Form GE Status as of: 2018-02-02

## DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)  Main trait group <sup>1</sup> NOTE! Only one trait group per form!	BELGIUM (Walloon Region) Production
	All dairy and dual-purpose breeds
Breed(s)  Trait definition(s) and unit(s) of measurement <sup>2</sup> Attach an appendix if needed	<ol> <li>Milk</li> <li>Fat</li> <li>Protein</li> <li>Records are kg of yield produced within a 24-hours test-day period and EBV are average 305-d yields (kg) across lactation 1,2 and 3</li> <li>Fat percentage</li> <li>Protein percentage</li> <li>EBV<sub>%</sub>=(EBV<sub>Yi</sub>*100)-(EBV<sub>M</sub>*%B<sub>i</sub>)/(EBV<sub>M</sub>+B<sub>M</sub>), where</li> <li>EBV<sub>%</sub>= estimated breeding value for fat or protein percentage</li> <li>EBV<sub>H</sub>= estimated breeding value for fat or protein yield</li> <li>EBV<sub>M</sub>= estimated breeding value for milk yield</li> <li>%B<sub>i</sub>= average fat or protein percentage of the base animals</li> </ol>
Method of measuring and collecting data	$B_M$ = average milk yield of the base animals  Milk recording
Time period for data inclusion	Data since 1973 (included, calving date)
Age groups (e.g. parities) included	3 parities
Other criteria (data edits) for inclusion of records	Valid birth date, time frame
Criteria for extension of records (if applicable)	No extension
Sire categories	All sires
Environmental effects <sup>3</sup> , pre- adjustments	Age inside lactation-stage-breed, additive
Method (model) of genetic evaluation <sup>3</sup>	ML-MT-TDM-RR-AM (multi-lactation-multi-trait)
Environmental effects <sup>3</sup> in the genetic evaluation model	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), Herd x year RR (R), PE (R)
Adjustment for heterogeneous variance in evaluation model	No
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 before INTERBULL, yes after
Genetic parameters in the evaluation	See appendices GE and PR
System validation	Trend Validation (method III)

Expression of genetic evaluations If standardised (e.g. RBV), give standardisation formula in the appendix	EBV defined as mean EBV of the three lactations for milk, fat and protein yields, respectively					
<b>Definition of genetic reference</b> base	All cows with production born in 2010					
Next base change	In 2020 cows born in 2015					
Calculation of reliability	Based on INTERBULL EDC computations					
Criteria for official publication of	REL ≥ 50% for:					
evaluations	<ul> <li>young sires</li> </ul>					
	<ul> <li>imported sires if only domestic results</li> </ul>					
	<ul> <li>imported sires with INTERBULL results</li> </ul>					
Number of evaluations / publications per year	3					
Use in total merit index <sup>4</sup>	$V \in G = V \in L + V \in F + V \in T$					
	$V \in G = V \in L + V \in F + V \in T$					
	$V \in L = -0.064 EBV_{milk} + 1.75 EBV_{fat} + 6.25 EBV_{prot}$					
	$V\!\!\in\!\! F \sim 0.71 * RBV_{SCS} + 4.30 \; RBV_{long} + 0.40 * RBV_{fert} + 0.20 * RBV_{CEd} + 0.24 * RBV_{CEm}$					
	- all functional traits expressed on a 10 unit scale, means of 100 subtracted					
	<ul> <li>coefficients only approximate as computations done using selection index procedure estimating jointly V€F, 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.</li> </ul>					
	$V \in T = V \in M + V \in C + V \in P$					
	V€M= -4.11 RBV <sub>rear leg set</sub> + $(2.06 \text{ RBV}_{rear leg rear view})$ + $(10.54 \text{ RBV}_{bone})$ quality) + $(9.00 \text{ RBV}_{feet\&legs})$					
	V€C=-4.32 RBV <sub>overall development</sub> + 11.11 RBV <sub>udder corrected final conformation</sub>					
	V€P= 8.64 RBV <sub>fore udder</sub> + 14.19 RBV <sub>rear udder height</sub> + 5.55 RBV <sub>udder support</sub> + 14.19 RBV <sub>udder depth</sub> + 2.47 RBV <sub>front teat placement</sub> + (-11.11 RBV <sub>rear teat placement</sub> ) + (-5.55 RBV <sub>teat length</sub> )					
Anticipated changes in the near	Heterogeneous variance adjustement					
future	Multi-lactation (>3)					
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# **Key reference on methodology applied**

Auvray, B. and Gengler N. [2002]. Feasibility of a Walloon test day model and study of its potential as tool for selection and management. INTERBULL Bulletin 29: 123-127.

Gengler, N. and Wiggans G. [2001]. Heterogeneity in (co)variance structure in test-day yields. INTERBULL Bulletin 27: 179-183.

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. 89: 2257-2267.

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

<sup>1)</sup> 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.

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

<sup>3)</sup> 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).

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

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### Parameters used in genetic evaluation

**Country (or countries):** BELGIUM (Walloon Region)

Main trait group: Production

**Breed (repeat as necessary):** All dairy and dual-purpose breeds

Trait	Definition	ITB <sup>a</sup>	$h^{2b}$	genetic variance <sup>b</sup>	official proof standardisation formula <sup>c</sup>
Milk yield			0.41	301265	
			0.30	296532	
			0.31	322263	
Po	oled	X	0.38	280425	EBV
Fat yield			0.43	502.6	
			0.37	581.6	
			0.34	595.7	
Po	oled	X	0.43	522.6	EBV
Protein yield			0.40	253.1	
			0.32	283.6	
			0.32	302.5	
Po	oled	X	0.41	261.5	EBV

<sup>&</sup>lt;sup>a</sup> Indicate, with X, traits that are submitted to Interbull for international genetic evaluations.

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.

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.

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

**Country (or countries):** BELGIUM (Walloon Region)

Main trait group: Production

**Breed(s):** All dairy and dual-purpose breeds

Trait		$h^{2a}$	genetic variance <sup>a</sup>	official proof standardisation formula <sup>b</sup>
Milk yield:		0.41	301265	
		0.30	296532	
		0.31	322263	
	Pooled	0.38	280425	EBV
Fat yield:		0.43	502.6	
		0.37	581.6	
		0.34	595.7	
	Pooled	0.43	522.6	EBV
Protein yield:		0.40	253.1	
		0.32	283.6	
		0.32	302.5	
	Pooled	0.41	261.5	EBV

If lactations, or part of lactations, are treated as separate traits, provide heritability estimates and genetic variances separately for each lactation, as well as for all lactations pooled, i.e. for the trait submitted to Interbull.

TABLE: Genetic correlations above, phenotypic below and heritabilities on diagonal.

	M1	F1	P1	M2	F2	P2	M3	F3	P3
M1	0.41	0.88	0.95	0.87	0.81	0.87	0.85	0.79	0.84
F1	0.80	0.43	0.91	0.82	0.89	0.85	0.79	0.88	0.82
P1	0.92	0.87	0.40	0.86	0.85	0.90	0.85	0.83	0.87
M2	0.76	0.64	0.73	0.30	0.90	0.95	0.90	0.84	0.90
F2	0.60	0.72	0.64	0.80	0.37	0.93	0.85	0.94	0.88
P2	0.66	0.64	0.68	0.90	0.89	0.32	0.90	0.87	0.94
M3	0.64	0.57	0.62	0.76	0.64	0.70	0.31	0.86	0.92
F3	0.56	0.67	0.60	0.64	0.72	0.66	0.85	0.34	0.90
P3	0.61	0.60	0.62	0.73	0.68	0.71	0.91	0.86	0.32

b 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.