Developing a Reduced SNP Panel for Low-cost Genotyping in Beef Cattle

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Summary and Implications
The objective of this study was to develop a low-density reduced SNP panel (RP) that could capture most of the predictive ability of a 50K panel for six important traits (birth, weaning and yearling weights; calving ease direct; marbling; and rib eye area) in beef cattle. More than 15,000 animals from six cattle breeds genotyped with 50K were used to select markers highly associated with target traits. Accuracies of direct genomic breeding values (DGV) were calculated for 3 independent validation populations using either 50K or RP. Accuracies of DGV obtained from RP were comparable with those obtained from 50K (>75% predictive ability of 50K) while the size of RP is <2% of 50K. These results offer promise for a low-cost low-density genotyping product in beef cattle.

Introduction
High-density SNP chip panels such as Illumina BovineSNP50 or BovineHD are currently price prohibitive for many applications and species. There is considerable interest in developing low-density, low cost SNP panels for a variety of purposes including: selection of breeding stock in species where individuals have comparatively low value relative to the cost of high-density panels; selection of replacement animals on commercial farms; parentage assignment; optimizing mate choice; and marker-assisted management (Van Eenennaam, 2012).

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. Imputation is a method of predicting unobserved genotypes.

Materials and Methods
The training data set, used for selection of the most informative markers, consisted of 50K genotypes and deregressed estimated breeding values (DEBV) of six target traits (birth, weaning and yearling weights; calving ease direct; marbling; and rib eye area) on more than 15,000 animals from six different cattle breeds (Angus, Gelbvieh, Hereford, Limousin, Red Angus and Simmental). The validation data set consisted of 8,654 animals from three independent populations with 50K genotypes and phenotypic information.

Preliminary analyses identified for each trait those 1-Mb windows with large effects, known as Quantitative Trait Loci (QTL). All markers within 12 such windows that were pleiotropic and segregating in most breeds were pooled with other highly associated single SNP from anywhere across the genome (20 markers per breed-trait combination) to develop the reduced-SNP panel (RP). Then, DGV for validation populations were calculated based on marker estimates obtained from training on either 50K or RP panels using GenSel software.

Accuracy of DGV was defined as the correlation between DGV and phenotype divided by the square root of trait heritability.

Results and Discussions
Several markers were selected more than one time across different traits (or different breeds), which reflect the existence of pleiotropic markers. The final RP comprised 699 markers.

Accuracies of DGV obtained from RP were comparable with those obtained from 50K (>75% predictive ability of 50K) despite the size of RP being <2% of 50K.

These results suggest that a low-density SNP panel can be developed for low-cost genotyping in beef cattle.

Table 1. The accuracies of DGV in CircleA, CMP and TCSF validation populations using 50K or RP SNP panels.

Trait	CircleA		CMP		TCSF	
	50K	**MRP**	**50K**	**MRP**	**50K**	**MRP**
Birth weight	0.53	0.43	-	-	-	-
Carcass weight	0.40	0.35	0.26	0.19	0.32	0.26
Fat thickness	-	-	0.33	0.28	0.43	0.35
Marbling	0.51	0.29	0.45	0.36	0.38	0.28
Rib eye area	0.43	0.34	0.37	0.28	0.40	0.21
Weaning weight	0.41	0.28	-	-	-	-
Yearling weight	-	-	-	-	0.22	0.29