64 The impact of putative causal variants and animal misidentification on genome-wide association studies for carcass traits in beef cattle. Lindsay R. Upperman, E. John Pollack, Matthew L. Spangler, *University of Nebraska - Lincoln*

Current genome-wide association studies (GWAS) are subject to misleading results given variation in linkage disequilibrium between SNP and causative variants and the potential for misidentification between genotypes and associated phenotypes. Consequently, the current study conducted a GWAS utilizing the Geneseek Genomic Profiler F250K panel to identify SNP associated with carcass traits, assess the effects of mismatching various percentages (5–50%) of phenotypes and genotypes, and to evaluate the benefits of the GGP F250K panel in comparison to a lower density panel. After editing, data were available on 745 animals for marbling (MARB), ribeye area (REA), carcass weight (CW), and backfat (FAT), and 221,115 SNP. A Bayes C model with fixed effects of birth year/season, harvest date, and linear covariate of age was employed with π set to 0.998. Results are the posterior means of 50,000 iterations after discarding 2,000 as burn-in. A lower density panel (LD) of 39,295 SNP in common between the Illumina 50K, GGP F250K, and Illumina BovineHD (777K) was created for comparison to the GGP F250K panel. To create mismatches between genotypes and phenotypes, a random sample (5–50%) of animals were selected from the phenotypes, permutated, then analyzed with the same model. This was repeated 5 times for each proportion of mismatches. As the proportion of mismatches increased, posterior heritability estimates decreased. Correlations between 1-Mb windows based on the proportion of variation between the GGP F250K and the LD panels were: 0.588 MARB, 0.764 REA, 0.797 CW, and 0.514 FAT. Ranges in posterior heritability estimates for mismatches of phenotypes and genotypes from 0–50% were: MARB (0.112-0.091), REA (0.477-0.172), CW (0.252-0.076), and FAT (0.085-0.080). Results suggest that re-ranking of 1-Mb windows would be expected between these two panels, and that GWAS studies with limited individuals are highly sensitive to mismatches between genotypes and phenotypes.

Key words: beef cattle, genome-wide association study, animal misidentification

60 Re-ranking of estimated breeding values using different panel densities with ssGBLUP in broiler chickens. Mayara Salvian[1], Gerson Barreto Mourão[2], Gabriel Costa Monteiro Moreira[2], Mônica Corrêa Ledur[3], Luiz Lehmann Coutinho[2], Matthew L. Spangler[1], *[1]University of Nebraska - Lincoln, [2]University of Sao Paulo - ESALQ, [3]Embrapa Suínos e Aves*

The aim of this study was to compare the rank of estimated breeding values (EBV) for organs (heart, liver, lungs and gizzard) and carcass (breast, thigh and drumstick) traits using pedigree-based BLUP (PBLUP) and single-step genomic BLUP (ssGBLUP) models. A total of 1,453 chickens (703 males and 750 females) from a paternal broiler (TT) reference population belonging to the Poultry Breeding Program from Embrapa Swine and Poultry were genotyped with the Axiom® Genome-Wide Chicken Genotyping Array (Affymetrix) 600K SNP panel. Samples with a call rate lower than 90% were removed. A SNP quality control was applied for removing SNP with call rate lower than 98%, MAF lower than 2% and significant deviations from HWE (p-value < 10^{-7}) leaving 370,608 SNP for further analysis. Estimated breeding values were predicted using the blupf90 family of programs whereby a series of bi-variate animal models that included sex and hatching as fixed effects were fitted. Heritability estimates for carcass and organ traits obtained through PBLUP varied from low (0.16) for lungs to moderate (0.34 to 0.47) for heart, liver, gizzard, breast, thigh and drumstick. The genomic heritability estimates through ssGBLUP varied from low (0.14) for lungs to moderate (0.30 to .041) for all other traits. Five subsets (5, 10, 20, 40 and 80% of SNP) were randomly selected from the full SNP set to determine the impact, in terms of EBV rank, of using reduced subsets of SNP to inform relationships among individuals. Although the 5% subset of SNP consistently had the lowest correlation with the full set of SNP, all correlations were greater than 0.995. Results suggest that a relatively limited proportion of SNP could be used to reliably predict EBV via ssGBLUP in this population.

Tables

Re-ranking of estimated breeding values using different panel densities with ssGBLUP in broiler chickens

Mayara Salvian[1]; Gerson Barreto Mourão[1]; Gabriel Costa Monteiro Moreira[1]; Mônica Corrêa Ledur[2]; Luiz Lehmann Coutinho[1]; Matthew L. Spangler[3]

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Table 1. EBV correlation for heart (above diagonal) and body weight (below diagonal) for 5, 10, 20, 40, 80 and 100% of SNP panel.

	5%	10%	20%	40%	80%	100%
5%	-	0.995	0.996	0.996	0.997	0.997
10%	0.996	-	0.998	0.998	0.998	0.998
20%	0.996	0.998	-	0.999	0.999	0.999
40%	0.996	0.998	0.999	-	1.000	1.000
80%	0.997	0.998	0.999	1.000	-	1.000
100%	0.997	0.998	0.999	1.000	1.000	-

Table 2. Mean, minimum and maximum EBVs values for heart (HRT) and body weight (BW) considering 5, 10, 20, 40, 80 and 100% of SNP panel.

SNP	HRT			BW		
(%)	EBV_{min}	EBV_{mean}	EBV_{max}	EBV_{min}	EBV_{mean}	EBV_{max}
5	-2.303	0.028	2.453	-310.839	5.479	288.653
10	-2.231	0.030	2.503	-324.081	5.667	309.894
20	-2.337	0.028	2.516	-330.295	5.568	297.288
40	-2.288	0.029	2.519	-330.761	5.594	299.054
80	-2.320	0.029	2.537	-333.801	5.653	303.430
100	-2.314	0.029	2.546	-334.116	5.658	301.900

Table 3. EBV correlation for liver (above diagonal) and body weight (below diagonal) for 5, 10, 20, 40, 80 and 100% of SNP panel.

	5%	10%	20%	40%	80%	100%
5%	-	0.996	0.997	0.997	0.997	0.997
10%	0.996	-	0.998	0.998	0.999	0.999
20%	0.996	0.998	-	0.999	0.999	0.999
40%	0.997	0.998	0.999	-	1.000	1.000
80%	0.997	0.999	0.999	1.000	-	1.000
100%	0.997	0.999	0.999	1.000	1.000	-

Key words: broiler chickens, genomic selection, single-step genomic BLUP.

61 The impact of selective phenotyping and genotyping over generations in beef cattle.

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The aim of this study was to investigate selective phenotyping to maintain adequate prediction accuracy. A simulation was conducted, with 10 replicates, using QMSim to mimic the structure and size of a Braford population. A population with 50 generations, 500 animals per generation, was created with phenotyping and genotyping beginning in generation 11. The scenarios investigated were: 1) Randomly phenotype and genotype 10, 25, 50, 75, and 100% of individuals each generation and; 2) Randomly phenotype and genotype 10, 25, 50, 75, and 100% of individuals in every-other generation. Estimated breeding values (EBV) were obtained using single-step GBLUP and accuracy was determined as the correlation between true BV from simulation and those estimated from the blupf90 family of programs. For scenarios where phenotyping and genotyping occurred every generation, EBV accuracies in generation 11 and 50 ranged from 0.32 to 0.32, 0.42 to 0.43, 0.49 to 0.51, 0.53 to 0.56 and 0.57 to 0.59 when 10, 25, 50, 75, and 100% of animals were chosen, respectively. The highest accuracies were 0.40 and 0.50 in generation 38 for scenarios 10 and 25%; 0.56, 0.61 and 0.64 in generation 40 for scenarios 50, 75 and 100%, respectively. When animals were selected every-other generation, EBV accuracy in generation 11 and 50 ranged from 0.24 to 0.26, 0.36 to 0.36, 0.43 to 0.42, 0.48 to 0.44 and 0.53 to 0.48 for 10, 25, 50, 75 and 100% of selected animals, respectively. The highest accuracies were in generation 23 for scenario 10% (0.31), in generation 37 for scenarios 25 (0.43), 50 (0.50) and 75% (0.55) and in generation 39 for 100% (0.59). Although increasing the density of phenotyped and genotyped animals increased prediction accuracy, some gains were marginal. These differences in accuracy must be contemplated in an economic framework to determine the cost-benefit of additional information.