

Genomic Selection Strategies in Breeds with Small Population Size

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Abstract

In small populations, the reference population size is the most limiting factor for implementation of genomic selection. Therefore, alternative strategies must be considered to increase accuracy of genomic selection in small populations. One strategy to increase the size of reference population in small population breeds is to blend individuals of two or more breeds with similar breeding objectives and recorded traits to create a multi-breed reference population. For transboundary breeds with similar breeding objectives, international genomic evaluation could increase reliability of predictions. Another strategy for breeds with crossbred data is to use this data in the reference population for genomic evaluation. However, when the mentioned strategies are not applicable to small population breeds, a single-step genomic method that integrates all available phenotypic, pedigree, and genomic information is recommended.

Keywords: Small population; Genomic breeding value; Reference population

Introduction

The availability of high-throughput and cost-effective SNP panels and the development of appropriate statistical methods have replaced traditional breeding programs with genomic selection. Several studies have shown that genomic selection increases the accuracy prediction of breeding values and shortening generation interval, thereby leading to higher genetic gain [1,2].

Genomic selection depends on the Linkage disequilibrium between QTLs and genome-wide markers and in capturing QTL variance by these markers. Calculation of genomic breeding values usually requires a population with information on both phenotypes and markers genotypes, called reference population. The marker effects in the reference population are estimated using different statistical methods that can later be used to accurately predict breeding values of individuals who are only genotyped [3,4]. Several studies have shown the effects of reference population size and structure, statistical methods, marker density, and genetic architecture of traits on the accuracy of genomic breeding values [1,2,5]. However, in small populations, the size of reference population is the most limiting factor for implementation of genomic selection [6]. Therefore, the aim of this review was to overview alternative strategies that should be considered to increase the accuracy of genomic selection in small populations.

Discussion

The possibility of genomic selection in breeds with small populations such as small ruminants have been demonstrated in New Zealand, Australia, France and UK [6]. Genomic prediction accuracy depends mainly on the number of animals included in the reference population and obtaining a large enough reference population is a challenge for breeds with limited number of populations. Several strategies have been proposed to take advantages of genomic selection in small populations.

One strategy to increase reference population size in breeds with small population is to blend individuals of two or more breeds with similar breeding objectives and recorded traits to create a multi-breed reference population. Several studies have reported that multi-breed reference population increased the accuracy of breeding values. The method used to estimate the effects of markers such as Bayesian methods, high density marker panels, close

genetic relationship of the breeds, and traits influenced by large QTL increased the accuracies of multi-breed reference population [5-8].

When breeds used in multi-breed reference population are not closely related, a proposed strategy is to use of multi-trait (MT) models, in which each trait in a breed considered as a correlated trait to a similar one in the other breed [8]. Another model is to use of multi-task Bayesian learning model for multi-breed genomic prediction [9].

For transboundary breeds with similar breeding objectives, international genomic evaluation can increase reliability of predictions, but this requires more cooperation than national programs and highly depends on the level of genetic relationship and connection between populations [10].

Another strategy for breeds with crossbred data is to use this data in the reference population for genomic evaluation. The accuracy of the crossbred reference population was affected by marker density, population size and genetic relatedness between breeds [5,11].

However, when the declared strategies are not applicable to small population breeds, a single-step genomic method that integrates all available phenotypic, pedigree, and genomic information is recommended. Moreover, impute available marker panels to higher densities with imputation techniques is a tool to maximize benefits of genomic selection.

Conclusion

In conclusion, this review study shows that for breeds with small populations size, there are several strategies to increase the accuracy of genomic selection.

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