Status as of 2023-12-06

Form GENO

DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS

Country (or countries)	the Netherlands
Main trait group[a]. NOTE. Only one trait group per form!	Production, conformation, fertility, calving traits, longevity, workability, udder health
Breed(s)	Holstein
Trait definition(s) and unit(s) of measurement Attach an appendix if needed	Production traits: milk_yield, fat_yield, prot_yield all Interbull conformation traits all Interbull calving traits longevity all Interbull workability traits all Interbull fertility traits all Interbull udder health traits
Source of genotypes (chips used)	Genotypes are generated using chips from various manufacturers (Illumina, GeneSeek/Neogen, Zoetis, etc), with densities varying from 3k (Illumina 3k) up to 139 k (GeneSeek HDv3)
Imputation method for missing genotypes	Findhap. Reference: https://www.aipl.arsusda.gov/software/findhap/
Propagation of genomic information to non-genotyped descendants and ancestors	Using pseudorecord methodology. (Eding et all, 2015, Interbull meeting, Using Pseudo-observations to combine Genomic and Conventional Data in the Dutch-Flemish National Evaluation)
Animals included in reference population (males, females, countries included, total number)	Males and females
Source of phenotypic data (DYD, de-regressed proofs, national EBVs and/or MACE evaluations)	Recorded phenotypic observation data (see NLD GE_form)
Other criteria (data edits) for inclusion of records	Based on genotypes, individuals that are incompatible with their declared parents are removed. Also, animals with call rate (fraction of markers with genotype results) < 0.90 were removed.
Criteria for extension of records (if applicable)	-
Sire categories	All progeny tested and genotyped bulls
Genomic model (linear, Bayesian, polygenic effect, genotypes or haplotypes)	Single step linear SNP BLUP (Liu *et al.*, 2014; Vandenplas *et al.* 2018), fitting SNP genotypes; model includes a random polygenic effect and a random effect for each SNP.
Blending of direct genomic value (DGV) with traditional EBV	Using pseudorecord methodology.
Environmental effects in the	Overall mean

genetic evaluation model	
Adjustment for heterogeneous variance in evaluation model	-
Computation of genomic reliability	Reliabilities computed based on increase in reliability from the validation test, and reliability of pedigree index
Blending of foreign/Interbull information in evaluation	De-regressed Interbull EBVs are used as phenotypic data in the SNP BLUP evaluation
Genetic parameters in the evaluation	See GE form for conventional genetic evaluation
Expression of genetic evaluations If standardized (e.g. RBV), give standardization formula in the appendix	Same expression as conventional genetic evaluation . See GE form for conventional genetic evaluation
Definition of genetic reference base	See GE form for conventional genetic evaluation
Labeling of genomic evaluations	
Criteria for official publication of evaluations	Minimum reliability of 30%,
Number of evaluations / publications per year	Weekly. 3 official publications for bulls. For cows weekly.
Use in total merit index	see GE form for conventional genetic evaluation
Anticipated changes in the near future	
Key reference on methodology applied	Meuwissen & Goddard (2004), GSE 36, 261-279 https://www.aipl.arsusda.gov/software/findhap/ Calus et al (2016), JDS 2016-11028 Liu et al. (2014) J. Dairy Sci. 97 :5833–5850 Vandenplas et al. Genet Sel Evol (2018) 50:51 Vandenplas et al. Genet Sel Evol (2019) 51:30
Key organization: name, address, phone, fax, e-mail, web site	CRV PO Box 454 6800 AL Arnhem the Netherlands +31 26 3898500 +31 26 3898888 aeu@crv4all.com www.crv4all.com

[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:	260 validation bulls
If including foreign reference bulls: 4-yr old de-regressed MACE EBVs, OR	Current

Current de-regressed MACE EBVs If including foreign test bulls (type of proof 21 or 22), provide the reason.	no
If using a truncation ≠ 4 years, provide the reason.	Approx. 2 years
If applying an age cutoff for test bulls ≠ (YYYY-8), provide the reason	Cut-of-date is chosen such that we have enough Dutch bulls for the test/validation set.

Appendix GENO

Parameters used in genetic/genomic evaluation

Country (or countries):					
Main trait group:					
Breed (repeat as necessary):					
Trait	Definition	ITB[a]	h^{2b}	Genetic variance[b]	Official proof standardisation formula[c]

[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.