

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)	United States of America
Main trait group	Health (SCS)
Breed(s)	AYS (RDC), BSW, GUE, HOL (B&W, R&W), JER, MSH (RDC); all breeds and crossbred cows evaluated together in a multibreed AM
Trait definition(s) and unit(s) of measurement	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
Method of measuring and collecting data	Collected by Dairy Herd Information Affiliates using ICAR-approved methods and quality certification standards administered by the Council on Dairy Cattle Breeding
Time period for data inclusion	First calvings from 1984 and later; pedigree from birth years 1950 and later
Age groups (e.g. parities) included	First 5 parities included
Other criteria (data edits) for inclusion of records	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
Criteria for extension of records (if applicable)	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	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
Method (model) of genetic evaluation	ST BLUP RP AM
Environmental effects³ in the genetic evaluation model	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
Adjustment for heterogeneous variance in evaluation model	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; PE variance, 0.18; herd \times sire interaction, 0.05; RP, 0.35
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	PTA SCS; all-breed PTAs adjusted to within-breed bases as within-breed PTA = (all-breed PTA – breed mean) + phenotypic mean of 3
Definition of genetic reference base	Cows born in 2010 (stepwise, 5 years)
Next base change	December 2019 (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	SCS receives 10% of total emphasis in lifetime net merit dollars (NM\$, all breeds) and 5% of total emphasis in Total-Performance Index (TPI, HOL)
Anticipated changes in the near future	None
Key reference on methodology applied	Schutz, M.M. 1994. Genetic evaluation of somatic cell scores for United States dairy cattle . J. Dairy Sci. 77:2113–2129. 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. VanRaden, P.M., and G.R. Wiggans. 1991. Derivation, calculation, and use of national animal model information . J. Dairy Sci. 74:2737–2746. 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. Cole, J.B., D.J. Null, and P.M. VanRaden. 2009. Best prediction of yields for long lactations . J. Dairy Sci. 92:1796–1810. 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. (in press).

**Key organisation: name,
address, phone, fax, e-mail,
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Form GE

Appendix SM

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), 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	—	—	—

^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.