Status as of: 2020-04-20

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)	BELGIUM (Walloon Region)			
Country (or countries) Main trait group ¹				
NOTE! Only one trait group per form!	Carcass weight - Female			
Breed(s)	Belgian Blue			
Trait definition(s) and unit(s) of	Hot carcass weight females (kg)			
measurement ²				
Attach an appendix if needed				
Method of measuring and collecting data	By technicians in abattoir			
Time period for data inclusion	Cows born in Wallonia since 2006			
Age groups (e.g. parities) included	All			
Other criteria (data edits) for inclusion of records	$24 \leq$ Slaughter age \leq 96, no heifers $300 \leq$ Slaughter weight \leq 800			
Criteria for extension of records (if applicable)	N/A			
Sire categories	AI sires			
Environmental effects ³ , pre-adjustments	Pre-adjustment for type of carcass trimming			
	Pre-adjustment for age, 60 months Animal model			
Method (model) of genetic evaluation ³				
Environmental effects ³ in the genetic	Fattening herd Year month of slaughter			
evaluation model	Slaughterhouse			
	Fat class			
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			
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, which are multiplied by a standard error of 10 and added to a mean value of 100			
Definition of genetic reference base	All cows born 7 years before the current year			
Next base change	Base changes every year			
Calculation of reliability	Reliabilities are calculated from PEV			
Criteria for official publication of	Sires : REL \geq 50 % ; At least 10 calves in minimum 5 herds			
evaluations	Females : $\text{REL} \ge 15 \%$			
Number of evaluations / publications per year	3			
Use in total merit index ⁴	No			
Anticipated changes in the near future	No			
Key reference on methodology applied				

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		
	Rue des Champs Elysées 4		
	B-5590 Ciney		
	0032/83/23.06.32.		
	eval_gen@awenet.be		
	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):	BELGIUN	BELGIUM (Walloon Region)			
Main trait group: Breed (repeat as necess		eight – Females lue			
Trait	Definition	ITB ^a	h ^{2b}	genetic variance ^b	official proof standardisation formula ^c

0.35

583

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

Carcass weight females

^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.