

M62 Impact of accounting for parent and genotyped daughters' average in the estimation of deregressed estimated breeding values used in multiple-step genomic evaluations. H. R. de Oliveira^{1,2}, L. F. Brito^{2,3}, M. Sargolzaei^{2,4}, F. Fonseca e Silva¹, J. Jamrozik^{2,5}, D. A. L. Lourenco⁶, and F. S. Schenkel^{*2}, ¹Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brasil, ²University of Guelph, Guelph, ON, Canada, ³Purdue University, West Lafayette, IN, ⁴Select Sires Inc., Plain City, OH, ⁵Canadian Dairy Network, Guelph, ON, Canada, ⁶University of Georgia, Athens, GA.

Cows have been genotyped and used to increase the size of the training population in multiple-step genomic evaluations of dairy cattle with limited number of proven bulls. However, some of the genotyped cows are daughters of progeny tested bulls, which have their estimated breeding values (EBVs) predicted based on the parent average (PA) and the phenotypic information from their daughters, which would cause double count of information. The objective of this study was to investigate the impact of accounting for PA and genotyped daughters' average (GDA; i.e., the contribution of genotyped daughters to the bull's EBV) in the estimation of deregressed EBVs (dEBVs) used as pseudo-phenotypes in genomic evaluations. In addition, an alternative deregression method was proposed (NEW). A simulated dairy cattle data set was used to compare 8 scenarios defined based on the number of bulls, genotyped bull's daughters, and genotyped cows not sired by the genotyped bulls. For all these scenarios, Genomic EBVs (GEBVs) were predicted using dEBVs estimated based on 4 methods: VR, that includes PA and GDA information in the dEBV; VRpa, that excludes PA; and JA and NEW, which exclude PA and GDA from the dEBVs using either all information available in the complete pedigree or only information from parents and genotyped daughters, respectively. The dEBVs estimated by the VR and NEW showed the lowest (0.24 to 0.36) and highest (0.33 to 0.50) validation reliabilities across scenarios, respectively. The VRpa and NEW methods produced the least biased GEBVs (inflation/deflation) and showed the most consistent bias estimates (regression coefficient) across scenarios (1.08 to 1.17). Among all methods, the JA method displayed the largest variability in bias (1.00 to 1.75) across scenarios. Therefore, it was shown that removing PA and GDA information from dEBVs can increase the reliability of genomic predictions for populations with limited number of proven bulls. In addition, the proposed NEW deregression method addresses the double counting of information and it is a feasible alternative to generate dEBVs used in multiple-step genomic evaluations.

Key Words: double-counting, genomic BLUP (GBLUP), training population

M63 Understanding the impact of technologies and novel phenotypes on breeding strategies for genetic progress in dairy cattle. C. Lynch^{*1}, F. Schenkel¹, K. Houlihan¹, G. de Oliveira Junior¹, L. Alcantara¹, and C. Baes^{1,2}, ¹Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON, Canada, ²Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Bern, Switzerland.

In recent years, cutting-edge genomic technologies, methodologies and phenotype collection methods for current and novel traits have emerged. Some of these technologies are in development, some are undergoing regulatory analysis, and some have already been implemented. Each of these new technologies could potentially contribute to improving production efficiency; however, each technology has an associated cost, and potential benefits vary. The widespread adoption of these new technologies, methodologies and phenotype collection methods could potentially alter the way animals are selected within genetic and genomic evaluations. However, medium and long-term effects of

incorporating these novel traits and technologies into routine breeding programs are largely unknown. Here we describe potential changes to current breeding strategies, and compare how those changes could affect the way we breed dairy cattle in the future. For example, we quantify the current use of reproductive management technologies and describe potential effects of wide-scale adoption on population structure, inbreeding, and production efficiency. A variety of comparisons are presented, and methods to compare the benefits of various schemes and tools for genetic improvement and selection are discussed. This study presents a systematic analysis of the implications of applying novel technologies and methodologies. Through analysis of current and potential future strategies, as well as outlining expected outcomes thereof, changes to dairy cattle breeding programs in short, medium and long term can be predicted, and useful insight on optimal paths forward can be gathered.

Key Words: novel traits, breeding strategies, sustainability

M64 Approximate generalized least squares method for large-scale genome-wide association study. L. Ma¹, J. Jiang¹, D. Prakashenka², J. Cole³, and Y. Da^{*2}, ¹University of Maryland, College Park, MD, ²University of Minnesota, Saint Paul, MN, ³USDA/ARS, Beltsville, MD.

The use of genomic relationships among individuals is an effective approach for population stratification correction in the analysis of genome-wide association study (GWAS), but the matrix inversion required for the statistical testing of SNP effects limits the sample size that can be analyzed by GWAS methods using relationship matrices. We propose an approximate generalized least squares (AGLS) method for GWAS using large samples. The AGLS utilizes the mixed model result that the least squares (LS) solution to fixed SNP effects is the GLS solution or best linear unbiased estimation if the best linear unbiased prediction of polygenic effects is removed from the phenotypic observations. Since the LS method is computationally efficient, no sample size limitation for this method is expected for the foreseeable future even though dairy genomic and phenotypic data are growing at a fast pace. Combined with a previous method and computing tool for epistasis testing, the AGLS method offers capability for testing and estimating additive, dominance and epistasis effects as well as estimating allelic and genotypic effects in large-scale GWAS. AGLS was compared with BOLT-LMM that is capable of large-scale GWAS for testing additive effects. The results showed that AGLS and BOLT-LMM identified the same significant additive effects with only minor differences in a sample of 294,079 cows. For the same sample analyzed by AGLS and BOLT-LMM, the GWAS without polygenic correction lacked sensitivity, i.e., different chromosomes and different SNP within each chromosome had similar effects, except for SNP in and around the *DGATI* gene on chromosome 14. These results showed that polygenic correction is necessary for large-scale GWAS and that AGLS is an efficient and versatile method for large-scale GWAS analysis, especially in dairy cattle where the polygenic animal effect is routinely estimated.

Key Words: genome-wide association study (GWAS), SNP, generalized least squares

M65 Computing pipeline for genomic prediction and estimation using haplotypes and SNP markers. D. Prakashenka* and Y. Da, University of Minnesota, Saint Paul, MN.

The haplotype analysis for genomic prediction and estimation requires considerably more data processing and has many more possible configurations of the prediction model than single-SNP analysis. To facilitate