Table 0295.

Table 1. Genotype and allele concordance rates (CR) prior and post imputation for all 493 animals with a poor (<90%) and subsequent high call rate (>99%).

	Pre Imputation		Post Imputation			
Call rate class	Genotype CR	Allele CR	Genotype CR Called SNPs	Allele CR Called SNPs	Genotype CR All SNPs	Allele CR All SNPs
<40	38.36	62.35	38.61	62.38	39.42	63.22
40-50	47.08	68.57	47.33	68.62	44.74	67.15
50-60	58.59	76.59	58.89	76.67	53.68	73.54
60-70	79.31	89.51	79.66	89.65	73.21	85.92
70-75	86.06	93.01	86.29	93.08	81.71	90.51
75-80	93.47	96.73	93.64	96.79	90.77	95.26
80-85	96.83	98.41	96.93	98.46	95.56	97.72
85-90	98.44	99.22	98.47	99.22	98.08	99.01

and allele concordance for samples with a call rate between 85 and 90% increased to 98.13% and 99.04%, respectively.

Key Words: call rate, quality-control, genotype panels

296 Strategy for incorporating newly discovered causative genetic variants into genomic evaluations. G. R. Wiggans*[1], P. M. VanRaden[1], D. M. Bickhart[2], and M. E. Tooker[1], *[1]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [2]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

With sequence data available for an increasing number of dairy cattle, discovery of causative genetic variants is expected to be frequent. Current genomic evaluation systems require genotypes for all markers that contribute to an evaluation. A minimum number of animals with an observation for a new marker is required for accurate imputation. The SNP calls derived from sequence data from the 1000 Bull Genomes Project for 444 Holsteins were combined with SNP genotypes from bulls in the predictor population for U.S. national genetic evaluations to impute candidate variants from the full sequence. From this imputed data, the set of SNP used in genomic evaluation along with the newly discovered causative variants were selected and stored. Those genotypes replaced the original genotypes for the bulls when extracting genotypes for genomic evaluation. The time required for imputation is substantially reduced in routine evaluation by using the haplotype library and assignments from the previous evaluation. To create suitable prior information for the expanded SNP set, genotypes for approximately 100,000 animals (including the predictor bulls and many cows with genotyped progeny) were imputed without priors. This step took about 1 d; if the full set of animals had been used, it would have taken over a week. The accuracy of this approximation was tested using the December 2015 Holstein genomic evaluation of nearly 1 million animals. Genotypes from 978,987 bulls and cows were used to create the priors, which were used to impute the December 2015 Holstein genotypes. Of the nearly 60 billion comparisons, 97.7% were identical, 1% differed by 1 allele, and 1.2% differed by a missing allele. Efficient methods that result in higher concordance may be possible. Adding new highly informative markers to the evaluation process is expected to improve prediction accuracy. In addition, excluding other markers may further increase accuracy if they contribute more noise than value when highly informative markers are included. The procedure developed enables newly discovered causative variants to be added to genomic evaluation almost immediately, which saves the time previously required for a marker to be added to a new genotyping chip as well as the time required for sufficient animals to be genotyped with the new chip to achieve adequate imputation accuracy. With this strategy, the benefits from adding new markers to genomic evaluation can be realized sooner.

Key Words: causative variant, sequence data, genomic evaluation

0297 High density marker panels, SNPs prioritizing and accuracy of genomic selection. L. Y. Chang*[1], S. Toghiani[1], S. E. Aggrey[2,3], and R. Rekaya[1,3], *[1]Department of Animal and Dairy Science, University of Georgia, Athens, [2]NutriGenomics Laboratory, Department of Poultry Science, University of Georgia, Athens, [3]Institute of Bioinformatics, University of Georgia, Athens.*

Availability of high density (HD) SNP marker panels, genome wide variants and even sequence data create an unprecedented opportunity of dissect the genetic basis of complex traits and to enhance selection in livestock and plant species. The disproportional increase in the number of parameters in the genetic association model compared with the number of phenotypes has led to further deterioration in the statistical power, and increase in co-linearity and false positive rates. HD panels do not improve the accuracy of GS in any significant manner and could even lead to reduction in accuracy using both regression and variance component methods. As a result, HD panels at best they did not improve significantly the accuracy of genomic selection and at worst they led to a reduction in accuracy. This is true for both regression and