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Genomic Tools for Improving Disease Resistance in Domestic Animals

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Disease resistance in farm animals is a major challenge with big effects on the economy, animal welfare, and human health. Infectious diseases cause heavy financial losses worldwide and can spread to people, making better control methods very important. Differences in natural disease resistance between species, breeds and individual animals give a good base for selective breeding, but traditional methods are limited because testing is expensive and health records are often incomplete. New genomic tools such as genome-wide association studies (GWAS), marker-assisted selection (MAS) and CRISPR/Cas9 gene editing make it possible to choose or create animals with stronger resistance without exposing them to disease. Precision livestock farming (PLF), which uses sensors and real-time monitoring, adds further benefits by collecting detailed health and performance data to guide breeding. Challenges still exist, such as handling large amounts of data and agreeing on clear rules for gene editing, but together these modern approaches offer a big step forward in producing healthier, stronger and more productive livestock.

Introduction

Disease resistance in domestic animals is a major challenge with significant economic and welfare consequences. Infectious diseases cause heavy financial losses, estimated at 17% of turnover in developed countries (£1.7 billion in the UK) and between 35–50% in developing nations, while also reducing livestock productivity and compromising animal welfare (Bishop *et al.*, 2002). Beyond their impact on production, these diseases present serious zoonotic risks, underscoring the critical importance of veterinary services in global disease control. Genetic variation in disease resistance is observed across all major domestic animal species, occurring between species, breeds, and individual animals (Jovanović *et al.*, 2009). Detailed investigations of specific diseases almost always reveal genetic differences in resistance, providing a valuable basis for selective breeding strategies. Many disease resistance traits are highly heritable and show wide variability among animals, making selective breeding a feasible and sustainable approach (Stear *et al.*, 2001). With advances in molecular genetics, DNA marker-based systems have made it possible to objectively identify animals carrying favorable resistance alleles (Gogolin-Ewens *et al.*, 1990).

Despite these opportunities, conventional breeding for disease resistance faces important limitations. The most significant barrier is the high cost and logistical difficulty of obtaining resistance phenotypes through challenge testing or natural infection (Pal and Chakravarty, 2020). In addition, the lack of accurate, systematically recorded data on individual animal disease susceptibility restricts the integration of health traits into national breeding goals (Berry et al., 2011). Traditional quantitative genetic models, which have been highly effective for production traits, are less reliable for predicting responses to selection for disease resistance due to the complex interplay between host genetics and pathogen transmission (Stear *et al.*, 2012). To overcome these challenges, genomic technologies have provided powerful new solutions, enabling DNA-based selection without the need for pathogen exposure. Approaches such as genomic selection, gene editing, and transgenesis are now central to the development of disease-resistant livestock (Pal and Chakravarty, 2020). These methods are particularly advantageous for traits with low heritability that appear later in life. However, the primary limitation remains the availability of high-quality phenotypic data rather than genomic resources themselves (Bishop and Woolliams, 2014).

Overview of Genomic Technologies

Genome-Wide Association Studies (GWAS)

Over the past two decades, genome-wide association studies (GWAS) have become powerful tools for identifying genetic loci linked to economically important traits and disease resistance in livestock (Sharma *et al.*, 2015). These studies have greatly expanded the pool of molecular markers available for marker-assisted selection and improved the understanding of genetic mechanisms underlying complex traits (Ying, 2013). Recent progress has seen the integration of multi-omics approaches, which combine proteome, transcriptome, epigenome and metagenome data with advanced analytical algorithms, thereby increasing the precision and scope of GWAS applications. Such studies have been widely applied across major livestock species, including cattle, pigs, chickens and sheep, targeting traits related to disease resistance, production performance and genetic disorders (Tan *et al.*, 2023). An important example is the GWAS conducted on Katahdin sheep, where resistance loci for gastrointestinal nematodes were identified. This study revealed significant associations on multiple chromosomes and highlighted the potential involvement of genes such as DIS3L2 (Becker *et al*., 2020). Collectively, these developments continue to advance modern animal breeding technologies.

Marker-Assisted Selection (MAS)

Marker-Assisted Selection (MAS) represents a modern breeding technology that relies on DNA markers to indirectly identify superior plants and animals by detecting associations between genetic markers and quantitative trait loci (QTL). Often described as “smart breeding,” this approach facilitates the direct selection of desirable traits through molecular markers, proving especially advantageous for traits that are difficult to evaluate phenotypically, have low heritability, or are controlled by recessive genes (Wakchaure *et al.*, 2015). MAS has been widely utilized in breeding programs for improving disease resistance, with notable applications in rice for bacterial blight, blast disease and drought tolerance (Henkrar, 2020). In addition, for nematode resistance in crop plants, MAS provides a faster and more efficient alternative to conventional breeding methods, which are often labor-intensive and time-consuming (Banu *et al.*, 2017). By employing molecular markers at the seedling stage, breeders can achieve high-precision selection while reducing costs and bypassing traditional phenotype-based approaches. Despite its advantages, the broader implementation of MAS is sometimes limited by factors such as small QTL effects and economic constraints in breeding programs.

CRISPR/Cas9 and Gene Editing

CRISPR/Cas9 technology has brought a major transformation in livestock genetic engineering by enabling precise genome modifications aimed at improving disease resistance, productivity, and animal welfare (Liu *et al*., 2022). Its applications are diverse, including the development of pigs resistant to Porcine Reproductive and Respiratory Syndrome Virus through targeted modification of the CD163 gene, as well as the production of chickens with resistance to avian influenza. Another notable use is the introduction of hornless traits in cattle, which eliminates the need for painful dehorning procedures and directly contributes to animal welfare. A key advantage of this approach is that genome-edited animals can be developed with desired traits within a single generation, offering a much faster alternative compared to conventional breeding methods (Bhat *et al.*, 2017). Despite these advantages, several challenges hinder broader adoption of the technology. Ethical issues such as its potential impact on biodiversity and long-term animal welfare remain central to ongoing debates. Technical limitations, particularly the risk of off-target effects, add further complexity, while uncertainties in regulatory frameworks also pose obstacles to global implementation. International regulations vary widely, with significant differences in how legal authorities interpret the need for oversight and control of genome-edited animals (Kumar and Kues, 2022).

Integration with Precision Livestock Farming

The integration of genomics with precision livestock farming (PLF) is bringing major changes to livestock breeding and management. Livestock phenomics focuses on the systematic collection of large amounts of phenotypic data, helping to address the "phenomic gap" caused by falling genomics costs (Juárez, 2020). PLF makes use of continuous, automated monitoring systems with sensors and Internet of Things technology to improve the health, welfare, and productivity of individual animals (Tedeschi et al., 2021). When combined with artificial intelligence and machine learning, these systems provide real-time monitoring and predictive modeling, creating strong synergies between the fields. Genomic selection uses genome-wide markers and statistical tools to calculate genomic estimated breeding values, which speeds up genetic progress (Shoyombo et al., 2024). The merger of genomics and phenomics also supports high-throughput phenotyping and more effective genomic selection strategies. Despite these benefits, there are challenges such as data standardization, creating integrated computational pipelines, and handling very large datasets (Shakshi et al., 2024). To succeed, there is a need for hybrid intelligent mechanistic models that combine both concept-driven and data-driven approaches.

Conclusion

Improving disease resistance in farm animals is very important for both the economy and animal welfare. Traditional breeding methods have made some progress, but they are often slow and limited. New genomic tools now provide faster and more accurate ways to breed disease-resistant animals, with GWAS and MAS helping to identify useful genetic markers and CRISPR gene editing allowing direct introduction of resistance genes. Precision livestock farming adds further value by collecting real-time health and performance data, which helps fill gaps in disease information. Challenges such as managing large data, addressing ethical concerns and dealing with different international rules still remain. Even so, combining genomics with modern farming technologies offers a clear way forward for livestock breeding, supporting global food security, improving animal health and ensuring safer human–animal interactions.

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