Status as of: 2023-01-03

**Form GENO**

**DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS**

|  |  |
| --- | --- |
| Country (or countries)  | DEA  |
| Main trait groupa. NOTE. Only one trait group per form!  | Production |
| Breed(s)  | Simmental |
| Trait definition(s) and unit(s) of measurementAttach an appendix if needed  | Milk, fat and protein yields in kg. |
| Source of genotypes (chips used)  | Illumina Infinium XT – DAC custom chip (see GenoEx: DAC-BS50, 43’376). |
| Imputation method for missing genotypes  | findhap.f90, version 2 (VanRaden, 2011) is used to impute non-called genotypes (no imputation from lower density). |
| Propagation of genomic information to non-genotyped descendants and ancestors  | Yes; current implementation is using single-step methodology |
| Animals included in reference population (males, females, countries included, total number)  | Single-step methodology; all genotyped animals with national phenotypes are reference (narrow sense); currently (Dec 2022) ~ 180’654 cows and ~ 24’447 bulls  |
| Source of phenotypic data (DYD, de-regressed proofs, national EBVs and/or MACE evaluations)  | Yield-deviations for cows derived from the conventional national RR-TD model |
| Other criteria (data edits) for inclusion of records  | no |
| Criteria for extension of records (if applicable)  | no |
| Sire categories  |  |
| Genomic model (linear, Bayesian, polygenic effect, genotypes or haplotypes)  | Standard Single-Step (BLUP) genomic model based on weighted yield-deviations, APY methodology (core ~ 30’596), 25% residual polygenic. |
| Blending of direct genomic value (DGV) with traditional EBV  | Single-step methodology |
| Environmental effects in the genetic evaluation model  | No (model based on preadjusted YD derived from conventional TDM) |
| Adjustment for heterogeneous variance in evaluation model  | No (model based on preadjusted YD derived from conventional TDM) |
| Computation of genomic reliability  | Approach described by Liu et al. (2017, 2018) and Erbe et al. (2018) assuming 25% residual polygenic. |
| Blending of foreign/Interbull information in evaluation  | no |
| Genetic parameters in the evaluation  | See Appendix GENO  |
| Expression of genetic evaluationsIf standardized (e.g. RBV), give standardization formula in the appendix  | kg |
| Definition of genetic reference base  | Same as in the national conventional evaluation. |
| Labeling of genomic evaluations  | Lowercase ‘g’ for ‘genomic’ for animals with valid genotype. |
| Criteria for official publication of evaluations  | a) registered AI-bull, b) valid genotype, c) confirmed ancestry |
| Number of evaluations / publications per year  | Three major recalibration-runs a year; genomic evaluations for candidates conducted every month. |
| Use in total merit index  | Yes. Same index as used in the national conventional genetic evaluation. |
| Anticipated changes in the near future  |  |
| Key reference on methodology applied  | Aguilar, I. et al. (2010): Hot topic: A unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score. J. Dairy Sci. 93:743-752.Misztal, I. (2015): Efficient Inversion of Genomic Relationship Matrix by the Algorithm for Proven and Young (APY). Interbull Bulletin 49:111-116.Erbe, M. et al. (2018): Approximation of Reliability in Single Step Models using the Interbull Standardized Genomic Reliability Method. Interbull Bulletin 54:1-8. |
| Key organization: name, address, phone, fax, e-mail, web site  | Bavarian State Research Center for Agriculture, Institute forAnimal Breeding, Prof.-Dürrwaechter-Platz 1, 85586 Poing-Grub, Germany.Phone: ++49(0)8161 8640-7144Mail: Christian.Edel@LfL.bayern.de, Eduardo.Pimentel@LfL.bayern.de, Reiner.Emmerling@LfL.bayern.deWeb: http://www.lfl.bayern.de/ |

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

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| --- | --- |
| Approximate number of test bulls for this trait group: | 2’200 |
| 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. |  |
| If using a truncation ≠ 4 years, provide the reason. |  |
| If applying an age cutoff for test bulls ≠ (YYYY-8), provide the reason | Age cutoff 9 is used; reason: relevant amount of candidate bulls with byear 2013 |

# Appendix GENO

## Parameters used in genetic/genomic evaluation

|  |  |
| --- | --- |
| Country (or countries):  | DEA |
| Main trait group:  | Production |
| Breed (repeat as necessary):  | Simmental (SIM) |
| Trait  | Definition  | ITBa  | h2b  | Genetic varianceb  | Official proof standardisation formulac  |
| mil | Milk yíeld (kg) |  | 0.4403 | 312927 |  |
| fat | Fat yield (kg) |  | 0.3969 | 478 |  |
| pro | Protein yield (kg) |  | 0.3495 | 269 |  |

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.