Status as of: 2019-09-05

**Form GENO**

**DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS**

|  |  |
| --- | --- |
| Country (or countries)  | Czech Republic |
| Main trait groupa. NOTE. Only one trait group per form!  | Production, conformation, udder health, fertility, longevity |
| Breed(s)  | Holstein |
| Trait definition(s) and unit(s) of measurementAttach an appendix if needed  | As conventional – Test day measured in KgMilk, Fat, and Protein yield |
| Source of genotypes (chips used)  | Illumina 54K |
| Imputation method for missing genotypes  | none |
| Propagation of genomic information to non-genotyped descendants and ancestors  | Via changed relationship matrix. More accurate relationship is spread to all animals related to the genotyped-ones.  |
| Animals included in reference population (males, females, countries included, total number)  | All genotyped animals. Include:-- |
| Source of phenotypic data (DYD, de-regressed proofs, national EBVs and/or MACE evaluations)  | Test day records like in conventional evaluation.Lactations(TD records) with calving since January 1st 1995.MACE |
| Other criteria (data edits) for inclusion of records  | None - no difference from conventional run. |
| Criteria for extension of records (if applicable)  | Not applicable |
| Sire categories  | All sires |
| Genomic model (linear, Bayesian, polygenic effect, genotypes or haplotypes)  | Single-step GBLUP  |
| Blending of direct genomic value (DGV) with traditional EBV  | Conventional pedigree matrix “corrected” by genotype based relationship |
| Environmental effects in the genetic evaluation model  | Same like conventional model |
| Adjustment for heterogeneous variance in evaluation model  | none |
| Computation of genomic reliability  | The procedure calculates reliability of genomic breeding values on basis of effective number of records resulting from test-day records and information about related animals described by pedigree- and genomic relationship matrix in single-step genomic BLUP method (Misztal et al., 1993 and 2013). |
| Blending of foreign/Interbull information in evaluation  | yes |
| Genetic parameters in the evaluation  | Use Appendix GENO for heritability/genetic variance estimates;  |
| Expression of genetic evaluationsIf standardized (e.g. RBV), give standardization formula in the appendix  | Same like conventional.  |
| Definition of genetic reference base  | All cows born 2010  |
| Labeling of genomic evaluations  | Published separately, labeled with ”G” |
| Criteria for official publication of evaluations  | Daughters in less than 10 herds, no official MACE released.  |
| Number of evaluations / publications per year  | 6 times per year, all official. |
| Use in total merit index  | yes |
| Anticipated changes in the near future  | none |
| Key reference on methodology applied  | Misztal, I., Legarra, A., Short, T. H. 1993. Implementation of single- and multiple-trait Animal models for genetic evaluation of Holstein type traits. Journal of Dairy Science. 76 (5). 1421–1432.Misztal, I., Tsuruta, S., Aguilar, I., Leggara, A., Van Raden, P. M., Lawlor, T. J.. 2013. Methods to approximate reliabilities in single-step genomic evaluation. Journal of Dairy Science. 96 (1). 647 – 654.Přibyl, J., Haman, J., Kott, T., Přibylová, J., Šimečková, M., Vostrý, L., Zavadilová, L., Čermák, V., Růžička, Z., Šplíchal, J., Verner, M., Motyčka, J., Vondrášek, L., 2012. Single-step prediction of genomic breeding value in a small dairy cattle population with strong import of foreign genes. Czech Journal of Animal Science. 57 (4). 151–159.Přibyl, J., Madsen P., Bauer J., Přibylová, J., Šimečková M., Vostrý, L., Zavadilová, L. 2013. Contribution of domestic production records, Interbull estimated breeding values, and single nucleotide polymorphism genetic markers to the single-step genomic evaluation of milk production. Journal of Dairy Science. 96 (2). 1865-1873. Bauer J., Vostrý L., Přibyl J., Svitáková A., Zavadilová L. 2014. Approximation of reliability of single-step genomic breeding values for dairy cattle in the Czech Republic. Animal Science Papers and Reports. 32, (4), 301-306.Bauer J., Přibyl, J., Vostrý, L. 2015. Reliability of single-step genomic BLUP breeding values in multi-trait test-day model analysis. Journal of Dairy Science. 98(7):4999-5003. |
| Key organization: name, address, phone, fax, e-mail, web site  | Plemdat sro, Benesovska 123, Hradisto, Czech Rep.splichal@plemdat.cz, [www.plemdat.cz](http://www.plemdat.cz), +420257896444 |

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: | 150 |
| 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. | none |
| If using a truncation ≠ 4 years, provide the reason. |  |
| If applying an age cutoff for test bulls ≠ (YYYY-8), provide the reason |  |

# Appendix GENO

## Parameters used in genetic/genomic evaluation

|  |  |
| --- | --- |
| Country (or countries):  | CZE |
| Main trait group:  |  |
| Breed (repeat as necessary):  |  |
| Trait  | Definition  | ITBa  | h2b  | Genetic varianceb  | Official proof standardisation formulac  |
| Milk | Milk yield for 6-306 days in kg |  | 0.39 | 367 291 | See appendix PR of conventional form GE |
| Fat | Milk yield for 6-306 days in kg |  | 0.38 | 574.48 |
| Protein | Milk yield for 6-306 days in kg |  | 0.37 | 349.64 |
|  |  |  |  |  |  |
|  |  |  |  |  |  |

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.

**Form GE Appendix CO**

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

|  |  |
| --- | --- |
| **Country (or countries):** | Czech Republic |
| **Main trait group:** | Conformation |
| **Breed(s):** | Holstein |
| Trait | Definition | h2a | geneticvariancea | official proofstandardisation formulab |
| Stature | See the Methodology | 0.490 | 0.79390 | Average 100, sd 12, BB2010 |
| Chest Width | of the Holstein | 0.182 | 0.30855 |  |
| Body Depth | Word Association | 0.247 | 0.42405 |  |
| Angularity |  | 0.294 | 0.40621 |  |
| Rump Angle |  | 0.316 | 0.45527 |  |
| Rump Width |  | 0.400 | 0.68787 |  |
| Rear Leg Set |  | 0.161 | 0.22245 |  |
| Rear Leg Rear View |  | 0.140 | 0.31558 |  |
| Foot Angle |  | 0.102 | 0.12172 |  |
| Fore Udder |  | 0.238 | 0.58973 |  |
| Rear Udder Height |  | 0.232 | 0.44848 |  |
| Udder Support |  | 0.183 | 0.18783 |  |
| Udder Depth |  | 0.316 | 0.57143 |  |
| Front Teat Placement |  | 0.271 | 0.39137 |  |
| Teat Length |  | 0.324 | 0.39389 |  |
| Rear Teat Placement |  | 0.267 | 0.55604 |  |
| Overall Conformation Score |  | 0.252 | 1.8767 |  |
| Overall Udder Score |  | 0.197 | 3.4871 |  |
| Overall Feet & Leg Score |  | 0.121 | 2.5055 |  |
| Locomotion |  | 0.070 | 0.14121 |  |
| Body Condition Score |  | 0.275 | 0.4049 |  |

**Form GE Appendix SM**

**Parameters for national genetic evaluations for udder health traits as provided to Interbull**

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| --- | --- |
| **Country (or countries):** | Czech Republic |
| **Main trait group:** | Udder Health |
| **Breed(s):** | Holstein |

|  |  |  |  |
| --- | --- | --- | --- |
| Trait | h2a | geneticvariancea | official proofstandardisation formulab \* |
| Somatic Cell Score:lactation 1lactation 2lactation 3lactations pooled | 0.2070.2250.1870.301 | 19 35024 25423 49321 468 | a = average of cows born in 2010b = standard deviation of cows born in 2010c = 12d = 100 |
| Clinical Mastitis: |  |  |  |

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.

\* Standardization formula is valid for each lactation separately and for EBV submitted to Interbull too, but for this one is a = 0.**Form GE Appendix GE**

**Parameters used in genetic evaluation**

|  |  |
| --- | --- |
| **Country (or countries): Czech Republic** |  |
| **Main trait group: Female fertility** |  |
| **Breed (repeat as necessary): Holstein** |  |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Trait | Definition | ITBa | h2b | geneticvarianceb | official proofstandardisation formulac |
|  |  |  |  |  |  |
| Maiden heifer’s ability to conceive : | Conception Rate (CR)1 barren / 100 pregnant |  X | 0.039 | 95.45 | See below the table |
| Lactating cow’s ability to conceive :  | Conception Rate (CR)1 barren / 100 pregnant |  X | 0.044 | 108.54 | See below the table |
|  |  |  |  |  |  |
|  |  |  |  |  |  |

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.

**a = average of bulls born in 2010, b = standard deviation of bulls born in 2010, c = 12, d = 100**

**Form GE Appendix LO**

**Parameters for national genetic evaluations for longevity traits as provided to Interbull**

|  |  |
| --- | --- |
| **Country (or countries):** | Czech Republic |
| **Main trait group:** | Longevity |
| **Breed(s):** | Holstein |

|  |  |  |  |
| --- | --- | --- | --- |
| Trait | h2 | geneticvariance | official proofstandardisation formulaa |
| Direct longevity: | 0.223463 | 0.30792 | See under the table |
| Combined longevity: |  |  |  |

a Expressed as follows:

**a = average of bulls born in 2010, b = standard deviation of bulls born in 2010, c = 12, d = 100**