Form GE

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)	United States of America
Main trait group	Longevity [direct (single trait) and combined (multitrait) PL]
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	PL defined as time in milking herd before removal by voluntary culling, involuntary culling, or death; credits for each month in milk obtained from standard lactation curves and then summed across all lactations; diminishing credits within lactation give cows more credit for beginning a new lactation than for continuing to milk in previous lactation; cows get 8 months credit for 305-day first-lactation records, 10 months credit for second lactations, 10.2 months credit for third and later lactations, partial credits for shorter records, and extra credits for longer records
Method of measuring and collecting data	Calving dates, disposal dates, reasons for disposal, and lactation lengths from data collected by Dairy Herd Information Affiliates; dead cows receive credit for months of production as stated above; live cows receive additional credit for predicted remaining life expectancy; prediction factors consider cow age and lactation stage; credits from >1 herd combined for cows that change herds; released PL combines information from direct longevity with evaluations from correlated traits
Time period for data inclusion	First calvings from 1960 and later; pedigree from birth years 1950 and later; cows must be born at least 3 years prior to evaluation to be included
Age groups (e.g. parities) included	All parities included
Other criteria (data edits) for inclusion of records	Valid sire identification required with first-lactation records
Criteria for extension of records (if applicable)	Records extended for cows still alive, sold for dairy purposes, or in herds that discontinued testing; cows sold for dairy purposes or in herds that discontinued testing receive extended records if they had opportunity to reach 3 years of age or otherwise have records discarded
Sire categories	All sires (AI and NS) evaluated together
Environmental effects, pre-adjustments	Genetic variance in censored and uncensored management groups equalized by pre-adjusting censored data using expansion factors
Method (model) of genetic evaluation	ST BLUP AM; records from censored management groups receive less weight than those from uncensored groups
Environmental effects[3] in the genetic evaluation model	Management group [flexible based on herd of first lactation and birth date (and registry status for HOL)] (F), regression on inbreeding (F), regression on general heterosis (F), herd × sire interaction (R); model produces PTA adjusted to 0 inbreeding, 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	None
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	Direct longevity for foreign bulls combined with PTA for other traits with same MT procedures used for domestic bulls
Genetic parameters in the evaluation	See Appendix LO for h^2 and genetic variance estimates; herd × sire interaction, 0.05; after direct longevity evaluation, information from 11 other traits and composites combined by selection index theory to increase PL REL based on genetic correlations with PL; selection index procedures use PTAs, parent averages (PAs), and PTA and PA RELs for the 12 traits and are applied to both bulls and cows in age order so that improved PL evaluations of parents are transferred to progeny
System validation	Direct PL obtained with same AM programs used for yield; combined PL programs produced evaluations similar to multitrait, across-country evaluations when tested on international yield data; trend validation methods 2 and 3 applied separately for each breed
Expression of genetic evaluations	PTA, months; all-breed PTAs adjusted to within-breed bases as within-breed PTA = (all-breed PTA – breed mean)
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 with opportunity to reach 8 years of age considered a completed observation and gets 1 daughter equivalent (**DE**); cows with less opportunity get fewer DE regardless of whether they are culled or alive; DEs are 0.22 at 36 months of age, 0.53 at 48 months, 0.75 at 60 months, 0.89 at 72 months, and 0.95 at 84 months; those DEs combined with DE from parent average to calculate direct REL and then DEs from other traits increase combined REL
Criteria for official publication of evaluations	All bulls evaluated for milk yield by USA or Interbull have official PL evaluations; Interbull longevity evaluations used if bull has foreign daughters or Interbull REL is higher than REL for ST domestic longevity evaluation
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 E.J.H. Klaaskate. 1993. Genetic evaluation of length of productive life including predicted longevity of live cows. J. Dairy Sci. 76:2758–2764. VanRaden, P.M. 2001. Methods to combine estimated breeding values obtained from separate sources. J. Dairy Sci. 84(E-Suppl.):E47–E55. VanRaden, P.M., C.M.B. Dematawewa, R.E. Pearson, and M.E. Tooker. 2006. Productive life including all lactations and longer lactations with diminishing credits. J. Dairy Sci. 89:3213–3220. 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. 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 VanRaden, P.M., J.R. Wright, M.E. Tooker, and H.D. Norman. Value of selecting for cow and calf livability. Interbull Bull. 50:30–33. 2016

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: joao.durr@uscdcb.com web site: https://www.uscdcb.com **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: john.cole@usda.gov web site: http://aipl.arsusda.gov

Form GE **Appendix LO**

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

Country (or countries):	United States of America
Main trait group:	Longevity (PL)
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]
Direct Longevity	0.08	SD = 4.52	
Combined Longevity	0.08	SD = 4.52	

[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.