

ulation size) and admixture within breeds or differentiation levels (e.g., fixation index) between breeds, can help to assign individuals to breeds.

**Key Words:** breed assignment, genetic diversity, genotypes

**W17 Genetic and environmental changes in dairy traits revealed from a genetic base update.** H. D. Norman\*<sup>1</sup>, P. M. VanRaden<sup>2</sup>, and J. W. Dürr<sup>1</sup>, <sup>1</sup>*Council on Dairy Cattle Breeding, Bowie, MD*, <sup>2</sup>*Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, MD*.

The genetic bases to which (most) dairy traits are expressed in the United States has been updated every 5 years since 1980. For a base change, the average predicted transmitting abilities (PTA) for cows born in the designated year is subtracted from the current PTAs for all animals; i.e., it's the gain (or loss) in PTAs for animals across the 5-year period. The rationale for changing the base is to make users of genetic evaluations aware the standards set for genetic selection in the past may no longer meet the quality needed to remain competitive. Eighty-one of the 102 breed-traits for yield and fitness traits showed favorable gains. The base change for Holsteins and Jerseys will reduce PTA milk by about 223 and 238 kg., respectively. PTAs for fat and protein will be adjusted down by about 8 to 11 kg. Changes in PTAs for somatic cell score (SCS) will be small for all breeds except Holsteins (0.08). PTAs for productive life will be reduced by 0.6 to 1.9 mo for 4 breeds. Changes among breeds in fertility trait were unexpected; only Holstein improved in the 3 traits. The PTAs for cow livability improved for 3 of the 6 breeds (0.74 mo for Holsteins). Holstein resistance against diseases improved for 5 of the 6 traits. The genomic revolution initiated in 2008 increased the rate of genetic improvement, primarily due to a reduction in the generation interval. Improvement in Brown Swiss, Holsteins and Jerseys were greater for milk traits (7 to 64%) than for the previous base change. The Guernseys, Holsteins, and Jerseys showed larger gains (43 to 100%) in the lifetime merit indexes than during the previous 5-years. Results show how much of the changes in phenotypes in dairy traits that had evaluation initiated since 2008 is attributed to genetics and environment. The genetic contribution accounted for 45%, but was greater for the 3 traits with the largest emphasis in net merit dollars (averaged 69%) and for the most populous breed, Holsteins (71%). These changes in productivity should help eliminate world hunger and reduce greenhouse gas emissions from requiring fewer animals.

**Key Words:** genetic base, national evaluation, predicted transmitting ability

**W18 Predicted feed efficiency index applied to Italian Holstein Friesian cattle population.** F. Omodei Zorini\*<sup>1</sup>, R. Finocchiaro<sup>2</sup>, G. Savoini<sup>1</sup>, G. Invernizzi<sup>1</sup>, and M. Cassandro<sup>3</sup>, <sup>1</sup>*Department of Health, Animal Science and Food Safety 'Carlo Cantoni', University of Milan, Milan, Italy*, <sup>2</sup>*Italian Holstein and Jersey Association (ANAFIJ), Research and Development Office, Cremona, Italy*, <sup>3</sup>*Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padua, Padua, Italy*.

Selection for feed efficiency is important to improve the economic and environmental sustainability of the dairy cattle industry. Many countries and international research projects are working on the possibility to select animals that efficiently transform feed into milk products. Feed efficiency matters on farms because it has a major influence on farm profitability and environmental stewardship in the dairy industry. The aim of this study was to describe a new selection index adopted by ANAFIJ for improving feed efficiency using data recorded by the official recording system. Predicted dry matter intake (pDMI) was derived from milk yield, fat content, and cow estimated BW. Energy milk content (FPCM) was derived from milk yield corrected for fat, protein and lactose content using the Sjaunja equation. Therefore, the predicted feed efficiency was estimated as ratio between FPCM and pDMI. Average predicted feed efficiency was equal to  $1.26 \pm 0.18$  with heritability equal to 0.32. Predicted feed efficiency index

(pFE), traditional and genomic, has been implemented in the Italian Holstein Friesian evaluation system. Results suggest that pFE may be a new breeding objective for Italian Friesian. At this time the trait is derived by exploiting the national recording system, without any new additional trait. The official selection index (PFT), in use since 2002, is positively correlated with pFE meaning that breeders have already started selecting for more efficient animals. However, the introduction of a the pFE index, as a direct "tool" will improve the positive feed efficiency trend. This approach will permit the Holstein Friesian breeders in Italy to improve feed efficiency, without increasing costs of recording system. However, to avoid the risk to select animals with an excessive negative energy balance after calving, it should be useful to include in the pFE a correction for BCS and reproductive performances. In the meanwhile, to increase the accuracy of the predicted phenotype, an Italian consortium is creating a consistent phenotypic critical mass of individual data for DMI in cows, heifers and young bulls.

**Key Words:** feed efficiency, Italian Holstein Friesian dairy cattle, dry matter intake

**W19 Quality control to improve properties of sequence genotypes from different sources.** D. J. Null\*, J. B. Cole, A. Al-Khudhair, and P. M. VanRaden, *USDA Animal Genomics and Improvement Laboratory, Beltsville, MD*.

Sequence genotypes from run7 of the 1000 Bull Genomes Project, high-density array genotypes for many of the same bulls, and additional sequence data were examined to determine optimal editing strategies. The 3,093 sequenced animals in the run7 *Bos taurus* analysis included 928 Holsteins, 175 Brown Swiss, 156 Ayrshires/Red Dairy Cattle, 105 Jerseys, 51 Montbéliardes, 22 Normandes, and 20 Guernseys; 1,429 were selected as animals of interest after editing or removing bulls with low coverage; incorrect identification, breed, or pedigree; duplicate sequence genotypes; or sequence genotypes that were inconsistent with chip genotypes. An additional 241 bulls had sequence variants identified locally by SAMtools rather than globally by GATK now used in run7. For chromosome 29 as an example, the raw global analysis identified 149,684 variants, and the local data identified 99,600; surprisingly, the overlap was only 48,266 variants. Thus, half of the variants in local data were not in the global data, which were expected to be a superset. Known lethal recessive alleles affecting fertility were present and retained. For quality control, array genotypes from the Council on Dairy Cattle Breeding (Bowie, MD) database included either 79,294 SNP from routine predictions or 643,059 SNP from imputed high-density genotypes. Sequence genotypes for 534 of the run7 animals had matching array genotypes from national data. Concordance of genotypes was better with run7 raw data (98.6% for 69,433 matching SNP) than from the run7 Beagle-imputed subset (98.0% for 61,299 SNP). After excluding multiallelic variants, which were 9% of the run7 raw variants, 48,056,551 variants were polymorphic in the 1,429 dairy animals and included 11% insertions and 4% deletions. Genotypes were then edited for missing rate, parent-progeny conflicts, excess heterozygotes, and minor allele frequency of > 1% in at least 1 breed. After removing loci in a few potentially mismapped regions of the ARS-UCD1 reference map, an edited total of 6,735,530 loci were available to impute genotypes for other animals and investigate phenotypic effects.

**Key Words:** variant calling, genotype concordance, sequence variant

**W20 Genome changes due to selection in US dairy cattle.** E. Freebern\*<sup>1</sup>, J. Jiang<sup>2</sup>, J. B. Cole<sup>3</sup>, P. M. VanRaden<sup>3</sup>, and L. Ma<sup>1</sup>, <sup>1</sup>*University of Maryland, College Park, MD*, <sup>2</sup>*North Carolina State University, Raleigh, NC*, <sup>3</sup>*Animal Genomics and Improvement Laboratory, Beltsville, MD*.

Genetic and genomic selection in the US dairy population has achieved successful phenotypic improvement across a comprehensive set of economically important traits that involve production, reproduction, health, and body conformation. While contemporary cows differ phenotypically

from their ancestors hundreds of years ago, the changes in the genome, especially those due to selection, remain to be discovered. The aim of this study is to investigate genome-wide and region-specific changes in the US Holstein-Friesian (HF) cattle population between the years of 1950 to 2015. Using the US dairy cooperator's phenotypic and genomic databases hosted at CDCB, we first extracted genotype and phenotype (PTA) data of 27,000 reference bulls and performed GWAS analyses to identify candidate QTLs. We then divided the 27,000 Holstein bulls into 9 bins based on birth year, before 1980, 1980–1990, 1990–1995, 1995–2000, 2000–2002, 2002–2005, 2005–2007, 2007–2010, and after 2010. The allele frequency changes between the 2 extreme time periods were calculated to capture the difference between the earliest and most recent populations. Finally, the genomic regions with the largest allele frequency changes were compared against the QTL regions identified in GWAS analyses. To identify true genome changes due to selection from those due to random genetic drift, we implemented a gene dropping simulation approach with real pedigree and calculated thresholds of allele frequency change. The process was executed by running a simulation program in Python, which will visualize systemic changes over individual SNPs and compare them to a distribution under pure genetic drift. Observation of changes above the 99.9% threshold on the distribution may be indicative of selection and affecting dairy traits. From this evaluation of genome-wide and region-specific changes due to selection, we will identify candidate QTL regions under selection and that are associated with economically important traits in the US dairy population.

**Key Words:** genomic selection, GWAS, allele frequency changes

**W21 Changes in early milk composition has subsequent effects on microbial composition of the rumen.** A. Nin-Velez<sup>\*1</sup>, J. Duncan<sup>1</sup>, H. Cunningham-Hollinger<sup>2</sup>, K. Austin<sup>2</sup>, K. Cammack<sup>2</sup>, W. Lamberson<sup>3</sup>, and R. Cockrum<sup>1</sup>, <sup>1</sup>Virginia Polytechnic Institute and State University, Blacksburg, VA, <sup>2</sup>University of Wyoming, Laramie, WY, <sup>3</sup>University of Missouri, Columbia, MO.

Components within early milk provide continual inoculation of microbial species within the calf gut. The gut microbiome stimulates development of epithelial tissue and immune cell differentiation. Though limited research suggests milk components are influenced by mode of birth, it is unknown how the maternal environment influences the composition of early milk. We hypothesized that mode of birth would impact early milk composition, and, in turn, influence the microbial taxa in the calf gut. Early milk samples were collected from Charolaise (n = 35) and Angus (n = 34) dams on d 1, 3, and 28 postpartum who underwent vaginal (VD) or cesarean (CD) delivery. Components and fatty acid composition were determined for milk samples. Calf rumen fluid samples were obtained for d 1, 3, and 28 and were used for metagenomic sequencing. Samples were run on the Illumina HiSeq 2500 platform as paired end reads. Mode of birth was regressed on milk composition for each day using the GLM procedure in SAS. The GENMOD procedure was conducted with milk components being regressed against microbial counts. Results indicated that VD dams were more likely to have increased protein, solid nonfat (SNF), and lactose ( $P = 0.001$ ) on d 1 and 3, but decreased urea concentrations ( $P < 0.001$ ). Similarly, short, medium, and long-chain fatty acids were increased ( $P = 0.051$ ) in VD d 3 milk. True protein elicited a decrease ( $P = 0.033$ ) in rumen fluid *Actinobacteria* and *Proteobacteria*; whereas, both SNF and lactose were associated with an increased ( $P = 0.049$ ) response in d 1 milk. Based on these results, we suggest that mode of birth influences protein concentrations in early milk, and even though we can see some changes to microbial abundance the overall dynamics of the calf rumen microbiome are relatively stable in response to changes in milk composition.

**W22 Relationship between milk production and indicator traits of robustness in first-parity Holstein cows.** C. H. F. Zago Dias<sup>\*1</sup>, L. El Faro<sup>2</sup>, M. L. Santana Jr<sup>3</sup>, R. A. Teixeira<sup>1</sup>, A. A. Valotto<sup>4</sup>, and L. T. Dias<sup>1</sup>,

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The current major challenges of dairy cattle improvement are to select animals with a greater capacity to overcome the metabolic disorders in postpartum. This study aimed to evaluate the association of the type traits angularity (ANG) and body conditions score (BCS) with test-day milk yield (TDMY) to identify more robust animals. In this study, 301,301 TDMY records from 33,543 first-parity Holstein cows, which belonged to 146 herds in the state of Paraná, Brazil, were analyzed. Angularity and BCS were classified at an average 88 d of lactation. A 2-trait random regression model between TDMY and the type traits was applied. The model included the fixed effects of contemporary group (herd, test-day year and month) and the linear and quadratic effects of cow age at calving and interval between classification date and calving (only for ANG and BCS) as covariates. The fixed lactation curve for TDMY was modeled using quadratic Legendre polynomials. For TDMY, additive genetic and animal permanent environmental effects were modeled as random effects using cubic Legendre polynomials, in addition to the residual effect. For ANG and BCS, only the additive genetic effects and residual were included as random effects. The (co)variance components were estimated by Bayesian inference using the GIBBS2F90 program (Misztal et al., 2002). The heritability for TDMY ranged from 0.22 to 0.36, with higher estimates close to peak yield. The heritability estimates for ANG and BCS were  $0.17 \pm 0.03$  and  $0.19 \pm 0.02$ , respectively. Genetic correlations between TDMY and ANG or BCS were negative and antagonistic throughout lactation, with stronger correlations between TDMY and BCS at 30 d of lactation ( $-0.72$ ) and between TDMY and ANG from 90 to 120 d (around  $-0.86$ ). A higher genetic association was observed between BCS and TDMY at the beginning of lactation, a critical period when cows are in negative energy balance, while ANG showed a higher genetic association close to peak yield. Thus, the type traits studied may be used as auxiliary measures to identify more robust animals considering the different lactation periods.

**Key Words:** random regression model, transition period, type traits

**W23 Evaluating the correlation of digital dermatitis infection and genetic variants to predict gene resistance in Holstein cattle.** G. M. Canny<sup>\*1</sup>, C. L. Hendley<sup>1</sup>, W. B. Smith<sup>1</sup>, B. W. Jones<sup>1,2</sup>, and J. N. Waddell<sup>1</sup>, <sup>1</sup>Tarleton State University, Stephenville, TX, <sup>2</sup>Texas A&M AgriLife Research, Stephenville, TX.

Digital dermatitis (DD) is a contagious bacterial hoof infection. Determining genetic resistance of DD will allow dairy producers to select for this trait, therefore reducing lameness and treatment cost. This study evaluated the correlation of infection and genetic variants to predict genetic resistance of DD resistance in Holstein cattle on a commercial dairy farm in central Texas. Lactating dairy cattle were scored on an M0 (early lesions) to M4 (chronic lesions) scale. Blood samples were collected on lactating cows (n = 45) from the coccygeal vein for genomic DNA isolation. Cows were identified as having a lesion (n = 35) and not having a lesion (n = 10). Four previously reported SNPs were tested on genomic DNA to determine correlation to DD resistance by qPCR melt curve analysis. SNPs in the 3'UTR of C94T, A22DG, interleukin-8 (*IL8*) and exon 3 of toll-like receptor 4 (*TLR4*) were analyzed by Chi-Square in SAS (Version 9.4 SAS Institute, Inc., Cary, NC) to determine the frequencies of different genotypes present among the resistant and affected animals. One SNP in *Bta-IL8* resulted in a significant chi-square analysis ( $P = 0.03$ ). These results indicate a genetic correlation to resistance to DD within the *Bta-IL8* gene. This qPCR melt curve analysis can lead to a fast, affordable genotyping assay to select for cows genetically resistant to this costly infection.

**Key Words:** digital dermatitis, gene resistance, interleukin-8