Breeding and Genetics Symposium: Is There Space for Genomic Selection in Small Populations?

595 Is genomic selection a one size fits all? I. Misztal*, *University of Georgia, Athens.*

Several methods are used for genomic selection (GS). A multi step method in dairy involves a regular BLUP, creation of pseudo-observations for animals with genomic information, genomic prediction (GP) for genotyped animals, and creation of an index with parent average. This method is successful when models for prediction are simple, genotyped animals include high accuracy bulls, and the number of genotypes is >2000. When genotyped animals have low or variable accuracy, approximations in pseudo-observations, GP and the index reduce the accuracy of prediction and create biases. Lack of the index results in lower accuracy especially for animals farther from the reference population. Another method of GS applies GP directly to phenotypes and genotypes of reference populations. The resulting equations are used for prediction, either directly or as a correlated pseudo-trait in a regular evaluation. This method is simple but less accurate because it ignores information from ungenotyped ancestors and from correlated traits. Also, accuracy of predictions for animals far from the reference populations may be very low. The newest method for GS is single-step GBLUP (ssGBLUP), which is conventional BLUP except that the pedigree-based relationship matrix is modified by SNP-derived relationships. In tests, ssGBLUP seems to be the most accurate one as it utilizes all the information with few approximations. Issues implicitly present in the other methods but explicit in ssGBLUP are proper scaling of genomic relationships, removal of genotype and pedigree conflicts, realistic approximation of accuracies, and optimal selection of animals for genotyping to minimize costs. The additional accuracy due to GS is approximately $\sim\sum[(a^{ij}-g^{ij})^2\ acc_j^2]$, where a_{ij} (g_{ij}) are pedigree (genomic) relationships between animal i and j, and acc_j is accuracy for animal j. The additional accuracy is maximized by selection of reference animals with high accuracy who are strongly related to candidates for selection. In populations where an individual is inexpensive, expanding progeny sizes may be more cost effective than extra genotyping.

Key words: genomic selection, accuracy, single step

596 Is there value in maintaining small populations? Example of the Dual-Purpose Belgian Blue breed. N. Gengler*[1,2], H. Soyeurt[1,2], C. Bastin[1], B. Buske[1], S. Vanderick[1], and F. Colinet[1], [1]*Ulg - GxABT, Gembloux, Belgium,* [2]*FNRS, Brussels, Belgium.*

Current status of thinking on genomic selection in dairy cattle is mostly major breed centric (e.g., Holstein) and only for traditional traits (e.g., milk yields). Once you depart from this, it becomes obvious that different, often related, issues appear (e.g., lack of large training populations, need for expensive recording of new phenotypes). Also, there is an urgent need to rethink issues that are important for sustainability of dairy production (e.g., added value foods, animal robustness). In this context, small populations (breeds/lines) could represent a potential source of extra information to justify their maintenance. As marker densities increase, efficient dissection of different selection histories of divergent breeds or lines, potentially identifying pockets of unexploited variability will increase. A current example from the Belgian (Walloon) perspective is the Dual Purpose (DP) line of the Belgian Blue Breed (BBB), with presently around 4500 breeding females, for historical reason of which only 1500 have good pedigrees, and which is present in Belgium and northern France. Recent research, done on this line, showed its tendency to produce less saturated milk fat and to have better fertility. Results indicated that it could stay competitive in specific markets, especially because of largely increased meat value. Currently, the myostatin mutation is largely used for breeding purposes. To assess the genetic diversity of the breed, recently, over 200 genotypes (SNP50K) for nearly all breeding bulls of the last 20 years became available. HD genotypes should be available in the near future, also allowing to access selection history of this breed as being in between the 2 extreme breeds: Beef BBB (with which it shares a recent history) and Holstein-Friesian (which is related through its geographic proximity over centuries). Finally, genomic selection for DP-BBB will need to consider a single step type approach without the need of reference population and potentially relying heavily on SNP3K of cows, also with the objective to recreate relationships between animals of interest.

Key words: genomic selection, milk quality, robustness

597 Overview of genomic selection in dairy cattle populations. P. M. VanRaden*[1] and J. R. O'Connell[2], [1]*Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD,* [2]*University of Maryland School of Medicine, Baltimore.*

Genomic selection is most successful for traits recorded over many years in large populations. Holstein breeders have reference populations >10,000 proven bulls via cooperation among major countries, and countries with smaller Holstein populations can contribute additional bulls. Scandinavian red dairy cattle breeders have 8,000 reference bulls, and Brown Swiss breeders have a global population of 4,500 reference bulls at Interbull. Jersey breeders have genotyped but have not yet merged their 6,000 reference bulls. Denser chips can transfer genomic information across breeds if all breeds are in the same data set. Less dense chips with imputation to higher densities allow affordable selection for smaller populations or more recently recorded traits. The North American database now includes Illumina 2,900 marker (3K) or 50,000 marker (50K) genotypes for 74,389 Holsteins, 8,905 Jerseys, and 2,008 Brown Swiss, plus 777,000 marker (HD) genotypes for 435 animals. To determine how many HD animals within each breed may be needed for imputation, 600,000 marker genotypes were simulated for either the youngest animals or for older bulls with highest reliability, and the other animals had 40,000 markers. After imputation using findhap.f90 version 2, percentages of estimated genotypes that matched true genotypes ranged from 96.1 to 98.7% when numbers of HD genotypes ranged from 250 to 1000 within each of the 3 breeds. Imputation accuracy was about 1% less if the youngest animals instead of the older bulls had HD. The value of matching cow phenotypes to their own genotype instead of to their sire's genotype was demonstrated by excluding bulls and using only the 13,935 cows in the Holstein reference population instead of all 25,131 reference bulls and cows (official). For milk yield of young animals, the correlation was 0.86 between cow-only and official evaluations vs. 0.71 between parent average and official. Smaller populations can increase genomic reliability by exchanging information with large populations and by lower cost genotyping.

Key words: genomic evaluation, reference populations, breeds