

Status as of: 2022-05-01

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!	Zootechnical traits (second visit)
Breed(s)	Belgian Blue
Trait definition(s) and unit(s) of measurement Attach an appendix if needed	<ul style="list-style-type: none">- Conformation score (1, very low meat → 9, very high meat)- Weight (kg)- Height (cm)
Source of genotypes (chips used)	Illumina BovineSNP10K, Illumina Bovine SNP50K, Illumina BovineHD , Illumina Bovine MD
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 animals : 28845 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	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 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 * Test date (F) Age (F) Year * season of birth (F) Body condition (F)
Adjustment for heterogeneous variance in evaluation model	No adjustment
Computation of genomic reliability	Genomic reliability is computed as polygenic reliability plus a gain provided by genomics. This gain expresses a number of

	<p>‘daughter equivalent’ that genomic brings compared to polygenic. It is calculated in two different ways, and it is always the smaller of the two that is kept.</p> <p>First gain is obtained by mean theoretical genomic reliabilities minus mean theoretical polygenic reliabilities.</p> <p>Second gain is obtained by cross-validation. Younger animals are removed from dataset and the predictive ability is tested with and without genotypes. Difference between genomic predictive ability and polygenic predictive ability is used to get this second gain.</p>
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 phenotyped animals 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 : $GREL \geq 50 \%$ Females : $GREL \geq 15 \%$
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	<p>Organisation responsible for genetic evaluations and computing centre:</p> <p>Elevéo asbl</p> <p>R&D Department - Genetic Evaluation Unit</p> <p>Rue des Champs Elysées 4</p> <p>B-5590 Ciney</p> <p>+32 (0)83 23.06.32.</p> <p>evalgen@awegroupe.be</p> <p>WEB site for publication of sire breeding values:</p> <p>http://www.eleveo.be</p>

^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:	<p>Cross-validation study : Younger animals are removed from dataset and the predictive ability is tested with and without genotypes.</p> <p>Genetic trends</p> <p>Correlations between consecutive evaluations</p>
<p>If including foreign reference bulls: 4-yr old de-regressed MACE EBVs, OR</p> <p>Current de-regressed MACE EBVs</p> <p>If including foreign test bulls (type of proof 21 or 22), provide the reason.</p>	
If using a truncation \neq 4 years, provide the reason.	
If applying an age cutoff for test bulls \neq (YYYY-8), provide the reason	

Appendix GENO

Parameters used in genetic/genomic evaluation

Country (or countries):		Belgium (Walloon Region)			
Main trait group:		Conformation and beef production (second visit)			
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	414.52	
Height			0,38	5.87	

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

^bIf 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.

^cExpressed 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.