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Advances in Animal Breeding Genetics and Reproductive Biotechnology: Integrating Genomic Innovations for Sustainable Livestock Improvement

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ARTICLE INFO	ABSTRACT
Received: April 25, 2026 Revised: May 07, 2026 Accepted: May 22, 2026 Available Online: June 12, 2026 Keywords: <i>animal breeding; quantitative genetics; genomic selection; reproductive biotechnology; artificial insemination</i> Corresponding Author: Qudratullah Kalwar Email: qudratullahkalwar@gmail.com	Genetic improvement and reproductive efficiency are the two fundamental drivers of sustainable livestock production, directly influencing productivity, adaptability, and economic returns. During the past two decades, conventional breeding strategies have been transformed by advances in molecular genetics, genomics, and reproductive biotechnology. Traditional selection methods are now complemented by marker-assisted and genomic selection, while artificial insemination has evolved into a broader platform that includes sexed semen, ovum pick-up and in vitro embryo production (OPU-IVP), embryo transfer, cryopreservation, somatic cell nuclear transfer (SCNT), and genome-editing technologies. Together, these innovations have accelerated the identification, multiplication, and dissemination of genetically superior animals. This review provides a comprehensive overview of recent advances in animal breeding genetics and reproductive biotechnology, emphasizing their complementary roles in modern livestock improvement. It discusses the genetic foundations of breeding, the principles and applications of assisted reproductive technologies, and the integration of genomic information into breeding programs. Particular attention is given to marker-assisted and genomic selection, the advantages and limitations of reproductive biotechnologies, the emerging role of epigenetic regulation in fertility and phenotypic variation, and the growing potential of CRISPR/Cas9-based genome editing for the rapid introduction of desirable traits. A regional case study focusing on South Asian buffalo production demonstrates how these technologies can be adapted to resource-limited and smallholder production systems while conserving valuable indigenous genetic resources. Although remarkable progress has been achieved, widespread implementation remains constrained by technical, economic, regulatory, ethical, and infrastructural challenges. Future advances are expected to arise from the integration of multi-omics technologies, precision reproductive management, and affordable genomic tools tailored to locally adapted breeds. Collectively, these developments offer a practical pathway toward more productive, resilient, climate-adaptive, and sustainable livestock production systems worldwide.

Introduction

Livestock production plays a fundamental role in global food security, rural livelihoods, and agricultural economies. The genetic merit of breeding animals is one of the most important, permanent, and cumulative factors influencing herd productivity and long-term genetic progress. Traditionally, animal breeding has relied on the selection of superior parents based on phenotypic performance and pedigree records, exploiting additive genetic variation to improve economically important traits over successive generations (Çelik, 2024). Although this approach has been highly successful, genetic progress is often slow for traits characterized by long generation intervals, low heritability, or expression late in life or in only one sex, particularly reproductive and fertility traits (Debay, 2025; Marker-Assisted and Genomic Selection of Beef Cattle, 2023).

Advances in molecular genetics and genomics have transformed livestock breeding by enabling the identification of superior animals with greater accuracy and at an earlier age. The completion of livestock genome sequences and the declining cost of single-nucleotide polymorphism (SNP) genotyping have accelerated the transition from conventional pedigree-based selection to marker-assisted selection (MAS) and, more recently, genome-wide genomic selection. These approaches have substantially improved breeding-value estimation while reducing generation intervals (Dekkers, 2004; Demircioglu, 2024; Marker-Assisted Selection in Animal Breeding: A Review, 2016). At the same time, reproductive biotechnologies—including artificial insemination (AI), embryo transfer (ET), in vitro embryo production (IVP), cryopreservation, and somatic cell nuclear transfer (SCNT)—have provided effective tools for rapidly disseminating superior genetics across livestock populations (Ferré et al., 2020; Zuidema et al., 2021; Cloning in Cattle: From Embryo Splitting to Somatic Nuclear Transfer, 1998). More recently, genome-editing technologies such as CRISPR/Cas9 have created opportunities to introduce or remove specific alleles within a single generation, thereby overcoming the lengthy backcrossing required in conventional breeding programs (Kadurumba et al., 2026; Rodriguez-Villamil et al., 2024). This review integrates advances in quantitative genetics, genomics, and reproductive biotechnology into a unified framework for modern livestock improvement. It examines the principles of genetic selection, recent developments in reproductive biotechnologies, and the growing integration of these disciplines within precision breeding programs. Particular emphasis is placed on their application in developing countries, using South Asian buffalo production as a representative example of how advanced breeding technologies can be adapted to resource-limited and smallholder production systems (Bilal et al., 2006; Kalwar et al., 2025).

Genetic Principles in Animal Breeding

Quantitative Genetics and Heritability

Most economically important traits in livestock including growth rate, milk production, carcass quality, disease resistance, and fertility are quantitative traits influenced by numerous genes, each contributing a relatively small effect, together with environmental factors. The response of these traits to selection depends largely on their heritability (h^2), defined as the proportion of phenotypic variation attributable to additive genetic variation. Traits with higher heritability respond more rapidly to selection because a larger proportion of the observed variation is genetically determined (Debay, 2025; Marker-Assisted and Genomic Selection of Beef Cattle, 2023).

Reproductive traits, including age at puberty, conception rate, calving interval, and fertility, generally exhibit low heritability (approximately $h^2 = 0.02$ – 0.15), making genetic improvement through conventional phenotypic selection relatively slow. In contrast, growth, carcass, and milk production traits usually possess moderate to high heritability, allowing more rapid and predictable genetic progress through selection (The Epigenetics of Gametes and Early Embryos and Potential Long-Range Consequences in Livestock Species, 2021; Marker-Assisted and Genomic Selection of Beef Cattle, 2023). Consequently, the integration of genomic selection with reproductive biotechnologies has become an effective strategy for accelerating genetic gain, particularly for traits with low heritability and complex inheritance.

Table 1. Representative heritability estimates and corresponding genetic improvement strategies for major trait categories in livestock.

Trait category	Representative trait	Approx. heritability (h^2)	Primary improvement strategy
Reproductive	Age at puberty / calving interval	0.05–0.15 (low)	Genomic selection, MAS, reproductive management
Reproductive	Conception rate / fertility index	0.02–0.10 (low)	Genomic selection combined with ART
Growth	Birth weight	0.30–0.45 (moderate)	Conventional + genomic selection
Growth	Weaning / yearling weight	0.25–0.40 (moderate)	BLUP, genomic selection

Trait category	Representative trait	Approx. heritability (h^2)	Primary improvement strategy
Production	Milk yield (dairy cattle/buffalo)	0.25–0.35 (moderate)	Progeny testing, genomic selection
Carcass/meat	Marbling / tenderness	0.30–0.50 (moderate–high)	Marker-assisted selection
Health	Disease resistance (e.g., mastitis)	0.05–0.15 (low)	MAS, gene editing, genomic selection

Marker-Assisted Selection (MAS)

Marker-assisted selection (MAS) utilizes DNA markers that are closely linked to quantitative trait loci (QTL) to identify genetically superior breeding candidates. This approach is particularly valuable for traits that are difficult, expensive, sex-limited, or impossible to measure directly in selection candidates, as well as traits that are expressed late in life (De Mori & Cipriani, 2023; JABB, 2024). By enabling indirect selection for economically important characteristics, MAS increases selection efficiency and reduces the time required to achieve genetic improvement. Commercial DNA-based tests are now available for several economically important traits, including meat quality, disease resistance, milk production, and reproductive performance in cattle and other livestock species (Çelik, 2024; Debay, 2025). Similar marker systems have also been successfully applied in plant breeding, highlighting the broad applicability of marker-assisted approaches across agricultural species. Although MAS focuses primarily on a limited number of major genes or QTL, it provided the scientific and technological foundation for the subsequent development of genome-wide genomic selection, which simultaneously evaluates thousands of genetic markers distributed throughout the genome (JABB, 2024).

Genomic Selection

Genomic selection represents one of the most significant advances in modern animal breeding. Unlike MAS, which targets a limited number of markers, genomic selection estimates breeding values using dense genome-wide SNP panels that capture the combined effects of thousands of quantitative trait loci. This approach substantially improves the accuracy of breeding-value prediction, particularly for young animals that have not yet expressed their productive or reproductive potential (Çelik, 2024; Debay, 2025). Bibliometric analyses demonstrate a rapid expansion of genomic selection research since 2010, with major contributions from research institutions in Europe, North America, and Asia. Today, genomic selection is widely implemented in dairy cattle, beef cattle, sheep, goats, pigs, and poultry breeding programs (Çelik, 2024). Furthermore, the integration of genomic selection with reproductive biotechnologies including sexed semen, embryo transfer, and in vitro embryo production—has further accelerated genetic gain by reducing generation intervals and increasing selection intensity. As genotyping costs continue to decline, these technologies are increasingly being adopted for indigenous and regionally important breeds in developing countries (Bilal et al., 2006; Figueroa et al., 2025). Despite these advances, successful implementation still depends on large reference populations with reliable phenotypic records, robust genomic databases, and statistical models capable of accounting for genotype-by-environment interactions (Debay, 2025).

Reproductive Technologies in Animal Breeding

Artificial Insemination and Sexed Semen

Artificial insemination (AI) remains the most widely adopted reproductive biotechnology in livestock production and has served as the cornerstone of genetic improvement programs for more than six decades. By allowing semen from genetically superior sires to be distributed to thousands of females, AI has substantially increased the rate of genetic gain while reducing the risk of disease transmission associated with natural mating (Zuidema et al., 2021). Continued improvements in semen evaluation, sperm selection, preservation techniques, and sperm-sexing technologies have further enhanced reproductive efficiency across cattle, sheep, goats, horses, and other domestic species (Agriculture, 2026; Zuidema et al., 2021). Flow cytometry-based sperm sexing enables the production of offspring of the desired sex with high accuracy, making it particularly valuable in dairy and beef breeding programs. However, the sorting process reduces sperm numbers and can decrease post-thaw fertility compared with conventional frozen semen (Pecu., 2024). Timed artificial insemination (TAI) protocols based on GnRH or progesterone–estradiol synchronization have further improved reproductive management by eliminating the need for estrus detection. Recent studies indicate that integrating genomic, transcriptomic, proteomic, and metabolomic information into TAI protocols may enable precision reproductive management tailored to the physiological status of individual animals (Ayantoye et al., 2025). In sheep and goats, laparoscopic AI remains the most reliable technique because the complex anatomy of the cervix limits the success of conventional cervical insemination. Although this method requires specialized equipment and expertise, it consistently achieves higher pregnancy rates than transcervical approaches. Similar reproductive challenges exist in buffalo, where continued refinement of fixed-time AI protocols is expected to improve fertility under tropical production conditions (Kalwar et al., 2015; Kolachi et al., 2025).

Embryo Transfer and in Vitro Embryo Production

Embryo transfer (ET) has become an indispensable tool for accelerating genetic improvement by increasing the reproductive output of genetically superior females. Initially developed through multiple ovulation and embryo transfer (MOET), ET has evolved to include ovum pick-up combined with in vitro maturation, fertilization, and embryo culture (OPU-IVP), enabling repeated embryo production from elite donor animals throughout the year (Betteridge, 2020; Ferré et al., 2020). Since 2016, the global number of embryos produced through in vitro techniques has exceeded those generated using conventional MOET, reflecting widespread adoption of OPU-IVP by commercial breeding programs. The technology is particularly effective when integrated with genomic selection and sexed semen, allowing rapid multiplication of elite maternal genetics (Ferré et al., 2020). Nevertheless, embryos produced in vitro continue to exhibit lower developmental competence than those produced in vivo. Pregnancy losses remain comparatively high during early gestation, and IVP embryos often display altered embryonic development, placentation, and fetal growth (Hansen, 2019). Consequently, ongoing research is focused on improving oocyte quality, embryo culture systems, cryotolerance, and maternal–embryo interactions to enhance pregnancy success and offspring health (Ferré et al., 2020).

Semen and Embryo Cryopreservation

Cryopreservation is an essential component of modern livestock breeding because it enables the long-term storage, transport, and global exchange of valuable genetic material. The technology supports artificial insemination, embryo transfer, germplasm conservation, and biodiversity preservation by maintaining viable semen and embryos for extended periods (Lonergan, 2023). Despite its widespread application, cryopreservation remains associated with cellular damage caused by osmotic stress, ice crystal formation, oxidative stress, and membrane disruption during freezing and thawing. These changes may reduce sperm motility, membrane integrity, DNA stability, and overall fertility (Sharafi et al., 2022). To minimize cryoinjury, various cryoprotective agents, including glycerol, trehalose, antioxidants, and more recently nanotechnology-based additives, have been incorporated into semen extenders. Considerable progress has been achieved in improving post-thaw sperm quality, particularly in cattle; however, effective cryopreservation of semen from sheep and goats remains more challenging because of species-specific differences in sperm membrane composition and cryosensitivity (Yáñez-Ortiz et al., 2022).

Table 2. Comparative overview of major reproductive and genetic biotechnologies used in livestock breeding programs.

Technology	Principle	Main advantage	Key limitation
Artificial insemination (AI)	Deposition of processed/frozen semen into the female tract	Rapid dissemination of elite sire genetics; disease control	Requires accurate estrus detection; variable conception rates
Sexed semen / TAI	Flow-cytometric sorting of X/Y sperm combined with synchronization	Predetermined offspring sex; precision breeding	Lower sperm dose and post-thaw fertility than conventional semen
MOET (superovulation + embryo transfer)	Hormonal superovulation of donor females, non-surgical embryo flushing	Multiplies offspring from genetically superior females	Variable donor response; labour- and cost-intensive
OPU-IVP (ovum pick-up / in vitro production)	Ultrasound-guided oocyte aspiration, IVM-IVF-IVC	Higher embryo output per donor; usable with sexed semen	Lower embryo cryotolerance and pregnancy rates than in vivo embryos
Semen/embryo cryopreservation	Controlled freezing with cryoprotectants for long-term storage	Global distribution; germplasm genetic banking	Post-thaw viability losses; cryodamage to membranes/DNA
Somatic cell nuclear transfer (cloning)	Transfer of a donor somatic-cell nucleus into an enucleated oocyte	Exact replication of elite/endangered genotypes	Low efficiency; epigenetic abnormalities, large-offspring syndrome
Genome/gene editing (CRISPR-Cas9)	Site-specific modification of the genome to install or remove alleles	Single-generation introduction of favourable traits (e.g., disease resistance)	Mosaicism, off-target effects, regulatory uncertainty

Integrating Genomics and Reproductive Biotechnology

The greatest benefit of genomic selection is achieved when it is integrated with reproductive biotechnologies that enable the rapid multiplication and dissemination of superior genetics. In modern breeding programs, phenotypic and pedigree information is combined with high-density SNP genotypes to estimate genomic-enhanced breeding values (GEBVs). Animals with the highest GEBVs are then selected as elite breeding stock, and their genetic merit is propagated through reproductive technologies such as artificial insemination (AI), sexed semen, multiple ovulation and embryo transfer (MOET), ovum pick-up coupled with in vitro embryo production (OPU-IVP), and embryo cryopreservation (Çelik, 2024; Ayantoye et al., 2025; Ferré et al., 2020). Cryopreservation further facilitates the long-term storage and international distribution of valuable germplasm, ensuring that elite genetics remain accessible across both time and geographical regions.

An integrated breeding program is not a one-way process but a continuous cycle of improvement. Performance records from the offspring are incorporated back into genomic databases, refining prediction models and improving the accuracy of future breeding-value estimates. Figure 1 (presented at the end of this manuscript) illustrates this workflow and highlights the feedback mechanism that drives sustained genetic progress. Gene-editing technologies complement this pipeline by enabling the introduction of desirable alleles that are absent or occur at low frequency within a population, thereby accelerating genetic improvement beyond the limits of conventional selection (Kadurumba et al., 2026; Rodriguez-Villamil et al., 2024).

Emerging Genome-Editing Technologies

Genome-editing technologies, particularly CRISPR/Cas9, together with newer platforms such as base editing and prime editing, have transformed livestock genetics by enabling precise modifications at specific genomic loci. Unlike conventional breeding, which requires several generations to introduce desirable traits through repeated backcrossing, genome editing allows favorable genetic variants to be incorporated within a single generation (Kadurumba et al., 2026). Successful applications include the development of pigs carrying the CD163 allele for resistance to porcine reproductive and respiratory syndrome (PRRS), cattle with enhanced heat tolerance, and other livestock possessing traits that improve productivity and disease resistance. Several of these applications are currently progressing through regulatory evaluation in different countries. Despite these promising advances, the routine application of genome editing in commercial breeding remains limited. Recent systematic reviews conclude that reliable evidence is still confined largely to a small number of monogenic traits, and additional studies are needed to validate long-term performance, inheritance, and safety across multiple generations (Kadurumba et al., 2026). Technical limitations also remain. Mosaicism in edited embryos can complicate the identification of correctly edited founder animals, while unintended off-target mutations continue to raise concerns regarding precision and biosafety. Both issues have been documented in CRISPR-edited bovine embryos. At the same time, regulatory policies governing intentional genomic alterations continue to evolve, with authorities such as the U.S. Food and Drug Administration developing frameworks that balance innovation with food safety, animal welfare, and public confidence (Rodriguez-Villamil et al., 2024).

Epigenetics in Reproduction and Breeding

Although genomic variation explains a substantial proportion of economically important traits, it does not fully account for the phenotypic diversity observed in livestock populations. Increasing evidence suggests that epigenetic mechanisms including DNA methylation, histone modifications, chromatin remodeling, and non-coding RNAs contribute to this unexplained or "missing" heritability by regulating gene expression without altering the underlying DNA sequence (Kordowitzki et al., 2021). Among these mechanisms, DNA methylation has received the greatest attention because of its dynamic role during primordial germ cell development and early embryogenesis, stages that are particularly sensitive to environmental conditions, maternal nutrition, and assisted reproductive procedures (Zhu et al., 2021). In cattle, differential methylation patterns in sperm have been associated with fertility, semen quality, and sperm motility, indicating their potential as biomarkers for selecting highly fertile breeding sires (De Mori and Cipriani, 2023). Likewise, genome-wide methylation studies have identified tissue-specific methylation signatures that distinguish reproductive tissues from somatic tissues (Hu et al., 2025). Recent advances have also led to the development of epigenetic clocks based on DNA methylation profiles, providing novel tools for estimating biological age and investigating reproductive aging in bovine oocytes (Ibeagha-Awemu, E. M., & Zhao, X. 2015). Because assisted reproductive technologies can influence normal epigenetic reprogramming during early embryonic development, understanding these effects has become an essential component of responsible reproductive biotechnology and livestock breeding (Zhang et al., 2023).

Somatic Cell Nuclear Transfer and Cloning

Somatic cell nuclear transfer (SCNT) is a cloning technique in which the nucleus of a differentiated somatic cell is transferred into an enucleated oocyte to generate a genetically identical individual. The technology gained worldwide recognition following the birth of Dolly the sheep in 1996, demonstrating that differentiated adult cells retain the genetic information necessary to produce an entire organism (Sattar et al., 2025). Today, SCNT is used primarily for preserving elite genetics, conserving endangered breeds, and producing genetically modified animals for agricultural and biomedical research. When combined with genome-editing technologies, SCNT provides an efficient platform for generating precisely modified livestock carrying desirable genetic traits (Alberio and Wolf, 2021).

Despite its scientific value, cloning remains constrained by relatively low efficiency and high developmental losses. Cloned animals frequently exhibit abnormalities such as large offspring syndrome, placental dysfunction, respiratory disorders, and metabolic complications, many of which are attributed to incomplete epigenetic reprogramming of the donor nucleus (Stice et al., 1998). Nevertheless, international regulatory agencies, including the World Organisation for Animal Health and several national food-safety authorities, have concluded that meat and milk obtained from healthy cloned animals and their offspring are comparable in safety to products from conventionally bred livestock, although issues related to public acceptance, ethics, and traceability continue to influence commercial adoption (Parnpai et al., 2010).

Regional Perspective: Genetic Improvement of Buffalo in South Asia

Buffalo play a pivotal role in the livestock economies of South Asia, serving as the principal dairy species in many regions. Pakistan alone maintains one of the world's largest buffalo populations, comprising indigenous breeds such as Nili-Ravi, Kundi, and Azi Khaili, while buffalo production also contributes substantially to food security and rural livelihoods in India, Bangladesh, and Nepal (Bilal et al., 2006). Despite their economic importance, genetic improvement programs for these breeds have progressed more slowly than those for commercial cattle because breeding has traditionally relied on smallholder production systems with limited pedigree recording, milk performance data, and organized selection programs.

Recent reviews suggest that integrating affordable SNP genotyping with reproductive technologies, including fixed-time AI, embryo transfer, and, in the future, genome editing, could substantially accelerate genetic improvement while preserving the unique adaptive characteristics of indigenous buffalo breeds (Bilal et al., 2006). Similar challenges have been reported across neighboring countries, where inadequate record-keeping, limited AI services, and shortages of genetically superior breeding stock continue to impede sustainable genetic progress (Coman et al., 2024). These regional experiences highlight an important principle: advanced breeding technologies should be adapted to local production systems, available infrastructure, and socioeconomic conditions rather than simply transferred from highly intensive livestock industries.

Challenges and Limitations

Despite remarkable advances in genomics and reproductive biotechnology, several challenges continue to limit their widespread implementation in livestock breeding. Effective genomic selection depends on large, accurately phenotyped reference populations, the development of which requires substantial investment and remains difficult for many indigenous or regionally important breeds (Debay, 2025; Bilal et al., 2006). Similarly, although assisted reproductive technologies such as in vitro embryo production and cryopreservation have improved considerably, embryo developmental competence and post-thaw viability still lag behind those achieved under natural or fresh-gamete conditions (Akhtar et al. 2022).

The adoption of genome editing and cloning also faces scientific, regulatory, ethical, and societal challenges. While these technologies hold considerable promise, evidence supporting their routine application in commercial breeding is still limited to relatively few traits and species, and broader acceptance will depend on continued improvements in safety, efficacy, and regulatory oversight (Kadurumba et al., 2026). In many developing countries, however, the most immediate constraints are not technological but infrastructural. Weak animal recording systems, limited veterinary support, inadequate AI coverage, and fragmented smallholder production systems continue to restrict the practical implementation of modern breeding strategies (Betteridge, K. J. 1998). Addressing these foundational challenges will be essential for ensuring that advances in genomic and reproductive technologies translate into sustainable genetic improvement and increased livestock productivity.

Future Perspectives

Future advances in animal breeding are expected to be driven by the integration of multi-omics technologies, including genomics, transcriptomics, proteomics, and epigenomics, into breeding-value estimation and reproductive management. This integrated approach will enable more precise selection decisions and allow reproductive protocols to be tailored to the metabolic and fertility status of individual animals rather than applying uniform herd-level strategies (Ayantoye et al., 2025). At the same time, improvements in the precision and efficiency of gene-editing technologies, coupled with the development of clear and harmonized regulatory frameworks, will play a critical role in determining the pace at which these innovations can be translated into commercial breeding programs (Kadurumba et al., 2026; Rodriguez-Villamil et al., 2024). In developing countries, expanding access to affordable genomic tools and reproductive biotechnologies for indigenous and locally adapted breeds presents a major opportunity to improve productivity while safeguarding valuable genetic diversity. Ongoing initiatives to enhance the genetic potential of South Asian buffalo populations illustrate how modern breeding technologies can be successfully integrated with conservation efforts, helping to narrow the productivity gap between native breeds and highly selected international populations without compromising their unique adaptive traits (Bilal et al., 2006).

Conclusion

Genetic and reproductive technologies have increasingly converged to form an integrated framework for modern animal breeding, in which genomic evaluation identifies genetically superior individuals and reproductive biotechnologies enable their rapid dissemination across livestock populations. Marker-assisted selection and genomic selection have significantly enhanced the accuracy, efficiency, and rate of genetic improvement, while artificial insemination, embryo transfer, and cryopreservation continue to serve as the cornerstone technologies for translating genetic gain into commercial production systems. Emerging approaches, including gene editing and somatic cell nuclear transfer (cloning), further expand the scope of genetic improvement by enabling precise genome modification and preservation of elite genotypes. However, these technologies still require additional research, technical refinement, and well-defined regulatory frameworks before they can achieve widespread commercial adoption. At the same time, advances in epigenetics are uncovering important non-sequence-based mechanisms that influence fertility, productivity, adaptability, and other economically important traits, offering new opportunities for precision breeding. When strategically integrated and tailored to regional production systems and infrastructural capacities—as demonstrated by ongoing initiatives to enhance the genetic potential of indigenous buffalo populations in South Asia these complementary technologies provide a robust pathway toward more productive, resilient, climate-adaptive, and sustainable livestock production systems worldwide.

Author Contributions

All authors have read and agreed to the published version of the manuscript. Conceptualization: JF, QK, and MMR; Literature search and data collection: ASB, SAL; Critical review of literature, AAK; Manuscript drafting: JF; Manuscript review: QK, MMR, and HS; Supervision: QK.

Conflict Statement

The authors declare no conflict of interest.

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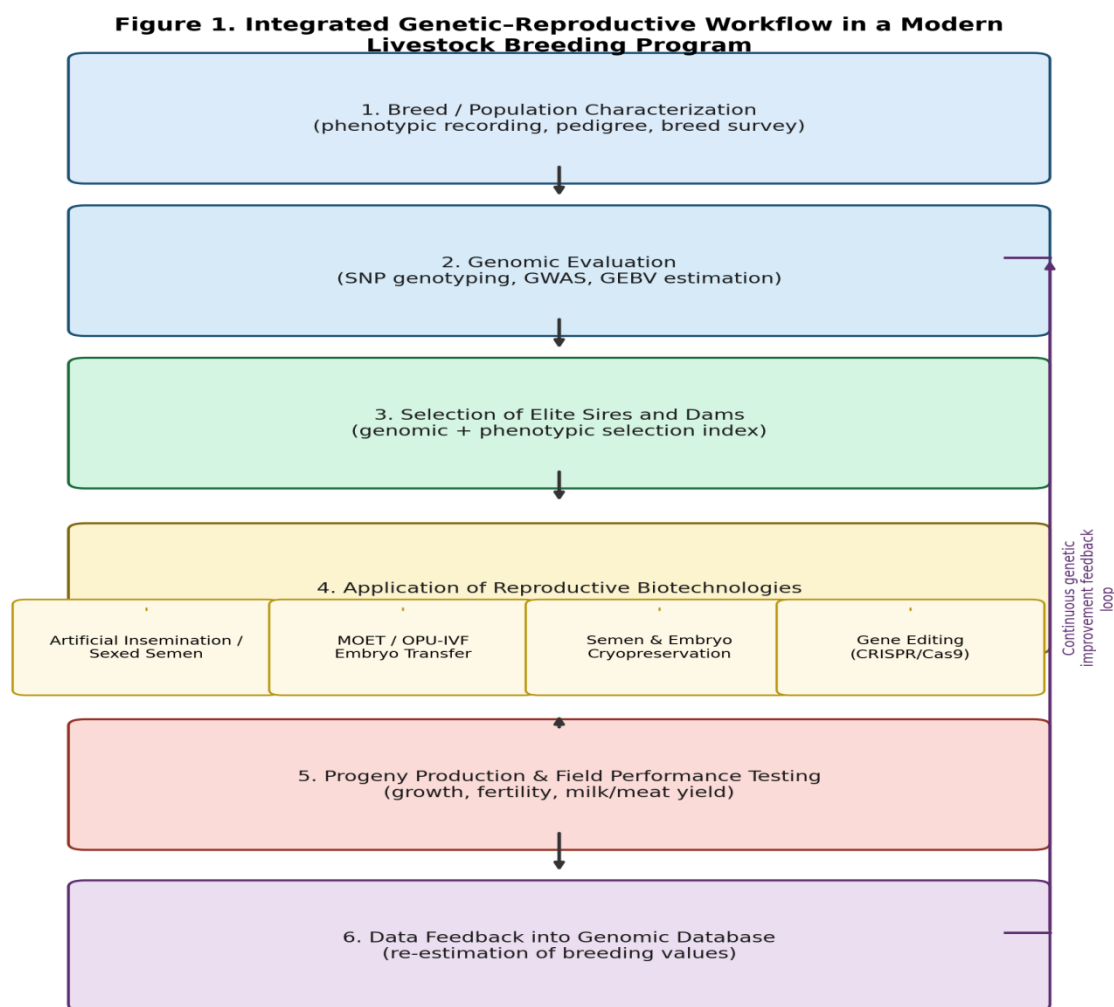


Figure 1. Integrated workflow linking genomic evaluation and reproductive biotechnologies in livestock breeding programs, including the feedback loop from field performance data to the genomic database.



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