

## 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!	Calving Traits
<b>Breed(s)</b>	Red and Black Holstein
<b>Trait definition(s) and unit(s) of measurement<sup>2</sup></b> Attach an appendix if needed	Calving ease scores range from 1 to 4 1 Caesarean /fetonomy 2 Hard pull 3 Easy pull 4 Normal
<b>Method of measuring and collecting data</b>	Scored by breeders on voluntary basis
<b>Time period for data inclusion</b>	All available data since 2000
<b>Age groups (e.g. parities) included</b>	Heifer (1 <sup>st</sup> calving) and cows (from 2 <sup>nd</sup> to 5 <sup>th</sup> calvings included)
<b>Other criteria (data edits) for inclusion of records</b>	Valid birth date Age checks for all parities Multiple births, calving interval < 270 days; calves with unknown dam and herds with low variability in calving scores are skipped
<b>Criteria for extension of records (if applicable)</b>	N/A
<b>Sire categories</b>	All
<b>Environmental effects<sup>3</sup>, pre-adjustments</b>	No pre-adjustments
<b>Method (model) of genetic evaluation<sup>3</sup></b>	Animal Model Single Trait – no covariance between direct and maternal effects
<b>Environmental effects<sup>3</sup> in the genetic evaluation model</b>	Herd (F) Herd – Year of calving (R) Season (F) Age at current calving (10 classes of age in months) by sex of calf, by group of calving (2 groups: 1 <sup>st</sup> calving and 2 <sup>nd</sup> -5 <sup>th</sup> calvings) (F) Maternal permanent environment (R)
<b>Adjustment for heterogeneous variance in evaluation model</b>	No Adjustment
<b>Use of genetic groups and relationships</b>	All known relationships of cows and sires are considered. No genetic groups
<b>Blending of foreign/Interbull information in evaluation</b>	No blending
<b>Genetic parameters in the evaluation</b>	Heritability for direct effect : 0.08 Heritability for maternal effect : 0.02
<b>System validation</b>	Trend validations
<b>Expression of genetic evaluations</b> If standardised (e.g. RBV), give standardisation formula in the appendix	Expressed in expected differences in percentage of “normal” calving. Transformed to RBV (average 100, SD 10)

<b>Definition of genetic reference base</b>	SD for all cows with calving ease scores 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>	First sire need to have production evaluation REL $\geq$ 30% for : <ul style="list-style-type: none"> <li>• young sires</li> <li>• imported sires if only 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 <math>V\epsilon F</math>, combined <math>RBV_{long}</math> and combined <math>RBV_{fert}</math> 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>	
<b>Key reference on methodology applied</b>	<p>Vanderick S, Troch T, Gillon A, Glorieux G, Faux P, Gengler N. Genetic evaluation of calving ease for Walloon Holstein dairy cattle. Interbull Bull. 2013;(47):32–7.</p> <p>Vanderick S, Troch T, Gillon A, Glorieux G, Gengler N. Genetic parameters for direct and maternal calving ease in Walloon dairy cattle based on linear and threshold models. J Anim Breed Genet. 2014;131(6):513–21.</p>

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

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<http://www.elinfo.be>

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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 used in genetic evaluation

**Country (or countries):** BELGIUM (Walloon Region)  
**Main trait group:** Calving Traits  
**Breed (repeat as necessary):** Red and Black Holstein

Trait	Definition	ITB <sup>a</sup>	h <sup>2b</sup>	genetic variance <sup>b</sup>	official proof standardisation formula <sup>c</sup>
Direct Calving Ease		X	0.077	0.028	
Maternal Calving Ease		X	0.023	0.009	

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

<sup>b</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>c</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.

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

**Country (or countries):** BELGIUM (Walloon Region)  
**Main trait group:** Calving Traits  
**Breed(s):** Red and Black Holstein

Trait	$h^2$	genetic variance	official proof standardisation formula <sup>a</sup>
Direct calving ease:	0.077	0.389	
Maternal calving ease:	0.023	0.389	

<sup>a</sup> Expressed as follows:

$\text{StandEval} = ((\text{eval} - a) / b) * c + d$  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.