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Review of Crossbreeding Methods in Lamb Production

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ABSTRACT

Optimising lamb production necessitates a comprehensive understanding of the relationship between genotype, nutritional inputs, and breeding methodologies in guiding growth performance, carcass traits, and overall productivity. The practice of crossbreeding, utilising heterosis and breed combination, is a reliable method of enhancing average daily gain, feed conversion rates, dressing percentages, and carcass traits. Research findings highlight the positive outcomes of crosses with these advantages further enhanced under high-energy and concentrate-rich feeding regimens. Advancements in reproductive biotechnologies, including in vitro embryo production, multiple ovulation and embryo transfer, and embryo cryopreservation, have significantly contributed to the proliferation of superior genetic lines and the minimisation of generation intervals. The development of genomic selection, marker-assisted breeding, and gene-editing technologies such as CRISPR/Cas9 has enabled advances in traits including prolificacy, carcass traits, wool characteristics, and disease resistance. The integration of genomic data with phenotypic and multi-omics datasets has enhanced selection accuracy, thereby generating opportunities for the development of customized breeding strategies to specific production systems. However, the effective application of these techniques must overcome several limitations. Financial concerns related to genotyping, the limited availability of crossbred reference groups, and the complexity of protecting genetic variation across different breeds and systems are significant difficulties. Also, the relationship between genotype and both nutrition and environmental factors necessitates careful evaluation to ensure the reliable expression of genetic potential in various management practices. A methodical breeding strategy that integrates phenotypic, genomic, and environmental data can lead to significant improvements in genetic gain, enhanced sustainability, and optimized lamb production based on market and welfare standards.

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Introduction

Research on the differences in nutrition, growth, carcass quality, and crossbreeding technologies of domestic versus crossbred lambs is critical to optimizing lamb production systems and meeting consumer demands. In earlier studies, researchers established basic knowledge on breed-specific growth and carcass traits, emphasizing the effect of genotype and nutrition on lamb performance (Lewis et al. 2004; Speijers et al. 2009). Historically, research focused on specific production systems, feeding regimens, and crossbreeding strategies. However, as global sheep production becomes increasingly complex, research programs are adapting to encompass a broader range of factors (Theron et al. 2024).

The practical significance of this field is underscored by the economic importance of lamb meat. Lamb meat is a valuable product, and crossbreeding shows potential to enhance growth rates, carcass yield, and meat quality. Therefore, crossbreeding shows promise in improving producer profitability and sustainability (Claffey et al. 2018; Issakowicz et al. 2018). For instance, crossbred lambs commonly show higher dressing percentages and carcass conformation in comparison to purebreds. This aligns with market preferences for leaner, well-muscled carcasses (Theron et al. 2024).

Research shows challenges in understanding how genotype, nutrition, and crossbreeding affect lamb growth and carcass traits under different production conditions. Some studies report significant genotype × diet interactions affecting growth and feed efficiency (Hegarty et al. 2006; Speijers et al. 2009). Others emphasize the role of feeding systems in modulating carcass fatness and meat quality (Huang et al. 2023).

The conceptual framework defines nutrition as the plane and composition of feed influencing growth and carcass development. Growth is defined as the rate of liveweight gain and meat production. Carcass quality is defined as the composite of yield, conformation, and fatness. Finally, crossbreeding technologies are defined as genetic strategies to combine desirable traits from different breeds (Claffey et al. 2018; Speijers et al. 2009). These concepts are associated with nutritional factors that affect the expression of genetic potential for growth and carcass traits. Crossbreeding, on the other hand, utilizes heterosis to enhance performance. Comprehension of these associations is imperative to assess the differences in production outcomes between native and crossbred lambs and to inform breeding and feeding practices (Annett et al. 2011; Hegarty et al. 2006).

Recent technological advancements combine molecular genetics and reproductive biotechnologies, such as gene editing and embryo transfer, to increase genetical gains (Falchi et al. 2022; Zhang et al. 2025). Nevertheless, there are still knowledge gaps regarding the integration of traditional crossbreeding with emerging molecular tools, the heterosis effects on growth and prolificacy, and the management of genetic mosaicism in edited animals (Ledesma and Eenennaam 2024; Salvesen et al. 2024; Vargas Jurado et al. 2022).

The objective of this comprehensive review is to synthesize current scientific knowledge on the differences in nutrition, growth, carcass quality, and crossbreeding technologies between native and crossbred lambs. Moreover, this study aims to clarify the interactive effects of genotype and nutrition on lamb performance and to assess the efficacy of crossbreeding strategies in diverse production systems. This review contributes to the existing body of knowledge by synthesizing the findings from multiple studies. Consequently, it addresses existing knowledge gaps and informs practical applications in lamb production.

Chronological Review

Research on sheep breeds and crossbreeding methods has advanced considerably over the decades, with initial studies focusing on fertility, reproduction, and survival rates in purebred and crossbred sheep. The development of genetic evaluation techniques has led to a shift in focus to the quantification of the effects of breeds on growth, carcass quality, and reproductive traits under various management systems. Recent research has integrated genomic tools, environmental adaptation, and farmer perceptions in order to optimise crossbreeding strategies for the purpose of achieving sustainable agricultural productivity. Crossbreeding strategies are increasingly designed to balance productivity gains with genetic diversity and environmental resilience. In preliminary studies (Table 1), the focus was on fertility, reproductive performance, and lamb survival in purebred and crossbred sheep. It was observed that improvements in reproductive performance and growth occurred with two- and three-way crossbreeding. Genetic effects, including heterosis, maternal ability, and breed-specific traits, were identified as the primary factors affecting growth and survival metrics. Research conducted between 1981 and 2000 was expanded to cover a wider range of breed and crossbreeding combinations, to evaluate carcass traits, growth rates, and reproductive performance. Mating and crossbreeding programs were used to evaluate additive and non-additive genetic effects, and the findings support the use of specific terminal breeding breeds to increase meat production and lamb growth. Following 2001, an increasing number of studies utilized national and regional genetic evaluation programs to assess crossbred lamb production in different grazing and feeding systems. Growth, carcass traits, wool traits, and reproductive performance were measured under changing environmental conditions, thereby highlighting the importance of breed selection and maternal genetics.

Since 2011, research has focused on the optimisation of crossbreeding strategies that combine native and exotic breeds, with a particular emphasis on specific regional conditions such as semi-arid climates and intensive and extensive production systems. The practical benefits of crossbreeding include improvements in growth rates, lamb survival, carcass quality, and reproductive traits, as well as addressing challenges related to breed compatibility and management. Recent research combines genomic tools, machine learning, and community-based breeding programs to enhance the sustainability and efficiency of breeding programs. In developing regions, particular emphasis is placed on environmental adaptability, the preservation of genetic diversity, and socioeconomic factors that influence the success of breeding programs in various agricultural contexts.

Crossbreeding Methods

Crossbreeding can enhance various traits, including growth, carcass yields, and overall production efficiency. These enhancements result from the combination of distinct genetic traits within the crossbreeding process, a phenomenon referred to as heterosis or the superior performance of crossbreds relative to their purebred counterparts. Additionally, breed complementarity, where the characteristics of different breeds are selectively combined to optimize specific performance traits, can contribute to enhanced efficiency in crossbreeding. (Bizjak and Cividini 2020; Paim et al. 2019; Theron et al. 2024).

Table 1. Chronological review of crossbreeding strategies.

Year Range	Research Direction
1970 – 1980	Foundational Crossbreeding Evaluations
1981 – 2000	Expansion of Breed Comparisons and Crossbreeding Effects
2001 – 2010	Genetic Evaluation and Production System Integration
2011 - 2020	Practical Applications and Regional Breed Adaptations
2021 - 2025	Integration of Genomics, Sustainability, and Farmer Perspectives

Various crossbreeding schemes, including terminal and maternal crosses, are evaluated for their impact on lamb growth efficiency and carcass quality. Crossbreeding with specialized meat breeds improves production traits and offers the potential to adapt to local breeds, enhancing performance (Annett et al. 2011; Boujenane 2015; Paim et al. 2019).

Phenotypic methods

Producers seeking to optimize their livestock production systems can take advantage of the complementary traits exhibited by different breeds to reduce finishing periods and enhance saleable meat production. Nutritional management is critical to realizing genetic potential. Across genotypes, concentrate-based or high-energy diets have been shown to consistently improve growth performance and carcass traits, suggesting that feeding strategies should be optimized alongside genetic selection to maximize returns. (Huang et al. 2023; Speijers et al. 2009; Tariq et al. 2024).

A number of studies indicate that crossbred lambs generally show higher average daily and live weight gains than purebreds. Breed-specific differences show superior growth rates, as shown by Texel and Suffolk crosses (Bizjak and Cividini 2020; Blasco et al. 2019; Speijers et al. 2009). In other studies, nutritional status and dietary composition were found to have a significant effect on growth performance. Diets with high energy or concentrate content led to increased growth rates across all genotypes. A number of studies emphasized genotype-by-nutrition interactions, whereby genetic potential for growth was more fully expressed under optimal nutritional conditions (Hegarty et al. 2006; Tariq et al. 2024).

Speijers et al. (2009) found that crossbred lambs showed higher growth rates, especially Texel crosses under conditions of high nutrition. The correlation between dressing percentage and fatness was found to vary according to genotype, with Texel crosses exhibiting the optimal conformation. The highest feed efficiency was observed in the Texel and Cheviot crosses. Crossbreeding resulted in significant improvements in growth and carcass traits. On the other hand, high level nutritional content significantly increased growth and fatness, while oilseed rape had no significant effect.

As stated in the study by Bizjak and Cividini (2020), the results indicated that Texel crossbreeding had a positive effect on growth and carcass characteristics. The crossbreds had higher daily gains, with males growing at a faster rate than females. Crossbreds were found to have higher dressing percentages, superior conformation, and larger rib eye areas. It emphasizes the significance of early concentrate feeding in supporting growth.

The results of the study by Mckibben et al. (2019) found that composite breeds consisting of Suffolk, Columbia, Texel, and Hampshire breeds showed similar trends in growth compared to Suffolk crosses. The carcass traits observed were consistent across both composite and Suffolk crosses. This suggests that composite breeds may be particularly suitable for use as terminal sires. The range production system affected the carcass traits.

In a study conducted by Paim et al. (2019), it was found that crossbreeds obtained from East Friesian, Santa Inês, Primera, Poll Dorset, Dorper, and White Dorper breeds reached slaughter weight faster than purebreds. The results of the study indicated that crossbreds exhibited higher carcass yields and commercial cut weights. Crossbreds were found to be particularly adaptable to intensive rearing systems.

The observed differences in growth and carcass traits between male and female lambs indicate that management and marketing strategies should consider sex-specific growth traits and carcass composition to optimize production efficiency and product quality (Bizjak and Cividini 2020; Theron et al. 2024). Finishing rams may be more profitable because of higher growth rates and carcass weights. Pasture-based finishing systems, particularly combined with crossbreeding, result in carcasses that satisfy consumer preferences for meat tenderness and quality. This makes them a suitable alternative to intensive feedlot systems (Armero and Falagán 2015; Theron et al. 2024). Consequently, it is imperative to consider the implications of these findings on sustainable production and marketing strategies, with a particular emphasis on animal welfare and product differentiation.

Vargas Jurado et al. (2022) reported that maternal age had a significant and positive effect on the birth and weaning weights of purebred and crossbred lambs. However, the predicted effect at birth was more pronounced in crossbred and Suffolk lambs. It was observed that both birth and rearing litter size had a significant negative effect on both traits. Lambs born and reared as twins or triplets showed lower birth and weaning weights compared to singletons. The effect size was consistent across breeds. Although environmental variances at birth and weaning were similar across breed types, additive genetic variances differed, with measurable heterogeneity observed among purebred and crossbred groups. This finding indicates that breed-specific genetic variation exerts an influence on trait expression and should, as a result, be considered in evaluation models. The integration of crossbred data with purebreds in genetic evaluations led to an enhancement in the accuracy of sire estimated breeding value (EBV) estimates. The collaborative evaluation enabled a direct comparison of purebred sires from different breeds, thereby enhancing the ability to estimate genetic value.

Heterosis

The level of heterosis observed varies among crosses, with some resulting in reduced fat deposition, while others produce higher levels of internal fat. (Issakowicz et al. 2018; Khaldari et al. 2008). The effect of genetic origin and crossbreeding strategies on meat quality and carcass composition is a subject of considerable interest (Khaldari et al. 2008; Paim et al. 2019). The level of heterosis, or the expression of heterotic characteristics in crossbreeding, is affected by parental breed combinations, heterozygosity levels, and production environments. Variation in experimental breeds and crossbreeding objectives also lead to variations in outcomes.

Vargas Jurado et al. (2022) present a robust multi-breed, multi-trait genetic evaluation framework that directly models both purebred and crossbred data, taking heterosis effects into clear consideration. In their study, the researchers developed a paternal line and quantified both direct and maternal heterosis. The results indicated that

crossbred lambs from breeds such as Suffolk, Columbia, Texel, Polypay, Rambouillet, and Targhee showed birth weights that were around 5% greater than those of purebreds. Furthermore, these crossbred lambs showed post-weaning weights that were up to 10% greater than those of purebreds.

Embryo

The development of advanced embryo-based technologies for the purpose of lamb breeding was a significant milestone in the field. In vitro embryo production (IVEP) using oocytes collected from post-mortem or live donor ewes or pre-pubertal lambs enables the controlled production of embryos from selected genotypes (Baldassarre 2021; Leoni et al. 2015). The utilisation of pre-pubertal lambs is a highly effective technique to reduce generation interval and increase genetic gain. As another technique to maximise the cumulative embryo yield per cycle, refined superovulation and oocyte recovery protocols in donor ewes can be useful (Grasa et al. 2004). Furthermore, IVM (in vitro maturation), IVF (in vitro fertilisation) and IVC (in vitro culture) systems can be optimised for sheep genotypes, ovarian status and donor age to improve blastocyst rates (ranging from 15-79%) and thus increase embryo transfer success (Zhu et al. 2018). The integration of embryo cryopreservation and transfer methodologies is a key aspect of the strategy aimed at enhancing the genetics of elite individuals, supporting the formation of combined or cross-breed flocks, and promoting the conservation of breeds (Shirazi et al. 2010). The integration of controlled embryo production and transfer mechanisms is a key aspect of these technologies, collectively facilitating the efficient and large-scale proliferation of superior lamb genetics and hybrid lines (Falchi et al. 2022).

In recent decades, reproductive biotechnologies such as artificial insemination, multiple ovulation and embryo transfer (MOET), and IVF have evolved from experimental procedures to commercially viable tools that accelerate genetic gain and reduce generation intervals (Dhangada et al. 2024; Fleming et al. 2018). A wide range of animal species, including cattle, sheep, goats and poultry, can be used as subjects in the application of these technologies. The results of research in this field demonstrate that the use of these technologies can improve reproductive performance and contribute to sustainable livestock production (Daly et al. 2020). For instance, the global application of MOET has enabled the production of over one million bovine embryos yearly, emphasising its significance in genetic dissemination (Lonergan and Sánchez 2022). The social and economic importance of these technologies is further emphasised by their role in enhancing animal welfare, reducing disease transmission, and supporting ethical breeding practices (Mankad et al. 2022; Otoikhian et al. 2022).

Assisted reproductive technologies must be complemented by optimal nutrition, effective healthcare, and environmentally sustainable practices in small ruminant production systems. The integration of marker-assisted selection with cross-breeding leads to an enhancement in the efficiency of selection, accomplished through the utilisation of markers rather than phenotype for the purpose of trait selection. Breeding strategies like artificial intelligence, selective breeding and IVF can accelerate genetic progress and improve lamb production (Ghosh et al. 2024).

Khan et al. (2022) stated several key findings, indicating the efficacy of various strategies designed to enhance MOET outcomes in ovine subjects. Immunization against inhibin led to a significant increase in the number of corpora lutea (CL) and transferable embryos. Specifically, treated ewes exhibited 14.0 CL and 6.3 transferable embryos per donor, while the control group showed 7.4 CL and 2.9 embryos. Melatonin implants also had a positive effect; in-season implantation resulted in an increase in CL count (13.4 vs. 8.8) and improved pregnancy (64.6% vs. 41.5%) and lambing rates (56.6% vs. 30.2%). The study found that the use of recombinant FSH (roFSH) in a single-dose protocol resulted in a comparable superovulatory response to conventional porcine FSH, with an average of 10.3 CL and 5.1 embryos per donor.

Genomic methods

Research on genomic methods in sheep crossbreeding stands as a significant area, given its capacity to improve genetic gain, enhance production traits, and optimize livestock breeding efficiency (Burrow and Goddard 2023; Zhang et al. 2024). The field has evolved from conventional marker-assisted selection (MAS) to more advanced genomic selection and gene-editing technologies, such as CRISPR/Cas9. This evolution signifies a considerable technological advancement over the past several decades (Sharma et al. 2024). These genomic approaches have gained practical significance as they enable more exact and efficient genetic improvement, which is essential to meet increasing global demands for animal protein and to adapt to environmental changes (Yáñez et al. 2022). Genomic selection is a breeding method that involves the use of molecular markers to select animals based on their genetic characteristics. This method is increasingly being adopted by sheep breeding programs worldwide due to its proven advantages over traditional methods in terms of accuracy and efficiency (Ibtisham et al. 2017; Martin et al. 2024).

In a study by Surov et al. (2023), it was concluded that the PCR-RFLP method is an effective means of identifying polymorphic variants in key genes growth hormone (GH), calpastatin (CAST) and growth differentiation factor 9 (GDF9) associated with quantitative traits in crossbred lamb populations, such as Russian meat merino crossed with Charollais, Ile-de-France, Poll Dorset, or other breeds. It was observed that lambs carrying favourable alleles, such as GHB, CASTN, and GDF9A genotypes, exhibited significantly higher live-weight gains at 2, 4, and 8 months. These lambs gained up to 10% more at 2 months and 6% more at 8 months. The study further indicates that animals possessing complex favourable genotype combinations (e.g., GHAB Moreno+ GDF9AA) exhibited live weights of 14.8–15.3 kg at 2 months and up to ~34–35 kg by 8 months, in comparison to lower-weight peers. The findings of this study emphasise the effectiveness of genomic selection and marker-assisted crossbreeding as tools for promoting genetic progress in the breeding of lambs. Thereby, these methods optimise both the growth performance and breed composition of the lambs, thus eliminating the reliance on phenotypic selection as the sole method of breeding.

In recent years with CRISPR-Cas application, targeted insertion of the Booroola fertility allele (FecB, BMPR1B) via CRISPR-Cas9 to improve reproductive performance in sheep (Zhou et al. 2023); knockout of the FGF5 gene to extend wool fiber length and density, increase cashmere or wool yield (Li et al. 2017); editing of growth-related genes (MSTN) (Guo et al. 2023; Zhou et al. 2023); alterations in lactation-related genes aimed at improving milk production traits (Ma et al. 2017); CRISPR-based edits in immunity-related genes to improve disease resistance in sheep (Eaton et al. 2019).

A recent work by Zhang et al. (2025) presents the generation and proliferation of fine-wool sheep edited with the FecB (BMPRIB) high-fecundity allele via CRISPR/Cas9-mediated homologous-directed repair (HDR). These findings are of particular relevance to the fields of sheep reproduction, crossbreeding, and management strategies, particularly with regard to prolificacy without compromising wool quality. In the study it was reported a high precision (≥31.6% editing rate) without compromising wool quality. This approach provides a compelling alternative – or complement – to traditional crossbreeding, allowing rapid, targeted enhancement of key reproductive traits.

In another study, Zhou et al. (2023) reported the first utilisation of prime editing (PE) in livestock, specifically sheep and pigs, with the aim of targeting economically significant mutations. FecB, in the sheep BMPR1B gene, is associated with enhanced prolificacy, and TBXT, associated with the short-tailed phenotype in sheep. Furthermore, the KCNJ5 mutation was induced in porcine blastocysts, with the aim of using this as a biomedical model. The study reported that sheep with two single base conversions at two different loci and pig blastocysts with two single base conversions in a single target gene were produced with high precision. The efficiency of defined point mutations was found to be 71.4% (5/7) at the animal level, and the editing frequency was reported to be as high as 14.7%. The editing efficiency for pig fibroblasts was found to reach up to 5.2%, but this did not match the efficiencies reported for other species.

Recent genome-wide association studies and genetic parameter estimations offer valuable insights into the heritability and genetic markers associated with carcass traits. These results support the potential for genomic selection in crossbred lambs (Kaseja et al. 2023; Stratz et al. 2018). The integration of molecular data with phenotypic traits has been demonstrated to enhance the accuracy of breeding programs.

Genome-wide association studies and genetic evaluation methods are increasingly being applied to crossbred lambs to identify loci associated with carcass traits and to improve breeding value estimations. These studies reveal polygenic models with moderate heritabilities for growth and carcass traits, emphasizing the necessity of integrating crossbred data for accurate genetic evaluation and selection (Kaseja et al. 2023; Lewis and Brown 2022; Vargas Jurado et al. 2022).

Recent researches combine genome-wide association studies with advanced carcass phenotyping techniques, including video image analysis and computed tomography, to identify genetic markers associated with carcass composition. The potential impact of genotype-by-Nutrition interactions on ruminal microbiota, metabolome, and growth performance is under consideration. The emphasis of the breeding program is on improving feed efficiency, reducing finishing periods, and optimizing carcass quality through the combined management of genetics and nutrition. The integration of advanced phenotyping techniques, including computed tomography (CT) and video image analysis (VIA), offers a more comprehensive understanding of carcass composition and the genetic factors that affect lean meat yield and fat distribution. (Gobbi et al. 2024; Kaseja et al. 2023). The employment of sophisticated phenotyping methodologies, including computed tomography (CT) and video image analysis (VIA), facilitates a more precise comprehension of carcass composition and the genetic underpinnings that influence the yield and distribution of lean meat. These technologies validate and extend classical carcass evaluation methods. As such, technology offers new opportunities for genetic selection and carcass quality improvement.

The polygenic nature of carcass traits, along with the relatively limited effect sizes of identified markers, has the potential to limit the practical uses of these traits in breeding schemes (Kaseja et al. 2023). As indicated by Kaseja et al. (2023) and Stratz et al. (2018), breed-specific genetic variations complicate the validation and transferability of markers. Further research is necessary to establish a connection between molecular findings and the development of practical breeding strategies.

Genomic and Phenotypic Integration

Recent studies show that integrating transcriptomic, epigenomic, and metabolomic data with genomic information has the potential to improve phenotype prediction and facilitate a more comprehensive understanding of biological mechanisms. Tissue-specific gene expression data can enhance the predictive abilities for certain traits (Li et al. 2024; Zhao et al. 2024).

Studies consistently indicate that accounting for population stratification and genetic diversity in crossbred sheep is imperative to avoid bias and enhance genomic analyses. Principal component analyses and admixture mapping methods are utilised to characterise genetic backgrounds and optimise reference populations (Kirichenko et al. 2022; Schmid et al. 2023). These approaches facilitate more accurate genomic predictions and marker discovery.

The application of genomic best linear unbiased prediction (GBLUP), Bayesian methods, and single-step GBLUP (ssGBLUP) techniques is known to enhance the precision of breeding value estimation, particularly when incorporating high-density genotypes and imputed whole-genome sequence data (Chen et al. 2020). Models accounting for additive and dominance effects can increase the accuracy of crossbred populations. The potential of multi-breed and combined reference populations to enhance prediction across breeds has been explored (Moghaddar et al. 2014).

The integration of genomic information into routine genetic evaluations, via methods such as ssGBLUP and selection index blending, is widely reported across numerous countries. This integration enhances the precision of genetic evaluations and reduces generation

intervals (Kaseja et al. 2023; Lewis and Brown 2022; Martin et al. 2024). Marker-assisted selection for specific traits such as growth, wool quality, and disease resistance is increasingly feasible (Surov et al. 2023). The findings of simulation studies support the cost-effectiveness of genotyping subsets of animals with a view to maximising genetic gain (Martin et al. 2024).

Nevertheless, the accuracy of predictions remains moderate and is highly dependent on the size of the reference population, the composition of the breed, and the trait inheritance (Brito et al. 2017). While inclusion of dominance and race-specific effects can enhance the efficacy of models, it tends to increase the complexity of the models and the computational requirements for their analysis. The accuracy of mixed-breed predictions is generally lower than that of purebred predictions, and the benefits of multi-breed reference populations are inconsistent. Furthermore, the integration of non-additive effects has not yet been standardised across studies (Moghaddar et al. 2014; Stock et al. 2020).

Despite the advances, the adoption of genomic selection in sheep breeding is comparatively slower than in other livestock due to higher genotyping costs relative to animal value and limited reference populations (Lewis and Brown 2022; Zhang et al. 2024). The challenges are identified as the management of large genomic datasets, the ensuring of consistent phenotyping, and the development of user-friendly tools for breeders (Kirichenko et al. 2022). The validation and evaluation of economic evaluations in various production environments remains inadequate (Martin et al. 2024).

The pooling data from multiple breeds or cross-breeds can reduce linkage disequilibrium and complicate association analyses, potentially leading to reduced power or precision (Schmid et al. 2023). When not adequately controlled, population composition may affect the accuracy of marker effect estimates because of its potential to create bias (Toosi et al. 2010). The genetic variance among breeds and crosses demands methodical configuration of training and validation sets, a practice that is frequently lacking (Schmid et al. 2023). The limitations resulting from the use of small sample sizes in certain populations are recognised as a factor that compromises the efficacy of these analyses (Deniskova et al. 2019).

Conclusion

Crossbreeding offers a viable pathway to enhance growth rate, carcass quality, and reproductive efficiency in lamb production systems, when implemented strategically. The evidence consistently supports the superiority of crossbred lambs, particularly those involving Texel, Suffolk, and Dorper breeds, in terms of achieving higher average daily gains, better feed conversion ratios, and more desirable carcass traits compared to purebred lambs. Nutritional factors, especially high-energy and concentrate-based diets, enhance these benefits and must be integrated with genetic intervention strategies.

The integration of genomic selection, transcriptomics, and advanced reproductive technologies such as in vitro embryo production and gene editing has expanded available breeding methodologies. These technological advancements provide the potential to enhance the genetic gain, reduce generation intervals, and adapt breeding objectives to regional and market-specific requirements. However, factors such as cost, infrastructure requirements, and the complexity of managing genetic diversity across breeds and production environments, limit their adoption.

It is recommended that future research should focus on the development of integrated selection indicators that combine phenotypic, genotypic and epigenetic data to improve prediction accuracy. Greater attention must also be directed toward understanding genotype-by-environment interactions, particularly under pasture-based or semi-intensive systems. In addition, ethical considerations, regulatory frameworks, and public acceptance of gene-edited animals must be addressed to ensure responsible application of emerging technologies.

Declarations

Ethical Approval Certificate

The author declares that the article does not require ethics committee approval and/or special legal permission.

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Conflict of Interest

The author declares no conflict of interest.

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