

duced. 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 dysmyelination, 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

0154 Gains in reliability with genomic information in US commercial holstein heifers. F. A. Di Croce*, J. B. Oosterstock, 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 GPA 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