

Just Veterinary

e- Magazine

Volume - 1

Issue - 3

September-October, 2025

www.justveterinary.co.in

AUTHORS' DETAILS:

Rakesh Nehra

*Assistant Professor,
Department of Animal Genetics &
Breeding, Shriganganagar
veterinary college, Tania
University, Sri Ganganagar,
Rajasthan.*

Pulkit Chugh

*Ph.D. Scholar,
Department of Livestock
Production Management, LUVAS,
Hisar, Haryana.*

Nikhil kumar

*Assistant Professor,
Department of Animal Nutrition,
SCVAS, Sanskaram University,
Jhajjar, Haryana.*

Anil

*Assistant Professor,
Department of Veterinary
Gynecology & Obstetrics, Apex
Institute of Veterinary Education
and Research, Tohana, Haryana.*

Hitesh

*Assistant Professor,
Department of Veterinary
Gynecology & Obstetrics,
SCVAS, Sanskaram University,
Jhajjar, Haryana.*

ARTICLE ID: 03

BREEDING FOR DISEASE RESISTANCE IN LIVESTOCK: STRATEGIES, CHALLENGES AND FUTURE PROSPECTS

Abstract

Developing disease-resistant livestock is essential for sustainable animal production and global food security. Selective breeding, strengthened by advancements in genomics, offers a long-term and environmentally sound solution. Classical selection based on traits such as faecal egg counts in sheep or somatic cell counts in dairy cattle laid the foundation for resistance improvement, while modern genomic tools including marker-assisted and genomic selection have enhanced the precision of identifying resilient animals. Recent innovations in gene editing technologies, such as CRISPR/Cas9 and base editing, now allow targeted modification of resistance genes with remarkable accuracy. However, low heritability, performance constraints, and evolving pathogens remain major challenges. Integrating modern genomic innovations with traditional breeding strategies can help develop healthier, more resilient, and productive livestock populations, ensuring sustainable animal health and food security.

Introduction

Improving disease resistance is critical not only for animal health and welfare but also for ensuring a safe, high-quality food supply for a growing global population. This is particularly evident, as animal diseases can severely damage farms, resulting in economic losses of 35–50% in developing countries and substantially lowering productivity worldwide. Traditional methods for controlling infectious diseases in livestock, such as vaccination, biosecurity, and culling, have limited success due to frequent boosters, pathogen mutations, and ethical concerns (Gao et al., 2023). Hence, new genetic and genomic approaches are essential to improve disease resistance and ensure sustainable livestock health. In recent years, genomic studies, such as GWAS and QTL mapping, have revealed candidate genes and markers linked to disease resistance in livestock (Goddard and Hayes, 2009). The use of these advanced tools for genetic improvement of animals can help create disease-resistant livestock herds. Thus, breeding for disease resistance is feasible, desirable, and sustainable, offering a reliable approach to improving animal health and productivity (Stear et al., 2001).

This article highlights possible ways for the selection and breeding of disease-resistant animals, highlighting key challenges and future prospects for sustainable livestock improvement. Mastitis is economically the most important disease of dairy cattle, while nematode infection is the most important disease of small ruminants. Mastitis is economically the most important disease of dairy cattle, while nematode infection is the most important disease of small ruminants.

Traditional Breeding Methods

Breeding animals for disease resistance involves several approaches aimed at identifying individuals that can naturally withstand infections. One of the simplest methods is to select animals that remain healthy under natural exposure to pathogens. This approach is low-cost, easy to implement, and free of ethical concerns, although its accuracy can be limited if animals are not sufficiently exposed (Gogoi et al., 2022). For example, Red Maasai sheep in Kenya have been observed to resist *Haemonchus* infections better than the South African Dorper breed (Mugambi et al., 1996). Accuracy can be improved by deliberately exposing animals to controlled doses of pathogens, ensuring uniform challenge and precise evaluation. Studies comparing resistant Barbados Black Belly lambs with susceptible INRA 401 lambs during *Haemonchus contortus* infection have shown that resistant breeds exhibit stronger immune responses (Terefe et al., 2007). In cases of highly lethal diseases, relatives or clones of breeding stock can be challenged under controlled conditions, though this is usually limited to research facilities and involves higher costs and ethical considerations (Gogoi et al., 2022).

Indirect selection is another widely used approach, based on indicator traits such as faecal egg counts, somatic cell counts, or other immune responses that are correlated with disease resistance. To be effective, these traits must be heritable, strongly associated with resistance, easy to measure, and cost-effective (Snowder, 2006). Successful examples include selecting sheep for

low internal parasite egg counts and dairy cattle for reduced somatic cell counts to decrease mastitis incidence (Woolaston et al., 1992; Shook and Schutz, 1994). By integrating these strategies, breeders can progressively develop livestock populations that are healthier, more productive, and better prepared to withstand emerging disease challenges.

Advanced Genomic methods

Classical breeding has long relied on selecting resilient animals or families based on observable traits, such as faecal egg counts in sheep or somatic cell counts in dairy cattle, to improve disease resistance. While effective, these methods were limited by the slow pace of selection and the difficulty of accurately identifying resistant individuals. Recent developments in genetics and genomics have markedly improved this process, facilitating more accurate, efficient, and accelerated selection of disease-resistant animals.

Modern approaches such as Marker-Assisted Selection (MAS) allow breeders to identify animals carrying specific DNA markers associated with resistance, including key genes like MHC, CD14, and TLR4. Single nucleotide polymorphisms (SNPs) in immune-response genes have been reported for the CD14 gene in goats and cattle (Pal and Chatterjee, 2009; Pal et al., 2011). Genomic Selection (GS) goes even further, analyzing thousands of genetic markers across the genome to predict which animals are most likely to resist infections. Coupled with bioinformatics and next-generation sequencing, these tools enable the analysis of massive datasets, helping pinpoint the most promising animals for future breeding programs. These strategies have already produced notable successes. Indigenous breeds like *Bos indicus* cattle and buffalo often display naturally higher resistance due to favorable gene variants. Specific genes, such as NRAMP1 in cattle, confer resistance to tuberculosis (Liu et al., 2017), while gene-edited pigs lacking CD163 are protected against PRRS virus (Whitworth et al., 2016). Disease resistance breeding has also benefited

poultry, improving defenses against Marek's disease, and small ruminants, enhancing protection against parasites and viral infections.

The newest frontier in disease resistance is precision gene editing. Technologies like CRISPR/Cas9 now allow scientists to insert, delete, or modify genes with unprecedented accuracy. For example, introducing the NRAMP1 gene into cattle strengthens their ability to control tuberculosis infection. These innovations have great potential, but ethical and safety issues must be considered to gain public trust.

Practical Challenges and Future Prospects

The main challenge in breeding for disease resistance is the accurate identification of resistant animals, as selection based solely on phenotype (observable health) may fail to detect subclinical carriers, limiting the reliable evaluation of resistance traits (Gogoi et al., 2022). Further, disease resistance traits often have low heritability (5–15%), making careful selection and the use of indicator traits crucial, as these traits are often more heritable and can serve as effective proxies for resistance (Uribe et al., 1995). Resistance traits for different diseases may also be negatively correlated, meaning improvement in one trait could reduce resistance to another. Rapid evolution of parasites and pathogens adds another layer of complexity, as enhancing host resistance to a specific disease may inadvertently increase susceptibility to other infections. Additionally, negative genetic correlations between disease-resistant traits and production traits must be considered, as improvements in resistance should not compromise overall productivity. Ongoing pathogen evolution thus requires flexible, genomics-driven breeding strategies to stay ahead of emerging threats while maintaining economically viable, healthy livestock.

Looking ahead, advances in genomics and gene editing offer promising solutions to these challenges. Tools such as marker-assisted selection, genomic selection, and precision gene editing (including CRISPR/Cas9, base editing, and prime editing) enable more accurate, efficient, and

targeted improvement of resistance traits. Emerging technologies, including multi-site CRISPR targeting, Type I CRISPR systems, and gene regulation approaches like RNA interference and CRISPR interference, offer greater precision and safety while addressing pathogen evolution (Tan et al., 2022). By integrating these modern approaches with classical breeding methods and environment-specific strategies, it is possible to develop livestock populations that are both resilient to diseases and economically viable, ensuring sustainable animal health, productivity, and food security (Gao et al., 2023).

Conclusion

Breeding for disease resistance has proven to be a sustainable and effective strategy for improving livestock health, productivity, and food security. Traditional selection methods, based on observable traits such as faecal egg counts in sheep or somatic cell counts in dairy cattle, laid the foundation for genetic improvement. Advances in genomics, marker-assisted selection, and genomic selection have significantly enhanced the precision and efficiency of identifying disease-resistant animals. Modern gene editing technologies, including CRISPR/Cas9, base editing, and prime editing, now provide unprecedented opportunities to introduce or modify genes associated with resistance. Evidence from nematode-resistant sheep, mastitis-resistant cattle, and disease-resistant poultry confirms that selective breeding for disease resistance is a practical and globally relevant strategy.

References

- Gogoi, A., Das, B., Chabukdhara, P., Phookan, A., & Phangchopi, D. (2022). Livestock breeding for disease resistance: a perspective review. *Agricultural Reviews*, 43(1), 116-121.
- Liu, K., Zhang, B., Teng, Z., Wang, Y., Dong, G., Xu, C., ... & Zhang, Y. (2017). Association between SLC11A1 (NRAMP1)

- polymorphisms and susceptibility to tuberculosis in Chinese Holstein cattle. *Tuberculosis*, 103, 10-15.
- Mugambi, J. M., Wanyangu, S. W., Bain, R. K., Owango, M. O., Duncan, J. L., & Stear, M. J. (1996). Response of Dorper and Red Maasai lambs to trickle *Haemonchus contortus* infections. *Research in Veterinary Science*, 61(3), 218-221.
 - Pal, A., & Chatterjee, P. N. (2009). Molecular cloning and characterization of CD14 gene in goat. *Small Ruminant Research*, 82(2-3), 84-87.
 - Pal, A., Sharma, A., Bhattacharya, T. K., Chatterjee, P. N., & Chakravarty, A. K. (2011). Molecular characterization and SNP detection of CD14 gene of crossbred cattle. *Molecular biology international*, 2011(1), 507346.
 - Shook, G. E., & Schutz, M. M. (1994). Selection on somatic cell score to improve resistance to mastitis in the United States. *Journal of Dairy Science*, 77(2), 648-658.
 - Snowden, G. (2006, April). Genetic selection for disease resistance: challenges and opportunities. In *Beef Improvement Federation Conference Proceedings* (Vol. 38, pp. 52-60).
 - Stear, M. J., Bishop, S. C., Mallard, B. A., & Raadsma, H. (2001). The sustainability, feasibility and desirability of breeding livestock for disease resistance. *Research in veterinary science*, 71(1), 1-7.
 - Tan, R., Krueger, R. K., Gramelspacher, M. J., Zhou, X., Xiao, Y., Ke, A., ... & Zhang, Y. (2022). Cas11 enables genome engineering in human cells with compact CRISPR-Cas3 systems. *Molecular cell*, 82(4), 852-867.
 - Terefe, G., Lacroux, C., Andréoletti, O., Grisez, C., Prévot, F., Bergeaud, J. P., ... & Jacquet, P. (2007). Immune response to *Haemonchus contortus* infection in susceptible (INRA 401) and resistant (Barbados Black Belly) breeds of lambs. *Parasite immunology*, 29(8), 415-424.
 - Uribe, H. A., Kennedy, B. W., Martin, S. W., & Kelton, D. F. (1995). Genetic parameters for common health disorders of Holstein cows. *Journal of dairy science*, 78(2), 421-430.
 - Whitworth, K. M., Rowland, R. R., Ewen, C. L., Tribble, B. R., Kerrigan, M. A., Cino-Ozuna, A. G., ... & Prather, R. S. (2016). Gene-edited pigs are protected from porcine reproductive and respiratory syndrome virus. *Nature biotechnology*, 34(1), 20-22.
 - Woolaston, R. R., Elwin, R. L., & Barger, I. A. (1992). No adaptation of *Haemonchus contortus* to genetically resistant sheep. *International Journal for Parasitology*, 22(3), 377-380.