

Breeding and Genetics Platform Session: Breeding for Sustainability and Environmental Efficiency

1329 International collaboration to improve sustainability and resilience in dairy: Current and future studies. C. F. Baes^{*1,2}, G. Kistemaker³, R. Baldwin⁵, A. Butty⁴, J. Burchard⁵, O. González-Recio⁶, J. Lassen⁷, M. VandeHaar⁸, D. Segelke⁹, R. Tempelman⁸, K. Weigel¹⁰, J. Koltes¹¹, F. Miglior^{1,3}, RDGP Consortium Partners¹, and FARR Consortium Partners⁸, ¹University of Guelph, Guelph, ON, Canada, ²Universität Bern, Bern, BE, Switzerland, ³Lactanet, Guelph, ON, Canada, ⁴Qualitas AG, Zug, ZG, Switzerland, ⁵CDCB, Bowie, MD, ⁶INIA-Madrid, Madrid, MD, Spain, ⁷Aarhus University, Aarhus, Denmark, ⁸Michigan State University, East Lansing, MI, ⁹VIT, Verden, NS, Germany, ¹⁰University of Wisconsin–Madison, Madison, WI, ¹¹Iowa State University, Ames, IA.

The global demand for dairy products is increasing continuously, however, the dairy industry is concurrently facing criticism for potential issues related to human and animal health, environmental impacts, sustainability, and overall social acceptability. The Resilient Dairy Genome Project (RDGP) is one of several large-scale international collaborations between research and industry partners with the goal of integrating genomic approaches to enhance dairy cattle resilience. In this project, resilience is defined as the capacity of an animal to adapt rapidly to changing environmental conditions, without compromising its productivity, health or fertility, while becoming more resource-efficient and reducing its environmental burden. Here we describe a strategy for incorporating data from multiple national and international partners for use in dairy cow genomic evaluation programs. We discuss current and future research studies and direct use of the data in routine genomic prediction. Potential long-term strategies for continuous data collection are also presented.

Key Words: resiliency, efficiency, international

1330 Accuracy of genomic predictions including or excluding foreign data in reference populations. R. R. Mota^{*1} and P. M. VanRaden², ¹Council on Dairy Cattle Breeding (CDCB), Bowie, MD, ²Animal Genomics and Improvement Laboratory, ARS, USDA, Beltsville, MD.

Genomic predictions often include foreign data obtained from Interbull's multi-trait across-country evaluation (MACE), but accuracy advantages may be reduced as domestic data sets grow and many cows are genotyped. To test this, accuracies of predictions were compared from truncated domestic data vs. a combined reference that also included truncated MACE (TMACE) data. The predictions used the current multi-step models instead of testing with previously official methods that may have been revised during the past 4 years. Predictions were tested for 10 traits and Net Merit \$. Genomic estimated breeding values (GEBV) were compared for 7,651 bulls born 2012 or later that had no daughter records in August 2017 but had > 75% reliability of conventional EBV in August 2021. The validation bulls consisted of 4 groups: 3,623 domestic Holsteins and 544 Jerseys with USA (or country code 840) identification and 3,386 foreign Holsteins and 98 Jerseys with other country identification. Smaller subsets of these bulls were used for traits with less reliability. Most squared correlations (R^2) were unexpectedly higher for predicting foreign than USA bulls, possibly because the foreign bulls were less selected or obtained less reliability than the USA bulls on USA scale. Inclusion of TMACE gave largest benefits to predict less heritable traits such as productive life and somatic cell score in both

breeds. Gains were larger for foreign bulls than for the same traits of USA bulls. For predicting higher heritability yield traits, benefits were near 0 for USA bulls, small (1 to 2%) for foreign Holsteins, and larger (5 to 11%) for foreign Jerseys. All regressions (B_1) were near 1.0 and changed only a little with the inclusion of TMACE. MACE can increase prediction reliability even when large domestic reference populations are available, and results from TMACE more accurately demonstrate that by comparing predictions using the same current model.

Key Words: genomic validation, dairy cattle, international evaluation

1331 Daily body weight of cows compared to estimates of body weight. B. Shonka-Martin, H. Templeton, A. Sewalem, L. Chang, J. Nani, R. Starkenburg, and M. McClure^{*}, ABS-Global, Deforest, WI.

Daily weights of cows on commercial dairy farms were collected to compare with current genetic estimates of body dimensions. Accurately estimating a cow's body weight has numerous benefits, including calculating body maintenance needs, feed efficiency and carbon footprint. Data were obtained from 61 Lely AMS farms that had body weight scales integrated into their milking systems. In total there were 23,960 females with 18,046,329 unique daily body weights recorded. These farms are located in Canada (4), France (11), Italy (12), the Netherlands (2), UK (28), and USA (4). Two USA located farms had 753 females with both CDCB genomic evaluations (Dec 2021 values) and scale weights ($n = 261,257$) across multiple lactations, with the majority of the genotypes provided by ABS. These data were analyzed to compare genomic evaluations for Body Weight Composite (BWC from Holstein Association USA) to actual daily live weight (pounds). Average weekly weights were calculated per animal to minimize random day-to-day variation. A cow's BWC values were correlated with her average weekly weight for the first 4 lactations from wk 9 to 44. Week 9 was chosen as the starting week because the data set showed that a cow regained her post-freshening weight loss by wk 9. The correlation between BWC and weekly weight increased in later lactations (Table 1). The highest weekly correlation values resulted from cows as they neared mature weight. By modeling changes in body weight measurements of cows from all 61 farms throughout and across lactations, further analysis can better assess the accuracy of body trait genetic evaluations in predicting the actual body weight of a cow over its lifetime.

Table 1. Analysis of weekly cow weights, week 9-44 in milk, and BWC

Lactation	Correlation: Scale weight and BWC		# Weekly weighted cows		Average weight	
	Average	SD	Average	Max	Week 9	Week 44
1	0.36	0.05	668	702	1248	1488
2	0.42	0.03	325	379	1407	1589
3	0.44	0.07	67	91	1465	1667
4	0.64	0.14	14	23	1499	1639

Key Words: body weight, robot milking, growth

1332 Estimates of genetic parameters for feeding behavior traits and its association with feed efficiency in Holstein cows. L. Cavani^{*1}, W. E. Brown¹, K. L. Parker Gaddis², R. J. Tempelman³, M.