0152 Calculation and delivery of US genomic evaluations for dairy cattle. G. R. Wiggans[*1], T. A. Cooper[1], P. M. VanRaden[1], D. J. Null[1], J. L. Hutchison[1], O. M. Meland[2], M. E. Tooker[`], and H. D. Norman[2], [1]*Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, [2]Council on Dairy Cattle Breeding, Columbus, OH.*

In April 2013, the responsibility for calculation and distribution of genomic evaluations for dairy cattle was transferred from the USDA to the US dairy industry's Council on Dairy Cattle Breeding; the responsibility for development of evaluation methodology remained with the USDA. The Council on Dairy Cattle Breeding has implemented a fee schedule to provide operational funds as well as an incentive for continued submission of phenotypic data necessary for estimation of genomic effects. Since April 2013, substantial improvements have been made to the evaluation system. The number of SNP used for all evaluations has been increased to 61,013 from 45,195. The Jersey reference population has been increased by 1186 Danish bull genotypes obtained through an exchange with Viking Genetics International (Skara, Sweden). Genomic evaluations for Ayrshires were released to the industry. Cutoff studies to assess the accuracy of data available 4 yr earlier for predicting current data showed the mean gain in reliability across traits for Holsteins was 0.5% points from adding 15,818 SNP, 1.2% points for adding the Jersey bulls, and 8.2% points over parent average for Ayrshires. The weighting for cow evaluations used to estimate SNP effects has been reduced. Also, the deregression of the traditional PTA is jointly across animals instead of 1 animal at a time. Each animal gets credit for its own records and for records of its non-genotyped progeny. This prevents double counting of traditional information when parents and progeny are both genotyped. For yield traits, genotyped-daughter evaluations are not removed because the cow adjustment made them incompatible. Adjustment of cow weights improved the regression of genomic evaluation on future performance and reduced bias. Multitrait traditional evaluations for heifer and cow conception rates are used to estimate SNP effects for those traits. Imputed values are now provided for gene tests for bovine leucocyte adhesion deficiency, complex vertebral malformation, deficiency of uridine monophosphate synthase, syndactyly, Weaver Syndrome, spinal dismyelination, spinal muscular atrophy, red coat color, and polledness. Four tests for haplotypes that affect fertility or stillbirth rate were added (HH4 and HH5 for Holsteins, BH2 for Brown Swiss, and AH1 for Ayrshires). As of February 2014, over 538,000 genotypes are used in genomic evaluation with a mean of 18,000 added monthly. Genomic evaluations are released for animals from 36 countries, an indication of the global demand for them.

Key Words: dairy cattle, genomic evaluation, holstein

0153 An updated version of lifetime net merit incorporating additional fertility traits and new economic values. J. B. Cole[*] and P. M. VanRaden, *Animal Improvement Programs Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD.*

Lifetime net merit (NM$) is an economic selection index intended for use by commercial dairy producers. The current version of NM$ was most recently updated in 2010 and includes information from 13 traits in Holsteins, 11 in Brown Swiss, and 9 in the other dairy breeds. A new version of the index, 2014 NM$, now includes heifer (HCR) and cow (CCR) conception rates to provide more complete information about fertility. Additional benefits of fertility that are not included in productive life (PL) are earlier age at first calving, decreased units of semen needed per pregnancy, decreased labor and supplies for heat detection, synchronization, inseminations, and pregnancy checks, additional calves produced, and higher yields because more optimal lactation lengths are achieved. The total value of HCR including age at first calving, insemination costs, heat detection, pregnancy checks, and reproductive culling was $2.25; CCR was $2.25; and DPR was $11. Replacement heifers were previously assumed to cost $1940, but current prices are only about $1200 to 1500. Lower replacement prices will reduce the value of PL and daughter pregnancy rate (DPR) because fewer lactations are needed to recover costs. Fertility traits will receive a combined emphasis of 8.6%, less than the 11% on DPR in 2010 NM$. Relative emphasis for PL will decrease to 17% from 22% in 2010. DHI mean SCC has decreased from 230,000 in 2002 to 200,000 in 2012. Therefore, the actual change in SCC from a 1-unit change in SCS and actual SCC differences among bull daughters are now much less than when SCC premiums were introduced. The premium/1,000 cells increased only slightly since 2010 and contributes much of the SCS economic value, but the smaller phenotypic mean and SD for SCC will decrease the relative emphasis to 8% on SCS from 10% in 2010. Only slight revisions are needed to the milk and components prices forecast in 2010 NM$, but yield traits will receive more relative emphasis if PL, SCS, and fertility get less emphasis. These changes will increase the relative emphasis on yield to 42% from 35% in 2010. The 2014 NM$ index is correlated by 0.966 with 2010 NM$ for recent progeny-tested bulls. An increase in genetic progress worth $8 million/year is expected on a national basis, assuming that all of the changes are improvements and that all breeders select on NM$.

Key Words: economic values, lifetime net merit, selection index

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0154 Gains in reliability with genomic information in US commercial holstein heifers. F. A. Di Croce*, J. B. Osterstock, D. J. Weigel, and M. J. Lormore, *Zoetis Inc., Kalamazoo, MI.*

Genomic selection allows producers to accurately identify genetically superior animals at a much earlier age than traditional parent averages. The objective of this study is to quantify the gain in reliability from including genomic information in a commercial US Holstein dairy female population. Genomic Predicted Transmitting Abilities (GPTAs) from two Zoetis Low Density Panels consisting of 6836 markers (LD) and 10,932 markers (ZLD) and Parent Averages (PAs) for 73,480 Commercial US Holstein heifers were available for this study. Predicted transmitting abilities (PTAs) from the December 2013 USDA-CDCB evaluation for non-parent animals born in 2012 and 2013 were compared to corresponding GPTA from the December 2013 predictor population. Means were derived and daughter equivalents (DE) were estimated as described by VanRaden and Wiggans (1991). Mean reliabilities for the LD and ZLD panels were 66.85%, 71.15%, 71.15%, 71.15%, 64.48%, 67.45% and 63.10% for Lifetime Net Merit (NM$), Milk, Fat, Protein, Productive Life (PL), Somatic Cell Score (SCS) and Daughter Pregnancy Rate (DPR), respectively (not shown). Average gains in reliability above parent average ranged from 42.69% to 45.44% for LD and from 44.93% to 47.62% for ZLD across the selected yield, health and fertility traits. Mean Daughter Equivalent (DE) above Parent Average across the selected traits ranged from 23.9 to 142.0 and 24.9 to 147.5 for LD and ZLD, respectively (Table 0154). These results suggest that including genomic information in the genetic evaluation of young commercial Holstein females substantially increases reliability over the traditional parent averages.

Key Words: dairy, genomic, reliability

Table 0154. Observed reliabilities in December 2013 for Traditional Parent Averages and their December 2013 Genomic Evaluation by trait and DNA panel (Chip)

Trait[1]	Chip[2]	Parent Average	Genomic Value	Gain[3]	DE[4]
NM$	LD	23.21	66.76	43.55	30.7
	ZLD	21.54	67.21	45.68	32.0
Milk	LD	25.61	71.05	45.44	23.9
	ZLD	23.93	71.56	47.62	24.9
Fat	LD	25.61	71.05	45.44	23.9
	ZLD	23.93	71.56	47.62	24.9
Protein	LD	25.61	71.05	45.44	23.9
	ZLD	23.93	71.56	47.62	24.9
PL	LD	20.44	64.39	43.95	74.4
	ZLD	18.72	64.84	46.12	77.5
SCS	LD	23.13	67.44	44.31	55.5
	ZLD	21.37	67.92	46.55	57.8
DPR	LD	20.34	63.03	42.69	142.1
	ZLD	18.47	63.40	44.93	147.6

[1]NM$ = Lifetime Net Merit Dollars, PL = Productive Life, SCS = Somatic Cell Score, DPR = Daughter Pregnancy Rate.
[2]LD = Low Density Panels consisting of 6836 SNPs, ZLD = Low Density Panels consisting of 10,932 SNPs.
[3]Gain = Genomic REL– Parent Average REL.
[4]DE = Daughter Equivalent.

0155 Genome-wide association analysis in Italian Simmental cows for lactation curve traits using a low density (7K) SNP panel. N. P. P. Macciotta*[1], D. Vicario[2], C. Dimauro[1], G. Gaspa[1], M. Cellesi[1], A. Puledda[3], S. Sorbolini[1], and P. Ajmone-Marsan[4], *[1]Università di Sassari, Sassari, Italy, [2]ANAPRI, Udine, Italy, [3]Dipartimento di Agraria, Università di Sassari, Sassari, Italy, [4]Università Cattolica del Sacro Cuore, Piacenza, Italy.*

In genomic selection (GS) programs of dairy cattle breeds, bulls are currently genotyped using medium or high density SNP platforms. Genome wide association studies (GWAS) are then performed on variables (as polygenic breeding values or deregressed proofs) that are derived from phenotypes recorded on females. It could therefore be of interest to perform GWAS directly on cows that now are being genotyped in GS programs, often by using low density SNP panels. In this study, GWAS was performed on 1211 lactations of 337 Italian Simmental cattle, genotyped with the 7K Illumina bead-chip. Edit on markers was performed on call rate (> .99) and minor allele frequency (> .01). After edits, 6891 markers were retained for the analysis. Phenotypes were scores of the first two principal components obtained by performing principal component analysis on the test day records (seven for each lactation) for milk yield, fat and protein percentages, and somatic cell scores (SCS). The first component describes the average level (LEVEL) of the lactation curve, i.e., the average level of milk yield and percentages along the whole lactation, whereas the second is related to the shape of the lactation curve (SHAPE). Data were analyzed with a mixed linear model that included fixed effects of calving month, calving year, parity, SNP genotype (coded as 0,1,2), and random effects of herd, animal additive, permanent environment. Multiple testing was accounted for by performing the Bonferroni correction (uncorrected P × number of tests). Two markers were associated to LEVEL for milk yield according to the Bonferroni corrected statistical significance ($P < 0.05$). One was located on BTAs 6, close to the casein cluster. Nine significant SNPs were highlighted for LEVEL of fat percentage. Most important ($P < 0.001$) were on BTA23, close to the desmoplakin gene, which is involved in the turnover of epithelial cells, and on BTA7 close to the Ring Finger protein 145. Moreover, two significant SNP were located on BTA14, close to the CYP11B1 gene, previously reported to be associated to dairy traits in Holstein. Six markers were associated to protein percentage. The most significant was on BTA12, close to the HSTRA locus, reported to be associated to type traits in Chinese Holstein. Finally, one marker was found to affect SCS on BTA22, close to the LANCL2 locus. No markers were found to be associated to the SHAPE component for any of the four considered traits

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0156 Genetic parameters for pre-calving feed intake.

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The objective of this study was to estimate genetic parameters for dry matter intake (DMI) measured during lactation and the dry period in Holstein cows. Daily individual feed intake data collection started approximately 30 d before the expected calving date and continued through the first half of lactation. Pre-calving DMI traits were defined as average DMI on d -17 through -15 (cows) or d -10 through −8 (heifers) relative to parturition (DRYDMI), average DMI for d -1 through -3 relative to parturition (CALVEDMI), and the slope of the regression line fit through the last 14 (cows) or 7 (heifers) days before parturition (DECLINE). These traits were compared to DMI during lactation, defined as average DMI for 100 through 102 d in milk (LACDMI). The final data set included 242 and 214 primiparous and multiparous cows, respectively. Genetic parameters were estimated by mixed model analyses using a 5-generation pedigree. Fixed effects included lactation, year by season of calving, age at calving, sex of calf (male, female or twin), and status of calf (live or dead). Heritability estimates were 0.37, 0.60, 0.28, and 0.41 for DRYDMI, CALVEDMI, DECLINE, and LACDMI, respectively. Genetic correlations between all traits except DECLINE and LACDMI were significantly greater than zero. The correlation between DRYDMI and DECLINE was 0.37, but all other correlations were greater than 0.70. In particular, the genetic correlation between DRYDMI and LACDMI was 0.93. Results from this study demonstrate that DMI measured during the dry period or lactation is a moderately heritable trait. The high genetic correlation between DRYDMI and LACDMI was unexpected because DMI during lactation is also highly influenced by milk production. However, results of this study suggest the genetic regulation of DMI during the dry period and lactation is very similar. This result has potential implications for the measurement of feed intake for the purpose of calculating feed efficiency because in some situations, measurement of feed intake during the dry period is more feasible than measurement during lactation. However, this study is based on a relatively small number of cows and would benefit from verification in a larger population.

0157 Phenotypic and genetic correlations among milk energy output, body weight, and feed intake, and their effects on feed efficiency in lactating dairy cattle.

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Continued improvements in feed efficiency are essential for a thriving and sustainable dairy industry. Gross efficiency (GrEff) is defined as the energy captured in milk and body tissues as a percentage of gross energy intake. Our objective was to characterize the relationships among component traits for feed efficiency in lactating Holsteins and to determine their relationships to GrEff. Milk energy output per day (MilkE), calculated from milk, fat, protein, and lactose yields, dry matter intakes (DMI), body weights (BW), and body condition scores (BCS), were collected on 4452 lactating Holstein cows ranging from 50 to 200 d in milk from Scotland, the Netherlands, and the United States. The first 42-d records were analyzed with multivariate animal model in ASREML 3.0. Daily body energy change (dBE) was estimated from body weight change and BCS. Metabolic BW (MBW) was BW to the 0.75 power. GrEff was calculated as (MilkE + dBE)/Gross Energy intake, assuming all diets were 4.5 Mcal/kg. For these cows, MilkE was 26 ± 6 Mcal/d, BW was 600 ± 70 kg, DMI was 22 ± 5 kg/d, and intake as a multiple of maintenance was 3.9 ± 0.6. Genetic correlations for feed efficiency traits were 0.07 ± 0.04 for MilkE and MBW, 0.73 ± 0.03 for MilkE and DMI, and 0.40 ± 0.03 for MBW and DMI. Phenotypic correlations for feed efficiency traits were 0.16 ± 0.02 for MilkE and MBW, 0.60 ± 0.01 for MilkE and DMI, and 0.37 ± 0.01 for MBW and DMI. All correlations were reasonably consistent across countries. Genetic correlations of GrEff with MilkE, MBW, and DMI were 0.61 ± 0.04, -0.14 ± 0.05, and 0.04 ± 0.06, respectively. Phenotypic correlations of GrEff with MilkE, MBW, and DMI were 0.47 ± 0.01, -0.05 ± 0.02, and -0.17 ± 0.01, respectively. We conclude that, for Holsteins at a multiple of maintenance around 4, selection for milk component yield remains the overwhelming determinant of feed efficiency, and that selection for smaller body size may benefit feed efficiency but its impact will be slight compared to selection for more milk. Moreover, selection for greater milk will have a

Table 0158. Conception rate (CR) by month for lactating Holstein (HO) and Jersey (JE) cows

Year Month	2011 Apr	2011 May	2011 Jun	2011 Jul	2011 Aug	2011 Sep	2011 Oct	2011 Nov	2011 Dec
CR-JE	47.2%[a]	45.3%[a]	42.3%[a]	34.5%[b]	34.0%[b]	31.2%[c]	35.6%[b]	41.0%[a]	43.2%[a]
CR-HO	37.3%[a]	37.5%[a]	33.2%[b]	28.2%[c]	27.6%[c]	25.9%[c]	28.7%[c]	35.0%[a]	38.5%[a]

[a,b,c] different letters within rows ($P < 0.05$).

greater impact on profitability than would selection for BW. We suggest that that direct selection for body size (either larger or smaller) is likely not warranted as a means to enhance milk production or feed efficiency.

Key Words: lactating dairy cow, feed efficiency, body weight

0158 Benchmarking reproductive efficiency in commercial dairy herds in California.

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Our objective was to benchmark reproductive efficiency for both Holstein (HO) and Jersey (JE) dairy herds in California (CA). Reproductive records from DHIA's database (AgriTech Analytics) for all cows that calved in CA in 2011 were used. The initial dataset included artificial insemination records from 511 dairy operations and 554,523 lactating cows (501,616-HO; 52,907-JE) in a total of 1377,729 breedings (1262,926-HO; 114,803-JE). Only herds reporting at least 200 breedings and having overall conception results within 15% to 75% were included in the analysis. Breeding intervals that were less than 3d or greater than 150 d were discarded from final analysis. In addition, cows that were sold or died before pregnancy confirmation or re-inseminated (and assumed non-pregnant) were disregarded. Conception rate (CR) was defined as number cows pregnant by total number of AIs. Service rate (SR) was calculated based on the average interval between breedings (Woods-index). Statistical analyses were performed with the Proc HP-MIXED of SAS (version 9.3), with herd and cow used as random effects in the model. Overall, milk production level 305ME did not affect ($P > 0.10$) CR or SR results for either HO or JE cows. However, CR and SR from JE cows (CR = 38.8%; SR = 66.7%) were better ($P < 0.05$) than in HO-cows (CR = 32.8%; SR = 60.1%), but with great variation in milk production and reproductive performance within each breed. As suspected, CR was drastically affected ($P < 0.05$) by season, with a major decrease for both breeds during the warmer months of the year—as shown in Table 0158. In contrast, SR remained fairly constant throughout seasons and this was independent from cow breed. In summary, these results indicate a major detrimental effect of summer heat stress on fertility of California dairies that seems to disturb both HO and JE cows.

Key Words: dairy cows, heat stress, breed

0159 [Withdrawn]

0160 [Withdrawn]

0161 [Withdrawn]

0162 [Withdrawn]