

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)	BELGIUM (Walloon Region)
Main trait group¹ NOTE! Only one trait group per form!	Longevity
Breed(s)	All dairy and dual-purpose breeds
Trait definition(s) and unit(s) of measurement² Attach an appendix if needed	Survival over successive lactations
Method of measuring and collecting data	Milk recording
Time period for data inclusion	Lactation since 1973 (included)
Age groups (e.g. parities) included	All parities
Other criteria (data edits) for inclusion of records	Age checks for all lactations. Cows need to have a known first lactation. Herd has at least one test-day record in the year following the calving year, if not current survival put to censored record.
Criteria for extension of records (if applicable)	No extension
Sire categories	All sires
Environmental effects³, pre-adjustments	No preadjustments
Method (model) of genetic evaluation³	Random regression lactation survival animal model
Environmental effects³ in the genetic evaluation model	Herd – quota year – lactation class (1 st , 2 nd , 3 rd , 4 th and later) (F) Birth year – lactation class (1 st , 2 nd , 3 rd , 4 th and later) (F)
Adjustment for heterogeneous variance in evaluation model	No adjustments
Use of genetic groups and relationships	Yes, genetics groups based on selection path, type of breed, degree of Holsteinisation, origin (North-America vs Europe) and time
Blending of foreign/Interbull information in evaluation	No blending
Genetic parameters in the evaluation	See Appendices GE and LO
System validation	Trend validations (Method III)
Expression of genetic evaluations If standardised (e.g. RBV), give standardisation formula in the appendix	Cumulative survival over first 5 lactations, expressed in lactations Transformed to RBV (average 100, SD 10)
Definition of genetic reference base Next base change	SD for all cows having survival records born in 2010 used to standardize to 10 points– mean adjusted to 100 for average active sire use in 2014 In 2020 cows born in 2015, sires used in 2019

Calculation of reliability	Based on INTERBULL EDC computations
Criteria for official publication of evaluations	First sire need to have production evaluation REL \geq 30 % for: <ul style="list-style-type: none"> • young sires • imported sires if only domestic results • imported sires with INTERBULL results
Number of evaluations / publications per year	3
Use in total merit index⁴	$VEG = VEL + VEF + VET$ $VEG = VEL + VEF + VET$ $VEL = -0.064 EBV_{milk} + 1.75 EBV_{fat} + 6.25 EBV_{prot}$ $VEF \sim 0.71 * RBV_{SCS} + 4.30 RBV_{long} + 0.40 * RBV_{fert} + 0.20 * RBV_{CEd} + 0.24 * RBV_{CEm}$ <ul style="list-style-type: none"> - all functional traits expressed on a 10 unit scale, means of 100 subtracted - coefficients only approximate as computations done using selection index procedure estimating jointly VEF, combined RBV_{long} and combined RBV_{fert} from EBVs for direct longevity, indirect longevity, SCS, indirect fertility and calving ease traits. $VET = VEM + VEC + VEP$ $VEM = -4.11 RBV_{rear\ leg\ set} + (2.06 RBV_{rear\ leg\ rear\ view}) + (10.54 RBV_{bone\ quality}) + (9.00 RBV_{feet\ \&\ legs})$ $VEC = -4.32 RBV_{overall\ development} + 11.11 RBV_{udder\ corrected\ final\ conformation}$ $VEP = 8.64 RBV_{fore\ udder} + 14.19 RBV_{rear\ udder\ height} + 5.55 RBV_{udder\ support} + 14.19 RBV_{udder\ depth} + 2.47 RBV_{front\ teat\ placement} + (-11.11 RBV_{rear\ teat\ placement}) + (-5.55 RBV_{teat\ length})$
Anticipated changes in the near future	
Key reference on methodology applied	Gengler, N., Vanderick, S., Mayeres, P., Gillon, A. and Croquet, C. (2005) Genetic evaluation of cow survival using a lactation random regression model. Interbull Bulletin 33: 176-180. Vanderick S., Croquet C., Soyeurt H., Hammami H., Mayeres P., Gengler N. (2006). Integration of longevity into the Walloon genetic evaluation system. INTERBULL Bulletin 35.

**Key organisation: name, address,
phone, fax, e-mail, web site**

Organisation responsible for genetic evaluations:
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WEB site for publication of sire breeding values:

<http://www.elinfo.be>

1) Either: Production (e.g. milk, fat, protein), Conformation, Health (e.g. mastitis resistance, milk somatic cell, resistance to diseases other than mastitis), Longevity, Calving (e.g. stillbirth, calving ease), Female fertility (e.g. non-return rate, interval between reproductive events, number of AI's, heat strength), Workability (e.g. milking speed, temperament), Beef production, Efficiency (e.g. body weight, energy balance, body conditioning score), or Other traits.

2) Indicate frequencies per category if the trait is categorical and specify transformation of data if practiced.

3) Use abbreviations for most common effects (see document with list of abbreviations at http://www-interbull.slu.se/service_documentation/General/list_of_abbreviations.rtf) and indicate random (R) or fixed (F).

4) Please give economic weights and indicate how they are expressed (preferably in genetic standard deviation units).

Parameters used in genetic evaluation

Country (or countries): BELGIUM (Walloon Region)
Main trait group: Longevity
Breed (repeat as necessary): All dairy and dual-purpose breeds

Trait	Definition	ITB ^a	h ^{2b}	genetic variance ^b	official proof standardisation formula ^c
Direct longevity		X	0.106	0.0797	

^a Indicate, with X, traits that are submitted to Interbull for international genetic evaluations.

^b If repeated records are treated as separate traits, provide heritability estimates and genetic variances separately for each trait, as well as for all traits pooled, i.e. for the trait submitted to Interbull.

^c Expressed as follows:

StandEval=((eval-a)/b)*c+d where a=mean of the base adjustment, b=standard deviation of the base, c=standard deviation of expression (include sign if scale is reversed), and d=base of expression.

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

Country (or countries): BELGIUM (Walloon Region)
Main trait group: Longevity
Breed(s): All dairy and dual-purpose breeds

Trait	h^2	Genetic Variance	official proof standardisation formula ^a
Direct longevity:	0.106	0.0797	
Combined longevity:			

^a Expressed as follows:
 $StandEval = ((eval - a) / b) * c + d$ where a=mean of the base adjustment, b=standard deviation of the base, c=standard deviation of expression (include sign if scale is reversed), and d=base of expression.

Table 1 : Genetic correlations and genetic variances (on diagonal) across selected lactations (1 to 7, 10 and 17).

	1	2	3	4	5	6	7	10	17
1	0.00232	0.850	0.972	0.858	0.694	0.604	0.561	0.525	0.523
2	0.850	0.00354	0.900	0.514	0.251	0.129	0.074	0.029	0.026
3	0.872	0.900	0.00386	0.835	0.645	0.545	0.497	0.458	0.455
4	0.858	0.514	0.835	0.00496	0.959	0.917	0.893	0.871	0.870
5	0.694	0.251	0.645	0.959	0.00650	0.992	0.984	0.975	0.974
6	0.604	0.129	0.545	0.917	0.992	0.00650	0.998	0.995	0.995
7	0.561	0.074	0.497	0.893	0.984	0.998	0.00650	0.999	0.999
10	0.525	0.029	0.458	0.871	0.975	0.995	0.999	0.00650	0.999
17	0.523	0.026	0.455	0.870	0.874	0.995	0.999	0.999	0.00650

Table 2 : Residual correlations and residual variances (on diagonal) across selected lactations (1 to 7, 10 and 17).

	1	2	3	4	5	6	7	10	17
1	0.0751	0	0	0	0	0	0	0	0
2	0	0.115	0	0	0	0	0	0	0
3	0	0	0.125	0	0	0	0	0	0
4	0	0	0	0.149	0	0	0	0	0
5	0	0	0	0	0.210	0	0	0	0
6	0	0	0	0	0	0.210	0	0	0
7	0	0	0	0	0	0	0.210	0	0
10	0	0	0	0	0	0	0	0.210	0
17	0	0	0	0	0	0	0	0	0.210