

# Genomic Approaches for Enhancing Disease Resistance and Climate Adaptation in Livestock

Carlos Eduardo de Carvalho Silva Oliveira\*, Raissa Pereira de Oliveira, Pedro Henrique Gonçalves de Carvalho

Department of Clinical and Veterinary Surgery, School of Veterinary Medicine, Federal University of Minas Gerais (UFMG), Belo Horizonte, Minas Gerais, Brazil

## INTRODUCTION & AIM

Climate change poses critical and escalating challenges to livestock productivity and welfare, especially within tropical and subtropical ecosystems. Genomic technologies have emerged as state-of-the-art, powerful tools capable of concurrently enhancing both disease resistance and environmental adaptability. Therefore, the primary aim of this review is to synthesize high-impact evidence from recent studies evaluating genomic adaptation and disease resilience across key livestock species, including cattle, sheep, goats, and pigs.

## METHOD

This study systematically evaluates evidence from seven recent, high-quality investigations addressing genomic adaptation under climate-induced stress. The methodological frameworks applied in the selected works include genome-wide association studies (GWAS), single nucleotide polymorphism (SNP) mapping, transcriptomic profiling, and selection signature analysis. These advanced approaches were critically analyzed in the context of major climate-related stressors, specifically focusing on heat tolerance, pathogen pressure, and overall environmental variability.

## RESULTS & DISCUSSION

Across the evaluated species, our analysis consistently identified critical genomic regions fundamentally associated with both heat stress tolerance and robust immune responses. In heat-adapted cattle populations, definitive selection signatures were found in essential thermoregulatory and oxidative stress-response genes, most notably *TRPM8*, *HSP70*, and *SOD2*.

The prominent expression of these genes underscores a vital genetic mechanism for maintaining cellular homeostasis under extreme thermal challenges. Furthermore, the application of advanced landscape genomics in caprine models has successfully established a direct link between climate adaptation and distinct immune-related loci, suggesting a complex evolutionary adaptation linking environmental survival and pathogen resistance. Similarly, robust studies in pigs and sheep have demonstrated that phenotypic resilience to polymicrobial diseases and severe weather variation is a highly heritable trait. This indicates that these complex traits are deeply embedded within the genetic architecture and can be selectively enhanced. Collectively, the integration of these sophisticated genomic tools provides an unprecedented resolution for identifying adaptive variants, thereby establishing a highly effective and scientifically rigorous pathway to accelerate the breeding of climate-resilient herds without compromising health or productivity.

## CONCLUSION

Genomic tools provide an unparalleled capacity to identify adaptive variants and accelerate precision breeding for combined resilience against infectious diseases and climate stress. Consequently, genomic-based breeding represents a highly sustainable and indispensable strategy to secure global livestock productivity and significantly improve animal welfare in the face of escalating climate change.

## FUTURE WORK / REFERENCES

Future advancements must prioritize the integration of multi-omics datasets and the expansion of large-scale genomic databases to further optimize precision livestock adaptation strategies. The insights presented in this review are grounded in foundational literature, including Boettcher et al. (2015), Knap & Doeschl-Wilson (2020), and pivotal recent genomic studies published between 2020 and 2024.