

Overcoming challenges to enable the practical implementation of genomic evaluations in sheep

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Application

The Texel is the leading terminal sire sheep breed in the UK and has significant influence on the national maternal flock. The implementation of genomic evaluations for this breed will help to predict future performance more accurately than using simple genetic pedigree information. This allows breeders to optimise the profitability of their flocks by informing animal selection and supporting breeding decisions.

There are benefits for individual animals and at the breed-level from genomic evaluations. All animals benefit from the genomic evaluation whether they have been genotyped or not, though those that have been genotyped will benefit more.

In addition, genomic information can confirm an animal's parentage where genomic data for the offspring and at least one parent is available.

Introduction

The expanding utilisation of DNA technologies in the livestock sector presents numerous opportunities to enhance genetic programs and accelerate genetic gain. However, in sheep breeding programs, the high relative cost of genotyping limits the adoption of genomic technologies to a subset of animals within a population. One effective method to address this challenge is the Single-Step Genomic evaluation (SSGBLUP), which integrates genomic data with genealogical information to assess the genetic potential of genotyped and non-genotyped animals.

This work aimed to assess the predicted and realised animal and population-level benefits of the implementation of genomics in a large commercial pedigree sheep breed.

Materials and Methods

A total of 19,494 animals were genotyped with different SNP arrays (Ovine_600K, GGP_Ovine_50K, OvineSNP50 and Ovine_15K) and imputed to 44,065 SNPs using findhap.f90 V3 software (VanRaden et al. 2011).

A quality control (QC) procedure was initiated to identify genotypes that were not suitable for inclusion, based on the approach of Kaseja et al. (2022). Parentage verification was based on 8,130 SNPs, using the 'opposing homozygote' method (Hayes, 2011) and parent-offspring pairs considered to fail if the proportion of inconsistencies were greater than 1%.

The prediction ability of SSGBLUP and pedigree-based genetic evaluation (PEDBLUP) were compared using a cross-validation method (Linear Regression (LR); Legarra and Reverter, 2018) prior to commercial release. The evaluated dataset included 1,900,000 Texel animals. SSGBLUP and PEDBLUP evaluations were conducted using a multi-trait model with nine traits: eight-week weight (8WW), scan weight (SW), muscle depth (MD), fat depth (FD), computed tomography

(CT) scan lean (CTLean), CT muscularity (CTMusc), CT fat (CTFat), CT eye muscle area (EMA) and CT-predicted intramuscular fat percentage (IMF).

Post commercial release, the realised benefits of the implementation of SSGBLUP were assessed by summarising the published breeding values, economic indices and their accuracies for animals born 2019-2023 (n=293,168).

Results

Out of the 19,494 genotypes analysed, the QC procedure identified 145 instances (0.7%) where the same animal ID was associated with a different genotype and 32 instances (0.2%) where two identical genotypes were associated with different IDs. The <1% overall error rate was acceptable. Reasons included poor genotype quality and sample mislabelling, and confirmed the importance of the QC procedure, as both technical and human errors are impossible to eradicate completely.

In total, 20,954 genotyped parent-offspring relationships were present in the data and 1,256 inconsistencies detected, suggesting a parentage error rate of 6.4%, similar to a preliminary analysis on the same population and rates observed in other UK livestock species (Kaseja et al. 2022).

Pre-release analyses were performed on complete and partial datasets (excluding phenotypes for animals born after 2021). The H-inverse was constructed with Quaas-Pollak transformation using HGINV V1.03 and the MIX99 V22.0228 package (Vuori et al. 2006). For the focal [validation] dataset (~1,350 genotypes) the prediction accuracy increased from 0.27 to 0.45 for individual traits when comparing SSGBLUP with PEDBLUP. The accuracy of IMF increased from 0.43 to 0.59, and SW accuracy increased from 0.41 to 0.59 when estimated using PEDBLUP and SSGBLUP, respectively.

Post-release, the population-level Terminal Index accuracy increase based on SSGBLUP was negligible (0.005) compared to the PEDBLUP evaluation. However, genotyping increased the average accuracy of the Terminal Index by more than 0.3 for individual animals and phenotyping specific traits increased this by a further 0.08.

Conclusions

SSGBLUP is a promising method for integrating genomic information into commercial sheep evaluations. The integration of this disruptive technology into a viable business model, supporting genetic progress and enhancing Breed Society services, represents a 'science into practice' success.

The initiative, drive and financial investment from the Breed Society to adopt the genomic service is unprecedented in the UK sheep industry and provides a valuable tool to support breeders in the breed's development. This provides significant value to the industry through improved rates of genetic improvement in traits of commercial value in an influential breed.

The ability to identify and correct pedigree errors offers integrity benefits to the commercial delivery of this technology in a Breed Society registry. This improves flock book authenticity and contributes to improved prediction accuracies by correcting parentage assignment.

The high relative costs of genotyping limits the uptake of the technology, however it has been demonstrated that genotyping offers significant benefits for individuals, particularly unproven animals [lambs] as their genetic potential can be determined, with a high level of accuracy, from birth. These benefits can be exploited by breeders to enhance genetic gain and produce animals better suited to the commercial market.

References

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