Form GENO

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)	United States of America
Main trait group	Udder health [somatic cell score (**SCS**)]
Breed(s)	BSW, HOL (B&W), JER
Trait definition(s) and unit(s) of measurement	SCS ($\log_2$ of somatic cell count)
Source of genotypes	Illumina BovineSNP50 (v1 and v2), Illumina Bovine3K, Illumina BovineLD, and GeneSeek Genomic Profiler-LD BeadChips as well as subsets of 45,188 single-nucleotide polymorphisms (**SNPs**) from Illumina BovineHD and GeneSeek Genomic Profiler-HD BeadChips
Imputation method for missing genotypes	Missing genotypes filled using a combination of population and pedigree haplotyping in findhap.f90; additionally, imputed genotypes of non-genotyped dams included if >90% of haplotypes can be determined from progeny genotypes (usually ≥4 progeny)
Propagation of genomic information to non-genotyped descendants and ancestors	Evaluations of non-genotyped progeny recomputed to include genomic information from parents if reliability gain is ≥1% based on methods developed previously for foreign information; genotypes for non-genotyped dams imputed using methods described above
Animals included in reference population	Reference animals included as of February 2013: BSW: 5,404 males and 494 U.S. females; 887 U.S. males as well as 4,517 males provided by Interbull from 8 other countries HOL: 20,819 males and 30,201 U.S. females; 11,839 U.S., 3,576 Canadian, 3,148 Italian, and 627 U.K. males as well as 1,629 males from 21 other countries JER: 2,802 males and 8,521 U.S. females; 2,529 U.S. and 273 Canadian, Australian, New Zealand, and Danish males
Source of phenotypic data	Deregressed proofs (**DP**s) calculated from PTA and parent average (**PA**) by the simple formula $DP = PA + (PTA - PA)/REL_{dau}$, where REL_{dau} is REL from daughters; traditional cow PTAs first adjusted (yield traits only) to provide means and variances comparable to those of bull PTAs before deregression; DP in genomic model weighted by $REL_{dau}/(1 - REL_{dau})$
Other criteria (data edits) for inclusion of records	45,188 selected SNPs had minor allele frequency of ≥1% for BSW, HOL, or JER, few parent–progeny conflicts (≤1%), and high call rate (≥90%); each animal's genotype required to have 90% call rate, validated against parent and progeny genotypes, and checked for correct breed and sex; identical twins and clones receive a common, combined genotyped derived from source genotypes
Criteria for extension of records	Not applicable

Sire categories	None
Genomic model	Iterative, nonlinear model with heavy-tailed prior for marker effects analogous to Bayes A used; base population allele frequencies subtracted from genotypes, and polygenic effect (poly) with 10% of additive variance fit in the model: DP = mean + Σgenotypes(effects) + poly + error
Blending of direct genomic value (DGV) with traditional EBV	For animals with non-genotyped ancestors such as sire, dam, or maternal grandsire, selection index with 3 terms used to combine direct genomic effect, traditional evaluation, and genotyped subset evaluation if REL gain is ≥1%; to reduce bias, coefficients adjusted by trait group to assign more weight to traditional evaluation and less weight to direct genomic effect
Environmental effects in the genetic evaluation model	Not applicable
Adjustment for heterogeneous variance in evaluation model	Not applicable
Computation of genomic reliability	DGV REL computed from traditional daughter equivalents plus genomic daughter equivalents, which differ for each animal depending on its average genomic relationship to reference population; final REL computed by selection index using RELs of DGV, traditional PTA, and subset PTA
Blending of foreign/Interbull information in evaluation	Calculation of DGV includes foreign information from previous Interbull evaluation; current Interbull evaluation used in 3-term selection index step
Genetic parameters in the evaluation	Not applicable
System validation	DPs for bulls evaluated after August 2008 predicted from evaluations available in August 2008
Expression of genetic evaluations	PTA (phenotypic mean of 3 added)
Definition of genetic reference base	Cows born in 2005 (stepwise, 5 years)
Labeling of genomic evaluations	Genomic indicator code (0 = no genomic information, 1 = genotyped, 2 = non-genotyped progeny of genotyped parent, and 3 = imputed dam genotype); industry reports often use G prefix to indicate genotyped (e.g., GPTA, GTPI)
Criteria for official publication of evaluations	All genomic evaluations (young, old, domestic, foreign, male, female) released as official; official distribution after March 1, 2013, controlled by Council on Dairy Cattle Breeding
Number of evaluations/ publications per year	3 full releases (April, August, December) plus monthly updates for newly genotyped animals between full releases

Use in total merit index	Net merit is sum of genomic PTAs times economic values for each trait [yield (milk, fat, protein), PL, SCS (minus phenotypic mean of 3), udder composite, feet & legs composite, DPR, calving ability (includes service-sire and daughter CE and SB as available)]
Anticipated changes in the near future	Expansion of used SNPs from 45,188 to 90,000
Key reference on methodology applied	VanRaden, P.M. 2008. Efficient methods to compute genomic predictions. J. Dairy Sci. 91:4414–4423. VanRaden, P.M., C.P. Van Tassell, G.R., Wiggans, T.S. Sonstegard, R.D. Schnabel, J.F. Taylor, and F.S. Schenkel. 2009. *Invited review:* Reliability of genomic predictions for North American Holstein bulls. J. Dairy Sci. 92:16–24. Wiggans, G.R., P.M. VanRaden, L.R. Bacheller, M.E. Tooker, J.L. Hutchison, T.A. Cooper, and T.S. Sonstegard. 2010. Selection and management of DNA markers for use in genomic evaluation . J. Dairy Sci. 93:2287–2292. VanRaden, P.M., J.R. O'Connell, G.R. Wiggans, and K.A. Weigel. 2011. Genomic evaluations with many more genotypes. Genet. Sel. Evol. 43:10. Wiggans, G.R., P.M. VanRaden, and T.A. Cooper. 2011. The genomic evaluation system in the United States: Past, present, future. J. Dairy Sci. 94:3202–3211. Boichard, D., H. Chung, R. Dassonneville, X. David, A. Eggen, S. Fritz, K.J. Gietzen, B.J. Hayes, C.T. Lawley, T.S. Sonstegard, C.P. Van Tassell, P.M. VanRaden, K.A. Viaud-Martinez, and G.R. Wiggans. 2012. Design of a bovine low-density SNP array optimized for imputation. PLoS ONE 7:e34130. Wiggans, G.R., T.A. Cooper, C.P. Van Tassell, T.S. Sonstegard, and E.B. Simpson. 2013. *Technical note:* Characteristics and use of the Illumina BovineLD and GeneSeek Genomic Profiler low-density bead chips for genomic evaluation. J. Dairy Sci. 96:1258–1263.
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