

Breeding and Genetics: Dairy Cattle Breeding

M60 Differences in the production and reproduction traits of embryo transfer full siblings living under different and identical conditions. J. Bezdicsek¹ and J. Riha², ¹*Agriresearch Rapotin Ltd., Rapotin, Czech Republic*, ²*Research Institute for Cattle Breeding, Ltd., Rapotin, Czech Republic*.

Embryo transfer plays an important role in terms of using valuable maternal genotypes. The offspring of such embryo transfers are found not only on donors' farms but also on other farms. The aim of this study was to evaluate differences in milk production and reproduction traits in full siblings living on different farms. Evaluation was made in first lactation for 110 sibling pairs (experimental group). For the evaluation, differences full siblings under different conditions comparison was made for milk production differences in full siblings (n = 620) living on identical farms (control group). For production traits we observed milk production in first lactation (in kg), fat production (in % and kg) and protein production (in % and kg). For reproduction we observed age at first calving. The data were analyzed with Statistica 8 (2008, StatSoft Inc., Tulsa, OK) using descriptive statistics and t-tests. Analyzed were Holstein cows (H100) born in the Czech Republic in the years 2000–2005. Observed differences between full sibling pairs under different and under identical conditions (farms) were the following (in parentheses standard deviation): milk production in kg 1149.9 vs. 998.9^{n.s.} (1122.8 vs. 798.1 kg); fat content in percent 0.42 vs. 0.38^{n.s.} (0.31 vs. 0.30%); fat production in kg 48.95 vs. 39.86* (40.81 vs. 31.29 kg); protein content in per cent 0.21 vs. 0.17* (0.16 vs. 0.14%); protein content in kg 38.9 vs. 31.6* (33.63 vs. 25.44 kg). For age at first calving the differences between experimental and control group were as follows: 76.6 vs. 65.4* (56.26 vs. 54.9 d). Significant differences is marked * ($P \leq 0.05$); n.s. (nonsignificant). Even though in full sibling pairs, living under different conditions, was found for milk production greater differences (1149.9 kg milk) these differences were not statistically significantly greater than full sibling pairs living under identical conditions. For milk composition and age at first calving the differences were statistically significant. Of the 2 groups there was greater variability in siblings living under different conditions.

Key words: milk production, full siblings

M61 Female fertility in a Guzerat dairy herd: Heterogeneity of variance components for calving intervals. J. C. C. Panetto^{1,2}, J. E. Val³, C. R. Marcondes⁴, M. G. C. D. Peixoto², R. S. Verneque², J. B. S. Ferraz⁵, and B. L. Golden⁶, ¹*Curso de Veterinária, Universidade de Uberaba, Uberaba, MG, Brazil*, ²*Embrapa Gado de Leite, Juiz de Fora, MG, Brazil*, ³*Faculdade de Medicina de Ribeirão Preto - USP, Ribeirão Preto, SP, Brazil*, ⁴*Embrapa Pecuária Sudeste, São Carlos, SP, Brazil*, ⁵*Faculdade de Zootecnia e Engenharia de Alimentos - USP, Pirassununga, SP, Brazil*, ⁶*Dairy Science Department, California Polytechnic State University, San Luis Obispo*.

Our objectives were to determine if variance components of calving intervals varied with age and if considering calving intervals as a longitudinal trait would be a superior approach for fertility analysis of zebu dairy herds. Calving records from females born from 1940 to 2006 in a Guzerat dairy subpopulation in Brazil were analyzed in the present study. Contemporary groups, formed by year and farm at birth or at calving, ages at calving, equivalent inbreeding coefficients and day of the year were included as fixed effects in the models. Calving interval (CI) was first analyzed by fitting a random regression model

with Legendre polynomials of order 3 for the fixed effect of age at calving, and random effects of animal and permanent environment. In a second approach, a multivariate analysis was conducted, including age at first calving (AFC), first calving interval (CI1), calving interval for young females (CIY) and calving interval for mature females (CIM). Finally, a bivariate analysis was performed for AFC and CI where calving intervals were considered as a single trait in a repeatability model. Additionally, ranking of sires were compared among approaches. Calving intervals decreased with age until females were about 80 mo old, remaining nearly constant after that age. A quasi-linear increase of 11.5 d on the calving intervals was observed for each 10% increase in the female's equivalent inbreeding coefficient. Heritability of AFC was 0.37 from both analyses. In the case of CI, the genetic variance ratios ranged from 0.064 to 0.141, depending on the approach and on the ages at calving. Differences among genetic variance components for calving intervals observed along the animal's lifetime confirmed the longitudinal aspect of this trait, indicating the importance of such consideration when accessing fertility of zebu dairy females in situations where the available information relies on their calving intervals. Changes observed in the ranking of sires suggested that the genetic progress of the population can be affected by the approach chosen for the analysis of calving intervals.

Key words: calving intervals, female fertility, heterogeneous variances

M62 Detection of early pregnancy and embryonic loss in dairy cows using BioPRYN and a NEW PSPB-based ELISA. J. R. Branen¹, J. O. Giordano², C. Passavant¹, J. M. Howard¹, P. M. Fricke², and R. G. Sasser¹, ¹*BioTracking LLC, Moscow, ID*, ²*University of Wisconsin, Madison*.

BioPRYN, a blood-based pregnancy test is used in reproductive management of cattle and utilizes antibodies developed against pregnancy-specific protein B (PSPB). There were 2 objectives of this study: 1) measure the number of days since insemination in dairy cows for a change in pregnancy classification using BioPRYN and a new PSPB-specific ELISA (NEW), 2) measure the number of days since induced embryonic loss (in a subset of cows from 1) for a change in pregnancy classification using BioPRYN and NEW. The NEW assay was developed using a PSPB obtained after Butler et al. (1982. *Biol. Reprod* 26:925–933). Serial blood samples, collected 3 times a week until 29d after timed AI (TAI) from 60 lactating crossbred (75% Holstein, 25% Jersey) cows, were analyzed and categorized for time of changing from an Open status or, changing, after embryonic death, from a Pregnant status (to recheck or open) using the BioPRYN and NEW assays. Sampling continued until 39d for 30 cows found pregnant at 29d using transrectal ultrasound (TUS) while open cows were not analyzed further. At 39d pregnancy was reconfirmed by TUS and 7 cows were treated with PGF2 α (PGF; 25 mg, i.m.; n = 4) or an infusion of 120 mL hypertonic saline (INF; 25%, v/v; n = 3) into the uterine horn containing the embryo. Blood samples were then collected every 12h for 6.5d and daily from 6.5d to 10d. Death of the embryo was confirmed by TUS by cessation of an embryonic heartbeat. BioPRYN categorized the 30 pregnant cows as positive at 25d (n = 20), 27d (n = 7) and 29d (n = 3). NEW was compared with BioPRYN for 11 of those cows and provided positive result of all at 25d while BioPRYN classified 5 at 25d, 4 at 27d and 2 at 29d. Following embryonic death in 7 cows, NEW changed the classification at 0, 1, 1, 2, 2, 3, and 4d

earlier than BioPRYN. The NEW can add to the value of BioPRYN in testing for early pregnancy and when there is early embryonic loss.

Key words: PSPB, pregnancy loss, blood-based pregnancy detection

M63 Comparison of BioPRYN and a new pregnancy-specific protein B (PSPB) enzyme-linked immunosorbent assay (ELISA) for determination of early pregnancy status in dairy cattle. J. R. Branen^{*1}, C. Passavant¹, A. Phatak², D. Snider³, J. Azevedo⁴, J. M. Howard¹, D. Pals¹, and R. G. Sasser¹, ¹BioTracking LLC, Moscow, ID, ²Consulting Veterinarian, Waterford, CA, ³Strategy Lab & Dairy Consulting, Visalia, CA, ⁴Alta California, Hilmer, CA.

Pregnancy specific protein B (PSPB) is a protein fraction derived from ruminant placenta that can be used to develop immuno-assays to detect placental proteins in the maternal circulation. Since 2002 a PSPB-based ELISA, BioPRYN, has been commercially used for detection of pregnancy in cattle at least 30 d since last heat (DSLH) and after 89 d in milk (DIM). The objective of this study was to compare the accuracy of BioPRYN and a new PSPB-based ELISA (NEW) for pregnancy status at 28 ± 2 DSLH. NEW was developed using a PSPB protein fraction isolated as described in 1982 (Biol. Reprod. 26:925–933). Lactating Holstein (n = 385) and Jersey (n = 67) cows 70 or more DIM from 10 commercial dairies in California were used in the study. Blood samples were collected at 28 ± 2 DSLH (T1). These and subsequent samples were assayed for pregnancy status using BioPRYN and NEW. A second blood sample was collected at 33–42 DSLH (T2) concurrently with rectal palpation (RP) or trans-rectal ultrasonography (TUS) by trained professionals. A matching result of T2 ELISAs with RP or TUS was considered the true value for pregnancy status. A mismatch at T2 was rectified by ELISA and RP or TUS at 3–10 d following T2 (T3). Animals not available for T3 analysis were removed from the study (n = 82), leaving a total of 370 cows used for analysis. BioPRYN showed 100% sensitivity (100 X pregnant or recheck at T1 or T2/ true pregnant at T2 or T3) at 28 DSLH or later (Truly pregnant, n = 137). NEW showed 100% sensitivity at 28 DSLH or later (Truly pregnant, n = 137) and >98% (95% CI: 95–99%) with the inclusion of 27 DSLH animals (Truly Pregnant, n = 196). Ten true open animals at T2 and positive by BioPRYN at T1 (between 70 and 88 DIM) were categorized open at T1 by NEW. NEW shows promise for earlier testing after insemination and earlier testing in the postpartum period.

Key words: PSPB, blood-based pregnancy detection

M64 Survey of genetic selection practices on pasture-based dairy farms in the United States. K. D. Gay^{*}, T. D. Nennich, and M. M. Schutz, *Purdue University, West Lafayette, IN.*

A survey was mailed to dairy graziers across the country to ascertain their genetic selection practices, but included background information on feeding, production, and health. The overall aim was to collect data to allow eventual development of a genetic selection index. Mailing addresses were obtained from extension cooperators, NRCS advisors, and commercial companies. Producers were able to respond to the survey by mail or internet. Respondents to the survey included 77 farmers in 22 states. Producers were asked questions about the grazing history of their herd and average milk and component production. They were also asked questions about breeding practices to determine number utilizing seasonal grazing and to gain an understanding of breeds present in their herds. Producers were asked to rank genetic traits by the amount of selection pressure they felt should be applied to those commonly available. Traits were ranked from negative 5 to posi-

tive 5 with negative being selection against a trait and positive being selection for a trait. Respondents averaged 15.95 ± 9.12 years of grazing history, 129.1 ± 128.52 milking head, and grazed 224.5 ± 60.47 d a year. Production was 20.9 ± 4.89 kg of milk per cow per day, 4.0 ± 0.42% milk fat, and 3.6 ± 0.23% milk protein. Also, 46.7% of producers participated in seasonal calving, defined as 75% of cattle calving in any 3 mo window. Further, 70% utilized crossbreeding to the extent that at least 10% of the herd was crossbred. Percentage of herds that included at least some genetics from major breeds were: 70% Jersey, 65% Holstein, 26.7% Ayrshire, 21.7% Swedish or Norwegian Red, and 20% Milking Shorthorn. The average rank of genetic traits were: productive life 3.87, udder composite 3.57, somatic cell count –3.15, feet and legs 3.08, daughter pregnancy rate 3.05, fat percentage 2.97, calving ability 2.95, protein percentage 2.83, body size –2.73, fat yield 2.69, protein yield 2.56, and milk yield 2.27. It appears that pasture-based dairy producers place more emphasis on traits relating to longevity and fertility and less on production traits than the most widely used US selection indexes.

Key words: grazing, genetics, management

M65 Estimating field conception rates for Holstein sires in US herds (ACE index) and conception rate correlation from the same sires used for AI after natural estrus and timed AI breedings. A. H. Souza^{*1,2}, H. Rivera², P. Crump¹, and V. Cabrera¹, ¹Department of Dairy Science, University of Wisconsin, Madison, ²Accelerated Genetics, Baraboo, WI.

The aim of this retrospective study was to validate a fertility index of Holstein sires from one AI stud in the United States (accelerated conception evaluation – ACE index), using for comparison the sire conception rate index (SCR, AIPL-USDA) as the industry official standard. A second objective was to compare conception rate (CR) rankings from same sires used for AI after natural estrus (EAI) and timed-AI (TAI) breedings. Confirmed CR records from 3 national data centers (AGSource, ATA, DRMS) and farm backups from non-testing herds were merged and used as basis for this data analysis. Criteria edits in the data set were: breedings from last 4 years with confirmed conception results; sires with 300 breedings minimum; herd's CR within 20 and 60%; 30 breedings per herd minimum; sires used in a minimum of 10 herds with no more than 40% breedings in one herd; 1 to 5 breedings occurring within 45 to 375 DIM; and cows within 1 to 5 lactations. After editing 1,142,859 breeding records were available for analysis. A subset of the data (n = 801,636) was used to classify breeding codes into either AI to estrus or timed-AI based on weekly insemination profile in each herd. The procedure Glimmix of SAS took into account effects of state, farm, cow id, breeding month, year, parity, DIM at breeding, and service sire. Then, sire fertility classification was based on standard deviations from the population mean. The Spearman-correlation between ACE and SCR was 0.79 ($P < 0.01$). The same model was used independently for the 2 differing breeding codes and fertility classification within breeding code was done for sires with >700 (94 sires) and again for >1,000 (n = 56 sires) breedings in both EAI and TAI. Spearman-correlation of the rankings produced with EAI and TAI were 0.81 ($P < 0.01$; for >700 breedings) and 0.84 ($P < 0.01$; for >1,000 breedings). Thus, these results indicate a significantly good correlation between ACE and the industry gold standard index-SCR. In addition, conception rankings of the same sires used for EAI and TAI were highly correlated.

Key words: sire fertility, conception rate, dairy cow

M66 Effects of dam's dry period length on heifer development.

H. D. Norman and J. L. Hutchison*, *Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD.*

Effect of dam's days dry (DD) on calving ease (CE) score (1–5), still-birth (SB) rate, heifer age at first breeding (AFB), and heifer survival to first calving (SURV1) was investigated with US Holstein records from 1997 through 2010: 774,821 for CE, 347,462 for SB, 27,932 for AFB, and 300,725 for SURV1. The small number of records for AFB was because breeding records for heifers were not stored until 2003 and reporting is minimal. Heifer SURV1 was a binary trait (0 = no, 1 = yes) and included only female calves. Dam calving date was required to be within 10 d of expected calving date (previous calving date + previous days open + 280) to ensure producers knew calving date and dry period length. Dam DD were grouped into 12 categories: 0–30, 31–35, 36–40, ..., 66–70, 71–80, 81–90, 91–120 d. The linear fixed-effects model for analysis of CE and SB included dam calving herd-year and year-state-month, parity, calf sex, and DD category; the AFB model included heifer breeding herd-year and year-state-month as well as DD category. The SURV1 model included dam calving herd-year and year-state-month, dam parity, and heifer parent average for daughter pregnancy rate. For AFB and SURV1 analyses, heifer birth dates were required to be before January 2008 to allow time for completion of a first lactation. Calving difficulty increased linearly as dam DD increased until about 70 d and then leveled off: 1.29 for 0–30 DD, 1.36 for 56–60 DD, and 1.42 for 91–120 DD; corresponding SB were 4.15, 2.36, and 3.33%. Differences between DD categories were all significant ($P < 0.0001$) for CE and SB. For corresponding dam DD, heifer AFB were 463, 458, and 458 d; corresponding heifer SURV1 were 64.6, 70.1, and 68.8%. Heifer AFB and SURV1 differences were significant ($P < 0.05$) between 0 and 30 and 56–60 DD but nonsignificant between 56 and 60 and 91–120 DD.

Key words: days dry, calving ease, heifer survival

M67 Changes in the use of young bulls. K. M. Olson¹, J. L. Hutchison², P. M. VanRaden², and H. D. Norman², ¹*National Association of Animal Breeders, Columbia, MO*, ²*Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD.*

Availability of genomic information since 2008 has increased accuracy of genetic evaluations for young bulls in Holstein (HO), Jersey (JE), and Brown Swiss (BS). As a result, AI organizations have been aggressively promoting young bulls and producers have been using young bulls more extensively. Number of inseminations by breeding year and service sire (SSR) age at the time of insemination was investigated using US breeding records from 2007 through 2010. There were a total of 65,686 BS, 14,319,994 HO, and 771,766 JE inseminations. Age of SSR was categorized into 3 groups: young bulls (0.8 to 3.9 yr), first crop sires (4.0 to 7.9 yr), and older sires (≥ 8.0 yr). There was an increased use of young bulls between 2007 and 2010 for HO and JE (Table 1); increase in inseminations by young bulls was 14 percentage units for HO and 7 percentage units for JE. This was not surprising, because HO gain more in accuracy from genomics than the other breeds. First crop sire usage decreased for HO (14 percentage units) and JE (3 percentage units). Older sire usage remained constant at 15 to 18% for HO, 16 to 23% for JE, and 33 to 36% for BS. Economic (\$) rankings have been converted to percentile rankings since 1980 with the average of proven bulls being 50%; as a comparison, the 294 young HO bulls currently being marketed averaged +459 Net Merit and a 83 percentile ranking. When young bulls have reliabilities $>60\%$, simulations indicate that the optimum usage of young bulls may increase to >

90% of the market share. Current average genomic reliabilities for Net Merit are 73, 60, and 48% for HO, JE, and BS, respectively. The shift to increased inseminations to young bulls is likely to continue.

Table 1. Percentages of inseminations by breeding year, service sire (SSR) age, and breed

Breeding year	Service-sire age (yr)	Brown Swiss	Holstein	Jersey
2007	0.8 - 3.9	35	29	25
	4.0 - 7.9	29	56	55
	≥ 8.0	36	15	19
2008	0.8 - 3.9	32	30	27
	4.0 - 7.9	33	52	50
	≥ 8.0	35	18	23
2009	0.8 - 3.9	33	39	31
	4.0 - 7.9	33	44	50
	≥ 8.0	34	17	19
2010	0.8 - 3.9	33	43	32
	4.0 - 7.9	34	42	52
	≥ 8.0	33	15	16

Key words: breeding, insemination, service-sire age

M68 Body condition score comparisons of crossbred Normande-sired cows with herd mates sired by Ayrshire, Holstein, and Jersey. D. E. Brown* and C. D. Dechow, *The Pennsylvania State University, University Park.*

The objective of this study was to investigate the body condition score (BCS) of Normande sired crossbred cows with their herd mates sired by Ayrshire, Holstein, and Jersey. Eight farms in the Northeastern states of Massachusetts, New York, Pennsylvania, and Vermont were visited once during the months of January or February to BCS. The farms varied from year round confinement with large amounts of concentrate supplementation to herds with little confinement and minimal concentrate or silage supplementation. Data included observations for 46 Normande sired crossbreds, 52 Ayrshire sired, 263 Holstein sired, and 55 Jersey sired cows. 42 of the Ayrshire sired cows, 254 Holstein sired cows, and 42 Jersey sired cows were purebred. The Mixed procedure of SAS 9.1.3 was used to analyze the data. Significant fixed effects included days in milk ($P < 0.05$) and sire breed ($P < 0.0001$). Random effects included dam breed and farm. The Normande sired crossbreds had a significantly higher least-square-means for BCS (3.64) than cows from other breeds. Ayrshire cattle had the second highest least-squares-means estimate (2.76), followed by Holstein (2.61) and Jersey (2.35). The Ayrshire sired cow's estimated BCS was significantly higher than Jersey, but not significantly higher than Holstein. Holstein and Jersey sired cows were not significantly different from each other. These results suggest that crossbreeding with Normande may result in substantially higher levels of BCS in a range of herd environments.

Key words: Normande, crossbreed, Ayrshire

M69 Use of cow culling to help meet compliance for somatic cell standards. H. D. Norman and J. R. Wright*, *Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD.*

Stricter SCC standards are expected in the United States. The relationship between a single high herd test-day SCC and SCC noncompliance was examined for US DHI herds, and the use of cow culling for maintaining herd compliance was investigated. Data were SCS from 14,346 herds with 15 to 26 tests from January 2009 through October 2010 and ≥ 10 cows for all tests. Cow SCC were derived from cow SCS by $SCC = 2^{(SCS - 3)}(100,000)$. Herd test-day SCC was a proxy for bulk tank SCC and was determined by weighting individual cow SCC by test-day milk yields. Herd test-day SCC was used to determine whether a herd would be SCC noncompliant under current or proposed US standards because 3 of 5 consecutive SCC tests exceeded 750,000, 600,000, 500,000, or 400,000 cells/mL. Percentage of herds that were SCC noncompliant 4 mo later for each SCC limit was determined for starting dates of October 2009, February 2010, and June 2010. Effectiveness of 3 different culling approaches was examined: culling cows with a high (above limit) current SCC, culling cows with a high index of previous and current SCC, and culling all cows above a designated parity. The culling objective was to eliminate cows that were likely to have a high SCC for each of their next 4 tests. Culling was simulated by deleting various percentages (1 to 5) of cows with high SCC from the herd when a herd test-day SCC exceeded one of the alternative limits. Herd-test-day SCC were recalculated without the high-SCC cows so that herd compliance for the next 4 tests could be compared with compliance without simulated culling. For herds with a starting test-day SCC of $>400,000$ cells/mL and no subsequent culling for SCC, percentage of noncompliant herds 4 mo later was 55% for October 2009, 62% for February 2010, and 66% for June 2010. Culling 5% of high-SCC cows lowered herd noncompliance to 46, 50, and 55% for the same starting months; culling cows with parity >4 reduced herd noncompliance to 48, 53, and 56%, respectively.

Key words: culling, somatic cell count, milk quality

M70 The association of high and low parent average with performance for yield, somatic cell score, and productive life in individual herds. C. D. Dechow^{*1}, H. D. Norman², R. C. Goodling¹, and J. R. Wright², ¹Pennsylvania State University, University Park, ²Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD.

There have been efforts to demonstrate to dairy producers the value of genetic selection by evaluating response to selection within their own herds. The objective of this study was to evaluate how frequently results conform to expectations for various traits and for herds of varying sizes. Parent averages (PA) and standardized records of milk yield, fat yield, protein yield, somatic cell score (SCS), and productive life (PL) were obtained from the Animal Improvement Programs Laboratory at USDA for 1,042,361 sire-identified Holstein cows that calved from 2005 through 2009 in 3334 Pennsylvania herds. Parent averages were obtained from evaluations occurring before a cow's first calving date to prevent part-whole bias. The top 25% (Q1) and bottom 25% (Q4) of cows for PA were identified within each herd and year of calving for each trait. The mean milk, fat and protein yield, SCS, and PL in Q1 and Q4 was determined for all herd-years. Results conformed to expectations when the average for Q1 exceeded the average for Q4. Most herd-years had higher values for Q1 cows than Q4 cows regardless of the number of sire-identified daughters present in the herd, with results ranging from 60% for PL to 78% for fat yield. The mean difference in PA from Q1 to Q4 for fat yield was 34 kg, which was close to the phenotypic difference in fat yield (36 kg). For productive life, the mean difference in average PA from Q1 to Q4 (4.8 mo) was greater than the phenotypic difference (1.5 mo). Greater than 89% of herd-years met expectations for yield traits when the number of cows

exceeded 10 per quartile, compared with 74% of herd-years for SCS and 67% of herd-years for PL. All herds with 125 or more cows per quartile met expectations for yield traits compared with 98% for SCS and 68% for PL. Within-herd comparison of top and bottom cows for PA demonstrated a favorable response to selection for yield traits even in herds with relatively few sire-identified daughters. Results were less predictable for lower heritability traits, but the majority of herd-years still conformed to expectations.

Key words: parent average, genetic selection

M71 Genetic differences between New Zealand and North American dairy cows alter milk production and gluconeogenic enzyme expression. H. M. White^{*1}, S. S. Donkin¹, M. C. Lucy², T. M. Grala³, and J. R. Roche³, ¹Purdue University, West Lafayette, IN, ²University of Missouri, Columbia, ³DairyNZ Ltd., Hamilton, New Zealand.

Continuous selection of dairy cows for production traits may alter the regulation of metabolic pathways. High-producing North American (NA) cows produce more milk and have a larger degree of somatotrophic axis uncoupling than less intensively selected New Zealand (NZ) cows. The objective of this study was to determine if production-based selection priorities (i.e., NA cows) have altered the regulation of the gluconeogenic pathway differently than selection priorities based on production and longevity traits (i.e., NZ cows). In this study, NZ (n = 27) and NA cows (n = 27) were monitored from 1 wk before calving to 12 wk post calving. Cows were pasture-fed and supplemented with 0, 3, or 6 kg DM of concentrate/d. Liver biopsy samples were collected at -7, +7, and +28 d relative to calving (DRTC) for mRNA analysis. Milk production of NA cows was greater ($P < 0.05$) during wk 5 to 11 postpartum and concentrate supplementation increased ($P < 0.05$) milk production for both NA and NZ cows. There was no genotype (NA vs. NZ) by diet interaction on blood glucose, NEFA, or insulin. Expression of pyruvate carboxylase (PC) mRNA was increased ($P < 0.001$) at +7 and +28 DRTC relative to -7 DRTC (3.04 and 2.42 vs. 1.25 ± 0.13 arbitrary units) and expression of cytosolic phosphoenolpyruvate carboxykinase (PEPCK-C) mRNA was increased at +28 compared with -7 and +7 DRTC (4.78 vs. 2.18 and 2.48 ± 1.41 arbitrary units). Expression of PC mRNA tended to be greater ($P = 0.12$) in NZ cows and declined with concentrate supplementation ($P < 0.05$) in both NZ and NA cows. Gluconeogenic enzyme expression in liver increased postpartum in both NZ and NA cows, with the 2 strains tending to differ for PC expression (greater in NZ cows). Grain supplementation reduced PC mRNA expression regardless of genetic strain. This project was supported in part by DairyNZ, Ltd. and in part by Grant no. 2009-35900-05970 from the USDA National Institute of Food and Agriculture.

Key words: pyruvate carboxylase, genetic selection, concentrate supplementation

M72 Verification of factors to estimate daily milk yield from one milking of cows milked twice daily. M. M. Schutz^{*1} and H. D. Norman², ¹Purdue University, West Lafayette, IN, ²USDA-ARS Animal Improvement Programs Laboratory, Beltsville, MD.

The objective of this research was to verify factors to predict daily milk yield when milk is sampled once per day for cows milked twice (2x) per day. Milk weights for both milkings were recorded automatically by 30 herds and collected by Dairy Herd Improvement supervisors. Data was split into 2 subsets for developing (FACT) and testing

(TEST) factors. Following edits, 179,064 daily milk weight records of 2941 first lactation (L1) cows and 298,905 records of 4757 later lactation (L2) cows remained in FACT and 177,299 records of 2120 L1 cows and 335,692 records of 3319 L2 cows remained in TEST. Factors currently in use to adjust single milking yields for milking interval (MINT) were applied. Also, 3 methods were compared with estimate factors or equations to predict daily milk yield. First, factors were estimated as the ratio of the sum of daily yield to the sum of partial yield within a parity-MINT class (13 intervals in 2 parities) [Method 1] or as the sum of the ratios of daily yield to partial daily yield for each cow-day divided by the number of cow-days within parity-MINT class [Method 2]. Resulting factors from both methods were smoothed, applied to data, and residuals were regressed on days in milk (DIM) for FACT and applied to TEST. Regression equations ($n = 168$) were also developed within parity-MINT-DIM classes ($2 \times 7 \times 12$) [Method 3] to jointly account for MINT and DIM. Separate factors were derived for milking 1, and 2, for L1 and L2. Method 3 resulted in consistently strongest correlations between estimated and actual yields, and smallest variances of estimates, and root mean squared errors (rMSE) for milkings in L1 and L2 for FACT. When applied to TEST, Method 1 resulted in rMSE of 2.07 (Milking 1, L1), 2.12 (Milking 2, L1), 2.64 (Milking 1, L2), and 2.85 kg (Milking 2, L2); compared with rMSE of 2.13, 2.26, 2.68 and 2.83 kg, respectively, from current factors for the same milkings for L1 and L2. Methods 1 and 3 provide more accurate prediction of daily milk weight from a single milking for herds milking 2x daily than factors currently in use.

Key words: milking interval, adjustment factor, milking frequency

M73 Estimation of daily yield of major fatty acids from single milking. V. Arnould^{1,2}, E. Froidmont⁴, H. N. Nguyen⁵, F. Dehareng⁵, P. Dardenne⁵, A. Gillon^{2,6}, N. Gengler^{2,3}, and H. Soyeurt^{2,3}, ¹CONVIS, Herdbuch Service Élevage et génétique, Ettelbruck, Luxembourg, ²University of Liège, Gembloux Agro Bio-Tech, Animal Science Unit, Gembloux, Namur, Belgium, ³National Fund for Scientific Research, Brussels, Belgium, ⁴Production and Sectors Department, Walloon Agricultural Research Centre, Gembloux, Namur, Belgium, ⁵Quality of Agricultural Products Department, Walloon Agricultural Research Centre, Gembloux, Namur, Belgium, ⁶Walloon Breeding Association, Ciney, Namur, Belgium.

There are cost savings when the frequency of milk recording is reduced. Milk recording organizations have implemented alternative schemes that rely on milking interval (MI), but MI can be unreliable. Moreover, nothing is available for milk fatty acids (FA). The aim of this study was to build a model for estimating accurately the daily yields of major FA from single milking without using the MI. The hypothesis was that MI can be reflected by the changes of milk yield and composition. Five Holstein cows were followed generally every day at each milking between March 2008 and December 2010. FA were measured by mid-infrared. The database contained 1,440 records. Eight models were tested to estimate daily yields from morning or evening milking. Different effects were included progressively. The first ones were related to the characterization of the milk production (i.e., days in milk, month of calving, month of test, milk yield, and lactation number). The other effects were related to the milk composition (i.e., fat and protein contents). Models were compared from the coefficient of determination and the mean square errors between estimated and observed daily yields. Results showed that R^2 were higher when the milk composition effects are introduced in the model. For the different studied FA traits, R^2 ranged between 0.87 and 0.88, when daily yields were estimated from morning milking and between 0.75 and 0.86

when daily yield were estimated from evening milking. By comparison, the model approved by ICAR and proposed by Liu et al. in 2000 gave R^2 ranged from 0.81 to 0.84 from morning milking; and from 0.74 to 0.85 from evening milking. Therefore, the introduction of these milk composition effects permit to replace the MI. It was also observed that daily yields estimated from evening data are less accurate than those estimated from morning data. After a larger validation, the best accurate model could be used to evaluate the fatty acid data collected in alternate milking recording and used for breeding purposes.

Key words: milk, fatty acid, daily prediction

M74 Comparison of lactation performance in a panel of genetically diverse inbred mouse strains. D. L. Hadsell^{*1}, W. Olea¹, J. Wei², L. A. Hadsell¹, and P. Williamson², ¹Baylor College of Medicine, Houston, TX, ²The University of Sydney, Sydney, NSW, Australia.

Inbred mouse lines have been a powerful tool in the mapping and identification of genes underlying a variety of different qualitative and quantitative traits. Their use in mapping lactation-related traits has been limited. Recently, the application of mapping panels based on existing inbred mouse strains has had some success in identifying quantitative trait loci. The current study compared quantitative indices of lactation performance among a panel of inbred mouse strains with the ultimate goal of apply this data with association mapping strategies to identify potential genes determining variation in milk production. Females from each of 32 inbred strains ($n = 8$ mice/strain) were studied during the first 8 d of their second lactation. Weight gain (LWG) of cross-foster litters (10 pups/litter) served as the primary indicator of milk production (19.9 ± 8.9 g, mean \pm S.D.) and varied ($P < 0.0001$) among strains (range 5.3 – 32.1 g). The number of pups born per litter (7 ± 3) also varied ($P < 0.0001$) among strains (range 4 – 13) and was significantly correlated to crossfoster litter gain ($r = 0.47$, $P < 0.0001$). Maternal body weight and maternal food intake also had significantly positive correlations to crossfoster litter gain ($P < 0.0001$). Initial haplotype association analysis using the 132 k SNP database publicly available from the Broad Institute identified suggestive ($P < 10^{-5}$) associations to LWG on chromosomes 4, 11, and 13. These data indicate that significant phenotypic variation exists among genetically inbred mouse strains for traits indicative of milk production. Such variation should be useful to map QTL genes for lactation. Supported by NICHD grant #1R21HD059746-01A1.

Key words: milk production, variation, mouse

M75 Statistical comparison of persistency among calving seasons of Iranian Holsteins. R. Izadkhan^{*}, H. Farhangfar, M. H. Fathi Nasri, and H. Naeemipour, Birjand University, Birjand, Iran.

In this study, Wilmlink exponential function ($y = a+bt+ce(-0.05*t)$) was utilized to evaluate the effect of calving season on persistency. The function was fit on 130,668 monthly test-day milk yields belonging to 15,183 first lactation Iranian Holstein cows calving between 2000 and 2009. Persistency was calculated based upon predicted milk yield by the function [(milk305/peak yield*305)*100]. Effect of calving season on persistency was analyzed by a linear mixed model. In the model, fixed effect of geographical location, herd, year, season, sire's sperm origin, as well as linear covariables of calving age, peak yield, peak time, days to first milk recording, and sire random effect were included. The model was fit by Mixed Procedure of SAS software. The results indicated that all factors had significant ($P < 0.001$) affect on persistency. Least squares means of persistency were 84.68, 85.45,

85.77 and 84.75% for spring, summer, autumn and winter calvers, respectively. There were no significant differences between spring and winter seasons and between summer and autumn seasons. With respect to positive correlation between persistency and total lactation milk yield, providing constant peak yield, cows calving in autumn and summer are expected to have higher milk yield as compared with spring and winter calvers.

Key words: Wilmink function, persistency, Iranian Holstein

M76 Genetic parameters estimates to Colombian buffalo milk yield under random regression models. N. Hurtado-Lugo^{*1,2}, S. Sousa Júnior¹, M. Cerón², R. Aspilcuelta¹, E. Acevedo¹, S. Gutierrez², L. Albuquerque¹, G. de Camargo¹, D. Santos¹, and H. Tonhati¹, ¹UNESP Faculty of Agriculture and Veterinary Sciences, State University of São Paulo, Jaboticabal, SP, Brazil, ²Genetics and Animal Improvement Group, Faculty of Agriculture Sciences, University of Antioquia, Medellín, Colombia.

The random regression model (RRM) has been proposed as an alternative approach to analyze longitudinal data, for instance milk yield records that are collected repeatedly over a lactation, because it considers such data as repeated measures. Buffalo production is part of the agribusiness in developing countries such as Colombia, and there is still little research using RRM. This study has the aim to estimate the genetic parameters using RRM for test-day milk yield in dairy buffalo in Colombian northern coast. First lactations from 10,929 buffalo were recorded monthly from 1998 to 2008. The archive was composed of 11,148 animals, 10,929 female buffaloes and 219 bulls. The fixed effects were contemporary group that was composed of month and year of control, and milking days (the fixed regression to the population mean). The age at calving was used as covariate (linear and quadratic regression) and the random effects were the direct genetic and the permanent environment. The most appropriate model was the one using a Legendre's polynomial function of 3rd order for the genetic effect and 6th order for the permanent environmental effect. The residual variances were heterogeneous, modeled by a step function, containing 2 classes of variances. The variance components were estimated using the statistical package WOMBAT. Models were compared by Akaike Information and Schwarz Bayesian's criteria. The heritability varied from 0.33 to 0.17; the highest values were observed at the beginning of the lactation, and the lowest at the end. The genetic and phenotypic correlations were high and positive; it indicates the neces-

sity to model the residual with a heterogeneous structure. Financial support: FAPESP, Foundation for Research Support of São, SP, Brazil.

Key words: Legendre's polynomial, regression, buffaloes

M77 Mathematical modeling of the lactation curve of domestic donkey (*Equus asinus*). A. M. Guastella^{*1}, A. Criscione¹, S. Bordonaro¹, D. Marletta¹, R. Steri², and N. P. P. Macciotta¹, ¹Università di Catania, Catania, Italy, ²Università di Sassari, Sassari, Italy.

Donkey farming for milk production is getting an increasing interest in Italy mainly for pharmaceutical and cosmetic purposes but also for human nutrition. Actually donkey milk is suitable for people intolerant to cow milk protein and is able to fulfill nutritional requirements of babies. The knowledge of the lactation curve may be of interest for a first definition of production attitudes and nutrition requirements of this species. Data were 453 test day records for milk yield, fat and protein percentage and somatic cell count (SCS) of 62 donkeys farmed in 2 commercial herds located in Sicily. Animals were grouped according to age classes (<5, 5, 6, 7–10 and >10 years respectively). Average lactation curves for age class were estimated with a mixed linear model that included fixed effects of herd, calving season, age class, days in milk interval (9 intervals of 30 d each) and the random effect of the animal. Repeatability was 0.55, 0.14, 0.10 and 0.07 for milk yield, fat and protein percentage and scc logarithm, respectively. Almost all factors included in the model significantly affect milk yield and protein percentage. Youngest donkeys had curves with lower peak and higher persistency compared with older animals. Average curves for fat percentage showed an opposite trend compared with milk yield, even though with a high variability between classes of age. Protein content was characterized by a continuous decreasing trend along the lactation. Somatic cell count was constant throughout the lactation, below 20,000 cell/mL, with a slight increase only at the end. The fitting of individual patterns for milk yield with the incomplete gamma function of Wood resulted in a frequency of 0.43 of curves without a lactation peak. This result is mainly due to the scarce availability of data in early lactation, being the milk of the first month suckled by the foal. Standard curves had an overall mean of 68 d for time at peak occurrence and a peak yield of 2.28 kg/d. Younger animals have later peak occurrence (160 d) than older animals (between 45 and 76 d) and lower peak productions (1.6 kg/d vs. 2.3 kg/d) respectively.

Key words: donkey, lactation curve, mathematical modeling