

Meanwhile, the controllability of insertion sites directly determines the stability and consistency of exogenous gene expression. The “position effect” caused by traditional random integration remains a major source of phenotypic variation. Although the discovery of “safe harbor” loci (e.g., Rosa26, H11) has greatly improved this issue, safe sites in different species have yet to be systematically identified, and their tissue specificity and transcriptional activity still require further validation. In the future, site-specific targeting systems based on genome editing and precise recombination are expected to become a research focus. By combining high-fidelity Cas variants (such as Cas12, Cas13) with recombinase systems, precise chromosomal integration of exogenous genes at predetermined locations can be achieved, fundamentally eliminating random insertion risks. Furthermore, the use of long-read sequencing and whole-genome validation technologies will enable real-time verification and risk screening of editing results, establishing a safer and more traceable construction process for transgenic livestock.

8.2 Management and ethics: animal welfare and public acceptance

Beyond technical issues, transgenic livestock development faces complex management and ethical challenges. Animal welfare remains a central social concern. While gene editing improves traits, it may also cause physiological burdens and health risks such as metabolic overload, reproductive disorders, or shortened lifespan. For example, certain pigs with high growth hormone expression exhibited myocardial hypertrophy and endocrine imbalance, prompting ethical reflections within the scientific community on the moral boundaries of human intervention in nature. Therefore, in research and breeding practices, animal welfare assessment standards should be established, and the physiological conditions of edited animals should be monitored long-term to ensure that improved traits are not achieved at the cost of animal health.

Public acceptance and regulatory frameworks directly influence the future of transgenic livestock applications. Due to differing public perceptions of “genetically modified animal products”, some regions maintain a cautious or even resistant stance toward commercialization. Western countries have implemented limited market access through comprehensive approval and labeling systems, while Asian nations remain in the exploratory phase of regulatory development. In recent years, China has strengthened legal regulation and ethical review of transgenic technology, though improvements in research transparency, public science communication, and risk dialogue are still needed. Enhancing public understanding of genetic science and promoting openness and consistency in regulatory systems are key to fostering rational social consensus and effective policy implementation.

From a global governance perspective, ethical issues surrounding transgenic livestock involve not only animal rights but also biodiversity conservation and food safety. In the future, an international framework for ethical evaluation and information sharing should be established to promote unified standards among nations in technology assessment, data transparency, and ecological risk evaluation, balancing scientific innovation with ethical responsibility.

8.3 Future research trends: multi-omics integration, digital phenotyping, and artificial intelligence evaluation

Future research on transgenic livestock will enter a data-driven and intelligent decision-making era. Multi-omics integration will become the core approach for evaluating genetic stability and phenotypic consistency. By systematically integrating data from genomics, transcriptomics, methylomics, proteomics, and metabolomics, researchers can uncover the dynamic molecular behavior of exogenous genes and their regulatory networks. For instance, combined analysis of DNA methylation and mRNA expression profiles can identify epigenetic regulation of gene silencing; integrating metabolomic and proteomic data can trace the physiological origins of phenotypic variation. This cross-level data fusion will shift research from “gene presence” to “functional realization.”

The development of digital phenotyping provides new technological pathways for phenotypic evaluation. Using high-resolution imaging sensors, infrared scanning, behavior recognition, and automated monitoring systems,