

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

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| Country (or countries) | United States of America |
| Main trait group | Production (milk, fat, protein) Longevity [productive life (PL)] Udder health [somatic cell score (SCS)] Fertility [daughter pregnancy rate (DPR)] Conformation (final score, linear type traits) Calving traits [service sire and daughter calving ease (CE) and stillbirth (SB)] |
| Breed(s) | BSW, HOL (B&W), JER |
| Trait definition(s) and unit(s) of measurement | Milk (lb), fat and protein (lb, %); 305-day lactation yields PL (months) SCS (\log_2 of somatic cell count) DPR (percentage of non-pregnant cows that become pregnant during each 21-day period) Final score and linear type traits (50-point scale, except for 80-point scale for JER stature) Service sire and daughter CE [percentage of births of bull calves that are difficult in primiparous heifers (%DBH)] and SB [percentage of births of bulls calves that are stillborn in primiparous heifers (%SB)] |
| Source of genotypes | Illumina Bovine SNP50 BeadChip |
| Imputation method for missing genotypes | Missing genotypes filled using a combination of population and pedigree haplotyping; 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 $\geq 1\%$ 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 June 2010: BSW: 1,215 males and 116 females; 792 U.S., 403 Swiss, and 136 animals from 6 other countries HOL: 9,958 males and 8,122 females; 13,382 U.S., 3,837 Canadian, and 861 animals from 16 other countries JER: 2,088 males and 740 females; 2,611 U.S., 179 Canadian, and 38 Australian, New Zealand, and Danish animals |
| Source of phenotypic data | Deregressed proofs (DPs) 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 $REL_{dau}/(1 - REL_{dau})$ |

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| Other criteria (data edits) for inclusion of records | 43,382 selected single-nucleotide polymorphisms had a minor allele frequency of $\geq 1\%$ for BSW, HOL, or JER, few parent–progeny conflicts ($\leq 1\%$), and a high call rate ($\geq 90\%$); 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: $DP = \text{mean} + \Sigma \text{genotypes}(\text{effects}) + \text{poly} + \text{error}$ |
| 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 $\geq 1\%$ |
| 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 2006 predicted from evaluations available in August 2006 |
| Expression of genetic evaluations | PTA: Yield (lb) Yield components, DPR, CE, SB (%) PL (months) SCS (phenotypic mean of 3 added) Conformation (points) |
| Definition of genetic reference base | Cows born in 2005 (stepwise, 5 years) |

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| 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) are released as official except for young Holstein and Jersey males, which are released only after enrollment with the National Association of Animal Breeders or after 2 years of age |
| 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 | Inclusion of genotypes from version 2 of Illumina Bovine SNP50 BeadChip, a 3,000-marker chip, and also higher density chips |
| Key reference on methodology applied | <p>VanRaden, P.M. 2008. Efficient methods to compute genomic predictions. J. Dairy Sci. 91:4414–4423.</p> <p>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. 2009.</p> <p>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.</p> |
| Key organisation: name, address, phone, fax, e-mail, web site | <p>Animal Improvement Programs Laboratory Agricultural Research Service, U.S. Dept. of Agriculture Bldg. 005, Room 306, BARC-West 10300 Baltimore Ave. Beltsville, Maryland 20705-2350, USA Voice: 301-504-8334; Fax: 301-504-8092 E-mail: aipl.inquiry@ars.usda.gov web site: http://aipl.arsusda.gov</p> |