MSRP: A Multi-Breed Selected Reduced Panel for Efficient Genomic Selection in Beef Cattle

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Summary and Implications

The objective of this study was to develop a low-density multi-breed selected reduced panel (MSRP) that could capture most of the predictive ability of a 50K panel for efficient low-cost genomic prediction in purebred and commercial crossbred beef cattle. More than 15,000 animals from six beef cattle breed associations and genotyped with a 50K panel were used to select 1,029 markers highly associated with 10 target traits. An additional 1,278 evenly spaced markers were selected for imputation purposes. The final MSRP comprised 2,307 markers. Accuracies of direct genomic breeding values (DGV) were calculated for 3 independent validation populations using either 50K or MSRP. Accuracies of DGV obtained from MSRP were comparable with those obtained from 50K (>80% predictive ability of 50K) while the size of MSRP is <5% of 50K. These results demonstrate the efficiency of MSRP for low-cost genomic prediction in beef cattle.

Introduction

High-density SNP chip panels such as Illumina BovineSNP50 or BovineHD may still be price prohibitive for applications in beef cattle such as selection of replacement animals on commercial farms; optimizing mate choice; and marker-assisted management. There is considerable interest in developing low-density, low-cost SNP panels for efficient genomic prediction in beef cattle.

Two basic approaches can be used to develop low-density panels. One involves selecting SNPs most highly associated with the trait of interest in the training data set. The other approach is to use a subset of evenly-spaced SNP to “impute” high-density genotypes. We combined these two approaches to develop a multi-breed selected reduced panel for efficient genomic selection in beef cattle.

Materials and Methods

We used reference populations consisted of 15,847 animals genotyped with a 50K panel from the six dominant beef cattle breed associations in US (3,570 Black Angus, 1,374 Gelbvieh, 2,779 Hereford, 2,239 Limousin, 1,761 Red Angus, and 4,124 Simmental) to select highly associated SNPs for 10 different traits (birth, weaning, yearling and carcass weights; calving ease direct; fat thickness; marbling; ribeye muscle area; heifer pregnancy rate and stayability). We validated the efficiency of our developed multi-breed selected reduced panel (MSRP) in comparison with 50K in several independent purebred and crossbred commercial beef cattle populations (some 200 animals from each of 6 reference breeds, 3,338 animals from CircleA population (CA), 2,036 animals from Carcass Merit Project (CMP) and 1,085 animals from Tri-county (TCSF) population).

For each trait in each reference population, the “Bayes-B” method with parameter π (the fraction of markers assumed to have no effect on the trait) set to 0.99 was used to obtain 41,040 MCMC samples to estimate marker effects and variances after discarding the first 1,000 samples to allow for burn-in. The largest effect markers with genetic contributions more than 0.3% additive genetic variance were selected as highly associated markers for each trait in each reference population. Some 1,278 evenly spaced markers from BovineSNP50 BeadChip (Illumina, San Diego, CA) which are in common with other panles such as GGP-uLD (GeneSeek, Lincoln, NE) were added to improve the coverage of selected markers across the genome as well as their use for imputation. All selected highly associated and evenly spaced markers were pooled together to develop the final MSRP. Then, direct genomic breeding values (DGV) for validation populations were calculated based on marker estimates obtained from multi-breed training on either 50K or MSRP panels using GenSel software.

Results and Discussions

Several markers met the selection criteria more than one time across different traits (or different breeds), which reflects the existence of pleiotropic markers. The total number of highly associated markers for all traits over all six reference populations comprised 1,029 markers. The final MSRP comprised 2,307 markers including the evenly spaced markers.

The efficiency of MSRP in comparison with 50K (measured as the accuracy of DGV from MSRP training vs. 50K training) for each of trait within each of 6 US cattle breed associations is reported in Table 1. These results demonstrate that on average, MSRP has >80% predictive ability of 50K in all 6 US cattle breed associations despite the size of MSRP being <5% of 50K.

The efficiency of MSRP in comparison with 50K was also validated in independent CA, CMP, and TCSF populations using a multi-breed reference population of all 6 US cattle breed associations animals. These results also showed that on average, MSRP has about 80% predictive ability of 50K in independent CA, CMP, and TCSF populations (Table 2). On average, the accuracies of genomic predictions increased 5% by adding the evenly spaced markers from GGP-uLD to the model. These results demonstrate the efficiency of MSRP for low-cost genomic selection in beef cattle. The MSRP set has been implemented for multi-breed genetic evaluation at International Genetic Solutions (http://www.internationalgeneticsolutions.com) and is used for GeneSeek's Igenity Gold and Silver DNA profiles for commercial beef cattle.

Table 1: The efficiency (% of predictive ability) of MSRP vs. 50K in 6 US cattle breed association populations.

Trait	Black Angus	Hereford	Gelbvieh	Limousin	Red Angus	Simmental
Birth weight	93	84	81	76	100	93
Calving ease direct	85	90	85	93	96	91
Carcass weight	91	-	90	92	87	87
Fat thickness	81	83	70	-	57	105
Heifer pregnancy rate	-	-	-	-	108	-
Marbling	95	73	87	71	95	99
Rib eye area	85	83	51	79	99	92
Stayability	-	-	-	-	94	88
Weaning eight	91	84	87	77	84	91
Yearling weight	97	84	91	80	84	83
Average	90	83	80	81	90	92

Table 2: Accuracies[1] of direct genomic breeding values and efficiencies (% of predictive ability) of MSRP[2] in comparison with 50K in CircleA, Carcass Merit Project and Tri-county beef populations.

	CircleA			Carcass Merit Project			Tri-county		
Trait	50K	MSRP	Eff.	50K	MSRP	Eff.	50K	MSRP	Eff.
Birth weight	0.54	0.44	82	-	-	-	-	-	-
Carcass weight	0.40	0.36	90	0.27	0.23	85	0.32	0.22	70
Fat thickness	-	-	-	0.34	0.34	100	0.43	0.36	82
Marbling	0.51	0.36	70	0.45	0.35	79	0.38	0.26	68
Rib eye muscle area	0.42	0.35	84	0.37	0.24	66	0.40	0.28	73
Weaning weight	0.40	0.33	81	-	-	-	-	-	-
Average	0.45	0.36	81	0.36	0.29	83	0.38	0.28	73

[1] Defined as correlation between direct genomic values and phenotype divided by the square root of trait heritability;
[2] Multi-breed selected reduced panel