## DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

| | |
|---|---|
| **Country (or countries)** | United States of America |
| **Main trait group** | Longevity [direct (single trait) and combined (multitrait) productive life (**PL**)] |
| **Breed(s)** | BSW, HOL (B&W), JER |
| **Trait definition(s) and unit(s) of measurement** | PL (months) |
| **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:<br><br>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<br>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<br>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 (months) |
| **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.<br>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.<br>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.<br>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.<br>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.<br>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.<br>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. |
| **Key organisation: name, address, phone, fax, e-mail, web site** | Animal Improvement Programs Laboratory<br>Agricultural Research Service, U.S. Dept. of Agriculture<br>Bldg. 005, Room 306, BARC-West<br>10300 Baltimore Ave.<br>Beltsville, Maryland 20705-2350, USA<br>Voice: 301-504-8334; Fax: 301-504-8092<br>E-mail: aipl.inquiry@ars.usda.gov<br>web site: http://aipl.arsusda.gov |