

Abstract

Due to genetic differences between pure and crossbreeds and the differences in environmental conditions between the nucleus and commercial flocks, pure parental performance is a poor predictor of their progeny yield. To determine the possibility and technical benefit of including cross data in genomic evaluation, various selection strategies in sheep cross-breeding production systems were simulated and evaluated in the framework of 1250 scenarios using a modified BGLR and xbreed software packages. The effect of various levels of cross performance contribution to training set and selection scheme, training method, train set selection method and base-cross population structure on accuracy of genomic evaluation, cross and base cross performance were evaluated. Results showed that the accuracy of genomic values and base-cross performance were more influenced by population structure and population used as train set. Unlike generation performance of base-cross, cumulative performance and accuracy of the genomic evaluations decreased by increasing the participation rate of the cross performance in the genomic evaluation. Participation of 25-50% of cross performance in short term had no negative effect on the cumulative performance of the base-crosses. Cumulative and generation performance of crosses in addition to training set were influenced by training method and population structure. The estimation of marker effects using Bayesian ridge regression method compared with other Bayesian methods led to an increase in the accuracy of genomic evaluations. Using the cross performance in genomic evaluation increased the cumulative and generation performance of crosses in both short and long term. The results showed that the population structure of base-cross breeds and their genetic distance is a key factor in using cross performance for genomic selection. Including cross performance in genomic evaluation can provide more advantage, when breeds are not distantly close. Using cross data although has small negative effects on genomic prediction accuracy and base-cross performance but led to increase crosses performance and it is particularly useful when there is limited information on purebreds.

Keywords: Crossbreeding, Genomic Evaluation, Reference Population, Selection Scheme, Sheep



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Thesis Submitted for the Degree of Ph.D
In Genetic and Animal Breeding

Genomic selection strategies in sheep crossbreeding systems

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Spring 2019