

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)	BELGIUM (Walloon Region)
Main trait group¹	Zootechnical traits (second visit)
NOTE! Only one trait group per form!	
Breed(s)	Belgian Blue
Trait definition(s) and unit(s) of measurement²	<ul style="list-style-type: none"> - Conformation score (1, very low meat → 9, very high meat) - Weight (kg) - Height (cm)
Attach an appendix if needed	
Method of measuring and collecting data	By technicians Weight = real weight or calculated from chest girth
Time period for data inclusion	All available data since 1 st December 1999
Age groups (e.g. parities) included	Data are collected between 10 and 22 months of age
Other criteria (data edits) for inclusion of records	Only female data. Height and weight : elimination of erroneous data based on mean and standard deviation calculated by age group. At least data from 5 animals in a given herd * test date.
Criteria for extension of records (if applicable)	N/A
Sire categories	All
Environmental effects³, pre-adjustments	No pre-adjustments
Method (model) of genetic evaluation³	Multiple trait animal model
Environmental effects³ in the genetic evaluation model	Herd * Test date (F) Age (F) Year * season of birth (F) Body condition (F)
Adjustment for heterogeneous variance in evaluation model	No Adjustment
Use of genetic groups and relationships	No
Blending of foreign/Interbull information in evaluation	No blending. Only local information
Genetic parameters in the evaluation	See Appendix GE
System validation	Genetic trends, correlations between consecutive evaluations
Expression of genetic evaluations If standardised (e.g. RBV), give standardisation formula in the appendix	Standardized breeding values: animals from genetic reference base are put to a mean of 100 and a standard error of 10
Definition of genetic reference base	All phenotyped animals born 4 years before current year
Next base change	Base changes every year
Calculation of reliability	Reliabilities are calculated from PEV
Criteria for official publication of evaluations	Sires : REL \geq 50 % ; At least 10 calves in minimum 5 herds Females : REL \geq 15 %
Number of evaluations / publications per year	3
Use in total merit index⁴	No
Anticipated changes in the near future	No
Key reference on methodology applied	

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

Organisation responsible for genetic evaluations and computing centre:

Elevéo asbl

R&D Department - Genetic Evaluation Unit

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B-5590 Ciney

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WEB site for publication of sire breeding values:

<http://www.awenet.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: Conformation and beef production
Breed (repeat as necessary): Belgian-Blue

Trait	Definition	ITB ^a	h ^{2b}	genetic variance ^b	official proof standardisation formula ^c
Conformation score			0.37	0,25	
Body Weight			0.25	414,5	
Height at withers			0.38	5,9	

^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.