

## DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

<b>Country (or countries)</b>	United States of America
<b>Main trait group</b>	Calving traits [service sire and daughter calving ease ( <b>CE</b> ) and stillbirth ( <b>SB</b> )]
<b>Breed(s)</b>	BSW, HOL (B&W)
<b>Trait definition(s) and unit(s) of measurement</b>	Service sire and daughter CE [percentage of births of bull calves that are difficult in primiparous heifers ( <b>%DBH</b> )] and SB [percentage of births of bulls calves that are stillborn in primiparous heifers ( <b>%SB</b> )]
<b>Source of genotypes</b>	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 ( <b>SNPs</b> ) from Illumina BovineHD and GeneSeek Genomic Profiler-HD BeadChips
<b>Imputation method for missing genotypes</b>	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 $\geq 4$ progeny)
<b>Propagation of genomic information to non-genotyped descendants and ancestors</b>	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
<b>Animals included in reference population</b>	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
<b>Source of phenotypic data</b>	Deregressed proofs ( <b>DPs</b> ) calculated from PTA and parent average ( <b>PA</b> ) 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 $REL_{dau}/(1 - REL_{dau})$
<b>Other criteria (data edits) for inclusion of records</b>	45,188 selected SNPs had minor allele frequency of $\geq 1\%$ for BSW, HOL, or JER, few parent–progeny conflicts ( $\leq 1\%$ ), and 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
<b>Criteria for extension of records</b>	Not applicable

<b>Sire categories</b>	None
<b>Genomic model</b>	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: $DP = \text{mean} + \Sigma \text{genotypes}(\text{effects}) + \text{poly} + \text{error}$
<b>Blending of direct genomic value (DGV) with traditional EBV</b>	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 $\geq 1\%$ ; to reduce bias, coefficients adjusted by trait group to assign more weight to traditional evaluation and less weight to direct genomic effect
<b>Environmental effects in the genetic evaluation model</b>	Not applicable
<b>Adjustment for heterogeneous variance in evaluation model</b>	Not applicable
<b>Computation of genomic reliability</b>	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
<b>Blending of foreign/Interbull information in evaluation</b>	Calculation of DGV includes foreign information from previous Interbull evaluation; current Interbull evaluation used in 3-term selection index step
<b>Genetic parameters in the evaluation</b>	Not applicable
<b>System validation</b>	DPs for bulls evaluated after August 2008 predicted from evaluations available in August 2008
<b>Expression of genetic evaluations</b>	PTA (%)
<b>Definition of genetic reference base</b>	Cows born in 2005 (stepwise, 5 years)
<b>Labeling of genomic evaluations</b>	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)
<b>Criteria for official publication of evaluations</b>	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
<b>Number of evaluations/publications per year</b>	3 full releases (April, August, December) plus monthly updates for newly genotyped animals between full releases

<b>Use in total merit index</b>	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)]
<b>Anticipated changes in the near future</b>	Expansion of used SNPs from 45,188 to 90,000
<b>Key reference on methodology applied</b>	<p>VanRaden, P.M. 2008. <a href="#">Efficient methods to compute genomic predictions</a>. 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. <a href="#">Invited review: Reliability of genomic predictions for North American Holstein bulls</a>. J. Dairy Sci. 92:16–24.</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. <a href="#">Selection and management of DNA markers for use in genomic evaluation</a>. J. Dairy Sci. 93:2287–2292.</p> <p>VanRaden, P.M., J.R. O’Connell, G.R. Wiggans, and K.A. Weigel. 2011. <a href="#">Genomic evaluations with many more genotypes</a>. Genet. Sel. Evol. 43:10.</p> <p>Wiggans, G.R., P.M. VanRaden, and T.A. Cooper. 2011. <a href="#">The genomic evaluation system in the United States: Past, present, future</a>. J. Dairy Sci. 94:3202–3211.</p> <p>Boichard, D., H. Chung, R. Dasonneville, 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. <a href="#">Design of a bovine low-density SNP array optimized for imputation</a>. PLoS ONE 7:e34130.</p> <p>Wiggans, G.R., T.A. Cooper, C.P. Van Tassell, T.S. Sonstegard, and E.B. Simpson. 2013. <a href="#">Technical note: Characteristics and use of the Illumina BovineLD and GeneSeek Genomic Profiler low-density bead chips for genomic evaluation</a>. J. Dairy Sci. 96:1258–1263.</p>
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