator genes for pleiotropic effect on fertility and production traits in beef cattle. *PLoS One* 13 (10), e0205295. doi:10.1371/journal.pone.0205295

Franco, D., Mato, A., Salgado, F. J., Lopez-Pedrouso, M., Carrera, M., Bravo, S., et al. (2015). Tackling proteome changes in the longissimus thoracis bovine muscle in response to pre-slaughter stress. *J. Proteomics* 122, 73–85. doi:10.1016/j.jprot.2015.03.029

Fu, W., Wang, R., Xu, N., Wang, J., Li, R., Asadollahpour Nanaei, H., et al. (2022). Galbase: a comprehensive repository for integrating chicken multi-omics data. *BMC Genomics* 23 (1), 364. doi:10.1186/s12864-022-08598-2

Galbraith, D. A., Yang, X., Nino, E. L., Yi, S., and Grozinger, C. (2015). Parallel epigenomic and transcriptomic responses to viral infection in honey bees (apis mellifera). *PLoS Pathog.* 11 (3), e1004713. doi:10.1371/journal.ppat.1004713

Ge, K., and Geng, Z. (2022). Proteomic analysis of the liver regulating lipid metabolism in chaohu ducks using two-dimensional electrophoresis. *Open Life Sci.* 17 (1), 960–972. doi:10.1515/biol-2022-0101

Generalovic, T. N., McCarthy, S. A., Warren, I. A., Wood, J. M. D., Torrance, J., Sims, Y., et al. (2021). A high-quality, chromosome-level genome assembly of the black soldier fly (Hermetia illucens L.). *G3 (Bethesda)* 11 (5), jkab085. doi:10.1093/g3journal/jkab085

Geng, X., Li, W., Shang, H., Gou, Q., Zhang, F., Zang, X., et al. (2017). A reference gene set construction using RNA-seq of multiple tissues of Chinese giant salamander, *Andrias davidianus*. *Gigascience* 6 (3), 1–7. doi:10.1093/gigascience/gix006

Georges, M., Charlier, C., and Hayes, B. (2019). Harnessing genomic information for livestock improvement. *Nat. Rev. Genet.* 20 (3), 135–156. doi:10.1038/s41576-018-0082-2

Gerber, P. J., Steinfeld, H., Henderson, B., Mottet, A., Opio, C., Dijkman, J., et al. (2013). Tackling climate change through livestock: a global assessment of emissions and mitigation opportunities.

Ghosh, S., Meyer-Rochow, V. B., and Jung, C. (2021). Farming the edible aquatic snail Pomacea canaliculata as a mini-livestock. *Fishes* 7 (1), 6. doi:10.3390/fishes7010006

Gopinath, G., Srikeerthana, K., Tomar, A., Sekhar, S. M. C., and Arunkumar, K. P. (2017). RNA sequencing reveals a complete but an unconventional type of dosage compensation in the domestic silkworm *Bombyx mori*. *R. Soc. Open Sci.* 4 (7), 170261. doi:10.1098/rsos.170261

Greenberg, J. K., Xia, J., Zhou, X., Thatcher, S. R., Gu, X., Ament, S. A., et al. (2012). Behavioral plasticity in honey bees is associated with differences in brain microRNA transcriptome. *Genes Brain Behav.* 11 (6), 660–670. doi:10.1111/j.1601-183X.2012.00782.x

Grisel, J. E. (2000). Quantitative trait locus analysis. *Alcohol Res. Health* 24 (3), 169–174.

Gu, L., Chen, J., Hu, C., Wang, D., Huan, S., Rong, G., et al. (2024). Integrated transcriptomics and metabolomics study of embryonic breast muscle of Jiaji ducks. *BMC Genomics* 25 (1), 551. doi:10.1186/s12864-024-10452-6

Guilliet, J., Baudouin, G., Pollet, N., and Filee, J. (2022). What complete mitochondrial genomes tell us about the evolutionary history of the black soldier fly, Hermetia illucens. *BMC Ecol. Evol.* 22 (1), 72. doi:10.1186/s12862-022-02025-6

Guo, Y., Bao, Y., Meng, Q., Hu, X., Meng, Q., Ren, L., et al. (2012). Immunoglobulin genomics in the Guinea pig (*Cavia porcellus*). *PLoS One* 7 (6), e39298. doi:10.1371/journal.pone.0039298

Guo, H., Huang, C., Jiang, L., Cheng, T., Feng, T., and Xia, Q. (2018). Transcriptome analysis of the response of silkworm to drastic changes in ambient temperature. *Appl. Microbiol. Biotechnol.* 102 (23), 10161–10170. doi:10.1007/s00253-018-9387-5

Guo, Y., Zhang, Y., Liu, Q., Huang, Y., Mao, G., Yue, Z., et al. (2019). A chromosomal-level genome assembly for the giant African snail achatina fulica. *Gigascience* 8 (10), giz124. doi:10.1093/gigascience/giz124

Haider, S., and Pal, R. (2013). Integrated analysis of transcriptomic and proteomic data. *Curr. Genomics* 14 (2), 91–110. doi:10.2174/1389202911314020003

Hardouin, J. (1995). Minilivestock - from gathering to controlled production. *Biodivers. Conserv.* 4(3), 220–232. doi:10.1007/Bf00055969

Hardouin, J., Thys, E., Joiris, V., and Fielding, D. (2003). Mini-livestock breeding with Indigenous species in the tropics. *Livest. Res. Rural Dev.* 15 (4).

Hasin, Y., Seldin, M., and Lusis, A. (2017). Multi-omics approaches to disease. *Genome. Biol.* 18 (1), 83. doi:10.1186/s13059-017-1215-1

He, J., Xia, C., He, Y., Pan, D., Cao, J., Sun, Y., et al. (2019a). Proteomic responses to oxidative damage in meat from ducks exposed to heat stress. *Food Chem.* 295, 129–137. doi:10.1016/j.foodchem.2019.05.073

He, X. J., Jiang, W. J., Zhou, M., Barron, A. B., and Zeng, Z. J. (2019b). A comparison of honeybee (apis mellifera) queen, worker and drone larvae by RNA-seq. *Insect Sci.* 26 (3), 499–509. doi:10.1111/1744-7917.12557

Heckel, T., Schmucki, R., Berrera, M., Ringshandl, S., Badi, L., Steiner, G., et al. (2015). Functional analysis and transcriptional output of the gottingen minipig genome. *BMC Genomics* 16, 932. doi:10.1186/s12864-015-2119-7

Herault, F., Houee-Bigot, M., Baeza, E., Bouchez, O., Esquerre, D., Klopp, C., et al. (2019). RNA-seq analysis of hepatic gene expression of common pekin, muscovy, mule and hinny ducks fed ad libitum or overfed. *BMC Genomics* 20 (1), 13. doi:10.1186/s12864-018-5415-1

Herman, J. J., Spencer, H. G., Donohue, K., and Sultan, S. E. (2014). How stable "should" epigenetic modifications be? Insights from adaptive plasticity and bet hedging. *Evolution* 68 (3), 632–643. doi:10.1111/evo.12324

Herrera-Alvarez, S., Karlsson, E., Ryder, O. A., Lindblad-Toh, K., and Crawford, A. J. (2021). How to make a rodent giant: genomic basis and tradeoffs of gigantism in the capybara, the world's largest rodent. *Mol. Biol. Evol.* 38 (5), 1715–1730. doi:10.1093/molbev/msaa285

Herrero, M., Havlik, P., Valin, H., Notenbaert, A., Rufino, M. C., Thornton, P. K., et al. (2013). Biomass use, production, feed efficiencies, and greenhouse gas emissions from global livestock systems. *Proc. Natl. Acad. Sci. U S A.* 110 (52), 20888–20893. doi:10.1073/pnas.1308149110

Hostiou, N., Fagon, J., Chauvat, S., Turlot, A., Kling-Eveillard, F., Boivin, X., et al. (2017). Impact of precision livestock farming on work and human-animal interactions on dairy farms. A review. *Biotechnol. Agronomie Soc. Environnement* 21 (4), 268–275. doi:10.25518/1780-4507.13706

Hou, X., Dai, P., Song, X., Long, X., Gao, J., and Chai, T. (2024). Understanding the effect of compound probiotics on the health of rabbits and its mechanisms through metagenomics. *Probiotics Antimicrob. Proteins* 16 (3), 815–828. doi:10.1007/s12602-023-10072-8

Hu, Z., and Liu, X. (2023). Integration of transcriptomics and non-targeted metabolomics reveals the underlying mechanism of skeletal muscle development in duck during embryonic stage. *Int. J. Mol. Sci.* 24 (6), 5214. doi:10.3390/ijms24065214

Hu, Z. L., Fritz, E. R., and Reecy, J. M. (2007). AnimalQTLdb: a livestock QTL database tool set for positional QTL information mining and beyond. *Nucleic Acids Res.* 35 (Database issue), D604–D609. doi:10.1093/nar/gkl946

Hu, S., Qiu, N., Liu, Y., Zhao, H., Gao, D., Song, R., et al. (2016). Identification and comparative proteomic study of quail and duck egg white protein using 2-dimensional gel electrophoresis and matrix-assisted laser desorption/ionization time-of-flight tandem mass spectrometry analysis. *Poult. Sci.* 95 (5), 1137–1144. doi:10.3382/ps/pew033

Hu, W., Chen, Y., Lin, Y., and Xia, Q. (2019). Developmental and transcriptomic features characterize defects of silk gland growth and silk production in silkworm naked pupa mutant. *Insect. Biochem. Mol. Biol.* 111, 103175. doi:10.1016/j.ibmb.2019.05.010

Hu, Z., Cao, J., Ge, L., Zhang, J., Zhang, H., and Liu, X. (2021a). Characterization and comparative transcriptomic analysis of skeletal muscle in pekin duck at different growth stages using RNA-Seq. *Anim. (Basel)* 11 (3), 834. doi:10.3390/ani11030834

Hu, Z., Cao, J., Zhang, J., Ge, L., Zhang, H., and Liu, X. (2021b). Skeletal muscle transcriptome analysis of hanzhong Ma duck at different growth stages using RNA-seq. *Biomolecules* 11 (2), 315. doi:10.3390/biom11020315

Huang, C., Feng, W. L., Xiong, J., Wang, T. L., Wang, W. G., Wang, C. W., et al. (2019). Impact of drying method on the nutritional value of the edible insect protein from black soldier fly (dev comp ImmunolL.) larvae: amino acid composition, nutritional value evaluation, *in vitro* digestibility, and thermal properties. *Eur. Food. Res. Technol.* 245 (1), 11–21. doi:10.1007/s00217-018-3136-y

Huang, X., Zhang, H., Cao, H., Zhou, W., Xiang, X., and Yin, Z. (2022). Transcriptomics and metabolomics analysis of the ovaries of high and low egg production chickens. *Anim. (Basel)* 12 (16), 2010. doi:10.3390/ani12162010

Huang, D., Wang, Y., Ding, H., and Zhao, H. (2024). Comparative analysis of angora rabbit colostrum and mature milk using quantitative proteomics. *Biol. (Basel)* 13 (8), 634. doi:10.3390/biology13080634

Huang, M., Sun, J., Wang, J., Ye, X., Chen, Z., Zhao, X., et al. (2025). Goose multi-omics database: a comprehensive multi-omics database for goose genomics. *Poult. Sci.* 104 (3), 104842. doi:10.1016/j.psj.2025.104842

Hyslop, J. (2008). Simuljated global warming potential and ammonia emission figures for a range of suckler herd breeding strategies and beef cattle finishing systems. *Livest. Glob. Clim. Change,* 127.

i5K Consortium (2013). The i5K initiative: advancing arthropod genomics for knowledge, human health, agriculture, and the environment. *J. Hered.* 104 (5), 595–600. doi:10.1093/jhered/est050

Ikeobi, C. O., Woolliams, J. A., Morrice, D. R., Law, A., Windsor, D., Burt, D. W., et al. (2002). Quantitative trait loci affecting fatness in the chicken. *Anim. Genet.* 33 (6), 428–435. doi:10.1046/j.1365-2052.2002.00911.x

Imoru, A., and Babadipe, S. (2019). Minilivestock-the invaluable underutilised genetic species for enhanced protein availability. *Afr. J. Agric. Food Sci.* 2 (2), 27–32.

Ingweye, J., and Kalio, G. (2020). Little known small animals of economic value: why calling them mini-livestock matters. *Niger. J. Animal Sci.* 22 (1), 241–252.

Ip, J. C. H., Mu, H., Chen, Q., Sun, J., Ituarte, S., Heras, H., et al. (2018). AmpuBase: a transcriptome database for eight species of apple snails (gastropoda: ampullariidae). *BMC Genomics* 19 (1), 179. doi:10.1186/s12864-018-4553-9

Ip, J. C. H., Mu, H., Zhang, Y., Sun, J., Heras, H., Chu, K. H., et al. (2019). Understanding the transition from water to land: insights from multi-omic analyses of the perivitelline fluid of apple snail eggs. *J. Proteomics* 194, 79–88. doi:10.1016/j.jprot.2018.12.014

Isa, A. M., Sun, Y., Li, Y., Wang, Y., Ni, A., Yuan, J., et al. (2022). MicroRNAs with non-additive expression in the ovary of hybrid hens target genes enriched in key reproductive pathways that may influence heterosis for egg laying traits. *Front. Genet.* 13, 974619. doi:10.3389/fgene.2022.974619

Ishii, Y., Toyoda, A., Lewis, A., Davison, A., Miura, O., Kimura, K., et al. (2025). Chromosome-level genome assembly of the Asian tramp snail Bradybaena similaris (stylommatophora: camaenidae). *Genome Biol. Evol.* 17 (5), evaf070. doi:10.1093/gbe/evaf070

Jassal, B., Matthews, L., Viteri, G., Gong, C., Lorente, P., Fabregat, A., et al. (2020). The reactome pathway knowledgebase. *Nucleic Acids Res.* 48 (D1), D498–D503. doi:10.1093/nar/gkz1031

Jastrzebski, J. P., Lipka, A., Majewska, M., Makowczenko, K. G., Paukszto, L., Bukowska, J., et al. (2022). *In silico* identification of lncRNAs regulating sperm motility in the Turkey (meleagris gallopavo L.). *Int. J. Mol. Sci.* 23 (14), 7642. doi:10.3390/ijms23147642

Jegou, M., Gondret, F., Vincent, A., Trefeu, C., Gilbert, H., and Louveau, I. (2016). Whole blood transcriptomics is relevant to identify molecular changes in response to genetic selection for feed efficiency and nutritional status in the pig. *PLoS One* 11 (1), e0146550. doi:10.1371/journal.pone.0146550

Jia, X., Kang, Z., Wang, G., Zhang, K., Fu, X., Li, C., et al. (2024a). Long-read sequencing-based transcriptomic landscape in longissimus dorsi and transcriptome-wide association studies for growth traits of meat rabbits. *Front. Vet. Sci.* 11, 1320484. doi:10.3389/fvets.2024.1320484

Jia, Y., Zhao, Y., Niu, M., Zhao, C., Li, X., and Chen, H. (2024b). Preliminary study of metabonomic changes during the progression of atherosclerosis in miniature pigs. *Anim. Model Exp. Med.* 7 (4), 419–432. doi:10.1002/ame2.12462

Jiang, D., Armour, C. R., Hu, C., Mei, M., Tian, C., Sharpton, T. J., et al. (2019). Microbiome multi-omics network analysis: statistical considerations, limitations, and opportunities. *Front. Genet.* 10, 995. doi:10.3389/fgene.2019.00995

Jiang, L., Peng, L. L., Cao, Y. Y., Thakur, K., Hu, F., Tang, S. M., et al. (2020). Transcriptome analysis reveals gene expression changes of the fat body of silkworm (*Bombyx mori* L.) in response to selenium treatment. *Chemosphere* 245, 125660. doi:10.1016/j.chemosphere.2019.125660

Jiang, M. Z., Aguet, F., Ardlie, K., Chen, J., Cornell, E., Cruz, D., et al. (2023). Canonical correlation analysis for multi-omics: application to cross-cohort analysis. *PLoS Genet.* 19 (5), e1010517. doi:10.1371/journal.pgen.1010517

Johnston, P. R., Makarova, O., and Rolff, J. (2013). Inducible defenses stay up late: temporal patterns of immune gene expression in *Tenebrio molitor*. *G3 (Bethesda)* 4 (6), 947–955. doi:10.1534/g3.113.008516

Kanehisa, M. (2002). The KEGG database. *Silico'Simulation Biological Processes Novartis Found. Symposium* 247, 91–103. doi:10.1002/0470857897.ch8

Karami, K., Sabban, J., Cerutti, C., Devailly, G., Foissac, S., Gourichon, D., et al. (2025). Molecular responses of chicken embryos to maternal heat stress through DNA methylation and gene expression: a pilot study. *Environ. Epigenet.* 11 (1), dvaf009. doi:10.1093/eep/dvaf009

Karczewski, K. J., and Snyder, M. P. (2018). Integrative omics for health and disease. *Nat. Rev. Genet.* 19 (5), 299–310. doi:10.1038/nrg.2018.4

Kataoka, K., Minei, R., Ide, K., Ogura, A., Takeyama, H., Takeda, M., et al. (2020). The draft genome dataset of the Asian cricket Teleogryllus occipitalis for molecular research toward entomophagy. *Front. Genet.* 11, 470. doi:10.3389/fgene.2020.00470

Kaur, S., Stinson, S. A., and diCenzo, G. C. (2023). Whole genome assemblies of Zophobas morio and *Tenebrio molitor*. *G3 (Bethesda)* 13 (6), jkad079. doi:10.1093/g3journal/jkad079

Kawahara-Miki, R., Sano, S., Nunome, M., Shimmura, T., Kuwayama, T., Takahashi, S., et al. (2013). Next-generation sequencing reveals genomic features in the Japanese quail. *Genomics* 101 (6), 345–353. doi:10.1016/j.ygeno.2013.03.006

Kawamoto, M., Jouraku, A., Toyoda, A., Yokoi, K., Minakuchi, Y., Katsuma, S., et al. (2019). High-quality genome assembly of the silkworm, Bombyx mori. *Insect. Biochem. Mol. Biol.* 107, 53–62. doi:10.1016/j.ibmb.2019.02.002

Khamis, F. M., Ombura, F. L. O., Akutse, K. S., Subramanian, S., Mohamed, S. A., Fiaboe, K. K. M., et al. (2020). Insights in the global genetics and gut microbiome of black soldier fly, hermetia illucens: implications for animal feed safety control. *Front. Microbiol.* 11, 1538. doi:10.3389/fmicb.2020.01538

Khatri, B., Kang, S., Shouse, S., Anthony, N., Kuenzel, W., and Kong, B. C. (2019). Copy number variation study in Japanese quail associated with stress related traits using whole genome re-sequencing data. *PLoS One* 14 (3), e0214543. doi:10.1371/journal.pone.0214543

Khaveh, N., Buschow, R., and Metzger, J. (2024). Deciphering transcriptome patterns in porcine mesenchymal stem cells promoting phenotypic maintenance and differentiation by key driver genes. *Front. Cell Dev. Biol.* 12, 1478757. doi:10.3389/fcell.2024.1478757

Klapwijk, C. J., Schut, M., van Asten, P. J. A., Vanlauwe, B., Giller, K. E., and Descheemaeker, K. (2020). Micro-livestock in smallholder farming systems: the role, challenges and opportunities for cavies in South Kivu, eastern DR Congo. *Trop. Anim. Health Prod.* 52 (3), 1167–1177. doi:10.1007/s11250-019-02112-9

Klein, A. H., Ballard, K. R., Storey, K. B., Motti, C. A., Zhao, M., and Cummins, S. F. (2019). Multi-omics investigations within the phylum mollusca, class gastropoda: from ecological application to breakthrough phylogenomic studies. *Brief. Funct. Genomics* 18 (6), 377–394. doi:10.1093/bfgp/elz017

Kwon, D. J., Lee, Y. S., Shin, D., Won, K. H., and Song, K. D. (2019). Genome analysis of Yucatan miniature pigs to assess their potential as biomedical model animals. *Asian-Australas J. Anim. Sci.* 32 (2), 290–296. doi:10.5713/ajas.18.0170

Kwon, D., Ahn, J., Kim, H., Kim, H., Kim, J., Wy, S., et al. (2024). Convergent dwarfism consequences of minipigs under independent artificial selections. *BMC Genomics* 25 (1), 761. doi:10.1186/s12864-024-10677-5

Labas, V., Grasseau, I., Cahier, K., Gargaros, A., Harichaux, G., Teixeira-Gomes, A. P., et al. (2015). Qualitative and quantitative peptidomic and proteomic approaches to phenotyping chicken semen. *J. Proteomics* 112, 313–335. doi:10.1016/j.jprot.2014.07.024

Lamichhaney, S., Catullo, R., Keogh, J. S., Clulow, S., Edwards, S. V., and Ezaz, T. (2021). A bird-like genome from a frog: mechanisms of genome size reduction in the ornate burrowing frog, Platyplectrum ornatum. *Proc. Natl. Acad. Sci. U S A.* 118 (11), e2011649118. doi:10.1073/pnas.2011649118

Lande, R., and Thompson, R. (1990). Efficiency of marker-assisted selection in the improvement of quantitative traits. *Genetics* 124 (3), 743–756. doi:10.1093/genetics/124.3.743

Langfelder, P., and Horvath, S. (2008). WGCNA: an R package for weighted correlation network analysis. *BMC Bioinforma.* 9 (1), 559. doi:10.1186/1471-2105-9-559

Le Roy, N., Combes-Soia, L., Brionne, A., Labas, V., Rodriguez-Navarro, A. B., Hincke, M. T., et al. (2019). Guinea fowl eggshell quantitative proteomics yield new findings related to its unique structural characteristics and superior mechanical properties. *J. Proteomics* 209, 103511. doi:10.1016/j.jprot.2019.103511

Lee, J. H., Chung, H., Shin, Y. P., Kim, M. A., Natarajan, S., Veerappan, K., et al. (2021). Uncovering antimicrobial peptide from using transcriptome analysis. *Int. J. Pept. Res. Ther.* 27 (3), 1827–1835. doi:10.1007/s10989-021-10213-z

Legrand, E., Basu, N., Hecker, M., Crump, D., Xia, J., Chandramouli, B., et al. (2021). Targeted metabolomics to assess exposure to environmental chemicals of concern in Japanese quail at two life stages. *Metabolites* 11 (12), 850. doi:10.3390/metabo11120850

Li, Y., Wang, G., Tian, J., Liu, H., Yang, H., Yi, Y., et al. (2012). Transcriptome analysis of the silkworm (*Bombyx mori*) by high-throughput RNA sequencing. *PLoS One* 7 (8), e43713. doi:10.1371/journal.pone.0043713

Li, J. Y., Ye, L. P., Che, J. Q., Song, J., You, Z. Y., Yun, K. C., et al. (2015). Comparative proteomic analysis of the silkworm middle silk gland reveals the importance of ribosome biogenesis in silk protein production. *J. Proteomics* 126, 109–120. doi:10.1016/j.jprot.2015.06.001

Li, J., Qin, S., Yu, H., Zhang, J., Liu, N., Yu, Y., et al. (2016). Comparative transcriptome analysis reveals different silk yields of two silkworm strains. *PLoS One* 11 (5), e0155329. doi:10.1371/journal.pone.0155329

Li, D., Li, Y., Li, M., Che, T., Tian, S., Chen, B., et al. (2019a). Population genomics identifies patterns of genetic diversity and selection in chicken. *BMC Genomics* 20 (1), 263. doi:10.1186/s12864-019-5622-4

Li, F., Zhao, X., Li, M., He, K., Huang, C., Zhou, Y., et al. (2019b). Insect genomes: progress and challenges. *Insect Mol. Biol.* 28 (6), 739–758. doi:10.1111/imb.12599

Li, P., Che, X., Gao, Y., and Zhang, R. (2020a). Proteomics and bioinformatics analysis of cartilage in post-traumatic osteoarthritis in a mini-pig model of anterior cruciate ligament repair. *Med. Sci. Monit.* 26, e920104. doi:10.12659/MSM.920104

Li, Y., Gao, G., Lin, Y., Hu, S., Luo, Y., Wang, G., et al. (2020b). Pacific biosciences assembly with Hi-C mapping generates an improved, chromosome-level goose genome. *Gigascience* 9 (10), giaa114. doi:10.1093/gigascience/giaa114

Li, Y., Wang, J., Elzo, M. A., Gan, M., Tang, T., Shao, J., et al. (2021). Multi-omics analysis of key microRNA-mRNA metabolic regulatory networks in skeletal muscle of Obese rabbits. *Int. J. Mol. Sci.* 22 (8), 4204. doi:10.3390/ijms22084204

Li, J., Chen, C., and Zha, X. (2022a). Midgut and head transcriptomic analysis of silkworms reveals the physiological effects of artificial diets. *Insects* 13 (3), 291. doi:10.3390/insects13030291

Li, L., Wang, Y. Q., Li, G. Y., Song, Q. S., Stanley, D., Wei, S. J., et al. (2022b). Genomic and transcriptomic analyses of chitin metabolism enzymes in *Tenebrio molitor*. *Arch. Insect Biochem. Physiol.* 111 (3), e21950. doi:10.1002/arch.21950

Li, W., Lan, Y., Wang, L., He, L., Tang, R., Price, M., et al. (2022c). Comparative transcriptomes of nine tissues for the Heilongjiang brown frog (*Rana amurensis*). *Sci. Rep.* 12 (1), 20759. doi:10.1038/s41598-022-24631-6

Li, Z., Cheng, Y., Chen, J., Xu, W., Ma, W., Li, S., et al. (2023). Widely targeted HPLC-MS/MS metabolomics analysis reveals natural metabolic insights in insects. *Metabolites* 13 (6), 735. doi:10.3390/metabo13060735

Li, T., Wang, Y., Zhang, Z., Ji, C., Zheng, N., and Huang, Y. (2024a). A comparative analysis reveals the genomic diversity among eight muscovy duck populations. *G3 Genes, Genomes, Genet.* 14, jkae112. doi:10.1093/g3journal/jkae112

Li, Y., Yao, J., Sang, H., Wang, Q., Su, L., Zhao, X., et al. (2024b). Pan-genome analysis highlights the role of structural variation in the evolution and environmental adaptation of Asian honeybees. *Mol. Ecol. Resour.* 24 (2), e13905. doi:10.1111/1755-0998.13905

Libbrecht, M. W., and Noble, W. S. (2015). Machine learning applications in genetics and genomics. *Nat. Rev. Genet.* 16 (6), 321–332. doi:10.1038/nrg3920

Lin, J., Guan, L., Ge, L., Liu, G., Bai, Y., and Liu, X. (2021). Nanopore-based full-length transcriptome sequencing of muscovy duck (*Cairina moschata*) ovary. *Poult. Sci.* 100 (8), 101246. doi:10.1016/j.psj.2021.101246

Liu, L., and Penagaricano, F. (2025). EnrichKit: a multi-omics tool for livestock research. *Front. Genet.* 16, 1573374. doi:10.3389/fgene.2025.1573374

Liu, Y., Zeng, B. H., Shang, H. T., Cen, Y. Y., and Wei, H. (2008). Bama miniature pigs (sus scrofa domestica) as a model for drug evaluation for humans: comparison of *in vitro* metabolism and *in vivo* pharmacokinetics of lovastatin. *Comp. Med.* 58 (6), 580–587.

Liu, P., Wang, Y., Du, X., Yao, L., Li, F., and Meng, Z. (2015). Transcriptome analysis of thermal parthenogenesis of the domesticated silkworm. *PLoS One* 10 (8), e0135215. doi:10.1371/journal.pone.0135215

Liu, C., Zhang, Y., Ren, Y., Wang, H., Li, S., Jiang, F., et al. (2018a). The genome of the golden apple snail Pomacea canaliculata provides insight into stress tolerance and invasive adaptation. *Gigascience* 7 (9), giy101. doi:10.1093/gigascience/giy101

Liu, Y., Jia, Y., Liu, C., Ding, L., and Xia, Z. (2018b). RNA-seq transcriptome analysis of breast muscle in pekin ducks supplemented with the dietary probiotic Clostridium butyricum. *BMC Genomics* 19 (1), 844. doi:10.1186/s12864-018-5261-1

Liu, Y., Zhang, M., Shan, Y., Ji, G., Ju, X., Tu, Y., et al. (2020). miRNA-mRNA network regulation in the skeletal muscle fiber phenotype of chickens revealed by integrated

analysis of miRNAome and transcriptome. *Sci. Rep.* 10 (1), 10619. doi:10.1038/s41598-020-67482-9

Liu, Q., Song, Y., Ma, J., Mabrouk, I., Zhou, Y., Hu, J., et al. (2024a). The combination of RNA-Seq transcriptomics and data-independent acquisition proteomics reveal the mechanisms and function of different gooses testicular development at different stages of laying cycle. *Poult. Sci.* 103 (10), 104007. doi:10.1016/j.psj.2024.104007

Liu, X., Zhang, Z., Hu, B., Chen, K., Yu, Y., Xiang, H., et al. (2024b). Single-cell transcriptomes provide insights into expansion of glial cells in *Bombyx mori*. *Insect Sci.* 31 (4), 1041–1054. doi:10.1111/1744-7917.13294

Liu, Y., Zhang, X., Wang, K., Li, Q., Yan, S., Shi, H., et al. (2024c). RNA-seq reveals pathways responsible for meat quality characteristic differences between two Yunnan Indigenous chicken breeds and commercial broilers. *Foods* 13 (13), 2008. doi:10.3390/foods13132008

Lu, L., Chen, Y., Wang, Z., Li, X., Chen, W., Tao, Z., et al. (2015). The goose genome sequence leads to insights into the evolution of waterfowl and susceptibility to fatty liver. *Genome. Biol.* 16 (1), 89. doi:10.1186/s13059-015-0652-y

Lu, M. D., Han, X. M., Ma, Y. F., Irwin, D. M., Gao, Y., Deng, J. K., et al. (2016). Genetic variations associated with six-white-point coat pigmentation in diannan small-ear pigs. *Sci. Rep.* 6, 27534. doi:10.1038/srep27534

Lu, X., Abdalla, I. M., Nazar, M., Fan, Y., Zhang, Z., Wu, X., et al. (2021). Genome-wide association study on reproduction-related body-shape traits of Chinese holstein cows. *Anim. (Basel)* 11 (7), 1927. doi:10.3390/ani11071927

Lu, J., Guo, Y., Muhmood, A., Lv, Z., Zeng, B., Qiu, Y., et al. (2022a). Food waste management employing UV-Induced black soldier flies: metabolomic analysis of bioactive components, antioxidant properties, and antibacterial potential. *Int. J. Environ. Res. Public Health* 19 (11), 6614. doi:10.3390/ijerph19116614

Lu, Y., Wang, Z., Lin, F., Ma, Y., Kang, J., Fu, Y., et al. (2022b). Screening and identification of genes associated with flight muscle histolysis of the house cricket *Acheta domesticus*. *Front. Physiol.* 13, 1079328. doi:10.3389/fphys.2022.1079328

Lu, Y., Luo, F., Zhou, A., Yi, C., Chen, H., Li, J., et al. (2024). Whole-genome sequencing of the invasive golden apple snail Pomacea canaliculata from Asia reveals rapid expansion and adaptive evolution. *Gigascience* 13, giae064. doi:10.1093/gigascience/giae064

Luan, Y., Zuo, W., Li, C., Gao, R., Zhang, H., Tong, X., et al. (2018). Identification of genes that control silk yield by RNA sequencing analysis of silkworm (*Bombyx mori*) strains of variable silk yield. *Int. J. Mol. Sci.* 19 (12), 3718. doi:10.3390/ijms19123718

Lyko, F., Foret, S., Kucharski, R., Wolf, S., Falckenhayn, C., and Maleszka, R. (2010). The honey bee epigenomes: differential methylation of brain DNA in queens and workers. *PLoS Biol.* 8 (11), e1000506. doi:10.1371/journal.pbio.1000506

Ma, Y., Zeng, W., Ba, Y., Luo, Q., Ou, Y., Liu, R., et al. (2022). A single-cell transcriptomic atlas characterizes the silk-producing organ in the silkworm. *Nat. Commun.* 13 (1), 3316. doi:10.1038/s41467-022-31003-1

Ma, B., Jin, W., Fu, H., Sun, B., Yang, S., Ma, X., et al. (2023). A high-quality chromosome-level genome assembly of a snail Cipangopaludina cathayensis (gastropoda: viviparidae). *Genes (Basel)* 14 (7), 1365. doi:10.3390/genes14071365

Ma, Y., Li, Q., Tang, Y., Zhang, Z., Liu, R., Luo, Q., et al. (2024). The architecture of silk-secreting organs during the final larval stage of silkworms revealed by single-nucleus and spatial transcriptomics. *Cell Rep.* 43 (7), 114460. doi:10.1016/j.celrep.2024.114460

Malila, Y., Carr, K. M., Ernst, C. W., Velleman, S. G., Reed, K. M., and Strasburg, G. M. (2014). Deep transcriptome sequencing reveals differences in global gene expression between normal and pale, soft, and exudative Turkey meat. *J. Anim. Sci.* 92 (3), 1250–1260. doi:10.2527/jas.2013-7293

Manfredini, F., Brown, M. J., Vergoz, V., and Oldroyd, B. P. (2015). RNA-Sequencing elucidates the regulation of behavioural transitions associated with the mating process in honey bee queens. *BMC Genomics* 16, 563. doi:10.1186/s12864-015-1750-7

Manzanilla-Pech, C. I. V., Difford, G. F., Sahana, G., Rome, H., Lovendahl, P., and Lassen, J. (2022). Genome-wide association study for methane emission traits in Danish holstein cattle. *J. Dairy Sci.* 105 (2), 1357–1368. doi:10.3168/jds.2021-20410

Mao, W., Schuler, M. A., and Berenbaum, M. R. (2015). A dietary phytochemical alters caste-associated gene expression in honey bees. *Sci. Adv.* 1 (7), e1500795. doi:10.1126/sciadv.1500795

Marasco, V., Herzyk, P., Robinson, J., and Spencer, K. A. (2016). Pre- and post-natal stress programming: developmental exposure to glucocorticoids causes long-term brain-region specific changes to transcriptome in the precocial Japanese quail. *J. Neuroendocrinol.* 28 (5), jne.12387. doi:10.1111/jne.12387

Marciniak, P., Pacholska-Bogalska, J., and Ragionieri, L. (2022). Neuropeptidomes of *Tenebrio molitor* L. and Zophobas atratus fab. (coleoptera, polyphaga: tenebrionidae). *J. Proteome Res.* 21 (10), 2247–2260. doi:10.1021/acs.jproteome.1c00694

Masuoka, Y., Jouraku, A., Tsubota, T., Ono, H., Chiba, H., Sezutsu, H., et al. (2024). Time-course transcriptome data of silk glands in day 0-7 last-instar larvae of *Bombyx mori* (w1 pnd strain). *Sci. Data* 11 (1), 709. doi:10.1038/s41597-024-03560-1

Maxwell, M., Soderlund, R., Hartle, S., and Wattrang, E. (2024). Single-cell RNA-Seq mapping of chicken peripheral blood leukocytes. *BMC Genomics* 25 (1), 124. doi:10.1186/s12864-024-10044-4

Mc Cartney, A. M., Formenti, G., Mouton, A., De Panis, D., Marins, L. S., Leitão, H. G., et al. (2024). The european reference genome atlas: piloting a decentralised approach to equitable biodiversity genomics. *NPJ Biodivers.* 3 (1), 28. doi:10.1038/s44185-024-00054-6

Mei, Y., Jing, D., Tang, S., Chen, X., Chen, H., Duanmu, H., et al. (2022). InsectBase 2.0: a comprehensive gene resource for insects. *Nucleic Acids Res.* 50 (D1), D1040–D1045. doi:10.1093/nar/gkab1090

Mesbah-Uddin, M., Guldbrandtsen, B., Capitan, A., Lund, M. S., Boichard, D., and Sahana, G. (2022). Genome-wide association study with imputed whole-genome sequence variants including large deletions for female fertility in 3 nordic dairy cattle breeds. *J. Dairy Sci.* 105 (2), 1298–1313. doi:10.3168/jds.2021-20655

Meuwissen, T. H., Hayes, B. J., and Goddard, M. E. (2001). Prediction of total genetic value using genome-wide dense marker maps. *Genetics* 157 (4), 1819–1829. doi:10.1093/genetics/157.4.1819

Miao, J., Wei, X., Cao, C., Sun, J., Xu, Y., Zhang, Z., et al. (2024a). Pig pangenome graph reveals functional features of non-reference sequences. *J. Anim. Sci. Biotechnol.* 15 (1), 32. doi:10.1186/s40104-023-00984-4

Miao, J., Zhang, K., Yang, Y., Xu, S., Du, J., Wu, T., et al. (2024b). Single-nucleus transcriptomics reveal cardiac cell type-specific diversification in metabolic disease transgenic pigs. *iScience* 27 (6), 110015. doi:10.1016/j.isci.2024.110015

Miglietta, P. P., De Leo, F., Ruberti, M., and Massari, S. (2015). Mealworms for food: a water footprint perspective. *Water* 7 (11), 6190–6203. doi:10.3390/w7116190

Minozzi, G., Lazzari, B., De Iorio, M. G., Costa, C., Carpana, E., Crepaldi, P., et al. (2021). Whole-genome sequence analysis of Italian honeybees (apis mellifera). *Anim. (Basel)* 11 (5), 1311. doi:10.3390/ani11051311

Misra, B. B., Langefeld, C., Olivier, M., and Cox, L. A. (2019). Integrated omics: tools, advances and future approaches. *J. Mol. Endocrinol.* 62 (1), R21–R45. doi:10.1530/JME-18-0055

Miura, N., Kucho, K., Noguchi, M., Miyoshi, N., Uchiumi, T., Kawaguchi, H., et al. (2014). Comparison of the genomic sequence of the microminipig, a novel breed of swine, with the genomic database for conventional pig. *Vivo* 28 (6), 1107–1111.

Moghaddar, N., Khansefid, M., van der Werf, J. H. J., Bolormaa, S., Duijvesteijn, N., Clark, S. A., et al. (2019). Genomic prediction based on selected variants from imputed whole-genome sequence data in Australian sheep populations. *Genet. Sel. Evol.* 51 (1), 72. doi:10.1186/s12711-019-0514-2

Mohammadi, H. (2024). A genome-wide association study based on pathway analysis related to the angle wing in pekin ducks using whole-genome sequencing data. *Res. Animal Prod.* 15 (2), 32–43. doi:10.61186/rap.15.2.32

Morales, H. E., Faria, R., Johannesson, K., Larsson, T., Panova, M., Westram, A. M., et al. (2019). Genomic architecture of parallel ecological divergence: beyond a single environmental contrast. *Sci. Adv.* 5 (12), eaav9963. doi:10.1126/sciadv.aav9963

Moreira, G. C. M., Boschiero, C., Cesar, A. S. M., Reecy, J. M., Godoy, T. F., Pertille, F., et al. (2018). Integration of genome wide association studies and whole genome sequencing provides novel insights into fat deposition in chicken. *Sci. Rep.* 8 (1), 16222. doi:10.1038/s41598-018-34364-0

Morris, K. M., Hindle, M. M., Boitard, S., Burt, D. W., Danner, A. F., Eory, L., et al. (2020). The quail genome: insights into social behaviour, seasonal biology and infectious disease response. *BMC Biol.* 18 (1), 14. doi:10.1186/s12915-020-0743-4

Mu, X., Zhang, Z., Liu, Q., Ma, J., Qin, Y., Lang, H., et al. (2025). Single-nucleus and spatial transcriptomics identify brain landscape of gene regulatory networks associated with behavioral maturation in honeybees. *Nat. Commun.* 16 (1), 3343. doi:10.1038/s41467-025-58614-8

Mukherjee, K., Twyman, R. M., and Vilcinskas, A. (2015). Insects as models to study the epigenetic basis of disease. *Prog. Biophys. Mol. Biol.* 118 (1-2), 69–78. doi:10.1016/j.pbiomolbio.2015.02.009

Mutale, B., Dai, S., Chen, Z., and Maulu, S. (2025). Enhancing food security amid climate change: assessing impacts and developing adaptive strategies. *Cogent Food Agric.* 11 (1), 2519800. doi:10.1080/23311932.2025.2519800

Mutryn, M. F., Brannick, E. M., Fu, W., Lee, W. R., and Abasht, B. (2015). Characterization of a novel chicken muscle disorder through differential gene expression and pathway analysis using RNA-sequencing. *BMC Genomics* 16 (1), 399. doi:10.1186/s12864-015-1623-0

Nanaie, H. A., Tian, J., Sun, G., Wang, X., Zhao, M., Li, H., et al. (2025). Decoding the beef cattle genome through whole-genome sequencing reveals the genetic basis of carcass and meat quality traits. *Sci. Rep.* 15 (1), 33815. doi:10.1038/s41598-025-04205-y

National Research Council (1991). *Micro Live stock little known small animals with a promising economic future*. Washington, D.C.: National Academy Press.

Neculai-Valeanu, A.-S., Sanduleanu, C., Amaritii, G., and Bruma, I. S. (2025). Precision livestock farming and its role for assuring a sustainable cattle management-a study case on connected cow. *Sci. Pap. Ser. Manag. Econ. Eng. Agric. and Rural Dev.* 25 (1).

Niu, M., Zhao, Y., Jia, Y., Xiang, L., Dai, X., and Chen, H. (2023). Whole-genome sequencing study to identify candidate markers indicating susceptibility to type 2 diabetes in bama miniature pigs. *Anim. Model Exp. Med.* 6 (4), 283–293. doi:10.1002/ame2.12317

Niu, H., Li, Z., Zhang, C., and Li, M. (2024). Sustainable food systems under environmental footprints: the delicate balance from farm to table. *Sci. Total Environ.* 954, 176761. doi:10.1016/j.scitotenv.2024.176761

Ober, U., Ayroles, J. F., Stone, E. A., Richards, S., Zhu, D., Gibbs, R. A., et al. (2012). Using whole-genome sequence data to predict quantitative trait phenotypes in *Drosophila melanogaster*. *PLoS Genet.* 8 (5), e1002685. doi:10.1371/journal.pgen.1002685

Ogunjimi, S., Obaniyi, K., and Adedeji, I. (2012). Peri-urban and urban farmers' perceptions of mini-livestock farming in Southwestern Nigeria. *Res. J. Soc. Sci. Manag.*

Omuse, E. R., Tonnang, H. E. Z., Yusuf, A. A., Machekano, H., Egonyu, J. P., Kimathi, E., et al. (2024). The global atlas of edible insects: analysis of diversity and commonality contributing to food systems and sustainability. *Sci. Rep.* 14 (1), 5045. doi:10.1038/s41598-024-55603-7

Oppenheim, S., Cao, X., Rueppel, O., Krongdang, S., Phokasem, P., DeSalle, R., et al. (2020). Whole genome sequencing and assembly of the Asian honey bee apis dorsata. *Genome Biol. Evol.* 12 (1), 3677–3683. doi:10.1093/gbe/evz277

Oppert, B., Stoss, S., Monk, A., and Smith, T. (2019). Optimized extraction of insect genomic DNA for long-read sequencing. *Methods Protoc.* 2 (4), 89. doi:10.3390/mps2040089

Oppert, B., Perkin, L. C., Lorenzen, M., and Dossey, A. T. (2020). Transcriptome analysis of life stages of the house cricket, *Acheta domesticus*, to improve insect crop production. *Sci. Rep.* 10 (1), 3471. doi:10.1038/s41598-020-59087-z

Oppert, B., Dossey, A. T., Chu, F. C., Satovic-Vuksic, E., Plohl, M., Smith, T. P. L., et al. (2023). The genome of the yellow mealworm, tenebrio molitor: it's bigger than you think. *Genes (Basel)* 14 (12), 2209. doi:10.3390/genes14122209

Orabek, O., Petrusek, A., and Rovatsos, M. (2019). The complete mitogenome of helixpomatia and the basal phylogeny of helicinae (gastropoda, Stylommatophora, helicidae). *Zookeys* 827, 19–30. doi:10.3897/zookeys.827.33057

Ottenburghs, J., Megens, H. J., Kraus, R. H. S., Madsen, O., van Hooft, P., van Wieren, S. E., et al. (2016). A tree of geese: a phylogenomic perspective on the evolutionary history of true Geese. *Mol. Phylogenet. Evol.* 101, 303–313. doi:10.1016/j.ympev.2016.05.021

Ouyang, J., Zheng, S., Huang, M., Tang, H., Qiu, X., Chen, S., et al. (2022). Chromosome-level genome and population genomics reveal evolutionary characteristics and conservation status of Chinese indigenous geese. *Commun. Biol.* 5 (1), 1191. doi:10.1038/s42003-022-04125-x

Ouyang, Q., Ran, M., Hu, S., Tu, J., Hu, X., Li, X., et al. (2025). Multi-omics joint analysis and identification of candidate genes for the rate of right ovarian degeneration in geese. *Poult. Sci.* 104 (4), 104966. doi:10.1016/j.psj.2025.104966

Paes, C., Beaumont, M., Gidenne, T., Bebin, K., Duperray, J., Gohier, C., et al. (2024). A multi-omics dataset of the response to early plant polysaccharide ingestion in rabbits. *Sci. Data* 11 (1), 684. doi:10.1038/s41597-024-03471-1

Paoletti, M. G., and Dreon, A. L. (2005). "Minilivestock, environment, sustainability, and local knowledge disappearance," in *Ecological implications of minilivestock: potential of insects, rodents, frogs, and snails*, 1–18.

Papadopoulos, G., Papantonatou, M.-Z., Uyar, H., Kriezi, O., Mavrommatis, A., Psiroukis, V., et al. (2025). Economic and environmental benefits of digital agricultural technological solutions in livestock farming: a review. *Smart. Agric. Technol.* 10, 100783. doi:10.1016/j.atech.2025.100783

Parejo, M., Wragg, D., Henriques, D., Charriere, J. D., and Estonba, A. (2020). Digging into the genomic past of Swiss honey bees by whole-genome sequencing museum specimens. *Genome Biol. Evol.* 12 (12), 2535–2551. doi:10.1093/gbe/evaa188

Parey, E., Fernandez-Aroca, D., Frost, S., Uribarren, A., Park, T. J., Zottl, M., et al. (2023). Phylogenetic modeling of enhancer shifts in African mole-rats reveals regulatory changes associated with tissue-specific traits. *Genome Res.* 33 (9), 1513–1526. doi:10.1101/gr.277715.123

Park, D., Jung, J. W., Choi, B. S., Jayakodi, M., Lee, J., Lim, J., et al. (2015). Uncovering the novel characteristics of Asian honey bee, apis cerana, by whole genome sequencing. *BMC Genomics* 16 (1), 1. doi:10.1186/1471-2164-16-1

Park, S., Kim, J., Lee, J., Jung, S., Pack, S. P., Lee, J. H., et al. (2024). RNA sequencing analysis of sexual dimorphism in Japanese quail. *Front. Vet. Sci.* 11, 1441021. doi:10.3389/fvets.2024.1441021

Patir, A., Raper, A., Fleming, R., Henderson, B. E. P., Murphy, L., Henderson, N. C., et al. (2023). Cellular heterogeneity of the developing worker honey bee (apis mellifera) pupa: a single cell transcriptomics analysis. *G3 (Bethesda)* 13 (10), jkad178. doi:10.1093/g3journal/jkad178

Pei, Y., Sun, M., Zhang, J., Lei, A., Chen, H., Kang, X., et al. (2023). Comparative metagenomic and metatranscriptomic analyses reveal the response of black soldier fly (Hermetia illucens) larvae intestinal microbes and reduction mechanisms to high concentrations of tetracycline. *Toxics* 11 (7), 611. doi:10.3390/toxics11070611

Peng, W. C., Zhai, Y. Y., Li, M. K., Zhang, C. X., Du, J. X., Jiang, Y. Y., et al. (2025). Evaluation of physiological integrity in six-gene-edited bama miniature pigs as a model for xenotransplantation. *Biotechnol. J.* 20 (5), e70030. doi:10.1002/biot.70030

Pertille, F., Guerrero-Bosagna, C., Silva, V. H., Boschiero, C., Nunes Jde, R., Ledur, M. C., et al. (2016). High-throughput and cost-effective chicken genotyping using next-generation sequencing. *Sci. Rep.* 6 (1), 26929. doi:10.1038/srep26929

Peters, K. J. (1987). Unconventional livestock: classification and potential uses. *ILCA Bull.*

Piorkowska, K., Zukowski, K., Nowak, J., Poltowicz, K., Ropka-Molik, K., and Gurgul, A. (2016). Genome-wide RNA-seq analysis of breast muscles of two broiler chicken groups differing in shear force. *Anim. Genet.* 47 (1), 68–80. doi:10.1111/age.12388

Polakof, S., Rémond, D., Rambeau, M., Pujos-Guillot, E., Sébédio, J. L., Dardevet, D., et al. (2015). Postprandial metabolic events in mini-pigs: new insights from a combined approach using plasma metabolomics, tissue gene expression, and enzyme activity. *Metabolomics* 11 (4), 964–979. doi:10.1007/s11306-014-0753-8

Poma, G., Cuykx, M., Da Silva, K. M., Iturrospe, E., van Nuijs, A. L. N., van Huis, A., et al. (2022). Edible insects in the metabolomics era. First steps towards the implementation of entometabolomics in food systems. *Trends. Food. Sci. Technol.* 119, 371–377. doi:10.1016/j.tifs.2021.12.018

Posbergh, C. J., and Huson, H. J. (2021). All sheeps and sizes: a genetic investigation of mature body size across sheep breeds reveals a polygenic nature. *Anim. Genet.* 52 (1), 99–107. doi:10.1111/age.13016

Qanbari, S., Rubin, C. J., Maqbool, K., Weigend, S., Weigend, A., Geibel, J., et al. (2019). Genetics of adaptation in modern chicken. *PLoS Genet.* 15 (4), e1007989. doi:10.1371/journal.pgen.1007989

Rabani, V., Cheatsazan, H., and Davani, S. (2019). Proteomics and lipidomics of black soldier fly (diptera: stratiomyidae) and blow fly (diptera: calliphoridae) larvae. *J. Insect Sci.* 19 (3), 29. doi:10.1093/jisesa/iez050

Rabbani, M. A. G., Vallejo-Trujillo, A., Wu, Z., Miedzinska, K., Faruque, S., Watson, K. A., et al. (2024). Whole genome sequencing of three native chicken varieties (common deshi, hilly and naked neck) of Bangladesh. *Sci. Data* 11 (1), 1432. doi:10.1038/s41597-024-04291-z

Ramzy, R. R., Goenka, V., El-Dakar, M. A., and Lee, J. S. H. (2025). Assessing the environmental impacts of the black soldier fly-based circular economy and decentralized system in Singapore: a case study. *Sustainability* 17 (13), 6115. doi:10.3390/su17136115

Reed, K. M., Mendoza, K. M., Kono, T., Powell, A. A., Strasburg, G. M., and Velleman, S. G. (2023). Expression of miRNAs in Turkey muscle satellite cells and differential response to thermal challenge. *Front. Physiol.* 14, 1293264. doi:10.3389/fphys.2023.1293264

Reeve, J., Butlin, R. K., Koch, E. L., Stankowski, S., and Faria, R. (2024). Chromosomal inversion polymorphisms are widespread across the species ranges of rough periwinkles (*Littorina saxatilis* and L. arcana). *Mol. Ecol.* 33 (24), e17160. doi:10.1111/mec.17160

Reimer, C., Rubin, C. J., Sharifi, A. R., Ha, N. T., Weigend, S., Waldmann, K. H., et al. (2018). Analysis of porcine body size variation using re-sequencing data of miniature and large pigs. *BMC Genomics* 19 (1), 687. doi:10.1186/s12864-018-5009-y

Rexroad, C., Vallet, J., Matukumalli, L. K., Reecy, J., Bickhart, D., Blackburn, H., et al. (2019). Genome to phenome: improving animal health, production, and well-being - a new USDA blueprint for animal genome research 2018-2027. *Front. Genet.* 10, 327. doi:10.3389/fgene.2019.00327

Richards, S., and Murali, S. C. (2015). Best practices in insect genome sequencing: what works and what doesn't. *Curr. Opin. Insect Sci.* 7, 1–7. doi:10.1016/j.cois.2015.02.013

Riggs, P. K., Tedeschi, L. O., Turner, N. D., Braga-Neto, U., and Jayaraman, A. (2017). The role of "omics" technologies for livestock sustainability. *Arch. Latinoam. Prod. Anim.* 25 (3-4).

Rotimi, E. A. (2025). Application of genomics in livestock production: a mini-review. *World News Nat. Sci.* 59, 69–76.

Roy, D. B., Alison, J., August, T. A., Belisle, M., Bjerge, K., Bowden, J. J., et al. (2024). Towards a standardized framework for AI-assisted, image-based monitoring of nocturnal insects. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 379 (1904), 20230108. doi:10.1098/rstb.2023.0108

Rumpold, B. A., and Schlüter, O. K. (2013). Potential and challenges of insects as an innovative source for food and feed production. *Innov. Food. Sci. Emerg. Technol.* 17, 1–11. doi:10.1016/j.ifset.2012.11.005

Sahm, A., Bens, M., Szafranski, K., Holtze, S., Groth, M., Gorlach, M., et al. (2018). Long-lived rodents reveal signatures of positive selection in genes associated with lifespan. *PLoS Genet.* 14 (3), e1007272. doi:10.1371/journal.pgen.1007272

Sarg, B., Lopez, R., Lindner, H., Ponte, I., Suau, P., and Roque, A. (2015). Identification of novel post-translational modifications in linker histones from chicken erythrocytes. *J. Proteomics* 113, 162–177. doi:10.1016/j.jprot.2014.10.004

Schanes, K., Giljum, S., and Hertwich, E. (2016). Low carbon lifestyles: a framework to structure consumption strategies and options to reduce carbon footprints. *J. Clean. Prod.* 139, 1033–1043. doi:10.1016/j.jclepro.2016.08.154

Schyman, P., Printz, R. L., Pannala, V. R., AbdulHameed, M. D. M., Estes, S. K., Shiota, C., et al. (2021). Genomics and metabolomics of early-stage thioacetamide-induced liver injury: an interspecies study between Guinea pig and rat. *Toxicol. Appl. Pharmacol.* 430, 115713. doi:10.1016/j.taap.2021.115713

Sellem, E., Paul, K., Donkpegan, A., Li, Q., Masseron, A., Chauveau, A., et al. (2024). Multitrait genetic parameter estimates in a *Tenebrio molitor* reference population: high potential for breeding gains. *Animal* 18 (6), 101197. doi:10.1016/j.animal.2024.101197

Shan, L., Wu, Q., Li, Y., Shang, H., Guo, K., Wu, J., et al. (2014). Transcriptome profiling identifies differentially expressed genes in postnatal developing pituitary gland of miniature pig. *DNA Res.* 21 (2), 207–216. doi:10.1093/dnares/dst051

Shao, Y., Wang, X. B., Zhang, J. J., Li, M. L., Wu, S. S., Ma, X. Y., et al. (2020). Genome and single-cell RNA-Sequencing of the earthworm *Eisenia andrei* identifies cellular mechanisms underlying regeneration. *Nat. Commun.* 11 (1), 2656. doi:10.1038/s41467-020-16454-8

Shen, Q. K., Peng, M. S., Adeola, A. C., Kui, L., Duan, S., Miao, Y. W., et al. (2021). Genomic analyses of unveil helmeted Guinea fowl (*Numida meleagris*) domestication in West Africa. *Genome Biol. Evol.* 13 (6), evab090. doi:10.1093/gbe/evab090

Shen, Y., Zeng, X., Chen, G., and Wu, X. (2022). Comparative transcriptome analysis reveals regional specialization of gene expression in larval silkworm (*Bombyx mori*) midgut. *Insect Sci.* 29 (5), 1329–1345. doi:10.1111/1744-7917.13001

Shi, T. F., Wang, Y. F., Liu, F., Qi, L., and Yu, L. S. (2017). Sublethal effects of the neonicotinoid insecticide thiamethoxam on the transcriptome of the honey bees (hymenoptera: apidae). *J. Econ. Entomol.* 110 (6), 2283–2289. doi:10.1093/jee/tox262

Shi, S., Shao, D., Yang, L., Liang, Q., Han, W., Xue, Q., et al. (2023). Whole genome analyses reveal novel genes associated with chicken adaptation to tropical and frigid environments. *J. Adv. Res.* 47, 13–25. doi:10.1016/j.jare.2022.07.005

Sierra, V., Gonzalez-Blanco, L., Dineiro, Y., Diaz, F., Garcia-Espina, M. J., Coto-Montes, A., et al. (2021). New insights on the impact of cattle handling on post-mortem myofibrillar muscle proteome and meat tenderization. *Foods* 10 (12), 3115. doi:10.3390/foods10123115

Silva-Vignato, B., Cesar, A. S. M., Afonso, J., Moreira, G. C. M., Poleti, M. D., Petrini, J., et al. (2022). Integrative analysis between genome-wide association study and expression quantitative trait loci reveals bovine muscle gene expression regulatory polymorphisms associated with intramuscular fat and backfat thickness. *Front. Genet.* 13, 935238. doi:10.3389/fgene.2022.935238

Son, D. H., Hwang, N. H., Chung, W. H., Seong, H. S., Lim, H., Cho, E. S., et al. (2020). Whole-genome resequencing analysis of 20 Micro-pigs. *Genes Genomics* 42 (3), 263–272. doi:10.1007/s13258-019-00891-x

Southey, B. R., Zhu, P., Carr-Markell, M. K., Liang, Z. S., Zayed, A., Li, R., et al. (2016). Characterization of genomic variants associated with scout and recruit behavioral castes in honey bees using whole-genome sequencing. *PLoS One* 11 (1), e0146430. doi:10.1371/journal.pone.0146430

Sukmak, R., Suttinun, C., Kovitvadhi, U., Kovitvadhi, A., and Vongsangnak, W. (2024). Uncovering nutrients and energy related gene functions of Black soldier fly Hermetia illucens strain KUP. *Gene* 896, 148045. doi:10.1016/j.gene.2023.148045

Sun, Y. B., Xiong, Z. J., Xiang, X. Y., Liu, S. P., Zhou, W. W., Tu, X. L., et al. (2015). Whole-genome sequence of the Tibetan frog Nanorana parkeri and the comparative evolution of tetrapod genomes. *Proc. Natl. Acad. Sci. U S A.* 112 (11), E1257–E1262. doi:10.1073/pnas.1501764112

Sun, Q., Guo, H., Xia, Q., Jiang, L., and Zhao, P. (2020). Transcriptome analysis of the immune response of silkworm at the early stage of *Bombyx mori* bidensovirus infection. *Dev. Comp. Immunol.* 106, 103601. doi:10.1016/j.dci.2019.103601

Sunde, R., and Taylor, R. M. (2019). Full transcriptome expression in liver of selenium-deficient and high-selenium turkeys (meleagris gallopavo) determined by RNA-seq (P24-025-19). *Curr. Dev. Nutr.* 3, nzz044.P24–025-19. doi:10.1093/cdn/nzz044.p24-025-19

Thornton, P. K. (2010). Livestock production: recent trends, future prospects. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* 365 (1554), 2853–2867. doi:10.1098/rstb.2010.0134

Titilola, O. L., Olaniyi, O. Z., and Adebusola, A. A. (2015). Mini-livestock farming as a strategy for food security in Oyo state of Nigeria. *J. Agric. Sustain.* 7 (2).

Torson, A. S., Hicks, A. M. A., Baragar, C. E., Smith, D. R., and Sinclair, B. J. (2022). The mitochondrial genomes of two gryllus crickets (grylloidea: gryllidae) *via* RNA-Seq. *Mitochondrial. DNA. B. Resour.* 7 (1), 106–107. doi:10.1080/23802359.2021.2010613

Traniello, I. M., Bukhari, S. A., Dibaeinia, P., Serrano, G., Avalos, A., Ahmed, A. C., et al. (2023). Single-cell dissection of aggression in honeybee colonies. *Nat. Ecol. Evol.* 7 (8), 1232–1244. doi:10.1038/s41559-023-02090-0

Tuggle, C. K., Giuffra, E., White, S. N., Clarke, L., Zhou, H., Ross, P. J., et al. (2016). GO-FAANG meeting: a gathering on functional annotation of an imal genomes. *Anim. Genet.* 47 (5), 528–533. doi:10.1111/age.12466

Tzertzinis, G., Ganatra, M. B., Ruse, C., Taron, C. H., Causey, B., Wang, L., et al. (2023). The AMP deaminase of the mollusk helix pomatia is an unexpected member of the adenosine deaminase-related growth factor (ADGF) family. *PLoS One* 18 (7), e0286435. doi:10.1371/journal.pone.0286435

Urgessa, O. E., and Woldesemayat, A. A. (2023). OMICs approaches and technologies for understanding low-high feed efficiency traits in chicken: implication to breeding. *Anim. Biotechnol.* 34 (8), 4147–4166. doi:10.1080/10495398.2023.2187404

Van Alfen, N. K. (2014). *Encyclopedia of agriculture and food systems*. Elsevier.

van Binsbergen, R., Calus, M. P., Bink, M. C., van Eeuwijk, F. A., Schrooten, C., and Veerkamp, R. F. (2015). Genomic prediction using imputed whole-genome sequence data in holstein friesian cattle. *Genet. Sel. Evol.* 47 (1), 71. doi:10.1186/s12711-015-0149-x

van Broekhoven, S., Oonincx, D. G., van Huis, A., and van Loon, J. J. (2015). Growth performance and feed conversion efficiency of three edible mealworm species (coleoptera: tenebrionidae) on diets composed of organic by-products. *J. Insect Physiol.* 73, 1–10. doi:10.1016/j.jinsphys.2014.12.005

Van Emon, J. M. (2016). The omics revolution in agricultural research. *J. Agric. Food Chem.* 64 (1), 36–44. doi:10.1021/acs.jafc.5b04515

Vaure, C., Gregoire-Barou, V., Courtois, V., Chautard, E., Degletagne, C., and Liu, Y. (2021). Gottingen minipigs as a model to evaluate longevity, functionality, and memory of immune response induced by pertussis vaccines. *Front. Immunol.* 12, 613810. doi:10.3389/fimmu.2021.613810

Vauterin, A., Steiner, B., Sillman, J., and Kahiluoto, H. (2021). The potential of insect protein to reduce food-based carbon footprints in Europe: the case of broiler meat production. *J. Clean. Prod.* 320, 128799. doi:10.1016/j.jclepro.2021.128799

Vazquez-Diosdado, J. A., Paul, V., Ellis, K. A., Coates, D., Loomba, R., and Kaler, J. (2019). A combined offline and online algorithm for real-time and long-term classification of sheep behaviour: novel approach for precision livestock farming. *Sensors (Basel)* 19 (14), 3201. doi:10.3390/s19143201

Veith, A. C., Meudt, J. J., Reichert, J. L., Frank, J. M., Pavelec, D. M., Ladell, B., et al. (2025). The draft genome of the Wisconsin miniature SwineTM, a valuable biomedical research tool. *G3 (Bethesda)* 15 (6), jkaf067. doi:10.1093/g3journal/jkaf067

Verardo, L. L., Brito, L. F., Carolino, N., and Magalhães, A. F. B. (2023). *Omics applied to livestock genetics*. Lausanne: Frontiers Media SA.

Vietmeyer, N. (1984). Livestock for the landless. *FAO Review Agriculture Development* 17 (2), 43–46.

Vignal, A., Boitard, S., Thebault, N., Dayo, G. K., Yapi-Gnaore, V., Youssao Abdou Karim, I., et al. (2019). A Guinea fowl genome assembly provides new evidence on evolution following domestication and selection in galliformes. *Mol. Ecol. Resour.* 19 (4), 997–1014. doi:10.1111/1755-0998.13017

Vitorino Carvalho, A., Hennequet-Antier, C., Brionne, A., Crochet, S., Jimenez, J., Courousse, N., et al. (2021). Embryonic thermal manipulation impacts the postnatal transcriptome response of heat-challenged Japanese quails. *BMC Genomics* 22 (1), 488. doi:10.1186/s12864-021-07832-7

Voulgari-Kokota, A., van Loon, M. S., and Bovenkerk, B. (2023). Insects as mini-livestock: considering insect welfare in feed production. *NJAS Impact Agric. Life Sci.* 95 (1), 2191797. doi:10.1080/27685241.2023.2191797

Wadood, A. A., Bordbar, F., and Zhang, X. (2025). Integrating omics approaches in livestock biotechnology: innovations in production and reproductive efficiency. *Front. Anim. Sci.* 6, 1551244. doi:10.3389/fanim.2025.1551244

Wall, E., Simm, G., and Moran, D. (2010). Developing breeding schemes to assist mitigation of greenhouse gas emissions. *Animal* 4 (3), 366–376. doi:10.1017/S175173110999070X

Wallberg, A., Schoning, C., Webster, M. T., and Hasselmann, M. (2017). Two extended haplotype blocks are associated with adaptation to high altitude habitats in East African honey bees. *PLoS Genet.* 13 (5), e1006792. doi:10.1371/journal.pgen.1006792

Wang, M., and Ibeagha-Awemu, E. M. (2020). Impacts of epigenetic processes on the health and productivity of livestock. *Front. Genet.* 11, 613636. doi:10.3389/fgene.2020.613636

Wang, Y., Ghaffari, N., Johnson, C. D., Braga-Neto, U. M., Wang, H., Chen, R., et al. (2011). Evaluation of the coverage and depth of transcriptome by RNA-Seq in chickens. *BMC Bioinforma.* 12, S5. doi:10.1186/1471-2105-12-S10-S5

Wang, Y., Lupiani, B., Reddy, S. M., Lamont, S. J., and Zhou, H. (2014). RNA-seq analysis revealed novel genes and signaling pathway associated with disease resistance to avian influenza virus infection in chickens. *Poult. Sci.* 93 (2), 485–493. doi:10.3382/ps.2013-03557

Wang, Z., Li, Q., Chamba, Y., Zhang, B., Shang, P., Zhang, H., et al. (2015). Identification of genes related to growth and lipid deposition from transcriptome profiles of pig muscle tissue. *PLoS One* 10 (10), e0141138. doi:10.1371/journal.pone.0141138

Wang, H., Fu, Y., Gu, P., Zhang, Y., Tu, W., Chao, Z., et al. (2020). Genome-wide characterization and comparative analyses of simple sequence repeats among four miniature pig breeds. *Anim. (Basel)* 10 (10), 1792. doi:10.3390/ani10101792

Wang, X., Zhang, Y., Zhang, Y., Kang, M., Li, Y., James, S. W., et al. (2021a). Amynthas corticis genome reveals molecular mechanisms behind global distribution. *Commun. Biol.* 4 (1), 135. doi:10.1038/s42003-021-01659-4

Wang, Z., Wang, Q., Wu, H., and Huang, Z. (2021b). Identification and characterization of amphibian SLC26A5 using RNA-seq. *BMC Genomics* 22 (1), 564. doi:10.1186/s12864-021-07798-6

Wang, J., Zhao, K., Kang, Z., Wang, M., Chen, Y., Fan, H., et al. (2022a). The multi-omics analysis revealed a metabolic regulatory system of cecum in rabbit with diarrhea. *Anim. (Basel)* 12 (9), 1194. doi:10.3390/ani12091194

Wang, T., Antonacci-Fulton, L., Howe, K., Lawson, H. A., Lucas, J. K., Phillippy, A. M., et al. (2022b). The human pangenome project: a global resource to map genomic diversity. *Nature* 604 (7906), 437–446. doi:10.1038/s41586-022-04601-8

Wang, H., Zhao, X., Wen, J., Wang, C., Zhang, X., Ren, X., et al. (2023a). Comparative population genomics analysis uncovers genomic footprints and genes influencing body weight trait in Chinese indigenous chicken. *Poult. Sci.* 102 (11), 103031. doi:10.1016/j.psj.2023.103031

Wang, Q., He, F., Huang, R. Y., Yang, X., Yang, D., Ngatia, J. N., et al. (2023b). Draft genome of the oriental garden lizard (*Calotes versicolor*). *Front. Genet.* 14, 1091544. doi:10.3389/fgene.2023.1091544

Wang, X., Wang, Y., Wang, Y., Guo, Y., Zong, R., Hu, S., et al. (2024a). Single-cell transcriptomic and cross-species comparison analyses reveal distinct molecular changes of porcine testes during puberty. *Commun. Biol.* 7 (1), 1478. doi:10.1038/s42003-024-07163-9

Wang, Y., Chen, G., Pan, D., Guo, H., Jiang, H., Wang, J., et al. (2024b). Pig-to-human kidney xenotransplants using genetically modified minipigs. *Cell Rep. Med.* 5 (10), 101744. doi:10.1016/j.xcrm.2024.101744

Wang, Z., Tian, W., Guo, Y., Wang, D., Zhang, Y., Zhi, Y., et al. (2024c). Dynamic alternations of three-dimensional chromatin architecture contribute to phenotypic characteristics of breast muscle in chicken. *Commun. Biol.* 7 (1), 910. doi:10.1038/s42003-024-06599-3

Wang, B., Meng, F., Song, S., Xie, B., Jia, S., Xiu, D., et al. (2025). Multi-omics analysis of Curculio dieckmanni (coleoptera: curculionidae) larvae reveals host responses to *Steinernema carpocapsae* infection. *Insects* 16 (5), 503. doi:10.3390/insects16050503

Warr, A., Affara, N., Aken, B., Beiki, H., Bickhart, D. M., Billis, K., et al. (2020). An improved pig reference genome sequence to enable pig genetics and genomics research. *Gigascience* 9 (6), giaa051. doi:10.1093/gigascience/giaa051

Wen, J., Li, H., Wang, H., Yu, J., Zhu, T., Zhang, J., et al. (2023). Origins, timing and introgression of domestic geese revealed by whole genome data. *J. Anim. Sci. Biotechnol.* 14 (1), 26. doi:10.1186/s40104-022-00826-9

Westfall, A. K., Telemeco, R. S., Grizante, M. B., Waits, D. S., Clark, A. D., Simpson, D. Y., et al. (2021). A chromosome-level genome assembly for the eastern fence lizard (sceloporus undulatus), a reptile model for physiological and evolutionary ecology. *Gigascience* 10 (10), giab066. doi:10.1093/gigascience/giab066

Weyrich, A., Schullermann, T., Heeger, F., Jeschek, M., Mazzoni, C. J., Chen, W., et al. (2014). Whole genome sequencing and methylome analysis of the wild Guinea pig. *BMC Genomics* 15 (1), 1036. doi:10.1186/1471-2164-15-1036

Wragg, D., Marti-Marimon, M., Basso, B., Bidanel, J. P., Labarthe, E., Bouchez, O., et al. (2016). Whole-genome resequencing of honeybee drones to detect genomic selection in a population managed for royal jelly. *Sci. Rep.* 6 (1), 27168. doi:10.1038/srep27168

Wu, Y., Cheng, T., Liu, C., Liu, D., Zhang, Q., Long, R., et al. (2016). Systematic identification and characterization of long non-coding RNAs in the silkworm, *Bombyx mori*. *PLoS One* 11 (1), e0147147. doi:10.1371/journal.pone.0147147

Wu, Y., Zhang, Y., Hou, Z., Fan, G., Pi, J., Sun, S., et al. (2018). Population genomic data reveal genes related to important traits of quail. *Gigascience* 7 (5), giy049. doi:10.1093/gigascience/giy049

Wu, X., Pan, X., Cao, S., Xu, F., Lan, L., Zhang, Y., et al. (2019). iTRAQ-based quantitative proteomic analysis provides insights into strong broodiness in muscovy duck (*Cairina moschata*) combined with metabolomics analysis. *J. Proteomics* 204, 103401. doi:10.1016/j.jprot.2019.103401

Wu, F., Sun, H., Lu, S., Gou, X., Yan, D., Xu, Z., et al. (2020a). Genetic diversity and selection signatures within diannan small-ear pigs revealed by next-generation sequencing. *Front. Genet.* 11, 733. doi:10.3389/fgene.2020.00733

Wu, X., Galbraith, D. A., Chatterjee, P., Jeong, H., Grozinger, C. M., and Yi, S. V. (2020b). Lineage and parent-of-origin effects in DNA methylation of honey bees (apis mellifera) revealed by reciprocal crosses and whole-genome bisulfite sequencing. *Genome Biol. Evol.* 12 (8), 1482–1492. doi:10.1093/gbe/evaa133

Wy, S., Kwon, D., Park, W., Chai, H. H., Cho, I. C., and Kim, J. (2024). A chromosome-level genome assembly of the Korean minipig (sus scrofa). *Sci. Data* 11 (1), 840. doi:10.1038/s41597-024-03680-8

Xia, X., Zhang, S., Zhang, H., Zhang, Z., Chen, N., Li, Z., et al. (2021). Assessing genomic diversity and signatures of selection in Jiaxian red cattle using whole-genome sequencing data. *BMC Genomics* 22 (1), 43. doi:10.1186/s12864-020-07340-0

Xiang, H., Li, X., Dai, F., Xu, X., Tan, A., Chen, L., et al. (2013). Comparative methylomics between domesticated and wild silkworms implies possible epigenetic influences on silkworm domestication. *BMC Genomics* 14, 646. doi:10.1186/1471-2164-14-646

Xiao, W., Chen, P., Xiao, J., Wang, L., Liu, T., Wu, Y., et al. (2017). Comparative transcriptome profiling of a thermal resistant vs. sensitive silkworm strain in response to high temperature under stressful humidity condition. *PLoS One* 12 (5), e0177641. doi:10.1371/journal.pone.0177641

Xing, D., Yang, Q., Jiang, L., Li, Q., Xiao, Y., Ye, M., et al. (2017). RNA-seq analyses for two silkworm strains reveals insight into their susceptibility and resistance to Beauveria bassiana infection. *Int. J. Mol. Sci.* 18 (2), 234. doi:10.3390/ijms18020234

Xiong, X., Liu, J., and Rao, Y. (2023). Whole genome resequencing helps study important traits in chickens. *Genes (Basel)* 14 (6), 1198. doi:10.3390/genes14061198

Xu, H., Chen, L., Tong, X. L., Hu, H., Liu, L. Y., Liu, G. C., et al. (2022a). Comprehensive silk gland multi-omics comparison illuminates two alternative mechanisms in silkworm heterosis. *Zool. Res.* 43 (4), 585–596. doi:10.24272/j.issn.2095-8137.2022.065

Xu, M. M., Gu, L. H., Lv, W. Y., Duan, S. C., Li, L. W., Du, Y., et al. (2022b). Chromosome-level genome assembly of the muscovy duck provides insight into fatty liver susceptibility. *Genomics* 114 (6), 110518. doi:10.1016/j.ygeno.2022.110518

Xue, R., Hu, X., Zhu, L., Cao, G., Huang, M., Xue, G., et al. (2015). Comparative transcriptomic analysis of silkworm Bmovo-1 and wild type silkworm ovary. *Sci. Rep.* 5, 17867. doi:10.1038/srep17867

Xue, B., Li, F., Hu, J., Tian, J., Li, J., Cheng, X., et al. (2017a). Differentially expressed genes in the silk gland of silkworm (*Bombyx mori*) treated with TiO(2) NPs. *Gene* 611, 21–26. doi:10.1016/j.gene.2017.02.022

Xue, Q., Zhang, G., Li, T., Ling, J., Zhang, X., and Wang, J. (2017b). Transcriptomic profile of leg muscle during early growth in chicken. *PLoS One* 12 (3), e0173824. doi:10.1371/journal.pone.0173824

Yamada, R., Okada, D., Wang, J., Basak, T., and Koyama, S. (2021). Interpretation of omics data analyses. *J. Hum. Genet.* 66 (1), 93–102. doi:10.1038/s10038-020-0763-5

Yang, Y., Zhou, R., Mu, Y., Hou, X., Tang, Z., and Li, K. (2016). Genome-wide analysis of DNA methylation in obese, lean, and miniature pig breeds. *Sci. Rep.* 6, 30160. doi:10.1038/srep30160

Yang, Y.-l., Zhou, R., and Li, K. (2017). Future livestock breeding: precision breeding based on multi-omics information and population personalization. *J. Integr. Agric.* 16 (12), 2784–2791. doi:10.1016/s2095-3119(17)61780-5

Yang, H., Xu, D., Zhuo, Z., Hu, J., and Lu, B. (2020a). Transcriptome and gene expression analysis of Rhynchophorus ferrugineus (coleoptera: curculionidae) during developmental stages. *PeerJ* 8, e10223. doi:10.7717/peerj.10223

Yang, Q., Yang, W., Shang, F., Ding, B., Niu, J., and Wang, J. (2020b). Sequencing of transcriptome and small RNA revealed the xenobiotic metabolism-related genes and potential regulatory miRNA in Asian tramp snail. *Front. Genet.* 11, 595166. doi:10.3389/fgene.2020.595166

Yang, X., Deng, F., Wu, Z., Chen, S. Y., Shi, Y., Jia, X., et al. (2020c). A genome-wide association study identifying genetic variants associated with growth, carcass and meat quality traits in rabbits. *Anim. (Basel)* 10 (6), 1068. doi:10.3390/ani10061068

Yang, J., Tong, C., Xiao, D., Xie, L., Zhao, R., Huo, Z., et al. (2022). Metagenomic insights into chicken gut antibiotic resistomes and microbiomes. *Microbiol. Spectr.* 10 (2), e0190721. doi:10.1128/spectrum.01907-21

Yang, P., Zheng, Y., Zou, X., Sun, Y., and Liu, Y. (2024a). Comparative transcriptomic analysis of gene expression profiles in the liver and spleen of American bullfrog (Lithobates catesbeianus) in response to Citrobacter freundii infection. *J. World. Aquac. Soc.* 55 (1), 353–372. doi:10.1111/jwas.12999

Yang, Y., Yang, C., Zhuang, Z., Mao, J., Chen, A., Zhou, T., et al. (2024b). RNA-seq analysis revealed circRNAs and genes associated with abdominal fat deposition in ducks. *Anim. (Basel)* 14 (2), 260. doi:10.3390/ani14020260

Ye, S., Chen, Z. T., Zheng, R., Diao, S., Teng, J., Yuan, X., et al. (2020). New insights from imputed whole-genome sequence-based genome-wide association analysis and transcriptome analysis: the genetic mechanisms underlying residual feed intake in chickens. *Front. Genet.* 11, 243. doi:10.3389/fgene.2020.00243

Ye, Y., Shi, Y. X., Jiang, Q., Jin, Y., Chen, F. X., Tang, W. H., et al. (2024). Transcriptome analysis reveals antioxidant defense mechanisms in the silkworm *Bombyx mori* after exposure to lead. *Anim. (Basel)* 14 (12), 1822. doi:10.3390/ani14121822

Yi, Y., and Wu, G. (2024). RNA-seq analysis of LPS-induced immune priming in silkworms (*Bombyx mori*) and the role of cytochrome P450 detoxification system in the process. *Int. J. Biol. Macromol.* 283 (Pt 3), 136551. doi:10.1016/j.ijbiomac.2024.136551

Yi, Y., Xu, H., Li, M., and Wu, G. (2019). RNA-seq profiles of putative genes involved in specific immune priming in *Bombyx mori* haemocytes. *Infect. Genet. Evol.* 74, 103921. doi:10.1016/j.meegid.2019.103921

Yin, C., Shen, G., Guo, D., Wang, S., Ma, X., Xiao, H., et al. (2016). InsectBase: a resource for insect genomes and transcriptomes. *Nucleic Acids Res.* 44 (D1), D801–D807. doi:10.1093/nar/gkv1204

Ylla, G., Nakamura, T., Itoh, T., Kajitani, R., Toyoda, A., Tomonari, S., et al. (2021). Insights into the genomic evolution of insects from cricket genomes. *Commun. Biol.* 4 (1), 733. doi:10.1038/s42003-021-02197-9

Yokoi, K., Tsubota, T., Jouraku, A., Sezutsu, H., and Bono, H. (2021). Reference transcriptome data in silkworm *Bombyx mori*. *Insects* 12 (6), 519. doi:10.3390/insects12060519

Yokoi, K., Wakamiya, T., and Bono, H. (2022). Meta-analysis of the public RNA-seq data of the Western honeybee apis mellifera to construct reference transcriptome data. *Insects* 13 (10), 931. doi:10.3390/insects13100931

Yurchenko, A. A., Recknagel, H., and Elmer, K. R. (2020). Chromosome-level assembly of the common lizard (Zootoca vivipara) genome. *Genome Biol. Evol.* 12 (11), 1953–1960. doi:10.1093/gbe/evaa161

Yuyan, F., Jie, L., Xiaojing, C., Binbin, G., Mingming, L., Huanxi, Z., et al. (2025). Changes in goose hypothalamus under different photocycles: RNA-seq reveals new pathways and molecules. *Poult. Sci.* 104 (5), 104883. doi:10.1016/j.psj.2025.104883

Zhan, S., Fang, G., Cai, M., Kou, Z., Xu, J., Cao, Y., et al. (2020). Genomic landscape and genetic manipulation of the black soldier fly Hermetia illucens, a natural waste recycler. *Cell Res.* 30 (1), 50–60. doi:10.1038/s41422-019-0252-6

Zhang, P., Aso, Y., Yamamoto, K., Banno, Y., Wang, Y., Tsuchida, K., et al. (2006). Proteome analysis of silk gland proteins from the silkworm, *Bombyx mori*. *Proteomics* 6 (8), 2586–2599. doi:10.1002/pmic.200500348

Zhang, L., Huang, Y., Wang, M., Guo, Y., Liang, J., Yang, X., et al. (2019). Development and genome sequencing of a laboratory-inbred miniature pig facilitates study of human diabetic disease. *iScience* 19, 162–176. doi:10.1016/j.isci.2019.07.025

Zhang, R., Cao, Y. Y., Du, J., Thakur, K., Tang, S. M., Hu, F., et al. (2021a). Transcriptome analysis reveals the gene expression changes in the silkworm (*Bombyx mori*) in response to hydrogen sulfide exposure. *Insects* 12 (12), 1110. doi:10.3390/insects12121110

Zhang, Y., Fan, G., Liu, X., Skovgaard, K., Sturek, M., and Heegaard, P. M. H. (2021b). The genome of the naturally evolved obesity-prone ossabaw miniature pig. *iScience* 24 (9), 103081. doi:10.1016/j.isci.2021.103081

Zhang, C., Zhao, J., Guo, Y., Xu, Q., Liu, M., Cheng, M., et al. (2022a). Genome-wide detection of copy number variations and evaluation of candidate copy number polymorphism genes associated with complex traits of pigs. *Front. Vet. Sci.* 9, 909039. doi:10.3389/fvets.2022.909039

Zhang, J., Liu, P., He, M., Wang, Y., Kui, H., Jin, L., et al. (2022b). Reorganization of 3D genome architecture across wild boar and bama pig adipose tissues. *J. Anim. Sci. Biotechnol.* 13 (1), 32. doi:10.1186/s40104-022-00679-2

Zhang, S., Xiong, P., Ma, Y., Jin, N., Sun, S., Dong, X., et al. (2022c). Transformation of food waste to source of antimicrobial proteins by black soldier fly larvae for defense against marine Vibrio parahaemolyticus. *Sci. Total Environ.* 826, 154163. doi:10.1016/j.scitotenv.2022.154163

Zhang, T., Xing, W., Wang, A., Zhang, N., Jia, L., Ma, S., et al. (2022d). Comparison of long-read methods for sequencing and assembly of lepidopteran Pest genomes. *Int. J. Mol. Sci.* 24 (1), 649. doi:10.3390/ijms24010649

Zhang, W., Wang, L., Zhao, Y., Wang, Y., Chen, C., Hu, Y., et al. (2022e). Single-cell transcriptomic analysis of honeybee brains identifies vitellogenin as caste differentiation-related factor. *iScience* 25 (7), 104643. doi:10.1016/j.isci.2022.104643

Zhang, Z., Wang, A., Hu, H., Wang, L., Gong, M., Yang, Q., et al. (2023). The efficient phasing and imputation pipeline of low-coverage whole genome sequencing data using a high-quality and publicly available reference panel in cattle. *Animal Res. One Health* 1 (1), 4–16. doi:10.1002/aro2.8

Zhang, B., Yang, R., He, S., Dai, S., Hu, Q., Li, X., et al. (2024a). Swill and pig manure substrates differentially affected transcriptome and metabolome of the black soldier fly larvae. *Int. J. Mol. Sci.* 25 (22), 12147. doi:10.3390/ijms252212147

Zhang, W., Liu, J., Zhou, Y., Liu, S., Wu, J., Jiang, H., et al. (2024b). Signaling pathways and regulatory networks in quail skeletal muscle development: insights from whole transcriptome sequencing. *Poult. Sci.* 103 (5), 103603. doi:10.1016/j.psj.2024.103603

Zhang, J., Tang, C., Liu, Y., Sun, J., Li, X., Long, K., et al. (2025a). Single cell transcriptome profiling of immune tissues from germ-free and specific pathogen-free piglet. *Sci. Data* 12 (1), 652. doi:10.1038/s41597-025-04957-2

Zhang, L., Li, J., Li, X., He, J., Zhou, J., Hou, J., et al. (2025b). Development and validation of sex-associated markers using whole-genome re-sequencing in frog Quasipaa spinosa. *Front. Genet.* 16, 1596192. doi:10.3389/fgene.2025.1596192

Zhao, M., Liu, H., Liu, M., Yue, Z., Li, C., Liu, L., et al. (2024). Metagenomics and metabolomics reveal that gut microbiome adapts to the diet transition in hyla rabbits. *Microbiol. Res.* 283, 127705. doi:10.1016/j.micres.2024.127705

Zhao, X., Yue, S., Sun, J., Zhang, Y., Peng, F., Ma, Z., et al. (2025a). RNA-seq reveals the effects of light on reproductive traits in domesticated Geese. *Rev. Bras. Cienc. Avic.* 27 (1). doi:10.1590/1806-9061-2024-2016

Zhao, Z., Zhang, Y., Yang, H., Wang, Z., Ai, Z., Yang, R., et al. (2025b). Transcriptomic analysis to identify differentially expressed genes of abdominal fat (AF) and breast muscle (BM) tissues based on RNA-seq in Zhijin white goose. *Trop. Anim. Health Prod.* 57 (6), 274. doi:10.1007/s11250-025-04524-2

Zheng, X., Liu, F., Shi, M., Li, S., Xie, X., Li, G., et al. (2022). Transcriptome analysis of the reproduction of silkworm (*Bombyx mori*) under dimethoate stress. *Pestic. Biochem. Physiol.* 183, 105081. doi:10.1016/j.pestbp.2022.105081

Zhong, Z., Nong, W., Xie, Y., Hui, J. H. L., and Chu, L. M. (2022). Long-term effect of plastic feeding on growth and transcriptomic response of mealworms (*Tenebrio molitor* L.). *Chemosphere* 287 (Pt 1), 132063. doi:10.1016/j.chemosphere.2021.132063

Zhou, N., Lee, W. R., and Abasht, B. (2015). Messenger RNA sequencing and pathway analysis provide novel insights into the biological basis of chickens' feed efficiency. *BMC Genomics* 16 (1), 195. doi:10.1186/s12864-015-1364-0

Zhou, Y., Liu, S., Hu, Y., Fang, L., Gao, Y., Xia, H., et al. (2020). Comparative whole genome DNA methylation profiling across cattle tissues reveals global and tissue-specific methylation patterns. *BMC Biol.* 18 (1), 85. doi:10.1186/s12915-020-00793-5

Zhou, Y., Yang, L., Han, X., Han, J., Hu, Y., Li, F., et al. (2022). Assembly of a pangenome for global cattle reveals missing sequences and novel structural variations, providing new insights into their diversity and evolutionary history. *Genome Res.* 32 (8), 1585–1601. doi:10.1101/gr.276550.122

Zhu, J. Y., Yang, P., Zhang, Z., Wu, G. X., and Yang, B. (2013). Transcriptomic immune response of *Tenebrio molitor* pupae to parasitization by Scleroderma guani. *PLoS One* 8 (1), e54411. doi:10.1371/journal.pone.0054411

Zhu, Z., Rehman, K. U., Yu, Y., Liu, X., Wang, H., Tomberlin, J. K., et al. (2019). *De novo* transcriptome sequencing and analysis revealed the molecular basis of rapid fat accumulation by black soldier fly (Hermetia illucens, L.) for development of insectival biodiesel. *Biotechnol. Biofuels* 12, 194. doi:10.1186/s13068-019-1531-7

Zhuo, Z., Lamont, S. J., Lee, W. R., and Abasht, B. (2015). RNA-seq analysis of abdominal fat reveals differences between modern commercial broiler chickens with high and low feed efficiencies. *PLoS One* 10 (8), e0135810. doi:10.1371/journal.pone.0135810