Status as of 2017-07-10

**Form GENO**

**DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS**

|  |  |
| --- | --- |
| Country (or countries)  | Hungary |
| Main trait groupa. NOTE. Only one trait group per form!  | Production, conformation, calving traits, longevity, udder health |
| Breed(s)  | Holstein |
| Trait definition(s) and unit(s) of measurementAttach an appendix if needed  | All Interbull traits send by Hungary:milk\_yield, fat\_yield, prot\_yieldstature, chest\_width, body\_depth, angularity, rump\_angle, rump\_width, rear\_legs\_rear, rear\_legs\_side, foot angle, fore\_udder\_attachment, front\_teat\_placement, front\_teat\_length, udder\_depth, rear\_udder\_height, udder\_support, overall\_udder\_score, overall\_feet\_leg, overall\_conformation, somatic\_cell\_count, udder\_health\_index, direct\_longevity, direct\_calving\_easematernal\_calving\_ease |
| 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  | no |
| Animals included in reference population (males, females, countries included, total number)  | Males  |
| Source of phenotypic data (DYD, de-regressed proofs, national EBVs and/or MACE evaluations)  | De-regressed EBVs of sires from MACE evaluations are obtained according to VanRaden et al. (2009) |
| 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  | Yes, weighted according to reliabilities |
| 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 MACE EBV’s are used as input for the SNP estimation and for the blending |
| 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  | Bull’s GEBVs are officially published if:* the bull must be qualified and registered as a breeding bull
* GEBV’s reliability > 0,3 for production traits
* and there are no available official progeny testing based EBV or ITB MACE results qualified for publication.
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| Number of evaluations / publications per year  | 3 official publications for bulls.  |
| Use in total merit index  | see GE form for conventional genetic evaluation |
| Anticipated changes in the near future  | New method for deregression |
| 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 2016-11028VanRaden et al (2009), JDS 2009. 92:16-24. |
| Key organization: name, address, phone, fax, e-mail, web site  | Nemzeti Élelmiszerlánc-biztonsági Hivatal = NÉBIH (since 15th March 2012.)National Food Chain Safety Office ([www.nebih.gov.hu](http://www.nebih.gov.hu))(Formerly: Central Agricultural Office = MgSzH) H-1024 Budapest, Keleti Károly u. 24.Contacts:1. Pál Gombácsi: Tel.: +36 1 336 9274  Fax.: + 36 336 9083 E-mail: gombacsip@nebih.gov.hu2. Péter Wellisch: E-mail: wellisch.peter@si.hu |

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: | 350 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. | CurrentYes, Hungarian AI is mainly import, for most traits <20 Hungarian locally tested bulls. |
| If using a truncation ≠ 4 years, provide the reason. | We use current MACE EBV and a cutoff. |
| If applying an age cutoff for test bulls ≠ (YYYY-8), provide the reason | Cut-of-date is chosen such that we have enough Hungarian bulls for the test/validation set. (20080101) |

# 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.