Form GENO

DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS

Country (or countries)	Walloon Region of Belgium
Main trait group[a]. NOTE. Only one trait group per form!	Production traits
Breed(s)	Black and Red Holsteins
Trait definition(s) and unit(s) of measurement Attach an appendix if needed	1. Milk 2. Fat 3. Protein Records are kg of yield produced within a 24-hours test-day period and EBV are average 305-d yields (kg) across lactation 1, 2 and 3. 4. Fat percentage 5. Protein percentage
Source of genotypes (chips used)	Illumina BovineSNP50 BeadChip (version 1 and 2)
Imputation method for missing genotypes	None
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: 4985 animals
Source of phenotypic data (DYD, de-regressed proofs, national EBVs and/or MACE evaluations)	National EBV and MACE evaluations integrated as external information
Other criteria (data edits) for inclusion of records	None
Criteria for extension of records (if applicable)	No extension
Sire categories	All sires
Genomic model (linear, Bayesian, polygenic effect, genotypes or haplotypes)	Single-step GBLUP modified to combine all available information following a Bayesian approach
Blending of direct genomic value (DGV) with traditional EBV	Performed during the Single Step GBLUP method (genotypes, EBV and pedigree information are simultaneously combined)

Environmental effects in the genetic evaluation model	None
Adjustment for heterogeneous variance in evaluation model	None
Computation of genomic reliability	Based on the genetic variance (σ^2G) used for the genomic evaluation and the predicted error variance (PEV) obtained from the inverse of the left-hand-side of the ssGBLUP REL = 1 – (PEV / (1 * σ^2G)
Blending of foreign/Interbull information in evaluation	MACE-EBV were blended with national EBV in the ssGBLUP
Genetic parameters in the evaluation	See Appendix GENO
Expression of genetic evaluations If standardized (e.g. RBV), give standardization formula in the appendix	Same expression than conventional production EBV
Definition of genetic reference base	All cows with production born in 2010
Labeling of genomic evaluations	GEBV
Criteria for official publication of evaluations	If no publishable conventional EBV then publication rules for GEBV are: REL ≥ 85% imported sires if domestic results REL ≥ 50% young sires or imported sires with INTERBULL results
Number of evaluations / publications per year	3
Use in total merit index	*Yes, see Form_GE_PR*
Anticipated changes in the near future	
Key reference on methodology applied	Vandenplas, J. and Gengler N. [2012]. Comparison and improvements of different Bayesian procedures to integrate external information into genetic evaluations. J. Dairy Sci. 95, 1513-1526 Vandenplas, J. and Gengler N. [2012]. Extension of Bayesian procedures to integrate and to blend multiple external information into genetic evaluations. J. Dairy Sci. 95, Supplement 2 Vandenplas, J., Misztal I., Faux P. and Gengler N. [2012]. Bayesian integration of external information into the single step approach for genomically enhanced prediction of breeding values. J. Dairy Sci. 95, Supplement 2 Colinet, F., Vandenplas, J., Faux, P., Vanderick, S., Renaville, R., Bertozzi C., and Gengler, N. [2013]. Walloon single-step genomic evaluation system integrating local and MACE EBV. INTERBULL Bulletin 47, 203-210
Key organization: name, address, phone, fax, e-mail, web site	Organization responsible for genetic evaluations: Association Wallonne de l'Elevage Asbl (AWE) 4, rue des Champs Elysées B-5590 Ciney Belgium

	Computing center
	University of Liège
	Gembloux Agro-Bio Tech (GxABT)
	AGROBIOCHEM Department
	Animal Science Unit
	Numerical Genetic, Genomic and Modeling
	Passage des Déportés, 2
	B-5030 Gembloux
	Belgium
	Phone: + 32/81/622206
	Fax: + 32/81/622115
	E-mail : nicolas.gengler@ulg.ac.be
	WEB site for publication of sire breeding values:
	http://www.elinfo.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:	78
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.	Foreign reference bulls were included in order to have enough candidate bulls.
If using a truncation $\neq$ 4 years, provide the reason.	
If applying an age cutoff for test bulls $\neq$ (YYYY-8), provide the reason	An age cutoff of YYYY-10 was applied in order to have enough candidate bulls.

Appendix GENO

Parameters used in genetic/genomic evaluation

Country (or countries):	BELGIUM (Walloon Region)				
Main trait group:	Production				
Breed (repeat as necessary):	Black and Red Holstein				
Trait	Definition	ITB[a]	h^{2b}	Genetic variance[b]	Official proof standardisation formula[c]
Milk yield		X	0.38	280425	
Fat yield		X	0.43	522.6	
Protein yield		X	0.41	261.5	

[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.