1499V   Phenotypic and genotypic impact of milk components and bodyweight composite on dry matter intake. S. Toghiani*[1], P. M. VanRaden[1], K. L. Gaddis[3], M. J. VandeHaar[2], and R. J. Tempelman[2], [1]*Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD,* [2]*Michigan State University, East Lansing, MI,* [3]*Council on Dairy Cattle Breeding, Bowie, MD.*

Large data sets enable accurate estimation of feed requirements for individual milk components or cow maintenance. Phenotypic regressions are useful for nutrition management whereas genetic regressions are typically more useful for breeding programs. Dry matter intake (DMI) records from 6,338 lactations of 5,094 Holstein cows were predicted from phenotypes or genomic evaluations for milk components and body size traits. Statistical models included days in milk, age-parity subclass, trial date, management group, and bodyweight change during 28- and 42 d feeding trials in mid-lactation. Phenotypic regression estimates of DMI on milk (0.007 ± 0.008), fat (2.82 ± 0.13), and protein (5.32 ± 0.31) were much smaller than corresponding genomic regression (0.076 ± 0.029, 10.82 ± 0.60, and 7.88 ± 1.34) or sire genomic regression estimates multiplied by 2 (0.043 ± 0.054, 6.43 ± 1.14, and 6.66 ± 2.35). For milk standardized to 3.5% fat and 3.0% protein, estimated marginal feed costs totaled 18% of milk revenue by phenotypic regression, 46% by genomic regression, and 31% by sire genomic regression multiplied by 2. The energy-corrected milk formula assumes that 69% more DMI is required for fat than protein production with regressions of 0.122 for milk, 4.82 for fat, and 2.85 for protein whereas the new net merit formula (NM$ 2021) assumes that 20% more DMI is needed for protein than fat production with regressions of 0.12 for milk, 5.0 for fat, and 6.0 for protein, and a marginal feed cost of 32% of the milk price ($36.38/100 kg). Estimates of annual maintenance in kg DMI/ kg bodyweight/lactation were similar from phenotypic regression (5.8 ± 0.2), genomic regression (6.0 ± 0.4), and sire genomic regression multiplied by 2 (5.7 ± 0.7) and were revised upward to 4.5 in NM$ 2021. Multiple regressions on genomic evaluations for the traits in bodyweight composite (BWC) showed that strength was most associated with both bodyweight and DMI, agreeing with the current BWC formula, whereas other traits were less significant predictors, especially for DMI. Breeding programs should select smaller cows with negative RFI and produce more milk, fat, and protein to improve profit.

Key Words: feed intake, maintenance, body weight

1500V   Variance parameter estimation for age at puberty phenotypes under 2 levels of phenotype censorship. M. Stephen*[1,4], S. Meier[1], M. Price[1], J. E. Pryce[2,3], C. Burke[1], C. Phyn[1], and D. Garrick[4], [1]*DairyNZ, Hamilton, Waikato, New Zealand,* [2]*Agriculture Victoria Research, Bundoora, Victoria, Australia,* [3]*School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, Australia,* [4]*AL Rae Centre for Genetics and Breeding - Massey University, Hamilton, Waikato, New Zealand.*

Age at puberty (AGEP) is a moderately heritable trait in cattle that may be beneficial as an early-in-life predictor of an animal's genetic merit for lifetime reproductive success. Unfortunately, AGEP is difficult to measure precisely as animals must be observed frequently over several months. However, it is possible that genetic selection for AGEP could be successful using censored phenotypes. That is, when observations are less frequent and/or occur over a shorter time period. Our objectives for this study were 2-fold. First, to produce variance components for AGEP. Second, to investigate the implications of a simplified phenotyping strategy on the genetic evaluation of AGEP, where censoring of the phenotype was increased. We measured AGEP in a closely monitored population of approximately 500 Holstein-Friesian heifers, born in 2015 and managed under a seasonal, pasture-based dairy system. Animals were blood tested weekly from approximately 240 to 440 d of age and were deemed to have reached puberty when blood plasma progesterone (BP4) elevation (>1 ng/mL) was detected in 2 of 3 consecutive blood tests (AGEP_Weekly). To simulate a simplified phenotyping strategy based upon monthly herd visits (AGEP_Monthly), we selectively disregarded data from all but 3 blood tests, when animals were approximately 300, 330 and 360 d of age (SD = 14.5 d). The posterior mean of estimated heritabilities for AGEP_Weekly was 0.54, with a 90% credibility interval (CI) of 0.41 to 0.66, whereas it was 0.44 (90% CI 0.32 to 0.57) for AGEP_Monthly. The correlation between EBV for AGEP_Weekly and AGEP_Monthly was 0.87 (90% CI, 0.84 to 0.89). We conclude that, in this population, AGEP is a moderately heritable trait. Further, increasing phenotype censorship from weekly to monthly observations over a shorter period did not alter the main conclusions of this analysis. Our results support the use of censoring to reduce costs and logistical challenges associated with collection of puberty phenotypes.

Key Words: puberty, fertility, heritability

1501V   The increasing popularity of embryo transfer has implications for US dairy cattle fertility evaluations. A. M. Miles*, J. L. Hutchison, and P. M. VanRaden, *Animal Genomics and Improvement Laboratory, USDA, Agricultural Research Service, Beltsville, MD.*

Embryo transfer (ET) use has grown exponentially, accounting for 11% of US dairy calves born in 2021. However, the trend in ET breeding event reporting does not parallel the ET calving rate and this lack of congruence can interfere with both national evaluations and on-farm fertility management. Completely censoring ET-associated records is not necessarily the desired approach, as these represent the most elite animals and herds, and unreported ET could also bias fertility trait evaluations in the population. New edits to account for incorrect ET reporting were developed and applied to data extracted from the National Cooperator Database, maintained by the Council on Dairy Cattle Breeding, in December 2021 representing the most current information available on ET usage. Impact on sire conception rate (SCR) is shown as an example. Reported mating types were matched with recorded birth types to assess ET reporting error rates. Only 1% of ET calves correspond to ET breeding events, 2% are incorrectly reported as artificial insemination, and 97% have no associated breeding event. Herdyears that reported > 10% of calves born by ET but less than half of the expected ET breeding events given the number of ET calves born were removed, maximizing data preservation while minimizing confounding bias. SCR was recalculated for this new data set and subsequent analysis showed that censoring herdyears with inconsistent ET reporting has a negligible effect on SCR overall, except in the case of elite young bulls popular for ET use. Similar edits for unreported ET had larger effects on heifer conception rate than cow conception rate or SCR and might be needed for other fertility-related traits. Censoring herdyears with inconsistent ET reporting will affect elite new bulls popular for ET use and having a huge influence on breeding programs, but differences for most other bulls were negligible. The rapid increase of ET is likely to continue as advanced reproductive technologies become more affordable. Improved ET reporting is also needed to facilitate the delivery of accurate fertility evaluations.

Key Words: embryo transfer, conception rate, fertility

1502V   Signatures of selection in Cholistani and Sahiwal cattle breeds of Pakistan. H. Mustafa*[1], H. Kaul[1], G. Bilal[2], K. Farooq[3], I. Mohsin[1], K. Jong-Joo[4], and T. Sonstegard[5], [1]*University of Veterinary*