

Predictive genome-wide association and economic analyses of pooled DNA in a commercial feedlot setting

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Introduction

Understanding the genetic profile of cattle allows producers to make predictions of performance and disease. However, it is often fiscally and logistically unfeasible for commercial cattle producers to individually genotype animals. As such, our objective was to utilize prospectively-pooled DNA from commercial feedlot cattle for a genome-wide association study (GWAS) of economically-important carcass traits and measure the economic efficiency of this technique.

Materials and methods

A total of 1,956 mixed-breed commercial feedlot steers (n = 1,715) and heifers (n = 241), accompanied by complete receival and carcass data, were prospectively genotyped via GGP Bovine 100K array (Illumina) in 79 pools stratified by entry weight within lot and receival date. To reduce high variation of final phenotype within pool, outlier filtering (OF), the removal of pools containing a phenotypic outlier assumed via Levene's test ($P < 0.10$), and repeated measures (RM), the replication of the pool genotype by the number of individuals within the pool, were analytically applied. Phenotype and genotype files used for GWAS were analyzed with mixed-linear models via the Genome Association and Prediction Integrated Tool from iPat ($P < 0.001$), identifying single nucleotide polymorphisms (SNPs) associated with calculated yield grade (CYG) and marbling (MARB) values. Economic analyses calculated a cost comparison of pooled and individual genotyping and the potential benefit-cost ratio (BCR) of using genomics to make marketing decisions.

Results

Four GWAS trials, OF CYG, OF MARB, RM CYG and RM MARB, identified 20, 10, 27 and 16 significantly-associated SNPs, respectively. Identified SNPs were related to carbohydrate metabolism, actin activity, and cellular cytoskeleton formation. The estimated pooled project total (\$23,460) was nearly 4.5 times cheaper than the total individual genotype estimate (\$105,354). The mean potential BCR was 2.33 (SD = 1.91).

Significance

Our research displayed a successful inclusion of pooled DNA in a prospective GWAS, signified by the biologically logical significant genes identified. Prospective pooling for genetic analyses should be explored further to capture the potential economic advantages for commercial cattle producers. Further application of pooled GWAS in animal health research could identify disease-related genes more quickly and economically than traditional studies.

