

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