

## DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

<b>Country (or countries)</b>	BELGIUM (Walloon Region)
<b>Main trait group<sup>1</sup></b> NOTE! Only one trait group per form!	Health
<b>Breed(s)</b>	All dairy and dual-purpose breeds
<b>Trait definition(s) and unit(s) of measurement<sup>2</sup></b> Attach an appendix if needed	Somatic Cell Score SCS = $[\log_2 (\text{SCC}/100000)] + 3$ EBV are average 1-d score across lactation 1,2 and 3
<b>Method of measuring and collecting data</b>	SCC through regular milk recording (A4 or A6)
<b>Time period for data inclusion</b>	Since 1979 (included, calving date)
<b>Age groups (e.g. parities) included</b>	3 parities
<b>Other criteria (data edits) for inclusion of records</b>	Valid birth date, time frame 10,000<SCC<10,000,000; SCS<0.1 put to 0.1
<b>Criteria for extension of records (if applicable)</b>	No extension
<b>Sire categories</b>	All sires
<b>Environmental effects<sup>3</sup>, pre-adjustments</b>	N/A
<b>Method (model) of genetic evaluation<sup>3</sup></b>	Weighted ML-TDM-RR-AM (multilactation) Record weights are proportional to mastitis infection likelihood. (SCS that are above expected SCS levels based on standardized residuals have higher weights and SCS that are below expected levels have lower weights)
<b>Environmental effects<sup>3</sup> in the genetic evaluation model</b>	Herd-test-day (F), Minor stage of lactation (F), Major stage of lactation x Age x Season (F), Stage of lactation x Days carried calf (F), PE (R)
<b>Adjustment for heterogeneous variance in evaluation model</b>	No
<b>Use of genetic groups and relationships</b>	Yes, genetics groups based on selection path, type of breed, degree of Holsteinisation, origin (North-America vs Europe) and time
<b>Blending of foreign/Interbull information in evaluation</b>	No before INTERBULL, yes after
<b>Genetic parameters in the evaluation</b>	See Appendices GE and SM
<b>System validation</b>	Trend Validation (method III),
<b>Expression of genetic evaluations</b> If standardised (e.g. RBV), give standardisation formula in the appendix	RBV (average 100, SD 10)

<b>Definition of genetic reference base</b>	SD for all cows with SCS born in 2010 used to standardize to 10 points– mean adjusted to 100 for average active sire use in 2014
<b>Next base change</b>	In 2020 cows born in 2015, sires used in 2019
<b>Calculation of reliability</b>	Based on INTERBULL EDC computations
<b>Criteria for official publication of evaluations</b>	Sire needs to have production evaluation REL ≥ 45% for: <ul style="list-style-type: none"> <li>• young sires</li> <li>• imported sires if domestic results</li> <li>• imported sires with INTERBULL results</li> </ul>
<b>Number of evaluations / publications per year</b>	3
<b>Use in total merit index<sup>4</sup></b>	$V\epsilon G = V\epsilon L + V\epsilon F + V\epsilon T$ $V\epsilon G = V\epsilon L + V\epsilon F + V\epsilon T$ $V\epsilon L = -0.064 EBV_{milk} + 1.75 EBV_{fat} + 6.25 EBV_{prot}$ $V\epsilon F \sim 0.71 * RBV_{SCS} + 4.30 RBV_{long} + 0.40 * RBV_{fert} + 0.20 * RBV_{CEd} + 0.24 * RBV_{CEm}$ <p>- all functional traits expressed on a 10 unit scale, means of 100 subtracted</p> <p>- coefficients only approximate as computations done using selection index procedure estimating jointly VεF, combined RBV<sub>long</sub> and combined RBV<sub>fert</sub> from EBVs for direct longevity, indirect longevity, SCS, indirect fertility and calving ease traits.</p> $V\epsilon T = V\epsilon M + V\epsilon C + V\epsilon P$ $V\epsilon M = -4.11 RBV_{rear\ leg\ set} + (2.06 RBV_{rear\ leg\ rear\ view}) + (10.54 RBV_{bone\ quality}) + (9.00 RBV_{feet\ \&\ legs})$ $V\epsilon C = -4.32 RBV_{overall\ development} + 11.11 RBV_{udder\ corrected\ final\ conformation}$ $V\epsilon P = 8.64 RBV_{fore\ udder} + 14.19 RBV_{rear\ udder\ height} + 5.55 RBV_{udder\ support} + 14.19 RBV_{udder\ depth} + 2.47 RBV_{front\ teat\ placement} + (-11.11 RBV_{rear\ teat\ placement}) + (-5.55 RBV_{teat\ length})$
<b>Anticipated changes in the near future</b>	Improvement of weights, heterogeneous variance
<b>Key reference on methodology applied</b>	<p>Gengler, N. and Mayeres, P. [2003]. Use of a weighted random regression test-day model to better relate observed somatic cell score to mastitis infection likelihood. INTERBULL Bulletin <b>31</b>: 92-96.</p> <p>Croquet C, Mayeres P., Gillon A., Vanderick S., and Gengler N. (2006). Inbreeding Depression for Global and Partial Economic Indexes, Production, Type, and Functional Traits. J. Dairy Sci. <b>89</b>: 2257-2267.</p> <p>Vanderick S., Croquet C., Soyeurt H., Hammami H., Mayeres P., Gengler N. (2006). Integration of longevity into the Walloon genetic evaluation system. INTERBULL Bulletin <b>35</b>.</p>

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**Key organisation: name, address,  
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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](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 for national genetic evaluations for udder health traits as provided to Interbull

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

Trait	$h^{2a}$	genetic variance <sup>a</sup>	official proof standardisation formula <sup>b</sup>
Milk Somatic Cell:	0.0998	0.1561	
	0.128	0.2147	
	0.162	0.2366	
	Pooled 0.135	0.2060	EBV
Clinical Mastitis:	N/A		

<sup>a</sup> 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.

<sup>b</sup> 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: Genetic correlations above, phenotypic below and heritabilities on diagonal.

	SCS1	SCS2	SCS3
SCS1	<b>0.0998</b>	0.949	0.879
SCS2	0.311	<b>0.128</b>	0.950
SCS3	0.337	0.424	<b>0.162</b>