Advancing British Texel Sheep Breeding: Integration of Genomics using Single-Step Evaluation

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Abstract

The expanding utilization of DNA technologies in the livestock sector presents numerous opportunities to enhance genetic programs and accelerate genetic progress. However, in sheep breeding programs, the high costs of genotyping limit the adoption of genomic technologies to only a subset of animals within the population. One effective method to address this challenge is the Single-Step Genomic evaluation (SSGBLUP), which integrates current genomic data with both recent and historical genealogical information. This approach uses all the available data for assessing the genetic potential of both genotyped and non-genotyped animals. This research aims to assess the impact of incorporating genomic information and to compare the prediction ability of pedigree-based genetic evaluation (PEDBLUP) and SSGBLUP using a cross-validation method (i.e. Linear Regression (LR)). The dataset evaluated included 1,900,000 Texel animals. Among them, 19,494 animals were genotyped with different SNP arrays (e.g. Ovine_600K, GGP_Ovine_50K, OvineSNP50 and Ovine_15K) and all imputed to 44,065 SNPs using findhap.f90 V3 software. The evaluations of both PEDBLUP and SSGBLUP were conducted using a multi-trait model with nine traits (eight-week weight (8WW: 392,648), fat depth (FD: 291,324), scan weight (SW: 304,138), muscle depth (MD: 291,482), computed tomography (CT) scan lean (CTLean: 5,394), fat (CTFat: 5,371), eye muscle area (EMA: 4,431), muscularity (Musc: 5,390) and predicted intramuscular fat percentage (IMF: 4,014). The analyses were performed on both complete and partial datasets (excluding phenotypes for animals born after 2021). The H-inverse was construed with Quaas-Pollak transformation using HGINV V1.03 program and the MIX99 V22.0228 package was used for the analyses. For the focal (validation) dataset (1,350 genotypes) the prediction accuracy increased from 27 up to 45% across the different traits when comparing PEDBLUP with SSGBLUP. The maximum increases were for the IMF and SW traits. 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. The lowest increase was observed for MD with an increase of accuracy from 0.69 to 0.87. The findings of this study indicate that SSGBLUP is a promising method for integrating genomic information to enhance economically important traits in the Texel sheep breed by improving prediction accuracy.