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Strategic Breeding for Parasitic Resistance in Sheep

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Abstract

Gastrointestinal nematodes (GINs) present a major challenge to global sheep and small ruminant production, with infections from parasites such as *Haemonchus contortus* leading to considerable economic losses. Dependence on anthelmintics has led to drug-resistant nematodes, underscoring the need for sustainable alternatives. Breeding for genetic resistance is a promising strategy, leveraging natural variation in resistance across sheep breeds. An integrated approach combining selective breeding, improved grazing practices, nutrition, and targeted anthelmintic use is key. Selection focuses on traits such as growth rate under parasite challenge, faecal egg count (FEC), and anaemia indicators. Ultimately, breeding for resistance offers lasting resilience against nematodes, reducing reliance on anthelmintics and minimizing pasture contamination in affected areas.

Key words: GINs; Anthelmintic resistance; Selective breeding; Sustainable parasite control

Introduction

Small ruminant farming, especially in low-input systems, is critical for sustainable global food security, as sheep effectively convert short pasture into meat, providing food, income, and non-market benefits. However, gastrointestinal nematodes (GINs) impose severe constraints, reducing productivity and impacting smallholder livelihoods. Control traditionally relies on anthelmintics, but widespread drug resistance and environmental residues limit effectiveness and sustainability. Many resource-constrained farmers, particularly in tropical and subtropical areas, lack access to new anthelmintic treatments or adequate grazing management practices. Consequently, genetic improvement is emerging as a viable and sustainable alternative, leveraging inherent resistance traits to bolster sheep resilience against GINs. This approach can minimize reliance on chemical treatments, providing a long-term strategy for parasite management and enhancing food security for smallholder farmers. This paper focuses on gastrointestinal parasitism, anthelmintic resistance, alternative methods of parasite control in these farming systems, with genetic improvement offering a more sustainable option.

Gastrointestinal Parasitism

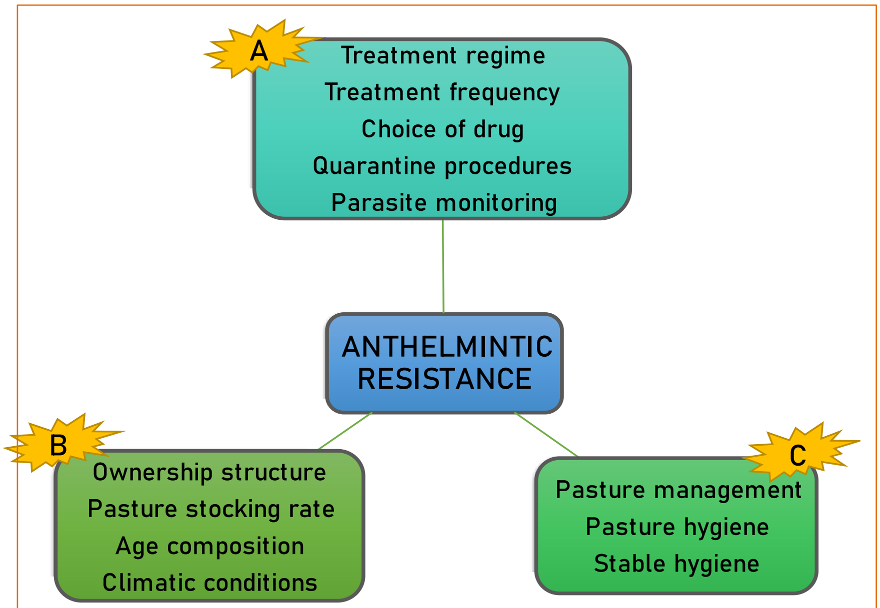


Figure 1: Factors influencing anthelmintic resistance in livestock

Gastrointestinal nematodes (GINs) are a significant health threat to ruminant livestock worldwide, notably reducing productivity in sheep through infections caused by species like *Haemonchus contortus*, *Teladorsagia circumcincta*, and *Trichostrongylus colubriformis*. These parasites infect the abomasum and small intestine, causing anaemia, hypoproteinaemia, and weight loss, which can lead to reduced productivity, high cortisol levels, and occasionally, death. Lesser-known species like *Nematodirus spp*. and *Strongyloides papillosus* have a minor economic impact but can also affect sheep health. Globally, GIN infections cause tens of billions of dollars in losses, including costs associated with anthelmintics, veterinary care, and lower growth and production rates. The repetitive and sometimes improper use of anthelmintics has led to widespread resistance among GIN populations, challenging effective parasite control. This resistance underscores the need for alternative strategies, such as selective breeding for resistance, to sustainably manage GIN infections and reduce reliance on limited anthelmintic options.

Anthelminthic Resistance

Nematode control faces challenges due to the parasites’ adaptations to changing climates, management practices, and the misuse of anthelmintic drugs. With large genomes, numerous genes, high polymorphism, and reproductive strategies favouring rapid population growth, nematodes easily adapt to both favourable and adverse conditions. Environmental shifts impact their free-living stages, while drug exposure accelerates resistance in parasitic stages. Growing concerns over food safety and environmental pollution underscore the urgency to find alternatives to reduce reliance on anthelmintics. The overarching goal of control methods is to limit nematode burden to a level that maintains host health and performance while fostering natural protective immunity.

Breeding For Parasitic Resistance

Selection Approach

The use of GIN-resistant animals in breeding is a longstanding strategy, modelled after natural selection, where resistant animals survive and reproduce, passing on traits that help combat infections. Certain sheep breeds worldwide, such as Santa Inês, Morada Nova, Katahdin, St. Croix, and Red Maasai, show natural GIN resistance. For susceptible breeds, selecting animals with greater resistance is possible due to genetic variation within populations. Traits like faecal egg count (FEC), haematocrit (HCT), packed cell volume (PCV), immunoglobulin levels, and FAMACHA scores are used to assess resistance. FEC, a reliable measure of GIN resistance, is especially favoured, as animals with lower FEC shed fewer eggs, thus reducing pasture contamination. The resistance trait is polygenic, making it difficult for parasites to overcome through adaptation. Conventional breeding strategies, while effective, are often costly and require significant infection levels to reveal genetic variation in FEC. Heritability of FEC ranges from low to high (0.01–0.65), indicating genetic gain potential through selection. Thus, breeding for GIN resistance in small ruminants offers a sustainable path to reduce reliance on anthelmintic drugs and mitigate parasite impacts on production.

Markers Associated with Host Gastrointestinal Parasite Resistance

A. QTLs Associated with Parasitic Resistance

Quantitative trait loci (QTL) mapping can help understand parasite resistance's complexity by identifying candidate genomic regions. Candidate gene studies and microarray and gene association studies have also been conducted in several small ruminant breeds to identify genes involved in the control of resistance and susceptibility. Several QTLs on different regions and chromosomes (OARs) have been reported in the literature for sheep, indicating a polygenic nature for the trait (OAR1, 3, 6, 14, and 20)

B. Candidate Gene Approach

Interest in the genetic basis for host resistance to gastrointestinal parasites was sparked by early observations of host resistance. Genetic selection offers cumulative, permanent gains and promotes sustainable resistance, helping to reduce reliance on anthelmintics. The candidate gene approach, used to identify DNA markers within genes linked to resistance, has identified key genes regulating immune responses, notably within the major histocompatibility complex (MHC) and interferon gamma (IFNG) genes. These genes, located on chromosomes OAR20 and OAR3, are associated with immune functions such as T-cell activation and cytokine responses. MHC genes are especially polymorphic and crucial for presenting antigens to T-cells, triggering immune responses against parasites. Despite the potential of QTL in advancing genetic progress, identifying major QTL for GIN resistance remains challenging since it appears to be a polygenic trait with many small-effect loci spread across the genome. Efforts continue with standard approaches that link resistance traits to polymorphisms in candidate genes, focusing on understanding the molecular mechanisms underlying anthelmintic resistance and advancing selective breeding strategies for improved resilience.

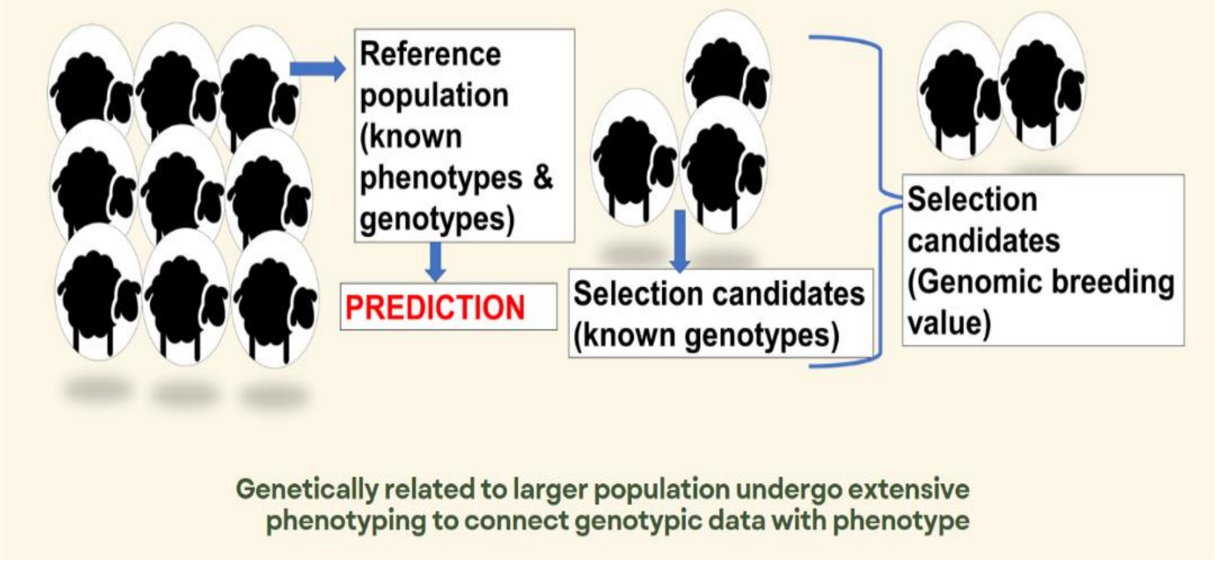
Genome Wide Association Studies

Genome-wide association studies (GWAS) analyse genetic variants like single nucleotide polymorphisms (SNPs) across populations to identify those associated with specific traits. Unlike previous methods, GWAS scans the entire genome without assumptions, reducing bias and improving reliability. Useful in both pedigreed and case-control studies, GWAS identifies genomic regions tied to traits such as faecal egg count (FEC) in sheep. A comprehensive tool, the OvineSNP50 Bead Chip, developed by Illumina with the International Sheep Genomics Consortium, covers 54,000 SNPs across the ovine genome and aids various applications in sheep genomics. Additionally, the OvineSNP600k chip, with 603,350 SNPs, further supports GWAS by enhancing SNP analysis across diverse breeds and traits.

Figure 2: Affymetrix Gene Chip used for high-throughput genomic analysis in livestock breeding.

Genomic Selection

Traditional genetic improvement programs rely on phenotypes and pedigrees to calculate estimated breeding values (EBVs). With the rise of SNP markers, it's now possible to compute genomic estimated breeding values (GEBVs) for traits like parasite resistance, provided there are adequate genotypic and phenotypic data. Understanding the genetic architecture of resistance enables risk prediction and selective breeding. Genomic selection, uses SNPs across the genome to predict complex traits, especially polygenic ones. The accuracy of these predictions depends on reference population size, genetic variance explained by markers, effective population size (Ne), and SNP chip density. To ensure reliable genomic prediction, the evaluation population should be closely related to the reference group.



Genetically related to larger population undergo extensive phenotyping to connect genotypic data with phenotype

Figure 3: Illustration of genomic breeding value estimation in livestock breeding

Conclusion

Breeding small ruminants with enhanced resistance to gastrointestinal nematodes (GINs) offers a sustainable approach to parasite control, reducing reliance on anthelmintics, treatment costs, and environmental contamination. Implementing genetic strategies, such as selecting for resistance and utilizing targeted selective treatments (TSTs), leverages the heritable nature of GIN resistance found across sheep population. In tropical regions, where phenotypic selection may be more feasible, identifying resistant breeds and evaluating traits like faecal egg counts (FEC) and anaemia under parasite pressure are effective steps forward. Advances in genomic tools and the decreasing cost of sequencing offer promising avenues for GIN-resistant breeding in low-input systems through SNP-based genetic markers. Countries incorporating genomic data into breeding programs have demonstrated accelerated genetic gains, reinforcing breeding as an effective strategy to combat anthelmintic resistance in livestock. Ultimately, combining selective breeding with improved grazing management, nutrition, and vaccination can create resilient flocks while contributing to sustainable, long-term parasite control.

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