

**Table 1 (Abstr. 389).** Feed efficiency between primiparous and multiparous crossbred and Holstein cows

Item	Primiparous		Multiparous	
	Holstein	Crossbred	Holstein	Crossbred
F+P/DMI	0.11	0.12**	0.12	0.13**
ECM/DMI	1.70	1.77**	1.89	2.01*
ECM/NEI	1.05	1.09*	1.16	1.23*
Protein/CPI	0.30	0.32**	0.32	0.35**
DMI/BW	5.31	5.03**	5.57	5.31*
IOFC	\$825	\$875**	\$1208	\$1296*
RFI	68.8	-65.5**	75.0	-64.5*

\*\* $P < 0.01$ , \* $P < 0.05$  for differences between breed groups.

**Key Words:** crossbreeding, feed efficiency

**390 Activity and rumination of Holstein versus crossbred cows in an organic grazing and low-input conventional herd.** G. M. Pereira\* and B. J. Heins, *University of Minnesota West Central Research and Outreach Center, Morris, MN.*

Holstein (HO) and crossbred cows from an organic grazing and low-input conventional herd were evaluated for activity and rumination from January 2014 to December 2017 at the University of Minnesota West Central Research and Outreach Center, Morris, MN. Within each herd (organic grazing or low-input), breed groups comprised HO ( $n = 114$ ), HO maintained at 1964 breed average level (H64;  $n = 83$ ); crossbreds comprised of Montbéliarde, Viking Red, and HO (MVH;  $n = 248$ ), and Normande, Jersey, and Viking Red (NJV;  $n = 167$ ). From May to October, organic grazing cows were on pasture, supplemented daily with 2.72 kg of corn per cow, and low-input cows were fed a TMR in an outdoor confinement lot. From November to April organic and low-input cows were fed a TMR in a compost barn or outwintering lot. Activity (reported in activity units per day) and rumination (reported in min per day) were monitored electronically using HR-LD Tags (SCR Engineers Ltd., Netanya, Israel). The PROC HPMIXED of SAS was used for statistical analysis and independent variables were herd, month, breed group, parity group and 2 and 3 way interactions of herd, month, breed group and parity group. Cow nested within breed group and herd was a random effect. All breed groups had similar daily activity in both herds. However, the H64 cows had lower rumination (495;  $P < 0.05$ ) compared with HO (529), MVH (519) and NJV (513) cows in the organic herd. In the low-input herd the H64 cows had lower rumination (483;  $P < 0.05$ ) compared with HO (512), MVH (507) and NJV (512) cows. In the primiparous group of the organic herd, H64 cows had lower rumination (495;  $P < 0.05$ ) than HO (520) cows, and multiparous H64 cows had lower rumination (496;  $P < 0.05$ ) than all other multiparous breed groups. In the primiparous group of the low-input herd, H64 cows had lower rumination (478;  $P < 0.05$ ) than HO (498) and MVH (497) cows, and multiparous H64 cows had lower rumination (489;  $P < 0.05$ ) than all other multiparous breed groups. In both herds, breed groups were active during the day and ruminated during the evening and night hours.

**Key Words:** crossbreeding, grazing, rumination

**391 Incorporation of feed efficiency into a selection index for Holstein cattle.** K. Houlahan\*<sup>1</sup>, F. Miglior<sup>1,2</sup>, M. Kargo<sup>3</sup>, Z. Wang<sup>4</sup>, C. Maltecca<sup>5</sup>, B. Gredler<sup>6</sup>, A. Fleming<sup>1</sup>, and C. F. Baes<sup>1</sup>, <sup>1</sup>*Centre for Genetic Improvement of Livestock, Department of Animal Bioscience, University of Guelph, Guelph, ON, Canada*, <sup>2</sup>*Canadian Dairy Network, Guelph, ON, Canada*, <sup>3</sup>*Center for Quantitative Genetics and*

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Feed efficiency (FE) is a trait currently under intense research worldwide. With feed costs accounting for over 50% of total operational costs on most dairy farms, there is a clear need for improvement in the efficiency of dairy cows' ability to convert feed to milk. Studies have shown there is genetic variation between FE of animals with similar production. Determining an optimal breeding strategy for improving FE in dairy cattle may be helpful in reducing feed costs, while maintaining or increasing production. The objective of this study was to estimate the expected genetic gains and monetary implications of including a measure of FE in a breeding program using different definitions of FE. Various breeding goals were modeled using ZPLAN+. A base scenario consisting of fat and protein yield, age at first service, first service to conception, days open and clinical mastitis was established. Five alternative scenarios of the base with the inclusion of various traits such as, RFI, DMI with a positive or negative economic value, production: feed intake ratio, and feed performance, were compared with results of the base scenario. Using genetic and phenotypic correlations, heritabilities and trait economic values, the effects of incorporating various measures of feed intake and FE were analyzed and compared. Annual genetic gain and monetary genetic gain were estimated for all scenarios. Long-term effects expected on both genetic gain and monetary genetic gain were assessed over a 20-year period. Preliminary results indicate an unfavorable trend for genetic gain and monetary genetic gain in relation to health and fertility traits when FE is included. The inclusion of various measures of FE appears to have minimal negative impact on the genetic gain and monetary genetic gain for production traits. Based on these results, further work is required to determine the optimal method to simultaneously improve health, fertility, production and FE.

**Key Words:** feed efficiency, breeding strategies, genetics

**392 Methods to compute reliabilities for genomic predictions of feed intake.** P. M. VanRaden and J. L. Hutchison\*, *USDA Animal Genomics and Improvement Lab, Beltsville, MD.*

For new traits without historical reference data, cross-validation is often the preferred method to validate reliability (REL). Time truncation is less useful because few animals gain substantial REL after the truncation point. Accurate cross-validation requires separating genomic gain from pedigree contributions and assuming that other animals with pedigrees less connected to the reference data will have less REL than validation cows. Fiveway cross-validation of residual feed intake (RFI) used data from 80% of the 3,965 US research cows to predict the other 20% and repeated the process 5 times to test predictions for all cows. However, RFI records were excluded from validation data if the cow had progeny in the reference data to ensure correct prediction direction. Pedigree REL for the validation cows was 13%, and their genomic REL was only 18% compared with 21% expected. Pedigree REL for elite young calves was 3%. After adjusting the discount factor to match expected with observed REL, their genomic REL was only 9%, which was less than the 12% previously estimated. Research cows often have paternal sibs, maternal sibs, or dams with RFI records, whereas most calves in other herds are  $> 2$  generations removed from any relatives with RFI records and thus have lower REL. Cross-validation of SCS records for these same 3,965 research cows gave REL estimates similar to those for RFI. Reliability of SCS was also estimated as genomic REL of national SCS predictions (72%) multiplied by the correlation of research herd

predictions with national predictions (0.39) squared, which resulted in 11% REL. Some evaluations report feed saved, which includes RFI plus the economic value for body weight composite (BWC). Inclusion of BWC added only about 7% to the REL of feed saved because RFI contributed much more genetic variance than BWC. Correlated yield traits contribute much variance to feed intake but not to RFI, which is independent of yield. Increases in genomic REL with further RFI data can be forecast. For young calves, such REL could be 12% with 5,000, 19% with 10,000, 31% with 20,000, and 52% with 50,000 cows in the reference population.

**Key Words:** feed efficiency, cross-validation, reliability

### 393 Indicator traits to predict dry matter intake in Holstein cattle.

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The cost of feed is the largest expense of a dairy farm, and this cost is rising. Feed intake traits such as DMI are highly desirable traits for dairy breeding programs. Measuring individual feed intake, however, is difficult and expensive. The use of predictor traits may be better suited to measure feed intake, as they are less expensive and easier to measure. Information such as mid-infrared spectroscopy (MIR), BW, and BCS have the potential to be predictor traits for DMI. MIR is used to analyze molecular vibration and rotation when a material is exposed to electromagnetic radiation. It is currently used worldwide to quantify milk components during routine milk analysis. MIR technology may provide a cost-effective opportunity to obtain predicted phenotypes for feed intake on many animals by taking advantage of technology that is currently used in regular milk recording. The objective of this study was to evaluate the efficacy of MIR, BW, and BCS to predict DMI and to determine the optimal predictor trait for DMI. Weekly milk samples were collected for 143 Canadian Holsteins ( $n = 2,775$ ) during routine milk recording and were sent to CanWest DHI for MIR spectral analyses. Milk, fat and protein yields ( $n = 2,775$ ), BW ( $n = 1,656$ ), and BCS ( $n = 1,656$ ) were also collected. Daily DMI (kg/d) for all cows ( $n = 2,775$ ) was recorded and averaged per lactation week with a mean (SD) of 85.33 (43.99). A prediction equation for DMI was produced using partial least squares regression from the MIR spectra of milk samples. Equations to predict DMI using BW and BCS were calculated to determine the optimal predictor trait for DMI. Further steps are needed to determine the ability of the prediction equations to estimate DMI.

**Key Words:** feed efficiency, mid-infrared (MIR), genetics

### 394 Dairy Wellness Traits from genomic testing with a control Holstein cow population compared to contemporary Holstein cows in a pasture production system.

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The University of Minnesota initiated a designed study of yield selection in 1964 that included an unselected control group of cows. The study continues at the West Central Research and Outreach Center (WCROC), Morris, Minnesota, and is currently part of the low-input sustainable and organic grazing dairy project. Control Holstein cows ( $n = 45$ ) were compared with contemporary Holstein cows ( $n = 64$ ) for wellness traits from the Clarifide Plus genomic test. Herd average

production during first lactation were 4,114 kg milk, 143 kg fat, 129 kg protein, and 3.2 SCS for the control cows and 6,563 kg milk, 241 kg fat, 209 kg protein, 2.5 SCS for the contemporary Holsteins. The control line of cows has not been evaluated in a pasture-based dairy production system. Cows were housed at the WCROC, a grazing herd, and calved for a first time from March 2011 to June 2017. All Holstein and control cows were tested during the summer of 2017 with Clarifide Plus and Dairy Wellness Traits (mastitis, lameness, metritis, retained placenta, displaced abomasum, and ketosis) were received during fall 2017 for all 109 cows. Independent variable for statistical analysis with PROC GLM was the fixed effect of genetic line. The control cows had significantly ( $P < 0.01$ ) lower Dairy Wellness Profit ( $-\$745$  vs.  $+\$402$ ) compared with the contemporary Holsteins cows, respectively. The control cows were significantly higher ( $P < 0.01$ ) for mastitis (108 vs. 102), lameness (106 vs. 101), and displaced abomasum (105 vs. 102) than contemporary Holstein cows, respectively. The control cows and contemporary Holsteins cows were not different for metritis (102 for both genetic lines) and retained placenta (101 for both genetic lines). The contemporary Holstein cows were higher ( $P < 0.05$ ) for ketosis (102 vs. 101) compared with the control cows. The control cows had a higher Wellness Trait Index ( $\$235$  vs.  $\$103$ ) compared with the contemporary Holstein cows. Future studies will compare the 2 genetic lines with genome-wide association analysis for production and health traits.

**Key Words:** genetic selection, organic, health

### 395 Heritability and genetic correlations of shape and size of lactation curves in Israeli Holsteins using geometric morphometrics.

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Routinely, genetic evaluations are based on 305-d lactations, which represent the size or magnitude of lactation curve but ignore the shape, an inherently multidimensional feature. We combined the methods of quantitative genetics and the geometric morphometrics (GM) to evaluate the heritability and genetic correlations of size and shape of lactation curves. The data were daily records of first parity milk production from January 2014 through January 2017 from 43 communal herds distributed throughout Israel. We proposed 2 geometrical shapes of lactation curves, one depicted by line graph and the other by orbital graph; using monthly records as the basis for estimating landmark coordinates, superimposition, and genetic evaluation. Lactation curve shapes were represented by a set of 2-dimensional coordinates. These landmarks were then superimposed using the Procrustes technique to extract shape information. The size of the line- and orbital-depicted lactation curve was recorded as the centroid size (CS), computed as the square root of the summed squared distances of each landmark from the centroid. Heritabilities and genetic and environmental correlations computed by the MTC REML individual animal model program for CS of the proposed shapes and total lactation are in Table 1. Similar heritability values and complete genetic and environmental correlations of the CS of the orbital lactation curve with the traditional method validate it as proxy for the size measure of lactation curves. The heritability of shape was 0.179 for the orbital-depicted lactation curve and 0.082 for the line-depicted lactation curve. These results demonstrate GM as a promising new approach to study the patterns of phenotypic and genetic variation of shape and size of lactation curve in dairy cattle.