

Genomic Prediction using Single or Multi-Breed Reference Populations in US Maine-Anjou Beef Cattle

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Summary and Implications

The objective of this study was to estimate accuracies of genomic predictions based on 50K SNP genotypes for 8 nationally evaluated traits in US Maine-Anjou beef cattle using single or multi-breed reference populations. The accuracies of direct genomic values (DGV) ranged from 0.22 to 0.45 for 8 studied traits when the reference populations comprised only 573 Maine-Anjou animals. Accuracies were slightly reduced and ranged from 0.21 to 0.38 when the reference population included over 9,000 animals from many other breeds as well as Maine-Anjou. These results demonstrate that including data from other populations does not generally increase accuracy of prediction in one particular population. This means every breed association must develop its own reference population if it intends to offer genomic prediction.

Introduction

The efficiency and advantage of predictors that use genomic information have been identified through previous papers, which reported worthwhile accuracy when the reference sets comprised thousands of individuals from their own purebreds. Several US beef cattle breed associations have been making an effort to take advantage of genomic predictors in their cattle evaluations. However, this is difficult for breeds with small numbers of registrations as they lack the animals, phenotypic data and financial resources to generate large reference populations. One alternative is for them to take advantage of other populations and pool the data to obtain a large reference population for training.

Materials and Methods

A total of 1,895 Angus, 31 Brangus, 54 Shorthorn, 30 Charolais, 1,254 Gelbvieh, 55 Hereford, 1,711 Red Angus, 573 Maine-Anjou, 3,930 Simmental were genotyped with bovineSNP50 BeadChip (Illumina, SanDiego, CA). In single breed analyses, only Maine-

Anjou animals were used as reference populations for training. Maine-Anjou animals were clustered into five-groups using K-means clustering for cross validation for the purpose of reducing the relationships between training and test populations. In the multi-breed reference population all other breeds were added to every Maine-Anjou reference population for training but results were only validated in Maine-Anjou animals.

BayesC with $\pi=0.95$ was used in all the analyses. Accuracies of genomic breeding values were calculated as simple correlations between deregressed estimated breeding values (DEBV) used as observation data and DGV.

Results and Discussion

Table 1 presents the accuracies of DGV in Maine-Anjou animals obtained by K-means clustering using single or multi-breed reference populations. Slightly lower accuracies were obtained except for weaning and maternal weaning weight traits, which improved slightly when predictions were obtained from multi breed reference populations.

These results indicate that adding animals from unrelated breeds to the reference population cannot improve the predictive accuracy in a small population. Accordingly, more animals should be obtained within the target breed or near relatives such as their crosses in order to improve the accuracy of genomic prediction.

Table 1. Accuracies of DGV for eight studied traits validated on Maine-Anjou animals for different reference populations.

Trait	Single breed	Multi breed
Carcass weight	0.23	0.21
Birth weight	0.38	0.34
Yearling weight	0.31	0.27
Weaning weight	0.29	0.30
Calving ease direct	0.45	0.38
Calving ease maternal	0.41	0.30
Milk	0.22	0.21
Maternal weaning weight	0.27	0.28