Form GENO

DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS

Country (or countries)	Wallon Region of Belgium
Main trait group[a]. NOTE. Only one trait group per form!	Linear Score
Breed(s)	Belgian Blue
Trait definition(s) and unit(s) of measurement Attach an appendix if needed	-Height (50-100) -Length (1-50) -Chest width (1-50) -Pelvis width (1-50) -Shoulder musculature (1-50) -Top muscling (1-50) -Rib (1-50) -Rump (1-50) -Pelvis length (1-50) -Tail set (1-50) -Thighs side view (1-50) -Thighs rear view (1-50) -Bone structure (1-50) -Top line (1-50) -Hocks (1-50) -Skin (1-50) -Muscling (50-100) -Meaty type (50-100) -General appearance (1-20) -Final score (50-100)
Source of genotypes (chips used)	Illumina BovineSNP10K BeadChip (version 4 to 9), Illumina Bovine SNP50K (version 2 and 3), Illumina BovineHD
Imputation method for missing genotypes	Beagle3 (allelic dosage)
Propagation of genomic information to non-genotyped descendants and ancestors	The propagation is performed during the Single-step GBLUP to all animals related to genotyped animals and their relatives.
Animals included in reference population (males, females, countries included, total number)	All genotyped males and females: 10296 animals
Source of phenotypic data (DYD, de-regressed proofs, national EBVs and/or MACE evaluations)	Phenotypes measured by technicians
Other criteria (data edits) for inclusion of records	Herd effective >= 5, age between 15-56 months, females only

Criteria for extension of records (if applicable)	N/A
Sire categories	All sires
Genomic model (linear, Bayesian, polygenic effect, genotypes or haplotypes)	Single step GBLUP, multiple trait animal model, use of allelic dosages.
Blending of direct genomic value (DGV) with traditional EBV	Performed during the Single Step GBLUP method
Environmental effects in the genetic evaluation model	Herd, date of evaluation, fatness
Adjustment for heterogeneous variance in evaluation model	No adjustment
Computation of genomic reliability	We used theoretical genomic reliability (contribution of record and relationships) or compute a "corrected" genomic reliability based on cross-validation study. The published value is always the smaller one of these two values. For the cross-validation study, 20% of the genotyped individuals are used in the validation group (the date of record is used to split the dataset) and the predictive ability (PA) is estimated as the correlation between breeding values and the masked performances. Then, the "corrected" genomic reliability is computed based on the difference in PA between polygenic and the genomic model.
Blending of foreign/Interbull information in evaluation	No blending. Only local information
Genetic parameters in the evaluation	See Appendix GENO
Expression of genetic evaluations If standardized (e.g. RBV), give standardization 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 cows with phenotype born 4 years before the current year Base changes every year
Labeling of genomic evaluations	GRBV
Criteria for official publication of evaluations	Genotyped animals Sires : GREL ≥ 50 % Females : GREL ≥ 15 % If reliability of height reaches the limit, height can be published. If reliability of muscling reaches the limit, all other traits can be published
Number of evaluations / publications per year	3
Use in total merit index	No
Anticipated changes in the near future	No
Key reference on methodology applied	Legarra A., Christensen O., Aguilar I. and Misztal I. [2014] Single Step, a general approach for genomic selection. Livestock Science 166, 54-65
Key organization: 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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	WEB site for publication of sire breeding values:
	http://www.eleveo.be

ªEither: 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.

System Validation

Approximate number of test bulls for this trait group:	Cross-validation study : 20% of the genotyped individuals are used in the validation group (the date of record is used to split the dataset) and the predictive ability (PA) is estimated as the correlation between breeding values and the masked performances.
If including foreign reference bulls: 4-yr old de-regressed MACE EBVs, OR Current de-regressed MACE EBVs If including foreign test bulls (type of proof 21 or 22), provide the reason.	
If using a truncation ≠ 4 years, provide the reason.	
If applying an age cutoff for test bulls ≠ (YYYY-8), provide the reason	

Appendix GENO

Parameters used in genetic/genomic evaluation

Country (or countries):	Belgium (Walloon Region)				
Main trait group:	Conformation				
Breed (repeat as necessary):	Belgian Blue				
Trait	Definition	ITB[a]	h[2b]	Genetic variance[b]	Official proof standardisation formula[c]
Height			0,39	23,19	
Length			0,18	0,6	
Chest width			0,2	1,96	
Pelvis width			0,26	0,89	
Shoulder musculature			0,3	2,35	
Top muscling			0,31	5,11	
Rib			0,25	4,99	
Rump			0,29	5,09	
Pelvis length			0,14	0,37	
Tail set			0,24	6,56	
Thighs side view			0,42	2,49	
Thighs rear view			0,39	2,4	
Bone structure			0,18	2,67	
Top line			0,14	0,25	
Hocks			0,19	2,47	
Skin			0,17	3,34	
Muscling			0,42	2,5	
Meaty type			0,31	1,4	
General appearance			0,39	0,6	
Final score			0,3	1,2	

[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.