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For low heritability traits, large reference populations are required to achieve high reliability of genomic EBV (GEBV). By including genotyped and non-genotyped animals simultaneously in the evaluation, the single-step GBLUP (ssGBLUP) has the potential to yield more accurate and less biased evaluations. The aim of this study was to compare the reliability and bias of genomic predictions for various workability and reproductive traits in Holstein cattle using 2-step GBLUP (tsGBLUP) and ssGBLUP. A total of 33,568 bulls and 6,849 cows were genotyped. Genomic predictions were assessed using genotypes only for bulls or for bulls and cows under different approaches: (1) GEBV estimated by ssGBLUP with a default blending of 5% of the pedigree relationship matrix among genotyped animals (A_{22}) and 95% of the genomic relationship matrix (G); (2) Direct genomic value (DGV) estimated by tsGBLUP where 5% or 20% of A_{22} was blended into G ; (3) GEBV as an index combining EBV and DGV, where the latter was obtained from tsGBLUP with 5% or 20% blending. Regular BLUP without genomic information were also carried out and EBV served as benchmark for comparisons. Reliabilities were obtained with forward prediction, following the Interbull validation method. Validation bulls had at least 50 daughters in 2014. Including genomic information improved reliability, on average, by 14.5 pts for ssGBLUP and 12 pts for tsGBLUP compared with BLUP. Overall, ssGBLUP predictions had 3.3 pts greater reliabilities and were 0.15 pts less biased compared with tsGBLUP. When a 20% blending was used in stGBLUP, predictions were less biased, but no differences in reliability were observed compared with a 5% blending. Adding genotypes for cows had a small, positive impact of 1.5 pts in reliability for ssGBLUP and 1.6 pts for tsGBLUP; bias was reduced by 0.002 and 0.023, respectively. When genomic information is available for cows, predictions for both workability and reproductive traits can be slightly improved. Single-step GBLUP leads to more accurate and less biased predictions compared with 2-step GBLUP.

Key Words: genomic EBV, reliability, single-step GBLUP

207 Value of thermal images as predictors of feed conversion efficiency in New Zealand Friesian dairy cattle. M. Camara*, K. McDonald, M. Olayemi, and J. Bryant, *DairyNZ, Hamilton, New Zealand.*

Feed conversion efficiency is important for the profitability of dairy farms, but measuring dry matter intake to estimate it directly is expensive and time consuming. Consequently, fast and inexpensive measurements of genetically correlated traits are desirable as predictors. In this study, we describe the utility of thermal imaging to predict feed conversion efficiency. We conducted a 30–40 d feeding trial on 6 to 9 mo old Friesian bulls ($n = 75$) and their half-sisters ($n = 246$) and estimated feed conversion efficiency as residual feed intake (RFI: the residual from a regression of daily dry matter intake on average daily gain and mid-trial metabolic weight). We also took thermal images to measure heat loss from the eye, cheek, and muzzle. Using univariate animal models, we estimated the heritability of RFI for each sex (0.13 for heifers and 0.18 for bulls), and using a bivariate animal model that treated RFI in bulls and heifers as different traits, we estimated the between-sex genetic correlation (0.93). To investigate the utility of thermal traits as predictors, we fit single-trait animal models for all 8 heat loss measurements (maximum and mean temperature of the eye, eye corner, cheek, and

muzzle) to estimate heat loss EBVs and then used multiple regression of heat loss EBVs on RFI EBVs to produce prediction equations. Even over-fit regression models using all 8 predictors resulted in low coefficients of determination (r^2) of 0.35, 0.40, and 0.19 for both sexes, heifers and bulls respectively. To simulate selective RFI phenotyping of bulls only, we fit a 3-trait animal model treating RFI and the first 2 principle components (PCs) of the 8 heat loss traits as separate traits using all data on bulls, but only the heat loss PCs on heifers to estimate RFI EBVs in both sexes. These RFI EBVs estimated using only 75 direct measurements on bulls were highly correlated with those from univariate models using 321 measurements on both sexes with r^2 values of 0.85, 0.84, and 0.94 for both sexes, heifers and bulls respectively but with lower reliabilities. Both strategies would require extensive independent validation to justify routine measurement of RFI and its incorporation into the national breeding objective.

Key Words: feed efficiency, dairy, genetics

208 Determining the economic value for efficiency traits. C. Richardson*¹, C. Baes¹, P. Amer³, C. Quinton³, F. Hely³, P. Martin¹, V. Osborne¹, J. Pryce^{4,5}, and F. Miglior^{1,2}, ¹University of Guelph, Guelph, ON, Canada, ²Canadian Dairy Network, Guelph, ON, Canada, ³AbacusBio Limited, Dunedin, Otago, New Zealand, ⁴Development, Jobs, Transport and Resources, AgriBio, Bundoora, VIC, Australia, ⁵La Trobe University, AgriBio, Bundoora, VIC, Australia.

Altering management practices and production designs to create a more sustainable global system has been highlighted in government policies and corporation objectives. In the dairy market, the inefficient utilization of feed and high production of emissions associated with raising and maintaining cattle are scrutinized for contributing to environmental degradation, and therefore, have become targeted areas for improvement. Feed is a major expense for the Canadian dairy industry, representing over 50% of all production costs. A new prospect for decreasing the environmental footprint of the dairy industry is to increase feed efficiency and decrease methane emissions through the selection of genetically superior animals, as these traits are favorably correlated. Current selection programs have been successful in achieving breeding objectives related to production, health and longevity. It is also important to develop a selection program that includes an aim to increase total system efficiency, thereby, maintaining a viable industry both economically and environmentally. Thus, the economic value of efficiency traits to be used in selection programs must be determined. The methodology introduced below was used to determine the total savings associated with selecting for a decrease in the total dry matter intake of a lactating first parity dairy cow; including the economic value of the reduction in feed-related methane production. The lifespan of a typical Canadian dairy animal was divided into stages based on significant changes in cost of ration or energy requirements by the animal. Regression coefficients defined as a ratio of the mean total feed intake across production animal life stages relative to a first parity lactating cow, were used to determine the economic effect of decreasing feed intake. The resulting coefficients were applied to determine the cost savings associated with the lower output of emissions. Using this approach, the approximate lifetime savings generated by a more feed efficient production animal can be estimated.

Key Words: feed efficiency, methane production, economics

209 Preliminary genomic predictions of feed saved for 1.4 million Holsteins. P. M. VanRaden*¹, J. R. Wright¹, E. E. Connor¹, M. J. VandeHaar², R. J. Tempelman², J. S. Liesman², L. E. Armentano³,

and K. A. Weigel³, ¹*Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD*, ²*Michigan State University, East Lansing, MI*, ³*University of Wisconsin, Madison, WI*.

Genomic predictions of transmitting ability (GPTAs) for residual feed intake (RFI) were computed using data from 4,621 42-d and 202 28-d feed intake trials of 3,947 US Holsteins born 1999–2013 in 9 research herds. The 28-d records had 8.5% larger error variance than 42-d records and received less weight (0.92 vs. 1.0) in the evaluation. The RFI averages were already adjusted to remove phenotypic correlations with milk energy output, metabolic body weight, and body weight change and for several environmental effects including other nutrition experiments during the feed intake trials. Traditional breeding values (BVs) for RFI of 74.3 million Holsteins were obtained by an animal model that also included effects for age-parity group, trial date, herd management group, permanent environment, herd-sire interaction, and regressions on inbreeding and on genomic evaluations for milk energy and body weight composite (BWC). The milk energy and BWC terms were specified with the intent to remove positive genetic correlations that remained after the phenotypic correlations were removed. Estimated heritability was 0.17 and repeatability across lactations was 0.42. Genomic BVs for RFI included 60,671 genetic markers for 1.4 million Holsteins and produced calculated genomic reliabilities for young animals averaging 19% compared with traditional reliabilities of 5%. A parallel test using somatic cell score (SCS) records for these same 3,947 cows indicated lower observed than expected genomic reliability (11% vs. 19%). The economic value of RFI is very large and could receive >20% of total emphasis in net merit, but the low reliability will limit the extra genetic progress to about 4% more than current progress. The RFI predictions were added to the extra feed associated with large BWC and then multiplied by –305 to convert from extra feed eaten per day to feed saved per lactation. Additional feed intake records could make feed saved a very important trait in future selection indexes for dairy cattle.

Key Words: feed intake, genomic evaluation, dairy efficiency

210 Breeding strategies for improving feed efficiency in Holstein cattle using ZPLAN+. K. Houlihan^{*1}, F. Miglior^{1,2}, C. Maltecca³, B. Gredler⁴, A. Fleming¹, and C. Baes¹, ¹*University of Guelph, Guelph, ON, Canada*, ²*Canadian Dairy Network, Guelph, ON, Canada*, ³*North Carolina State University, Raleigh, NC*, ⁴*Qualitas AG, Zug, Switzerland*.

Feed accounts for over 50% of the total costs on a dairy farm in North America, with feed prices expected to continue to rise in coming years. There is a clear need to improve the feed efficiency of dairy cattle. Studies have shown that there is variation in the amount of feed consumed between animals that have similar production. By exploiting this variation on a genetic level, there is an opportunity for greater and more permanent improvement in feed efficiency. Determining an optimal breeding strategy for improving feed efficiency in dairy cattle would be helpful in reducing feed costs, while maintaining or increasing output. Measuring feed intake can be expensive and time consuming. There are different ways to express feed efficiency, including residual feed intake (RFI) and dry matter intake (DMI). RFI and DMI are genetically correlated with milk yield. Using these genetic correlations, along with

phenotypic correlations and heritabilities, an optimal breeding strategy will be created and analyzed using ZPLAN+. ZPLAN+ is a software program that aids in the modeling and calculation of complex breeding scenarios using genomic information. This program will be used to assess the genetic gain, monetary gain, and costs associated with including feed efficiency in a selection index for the Canadian dairy industry. Both RFI and DMI will be simulated as measures of feed efficiency, and the results will be compared with determine which trait is optimal to include in the index. In addition to this work, long-term effects of including feed efficiency in the Canadian selection index on traits of economic interest such as milk yield, fertility and health will be analyzed. The results of this work will provide insight for the Canadian dairy industry as to the best method for including feed efficiency into the existing selection index.

Key Words: feed efficiency, breeding strategies, genetics

211 A comparison of feed intake, production, body condition score, body weight, and frame size of ProCROSS crossbred versus Holstein cows during the first 150 days of first lactation. B. N. Shonka-Martin^{*1}, B. J. Heins², and L. B. Hansen¹, ¹*University of Minnesota, St. Paul, MN*, ²*West-Central Research and Outreach Center, Morris, MN*.

Three-breed (Montbéliarde, Viking Red, Holstein) rotational crossbred (ProCROSS) cows (n = 44) were compared with Holstein cows (n = 41) for feed intake, production, and body traits during the first 150 d of first lactation. Cows calved in the University of Minnesota campus herd from September 2014 to April 2016. A total mixed ration (TMR) was fed twice daily, and refusals were weighed once daily. All cows were individually fed the same TMR on an ad libitum basis. Feed intake was recorded and dry matter intake (DMI) was calculated. Body weights were recorded twice weekly, body condition score (BCS) was evaluated once weekly, and height at both the withers and the hips was measured once a month. Best prediction (BP) was used to estimate production from data collected from routine milk recording. Mean body weight and BCS were calculated for monthly periods. Statistical analysis of total 150-d DMI included the fixed effects of year, age at calving, breed, and the interaction of year and age at calving and the random effect of cow nested within breed. A similar model was used for production traits except age at calving was removed because this variable is adjusted for by BP. Month nested within breed was an additional fixed effect for the body traits. Crossbred cows (2,770 kg) consumed significantly ($P < 0.01$) less DMI during the first 150 d of lactation than Holstein cows (2,922 kg). Fat plus protein production was not different ($P = 0.54$) for crossbred (338 kg) and Holstein cows (328 kg), but the crossbreds were numerically higher. Crossbred cows (3.39) had significantly higher ($P < 0.01$) BCS than Holstein cows (3.16) during the first 150 d of lactation. However, body weight was not different ($P = 0.33$) between the crossbreds (556 kg) and Holsteins (545 kg). Crossbred cows (136 cm) were shorter ($P < 0.01$) for height at the withers than Holstein cows (138 cm), but similar ($P = 0.51$) for height at the hips (143 cm vs. 144 cm, respectively).

Key Words: crossbreeding, feed intake