

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 effects³ 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 \times 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) \times (breed SD/HOL SD)
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 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 index⁴ Lifetime net merit dollars (**NM\$**, HOL) = (3.41 × protein yield) + (2.89 × fat yield) + (0.0001 × milk yield) + (35 × PL) – [182 × (SCS – 3)] + (32 × udder composite) + (15 × feet & legs composite) – (23 × size composite) + (27 × daughter pregnancy rate) + calving ability dollars (**CA\$**); relative values of traits are 16, 19, <1, 22, –10, 7, 4, –6, 11, and 5%, respectively; traits expressed as PTAs and weights as lifetime \$/PTA unit; CA\$ and SCS are deviations from base (i.e., not released PTA, which includes population average); CA\$ for HOL includes service-sire CE, daughter CE, service-sire stillbirth, and daughter stillbirth with relative emphasis of 25, 15, 15, and 45%, respectively; CA\$ for BSW includes only service-sire and daughter CE (50% emphasis each), receives only 3% emphasis in NM\$, and relative emphasis on all other traits increases by a factor of 1.02; CA\$ not included for all other breeds, and relative emphasis for all other traits increases by a factor of 1.05; relative emphasis of 25% for protein and 16% for fat yield in Total Performance Index (**TPI**, HOL)

Anticipated changes in the near future None

Key reference on methodology applied VanRaden, P.M., and G.R. Wiggans. 1991. [Derivation, calculation, and use of national animal model information](#). J. Dairy Sci. 74:2737–2746.

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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).

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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), 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 = 1518 HOL SD = 1487 RDC SD = 1268	
Milk yield BSW, JER	Varies with herd variance: 0.17 to 0.29, mean = 0.23	BSW SD = 1304 JER SD = 1240	
Fat yield GUE, HOL, RDC	Varies with herd variance: 0.15 to 0.25, mean = 0.20	GUE SD = 56 HOL SD = 54 RDC SD = 44	
Fat yield BSW, JER	Varies with herd variance: 0.17 to 0.29, mean = 0.23	BSW SD = 51 JER SD = 52	
Protein yield GUE, HOL, RDC	Varies with herd variance: 0.15 to 0.25, mean = 0.20	GUE SD = 41 HOL SD = 38 RDC SD = 34	
Protein yield BSW, JER	Varies with herd variance: 0.17 to 0.29, mean = 0.23	BSW SD = 40 JER SD = 37	

^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.