Status as of 2017-01-18

**Form GENO**

**DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS**

|  |  |
| --- | --- |
| Country (or countries)  | the Netherlands |
| Main trait groupa. 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 measurementAttach an appendix if needed  | Production traits: milk\_yield, fat\_yield, prot\_yieldall Interbull conformation traitsall Interbull calving traitslongevityall Interbull workability traitsall Interbull fertility traitsall Interbull udder health traits |
| Source of genotypes (chips used)  | Genotypes from custom Illumina 60K chip (de Roos et al, 2009), as well as Illumina BovineSNP50 BeadChip. Imputation (Druet & Georges, 2010) is applied to obtain genotypes for all animals for all markers on the custom Illumina 60K chip |
| Imputation method for missing genotypes  | Druet & Georges, 2010 |
| 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)  | De-regressed EBVs of sires from national and MACE evaluations are obtained according to Calus et all (2016).  |
| 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) < 0.85 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)  | Bayesian multiple QTL model (Meuwissen and Goddard, 2004), fitting SNP genotypes; model includes a random polygenic effect and a random effect for each SNP. The de-regressed EBV’s are weighted with EDC’s. |
| Blending of direct genomic value (DGV) with traditional EBV  | Using pseudorecord methodology. |
| Environmental effects in the genetic evaluation model  | Overall mean |
| 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 in case a bull has no domestic EBV. |
| Genetic parameters in the evaluation  | See GE form for conventional genetic evaluation |
| Expression of genetic evaluationsIf 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  | New method for deregression and usage of female reference population. |
| Key reference on methodology applied  | Meuwissen & Goddard (2004), GSE 36, 261-279Calus et al (2008), Genetics 178, 553-561de Roos et al (2009), INTERBULL bulletin 39, 47-50Druet & Georges (2010), Genetics 184, 789-798Calus et al (2016), JDS 2016-11028 |
| Key organization: name, address, phone, fax, e-mail, web site  | CRVPO Box 4546800 AL Arnhemthe Netherlands+31 26 3898500+31 26 3898888aeu@crv4all.com[www.crv4all.com](http://www.crv4all.com) |

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: | 260 validation bulls  |
| If including foreign reference bulls:4-yr old de-regressed MACE EBVs, ORCurrent de-regressed MACE EBVsIf including foreign test bulls (type of proof 21 or 22), provide the reason. | Currentno |
| 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  | ITBa  | h2b  | Genetic varianceb  | Official proof standardisation formulac  |
|  |  |  |  |  |  |
|  |  |  |  |  |  |

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.