Status as of: 2017-01-31

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!	Conformation
Breed(s)	Black and Red Holsteins
Trait definition(s) and unit(s) of measurement Attach an appendix if needed	Individual linear traits on scale1..9, composites between 50 and 99. Stature (transformed from measured cm), Chest width, Body depth, Angularity, Rump angle, Rump width, Rear leg, Rear leg rear view, Foot angle, Fore udder, Rear udder height, Udder support, Udder depth, Teat placement, Teat-length, Conformation composite, Udder composite, Feet and legs composite. Additional 10 linear and 5 composites evaluated
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: 5024 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 $REL = 1 – (PEV / (1 * \sigma^2G)$
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 and appendix CO
Expression of genetic evaluations If standardized (e.g. RBV), give standardization formula in the appendix	Same expression than conventional conformation RBV
Definition of genetic reference base	Cows classified and born in 2010
Labeling of genomic evaluations	GRBV
Criteria for official publication of evaluations	If no publishable conventional RBV then publication rules for GRBV are: GREL (stature) ≥ 85% imported sires if domestic results GREL (stature) ≥ 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_CO*
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

[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

Approximate number of test bulls for this trait group:	55
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 ≠ 4 years, provide the reason.	
If applying an age cutoff for test bulls ≠ (YYYY-8), provide the reason	An age cutoff of YYYY-10 was applied in order to have more 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^{2}[b]	Genetic variance[b]	Official proof standardisation formula[c]
Stature		X	0.522	1.1984	
Chest Width		X	0.141	0.1379	
Body Depth		X	0.288	0.2711	
Chest Depth			0.290	0.2353	
Loin Strength			0.209	0.2457	
Rump Length			0.189	0.1231	
Rump Angle		X	0.353	0.4568	
Hips Width			0.262	0.218	
Rump Width		X	0.310	0.2848	
Foot Angle		X	0.056	0.0439	
Rear Leg Set		X	0.150	0.1315	
Bone Quality			0.203	0.2397	
Rear Leg Rear View		X	0.094	0.0971	
Udder Balance			0.201	0.1556	
Udder Depth		X	0.286	0.2366	
Teat Placement Side			0.240	0.1971	
Udder Support		X	0.192	0.3212	
Udder Texture			0.128	0.1133	
Fore Udder		X	0.226	0.2917	
Front Teat Placement		X	0.316	0.3761	
Teat Length		X	0.344	0.3718	
Rear Udder Height		X	0.227	0.2099	

Rear Udder Width			0.189	0.1756	
Rear Teat Placement		X	0.285	0.3056	
Angularity		X	0.277	0.3056	
Overall Development			0.385	5.4834	
Overall Rump			0.187	2.3861	
Overall Feet & Leg Score		X	0.132	1.2953	
Overall Udder Score		X	0.238	1.4442	
Overall Fore Udder			0.215	2.3495	
Overall Rear Udder			0.208	1.4769	
Overall Dairy Character			0.332	3.4659	
Overall Conformation Score		X	0.359	1.4224	

[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.

Form GENO **Appendix CO**

Parameters for national genetic evaluations for conformation traits as provided to Interbull (all breeds except Brown Swiss)

Country (or countries): BELGIUM (Walloon Region)
Main trait group: Conformation
Breed(s): Red and Black Holstein

Trait	Definition	h^{2a}	genetic variance[a]	official proof standardisation formula[b]	
				a	b
Stature		0.522	2.895	0.758	0.643
Chest Width		0.141	5.970	-0.040	0.152
Body Depth		0.288	4.210	0.200	0.254
Angularity		0.277	4.439	0.461	0.262
Rump Angle		0.353	6.283	0.001	0.270
Rump Width		0.31	3.164	0.201	0.300
Rear Leg Set		0.15	6.610	0.069	0.141
Rear Leg Rear View		0.094	5.710	-0.034	0.130
Foot Angle		0.056	6.274	-0.004	0.084
Fore Udder		0.226	5.200	0.329	0.237
Rear Udder Height		0.227	3.679	0.411	0.239
Udder Support		0.192	4.148	0.260	0.278
Udder Depth		0.286	4.137	0.327	0.239
Front Teat Placement		0.316	3.804	0.405	0.314
Teat Length		0.344	4.076	-0.100	0.302
Rear Teat Placement		0.285	5.019	0.370	0.247
Overall Conformation Score		0.359	3.880	0.893	0.605
Overall Udder Score		0.238	4.055	0.947	0.597
Overall Feet & Leg Score		0.132	6.443	0.195	0.448
Locomotion	Considered as being rear leg rear view trait	0.094	5.710	-0.034	0.130

[a] 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.

[b] 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.