# Form GENO

## DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS

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|---|---|
| Country (or countries) | Wallon Region of Belgium |
| Main trait group[a]. NOTE. Only one trait group per form! | Conformation |
| 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 |

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| 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 $\geq$ 50 % Females : GREL $\geq$ 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 |

| | Rue des Champs Elysées 4 B-5590 Ciney +32 (0)83 23.06.32. eval_gen@awenet.be WEB site for publication of sire breeding values: http://www.eleveo.be |
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[a]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.

# System Validation

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| 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 $\neq$ 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 | | | | |
| 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.