Genomics and pig breeding: integrating molecular tools into selection programs

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Abstract. This mini-review examines the integration of modern molecular tools into pig breeding programs, with a focus on genomics, genome editing, epigenetics, and strategies for maintaining genetic diversity. Advances in genome-wide association studies (GWAS) and single nucleotide polymorphism (SNP) technologies have enabled the identification of key loci associated with economically important traits such as growth performance, carcass composition, and meat quality. These findings support the implementation of genomic selection (GS) to enhance breeding efficiency. In parallel, CRISPR-Cas9 genome editing has emerged as a transformative approach for developing disease-resistant pigs, particularly in the case of porcine reproductive and respiratory syndrome (PRRS), where targeted modifications of the CD163 gene confer robust resistance without compromising productivity. Furthermore, epigenetic mechanisms, including DNA methylation and histone modifications, mediate the interaction between environmental factors and gene expression, influencing phenotypic outcomes across generations. The review also highlights the importance of balancing genetic gain with the conservation of genetic diversity, emphasizing the role of optimal contribution selection (OCS) and genomic mating (GM) strategies in reducing inbreeding while sustaining long-term improvement. Collectively, these approaches represent a paradigm shift toward more precise, efficient, and sustainable pig breeding systems.

Keywords: GWAS, SNP, CRISPR-Cas9, PRRS resistance, epigenetics, genomic selection, genetic diversity, optimal contribution selection.

Introduction. The pig industry plays a critical role in global meat production, representing one of the most important livestock sectors for human nutrition and food security worldwide. Increasing demand for sustainable pork production has accelerated the adoption of advanced molecular breeding technologies aimed at improving productivity, animal health, and resource-use efficiency (Bergamaschi et al., 2019; Petrescu-Mag, 2023). In this context, integrating genomic and biotechnological tools into breeding programs has become essential for achieving higher genetic gains while maintaining long-term sustainability of pig populations (He et al., 2020; Zhao et al., 2021).

Traditional pig breeding programs have relied primarily on phenotypic selection and pedigree-based quantitative genetics, which, although effective, are limited by long generation intervals and moderate accuracy for complex traits (Petrescu-Mag, 2023). The advent of high-throughput genotyping and sequencing technologies has enabled a paradigm shift toward genomic-based selection, where genome-wide marker information is used to predict breeding values with higher precision (Bergamaschi et al., 2019; Wang et al., 2023). This transition has significantly improved the ability to select for economically important traits such as growth performance, carcass composition, fertility, and disease resistance at an earlier stage of life, thereby accelerating genetic progress and increasing selection efficiency (He et al., 2020; Gao et al., 2021).

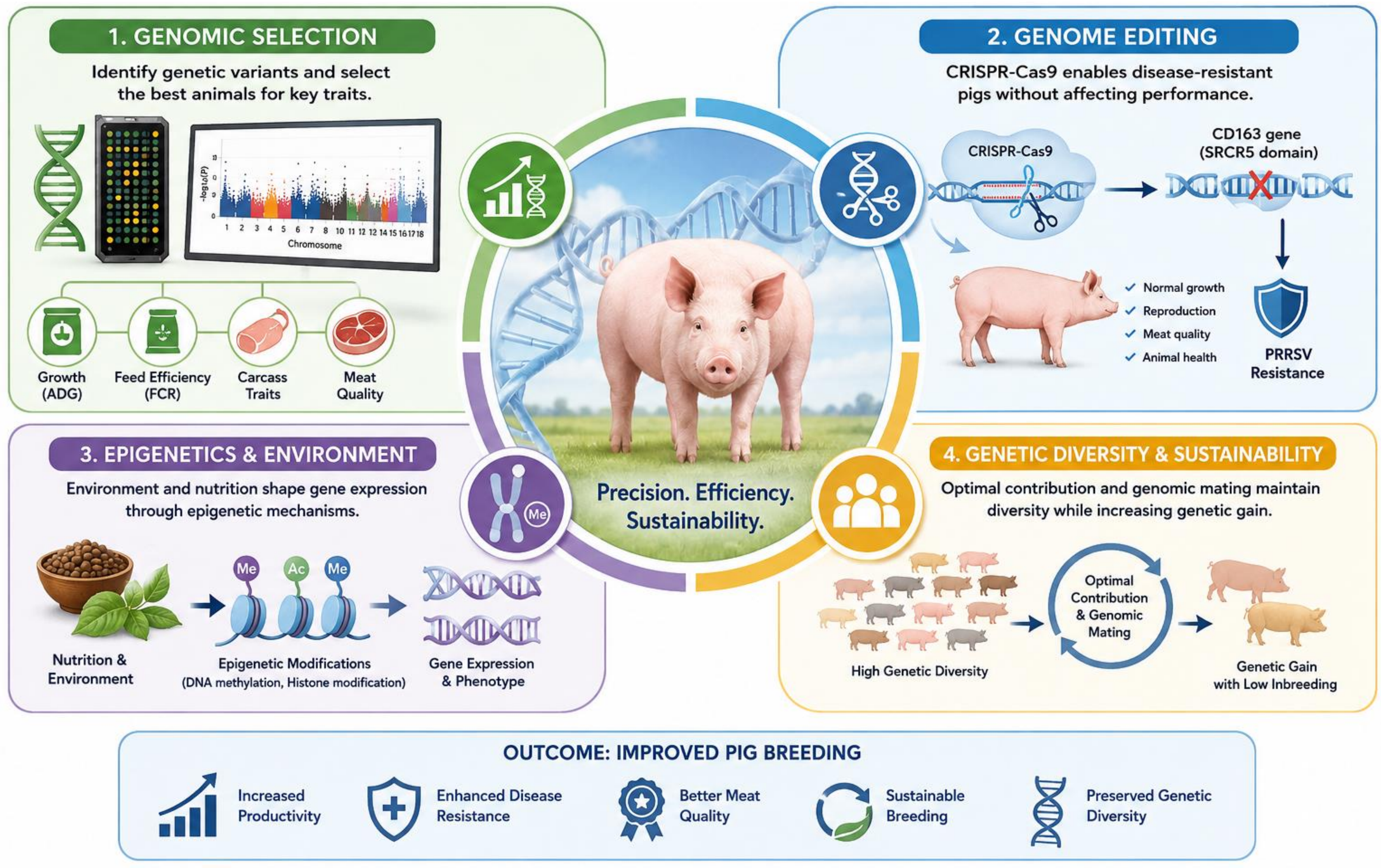

Figure 1. Integrated molecular framework of pig breeding programs.

Modern pig breeding increasingly combines quantitative genetics with genomic, gene-editing, and epigenetic information to improve production while preserving genetic diversity (Petrescu-Mag, 2023). Research covers genomic selection (GS) for economic traits, CRISPR-based disease resistance, environmentally responsive epigenetic regulation, and strategies to balance genetic gain with long-term diversity (Zhao et al., 2021; Zhao et al., 2023; Ji et al., 2026). Together, these approaches allow breeders to integrate classical selection principles with cutting-edge molecular tools, enabling more precise, efficient, and sustainable improvement of pig populations.

To provide a conceptual framework for this review, Figure 1 summarizes the main molecular tools, genomic selection, genome editing, and epigenetics, and their application in pig breeding programs. As shown in the Figure, genomic selection uses genome-wide markers to predict breeding values, CRISPR-Cas9 enables precise disease resistance, and epigenetic mechanisms mediate environmental effects on gene expression. Each of these approaches will be discussed in the subsequent sections of this review.

The aim of this mini-review is to synthesize current knowledge on the application of molecular and genomic tools in pig breeding and to evaluate their contribution to improving economically important traits while ensuring long-term sustainability. Specifically, the study seeks to: (i) assess the role of GS and genome-wide association studies (GWAS) in identifying genetic determinants of production traits, (ii) examine the potential of genome editing technologies, particularly CRISPR-Cas9, in enhancing disease resistance, (iii) analyze the influence of epigenetic mechanisms on gene expression and phenotypic plasticity in response to environmental factors, and (iv) explore strategies for maintaining genetic diversity under intensive selection regimes. By integrating these perspectives, the review aims to provide a comprehensive framework for the development of modern, efficient, and resilient pig breeding programs.

Genomic Selection in Pig Breeding. GS represents a major advancement in pig breeding, allowing breeders to estimate the genetic merit of animals based on genome-wide markers rather than solely on phenotypic records or pedigree information. By using single nucleotide polymorphisms (SNPs) across the genome, GS enables the calculation of genomic estimated breeding values (GEBVs) with higher accuracy, especially for traits with low heritability or measured later in life (Bergamaschi et al., 2019; Gao et al., 2021).

In pigs, GS has been successfully applied to improve growth traits, feed efficiency, carcass composition, and meat quality. Methods such as genomic best linear unbiased prediction (GBLUP)**,** single-step GBLUP (ssGBLUP), and Bayesian approaches integrate SNP genotypes with pedigree and phenotypic data, enhancing selection decisions and reducing generation intervals. GBLUP models using high-density SNP arrays or whole-genome sequencing data have increased selection accuracy for average daily gain (ADG), backfat thickness, and intramuscular fat content, accelerating genetic progress in commercial and crossbred populations (Bergamaschi et al., 2019; Gao et al., 2021; Wang et al., 2023; Ji et al., 2026). The integration of GS into breeding programs also provides opportunities to select simultaneously for multiple traits while controlling inbreeding. By combining GS with optimal contribution selection (OCS) and genomic mating (GM) strategies, breeders can maximize genetic gain while maintaining long-term genetic diversity, ensuring sustainable improvements in pig populations (Zhao et al., 2021; Zhao et al., 2023).

Genomic Tools for Economic Traits. GWAS using SNP chips or sequencing identify loci and candidate genes for growth and carcass traits such as backfat, loin depth, average daily gain (ADG) and meat quality (Bergamaschi et al., 2019; Gao et al., 2021; Wang et al., 2023; Ji et al., 2026). SNP arrays (PorcineSNP60K, GeneSeek 50K) and SLAF/WGS-derived SNPs have been used to detect regions explaining up to ~4% of variance per window, with moderate heritabilities for growth and quality traits (Bergamaschi et al., 2019; Gao et al., 2021; Wang et al., 2023). In crossbred pigs, GWAS has identified SNPs and genes affecting pH, marbling, meat color and intramuscular fat, supporting marker-assisted and GS for pork quality (Gao et al., 2021; Wang et al., 2023). Integrating GWAS with selection signatures in crossbreds has revealed key loci (e.g. ALOX15 for backfat), providing weighted SNP sets for GS in economic traits (Ji et al., 2026) (Table 1).

Table 1

Major genomic approaches and their applications in pig breeding programs

Trait / Category	*Main genomic resource / Approach*	*Key findings / Applications in breeding*	*References*
Growth traits (ADG, feed efficiency)	60K SNP arrays, ssGWAS, WGS	High heritabilities; SNP regions explaining variance for ADG and FCR; supports GS for growth	Bergamaschi et al., 2019; Ji et al., 2026
Carcass traits (backfat, loin depth)	60K SNP arrays, ssGWAS, selection signatures	Key loci identified (e.g., ALOX15 for backfat); weighted SNP sets for GS	Wang et al., 2023; Ji et al., 2026
Meat quality (pH, marbling, color, IMF)	50K SNP arrays in crossbreds	30+ significant SNPs; candidate genes identified for quality traits; supports marker-assisted and GS	Gao et al., 2021; Wang et al., 2023
Disease resistance (PRRS)	CRISPR-Cas9 editing of CD163	Exon 7/SRCR5 deletion confers PRRSV resistance without affecting performance; heritable, stable alleles	Whitworth et al., 2016; Burkard et al., 2017; Nesbitt et al., 2024
Genetic diversity / inbreeding control	Genomic OCS, genomic mating	Achieves high genetic gain while keeping inbreeding < 5% per generation; preserves heterozygosity	He et al., 2020; Zhao et al., 2021; Zhao et al., 2023

Note: ADG = average daily gain; FCR = feed conversion ratio; SNP = single nucleotide polymorphism; WGS = whole genome sequencing; ssGWAS = single-step genome-wide association study; GBLUP = genomic best linear unbiased prediction; GS = genomic selection; CRISPR-Cas9 = clustered regularly interspaced short palindromic repeats – Cas9 (genome editing technology); OCS = optimal contribution selection; IMF = intramuscular fat.

Genome Editing (CRISPR-Cas9) for PRRS Resistance. Porcine reproductive and respiratory syndrome virus (PRRSV) uses CD163 on macrophages to enter cells. Multiple CRISPR-Cas9 strategies deleting exon 7/SRCR5 of CD163 or replacing porcine exon 7 with a human ortholog generate pigs whose macrophages, and in several studies whole animals, are highly or fully resistant to PRRSV, including highly pathogenic strains (Whitworth et al., 2016; Burkard et al., 2017; Chen et al., 2019; Hung et al., 2022; Nesbitt et al., 2024). *In vivo* challenges show edited pigs lack viremia, clinical signs, lung lesions and antibody responses, yet maintain normal growth, health, reproduction and meat composition from birth to maturity (Whitworth et al., 2016; Nesbitt et al., 2024). Editing is achieved by zygote microinjection or other delivery of Cas9/sgRNA and produces heritable, stable alleles without transgenes (Whitworth et al., 2016; Burkard et al., 2017; Chen et al., 2019; Hung et al., 2022; Nesbitt et al., 2024). Reviews of molecular breeding emphasize that CRISPR now underpins rapid creation of disease-resistant, high-efficiency pigs and complements classical selection (Chen et al., 2025; Hassanine et al., 2025).

Despite its transformative potential, CRISPR-Cas9 genome editing has several limitations that must be considered. Off-target mutations can occur, potentially affecting unintended genomic regions and causing unforeseen phenotypic consequences. Consumer acceptance of gene-edited animals remains uncertain, and regulatory frameworks differ significantly between regions such as the European Union and the United States. Furthermore, the cost and technical complexity of implementing genome editing at scale may limit its immediate adoption in commercial breeding programs (Whitworth et al., 2016; Burkard et al., 2017; Chen et al., 2025).

Ethical and Regulatory Considerations. The application of genome editing and molecular breeding technologies in pigs raises complex ethical and regulatory challenges. Animal welfare must be prioritized, ensuring that edited animals do not experience unintended health or behavioral issues. Societal acceptance varies widely, influenced by public perceptions of naturalness, food safety, and transparency, which can affect market access. Traceability systems are crucial for labeling and monitoring gene-edited pigs, particularly in regions with strict consumer expectations. Regulatory frameworks differ globally: the European Union enforces stringent approval processes for genome-edited animals, whereas the United States permits certain modifications with less regulatory oversight. Ethical debates also consider the implications of altering animal genomes for human benefit, balancing innovation with moral responsibility. Integrating these considerations is essential for designing breeding programs that are sustainable, socially acceptable, and legally compliant (Chen et al., 2025; Hassanine et al., 2025)

Epigenetics, Environment and Gene Expression. Epigenetic mechanisms, including DNA methylation, histone modifications, and non-coding RNAs, mediate the interaction between environmental factors and gene expression in pigs (Thompson et al., 2020; Wang & Ibeagha-Awemu, 2021). Specific examples include methylation of the IGF2 gene affecting muscle growth, regulation of MSTN influencing myogenesis, and effects of prenatal nutrition on offspring growth and metabolic traits. Heat stress experienced by sows has also been shown to induce epigenetic changes that impact offspring performance and resilience. Incorporating epigenetic information into breeding models can improve predictions for traits that are environmentally sensitive or have low heritability, thus enhancing both productivity and animal welfare (Marín-García & Llobat, 2021; Liu et al., 2026).

Conserving Genetic Diversity Under Intense (Genomic) Selection. Simulation and applied work in local pig breeds show that conventional truncation selection rapidly increases inbreeding, whereas OCS and GM can simultaneously increase genetic gain and control inbreeding (He et al., 2020; Zhao et al., 2021; Škorput et al., 2022; Zhao et al., 2023; Zhao et al., 2024). Genomic OCS (using SNPs or runs of homozygosity) often achieves gains comparable to or exceeding unconstrained GS after several generations, while keeping inbreeding rates far lower (e.g. < 5% vs > 10% per generation) and preserving heterozygosity (He et al., 2020; Zhao et al., 2021; Zhao et al., 2023). Studies in conservation and commercial contexts conclude that pedigree- or genome-based OCS and GM are promising tools to make GS sustainable in small or indigenous pig populations, supporting both economic improvement and long-term diversity (He et al., 2020;; Zhao et al., 2021; Škorput et al., 2022; Zhao et al., 2023; Zhao et al., 2024).

Conclusions. The integration of genomics, genome editing, and epigenetics into pig breeding represents a paradigm shift toward precision livestock production. Future pig breeding programs will likely integrate genomic, epigenomic, transcriptomic, and gene-editing information into unified prediction models, supported by artificial intelligence and precision livestock farming technologies. Such integrated approaches are expected to enhance genetic gain, disease resistance, and adaptability, while maintaining genetic diversity and ensuring ethical and regulatory compliance. The strategic combination of molecular tools and sustainable breeding practices will be essential for meeting the increasing global demand for high-quality pork while safeguarding animal welfare and long-term population resilience.

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