

Form GE

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)	United States of America
Main trait group	Health (1. SCS; 2. Mastitis resistance (MAS), milk fever resistance (MFV), displaced abomasum resistance (DAB), ketosis resistance (KET), metritis resistance (MET), retained placenta resistance (RPL))
Breed(s)	1. AYS (RDC), BSW, GUE, HOL (B&W, R&W, SIM), JER, MSH (RDC); all breeds and crossbred cows evaluated together in a multibreed AM 2. HOL, JER
Trait definition(s) and unit(s) of measurement	1. SCS = $\log_2(\text{SCC}/100,000) + 3$, where SCC is somatic cells per milliliter; lactation SCS is mean of TD SCS across first 305 days of lactation 2. 100 = no event, 0 = at least 1 event reported. MAS = observed mastitis from 0 to 210 DIM MFV = observed milk fever from 0 to 30 DIM DAB = observed displaced abomasum from 0 to 60 DIM KET = observed ketosis from 0 to 60 DIM MET = observed metritis from 0 to 90 DIM RPL = observed retained placenta from 0 to 10 DIM
Method of measuring and collecting data	1. Collected by Dairy Herd Information Affiliates using ICAR-approved methods and quality certification standards administered by the Council on Dairy Cattle Breeding 2. Producer-recorded data collected by Dairy Herd Information Affiliates
Time period for data inclusion	1. First calvings from 1984 and later; pedigree from birth years 1950 and later 2. First calvings from 1986 and later; pedigree from birth years 1950 and later
Age groups (e.g. parities) included	1. First 5 parities included 2. First 5 parities included
Other criteria (data edits) for inclusion of records	1. Valid sire identification required; lactations from cows with >40 DIM and cows removed from the herd with >15 DIM included; TD by 90 DIM required 2. Valid sire identification required; minimum age of 18 months at calving; DIM must exceed window of occurrence; event occurs within DIM window; herd-year reporting specific event; maximum constraint by herd-year on incidence rate
Criteria for extension of records (if applicable)	1. Records with <305 days extended to 305 days using ST best prediction
Sire categories	All sires (AI and NS) evaluated together
Environmental effects, pre-adjustments	1. Multiplicative adjustments for calving age and month as well as differing SD by parity; unequal variances across time, across herds, and across breeds adjusted to HOL base variance calculated from standardized records of first lactation cows that calved in 2007 2. Variance pre-adjustment based on calving year, parity, and heritability (Wiggans & VanRaden, 1991)
Method (model) of genetic evaluation	1. ST BLUP RP AM 2. ST BLUP RP AM

Environmental effects³ in the genetic evaluation model	<p>1. Management group (flexible HYS, includes registry status for HOL) (F), parity × age (F), regression on inbreeding (F), regression on general heterosis (F), PE (R), herd × sire interaction (R); released PTA includes regression coefficient multiplied by expected future inbreeding and coefficient of heterosis when mated to purebred as a post-processing step</p> <p>2. Parity × age (F), year-season (F), regression on inbreeding (F), regression on heterosis (F), Herd-year (R), Herd-sire (R), PE (R); released PTA includes regression coefficient multiplied by the expected future inbreeding as a post-processing step</p>
Adjustment for heterogeneous variance in evaluation model	<p>1. Pre-adjustments for herd-year variance applied</p> <p>2. Pre-adjustments for herd-year variance applied</p>
Use of genetic groups and relationships	<p>1. Unknown parents grouped by birth year, breed, and, for HOL, separately for U.S. and foreign animals; unknown sires and dams of cows grouped separately, but unknown parents of bulls in a combined group; relationship matrix accounts for effects of inbreeding on Mendelian sampling variance</p> <p>2. Five unknown parent groups formed based on birth year</p>
Blending of foreign/Interbull information in evaluation	Foreign evaluations of parents not included
Genetic parameters in the evaluation	<p>See Appendix SM for h^2 and genetic variance estimates;</p> <p>1. PE variance, 0.18; herd × sire interaction, 0.05; RP, 0.35</p> <p>2. MAS: PE variance, 0.005; herd-year, 0.05; herd-sire, 0.03; RP, 0.09</p> <p>MFV: PE variance, 0.0003; herd-year, 0.05; herd-sire, 0.03; RP, 0.031</p> <p>DAB: PE variance, 0.0001; herd-year, 0.05; herd-sire, 0.03; RP, 0.012</p> <p>KET: PE variance, 0.0013; herd-year, 0.05; herd-sire, 0.03; RP, 0.045</p> <p>MET: PE variance, 0.0022; herd-year, 0.05; herd-sire, 0.03; RP, 0.053</p> <p>RPL: PE variance, 0.0009; herd-year, 0.05; herd-sire, 0.03, RP, 0.036</p>
System validation	Means and SDs for all variables calculated and examined overall; means for new bulls, changes for high bulls, largest changes, and key statistics for recent AI bulls checked; genetic trends for each breed validated by methods 1, 2, and 3
Expression of genetic evaluations	<p>1. PTA SCS; all-breed PTAs adjusted to within-breed bases as within-breed PTA = (all-breed PTA – breed mean) + phenotypic mean of 3</p> <p>2. PTA MAS - percentage points of resistance above or below the breed average (likewise for all other health traits)</p>
Definition of genetic reference base	Cows born in 2015 (stepwise, 5 years)
Next base change	April 2025 (when base will be cows born in 2020)
Calculation of reliability	Daughter equivalents from parents, progeny, and own records summed in an iterative process starting with REL from previous evaluation
Criteria for official publication of evaluations	At least 10 daughters with a usable first-lactation record; Interbull evaluations reported as official in the U.S. if they include data from an additional country, the U.S. has no evaluation, or Interbull excludes U.S. data and Interbull evaluation has higher REL

Number of evaluations/publications per year	3 (April, August, December)
Use in total merit index⁴	<p>1. SCS receives 4% of total emphasis in lifetime net merit dollars (NM\$, all breeds), 5% of total emphasis in Total-Performance Index (TPI, HOL), and 6% of total emphasis in Jersey Performance Index (JPI, JER)</p> <p>2. MAS receives 32.9% of the health trait subindex (HTH\$), 0.77% total emphasis in lifetime net merit dollars (NM\$). MFV receives 2.3% of HTH\$, 0.05% total emphasis in NM\$. DAB receives 23.3% of HTH\$, 0.54% of NM\$. KET receives 4.7% of HTH\$, 0.11% of HTH\$. MET receives 26.5% of HTH\$, 0.62% of NM\$. RPL receives 10.3% of HTH\$, 0.24% of NM\$. Further details available: https://aipl.arsusda.gov/reference/nmcalc-2018.htm</p>
Anticipated changes in the near future	None
Key reference on methodology applied	<p>Wiggans, G.R. and P.M. VanRaden. 1991. Method and effect of adjustment for heterogeneous variance. <i>J. Dairy Sci.</i> 74:4350-4357.</p> <p>Schutz, M.M. 1994. <u>Genetic evaluation of somatic cell scores for United States dairy cattle</u>. <i>J. Dairy Sci.</i> 77:2113– 2129.</p> <p>Schutz, M.M., P.M. VanRaden, G.R. Wiggans, and H.D. Norman. 1995. <u>Standardization of lactation means of somatic cell scores for calculation of genetic evaluations</u>. <i>J. Dairy Sci.</i> 78:1843–1854.</p> <p>VanRaden, P.M., and G.R. Wiggans. 1991. <u>Derivation, calculation, and use of national animal model information</u>. <i>J. Dairy Sci.</i> 74:2737–2746.</p> <p>VanRaden, P.M., M.E. Tooker, J.B. Cole, G.R. Wiggans, and J.H. Megonigal, Jr. 2007. <u>Genetic evaluations for mixed-breed populations</u>. <i>J. Dairy Sci.</i> 90:2434–2441.</p> <p>Cole, J.B., D.J. Null, and P.M. VanRaden. 2009. <u>Best prediction of yields for long lactations</u>. <i>J. Dairy Sci.</i> 92:1796–1810.</p> <p>VanRaden, P.M., M.E. Tooker, J.R. Wright, C. Sun, and J.L. Hutchison. 2014. <u>Comparison of single-trait to multi-trait national evaluations for yield, health, and fertility traits</u>. <i>J. Dairy Sci.</i> 97:7952-7962.</p> <p>Parker Gaddis, K.L., M.E. Tooker, J.R. Wright, J.H. Megonigal, Jr., J.S. Clay, J.B. Cole, and P.M. VanRaden. 2018. Development of national genomic evaluations for health traits in U.S. Holsteins. <i>Proc. 11th World Congr. Genet. Appl. Livest. Prod. Auckland, NZ.</i> 11:594.</p>

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Parameters for national genetic evaluations for udder health traits as provided to Interbull

Country (or countries):	United States of America
Main trait group:	Health (SCS)
Breed(s):	AYS (RDC), BSW, GUE, HOL (B&W, R&W, SIM), JER, MSH (RDC)

Trait	h^2	Genetic variance	Official proof standardisation formula ^a
Milk Somatic Cell (SCS)	0.12	BSW SD = 0.39 GUE SD = 0.41 HOL SD = 0.40 JER SD = 0.38 RDC SD = 0.41	StandEval = PTA SCS + 3
Clinical Mastitis	0.031	HOL SD = 2.6% JER SD = 2.6%	—
Milk fever (MFV)	0.006	HOL SD = 0.4% JER SD = 0.4%	
Displaced abomasum (DAB)	0.011	HOL SD = 0.7% JER SD = 0.7%	
Ketosis (KET)	0.012	HOL SD = 1.0% JER SD = 1.0%	
Metritis (MET)	0.014	HOL SD = 1.4% JER SD = 1.4%	
Retained placenta (RPL)	0.010	HOL SD = 0.9% JER SD = 0.9%	

^a Expressed as follows:

StandEval = ((Eval - a)/b) × c + d, where a = mean of base adjustment, b = SD of base, c = SD of expression (include sign if scale is reversed), and d = base of expression.