Form GE

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)	United States of America
Main trait group	Production (milk, fat, protein)
Breed(s)	AYS (RDC), BSW, GUE, HOL (B&W, R&W, SIM), JER, MSH (RDC); all breeds and crossbred cows evaluated together in a multibreed AM
Trait definition(s) and unit(s) of measurement	Milk (lb), fat and protein (lb, %); 305-day lactation yields
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 1960 and later; pedigree from birth years 1950 and later
Age groups (e.g. parities) included	First 5 parities included; first lactation required before later lactations can contribute to sire evaluation
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; owner-sampler records used from herds that meet identification, outlier, and bulk tank comparison limits
Criteria for extension of records (if applicable)	Records with <305 days extended to 305 days using MT best prediction for milk, fat, and protein
Sire categories	All sires (AI and NS) evaluated together; about 1900 AI and 1000 NS new bulls evaluated each year
Environmental effects, pre-adjustments	Multiplicative adjustments for calving age and month within each breed, times milked per day (adjusted to twice daily milking), previous DO, and heterogeneous variance; base age for mean and variance adjustments is 36-month-old, 2nd-parity cows; 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	MT BLUP RP AM
Environmental effects[3] in the genetic evaluation model	Management group [flexible HYS (2-12 months), includes registry status for HOL] (F), parity × age (F), regression on inbreeding (F), regression on general heterosis (F), PE (R), herd × sire interaction (R); model produces PTA adjusted to 0 inbreeding and 0 heterosis, but 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 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	Interbull sire evaluations and converted foreign dam evaluations with higher REL than current U.S. evaluation used to update parent averages and traditional evaluations
Genetic parameters in the evaluation	See Appendix PR for h^2 and genetic variance estimates and "calculation of reliability" section below for use in calculation; PE variance, 0.28; herd × sire interaction, 0.07; RP, 0.55
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, lb and component %; all-breed PTAs adjusted to within-breed bases as within-breed PTA = [(all-breed PTA – breed mean) + (breed inbreeding regression x Expected Future Inbreeding deviation) + (breed heterosis x heterosis)] × (breed SD/HOL SD)
Definition of genetic reference base **Next base change**	Cows born in 2015 (stepwise, 5 years) 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 using starting values for REL from previous evaluation; cows sired by JER or BSW bulls assumed to have h^2 of 0.23 instead of 0.20; instead of using differing h^2 within AM and REL calculations, lactation weights for such cows increased to reflect their decreased error variance
Criteria for official publication of evaluations	At least 10 daughters with a usable 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 index[4]	Used in Lifetime net merit dollars (**NM$**), Cheese Merit dollars (CM$), Fluid Merit dollars (FM$) and Grazing Merit dollars (GM$) with variable relative weighting. Latest merit information is available at: https://aipl.arsusda.gov/reference/nmcalc-2018.htm Production traits are also used in Total Performance Index (**TPI**, HOL) found in http://www.holsteinusa.com/genetic_evaluations/ss_tpi_formula.html , Jersey Performance Index (JPI, JER), Progressive Performance Ranking (PPR, BSW) , Production Type Index (PTI, RDC), and Production Type Index (PTI, GUE)
Anticipated changes in the near future	None

Key reference on methodology applied	VanRaden, P.M., and G.R. Wiggans. 1991. <u>Derivation, calculation, and use of national animal model information</u>. J. Dairy Sci. 74:2737–2746. VanRaden, P.M., G.R. Wiggans, and C.A. Ernst. 1991. <u>Expansion of projected lactation yield to stabilize genetic variance</u>. J. Dairy Sci. 74:4344–4349. Wiggans, G.R., and P.M. VanRaden. 1991. <u>Method and effect of adjustment for heterogeneous variance</u>. J. Dairy Sci. 74:4350–4357. VanRaden, P.M. 1997. <u>Lactation yields and accuracies computed from test day yields and (co)variances by best prediction</u>. J. Dairy Sci. 80:3015–3022. VanRaden, P.M., and L.A. Smith. 1999. <u>Selection and mating considering expected inbreeding of future progeny</u>. J. Dairy Sci. 82:2771–2778. 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>. J. Dairy Sci. 90:2434–2441. Cole, J.B., D.J. Null, and P.M. VanRaden. 2009. <u>Best prediction of yields for long lactations</u>. J. Dairy Sci. 92:1796–1810. 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>. J. Dairy Sci. 97:7952-7962.
Key organisation: name, address, phone, fax, e-mail, web site	**Evaluation calculation and distribution:** Council on Dairy Cattle Breeding One Town Center 4201 Northview Drive, Suite 302 Bowie, MD 20716 Ph: 240 334 4164 e-mail: <u>joao.durr@uscdcb.com</u> web site: <u>https://www.uscdcb.com</u> **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: <u>john.cole@usda.gov</u> web site: <u>http://aipl.arsusda.gov</u>

Parameters for national genetic evaluations for production traits as provided to Interbull

Country (or countries):	United States of America
Main trait group:	Production (milk, fat, protein)
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 yield GUE, HOL, RDC	Varies with herd variance: 0.15 to 0.25, mean = 0.20	GUE SD = 1547 HOL SD = 1428 RDC SD = 1402	
Milk yield BSW, JER	Varies with herd variance: 0.17 to 0.29, mean = 0.23	BSW SD = 1273 JER SD = 1359	
Fat yield GUE, HOL, RDC	Varies with herd variance: 0.15 to 0.25, mean = 0.20	GUE SD = 56 HOL SD = 53 RDC SD = 53	
Fat yield BSW, JER	Varies with herd variance: 0.17 to 0.29, mean = 0.23	BSW SD = 47 JER SD = 53	
Protein yield GUE, HOL, RDC	Varies with herd variance: 0.15 to 0.25, mean = 0.20	GUE SD = 43 HOL SD = 36 RDC SD = 40	
Protein yield BSW, JER	Varies with herd variance: 0.17 to 0.29, mean = 0.23	BSW SD = 38 JER SD = 41	

[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.