

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))
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
Trait definition(s) and unit(s) of measurement	1. SCS = \log_2 (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. MAS = observed mastitis from 0 to 210 DIM. 100 = no mastitis, 0 = at least 1 mastitis event reported.
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 \geq 201; MAST event occurs within 210 DIM; herd-year reporting MAS; 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 h^2 (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	1. Management group (flexible HYS, includes registry status for HOL) (F), parity \times age (F), regression on inbreeding (F), regression on general heterosis (F), PE (R), herd \times 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 2. Parity \times age (F), year-season (F), regression on inbreeding (F), Herd-year (R), PE (R)

Adjustment for heterogeneous variance in evaluation model	1. Pre-adjustments for herd-year variance applied
Use of genetic groups and relationships	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
Blending of foreign/Interbull information in evaluation	Foreign evaluations of parents not included
Genetic parameters in the evaluation	See Appendix SM for h^2 and genetic variance estimates; 1. PE variance, 0.18; herd \times sire interaction, 0.05; RP, 0.35 2. PE variance, 0.005; herd-year, 0.008; RP, 0.09
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	1. PTA SCS; all-breed PTAs adjusted to within-breed bases as within-breed PTA = (all-breed PTA – breed mean) + phenotypic mean of 3 2. PTA MAS - percentage points of resistance above or below the breed average
Definition of genetic reference base	Cows born in 2010 (stepwise, 5 years)
Next base change	April 2020 (when base will be cows born in 2015)
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	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) 2. MAS receives 32.9% of the health trait subindex (HTH\$), 0.77% total emphasis in lifetime net merit dollars (NM\$) Further details available: https://aipl.arsusda.gov/reference/nmcalc-2018.htm
Anticipated changes in the near future	None

<p>Key reference on methodology applied</p>	<p>Wiggans, G.R. and P.M. VanRaden. 1991. Method and effect of adjustment for heterogeneous variance. J. Dairy Sci. 74:4350-4357.</p> <p>Schutz, M.M. 1994. Genetic evaluation of somatic cell scores for United States dairy cattle. J. Dairy Sci. 77:2113– 2129.</p> <p>Schutz, M.M., P.M. VanRaden, G.R. Wiggans, and H.D. Norman. 1995. Standardization of lactation means of somatic cell scores for calculation of genetic evaluations. J. Dairy Sci. 78:1843–1854.</p> <p>VanRaden, P.M., and G.R. Wiggans. 1991. Derivation, calculation, and use of national animal model information. J. Dairy Sci. 74:2737–2746.</p> <p>VanRaden, P.M., M.E. Tooker, J.B. Cole, G.R. Wiggans, and J.H. Megonigal, Jr. 2007. Genetic evaluations for mixed-breed populations. J. Dairy Sci. 90:2434–2441.</p> <p>Cole, J.B., D.J. Null, and P.M. VanRaden. 2009. Best prediction of yields for long lactations. J. Dairy Sci. 92:1796–1810.</p> <p>VanRaden, P.M., M.E. Tooker, J.R. Wright, C. Sun, and J.L. Hutchison. 2014. Comparison of single-trait to multi-trait national evaluations for yield, health, and fertility traits. J. Dairy Sci. 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. Proc. 11th World Congr. Genet. Appl. Livest. Prod. Auckland, NZ. 11:594.</p>
<p>Key organisation: name, address, phone, fax, e-mail, web site</p>	<p>Evaluation calculation and distribution: Council on Dairy Cattle Breeding One Town Center, Suite 301 4201 Northview Dr. Bowie, MD 20716 Ph: 240-334-4164 e-mail: joao.durr@uscddb.com web site: https://www.uscddb.com/</p> <p>Evaluation methodology: Animal Improvement Program Animal Genomics and Improvement Laboratory Agricultural Research Service, U.S. Dept. of Agriculture 10300 Baltimore Ave. Bldg. 005, Room 306, BARC-West 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>

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 = 0.03	—

^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.