Status as of: 2020-04-20

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)	BELGIUM (Walloon Region)
Main trait group[1] **NOTE!** Only one trait group per form!	2nd visit Traits - Functionals
Breed(s)	Belgian Blue
Trait definition(s) and unit(s) of measurement[2] Attach an appendix if needed	- Death rate (0/1) - Straight hocks (0/1) - Bent hocks (0/1) - Defects at rear legs (0/1) - Deviation of the jaw (0/1) - Prognathism (0/1) - Brachygnathism (0/1)
Method of measuring and collecting data	By breeders on voluntary basis
Time period for data inclusion	All available data since 2000
Age groups (e.g. parities) included	All
Other criteria (data edits) for inclusion of records	Valid birth date Sex of the animal known
Criteria for extension of records (if applicable)	N/A
Sire categories	AI
Environmental effects[3]**, pre-adjustments**	No pre-adjustments
Method (model) of genetic evaluation[3]	Single trait – Sire model
Environmental effects[3] **in the genetic evaluation model**	Age of the animal at the visit (for Death: Year month of birth) (F) Province–Year month of visit (for Death: Province–Year of birth) (F) Sex (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
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 **Next base change**	No reference base
Calculation of reliability	Reliabilities are calculated from PEV obtained by direct inversion of the coefficient matrix
Criteria for official publication of evaluations	Sires : REL ≥ 50 % ; At least 10 calves in minimum 5 herds Females : NA
Number of evaluations / publications per year	1
Use in total merit index[4]	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 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): BELGIUM (Walloon Region)
Main trait group: 2nd visit Traits - Functionals
Breed (repeat as necessary): Belgian-Blue

Trait	Definition	ITB[a]	h^{2b}	genetic variance [b]	official proof standardisation formula[c]
Death rate			0.011	0.063	
Straight hocks			0.014	0.455	
Bent hocks			0.046	0.439	
Defect at rear legs			0.018	0.115	
Deviation of the jaw			0.037	0.205	
Prognathism			0.026	0.381	
Brachygnathism			0.041	0.146	

[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.