Status as of: 2025-01-07

**Form GENO**

**DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS**

|  |  |
| --- | --- |
| Country (or countries) | Switzerland |
| Main trait groupa. NOTE. Only one trait group per form! | Production |
| Breed(s) | Brown Swiss |
| Trait definition(s) and unit(s) of measurementAttach an appendix if needed  | see PREP Database for conventional genetic evaluation; same model but evaluated with ssGTaBLUP for genomic evaluation |
| Source of genotypes (chips used)  | Mainly own custom chip “SWISSLD” for domestic animals, but numerous Chips of various densities included |
| Imputation method for missing genotypes  | Missing genotypes are imputed using FImpute |
| Propagation of genomic information to non-genotyped descendants and ancestors  | PA of non-genotyped descendants calculated with GEBVs of parents |
| Animals included in reference population (males, females, countries included, total number)  | GEBV derived from single-step model: All available genotypes included in full model |
| Source of phenotypic data (DYD, de-regressed proofs, national EBVs and/or MACE evaluations)  | National phenotypes and MACE EBVs blended according to Pitkänen et al. 2020 in the single step model |
| Other criteria (data edits) for inclusion of records  | Genotypes need a minimum callrate of 0.95  |
| Criteria for extension of records (if applicable)  | - |
| Sire categories  | - |
| Genomic model (linear, Bayesian, polygenic effect, genotypes or haplotypes)  | Single step model with polygenic effect of 0.1For the bi-weekly prediction SNP effects are estimated in the single step model using MiX99 and the program predict\_GEBV is used to derive GEBV including the polygenic effect. |
| Blending of direct genomic value (DGV) with traditional EBV  | Done within single step model |
| Environmental effects in the genetic evaluation model  | For details go to prep data base to view the model description |
| Adjustment for heterogeneous variance in evaluation model  | For details go to prep data base to view the model description |
| Computation of genomic reliability  | Calculation from the single step model using scheme E by Gao et al. 2023  |
| Blending of foreign/Interbull information in evaluation  | Blending with MACE information according to Pitkänen et al. 2020 using the previous MACE release |
| Genetic parameters in the evaluation  | Same values used as for traditional EBV's. See PREP database for details. |
| Expression of genetic evaluationsIf standardized (e.g. RBV), give standardization formula in the appendix  | EBV in kgs (305-day yield) within each lactation then averaged across lactations. See PREP Database for more details |
| Definition of genetic reference base  | Rolling base yearly updated in April, defined by cows born 6 to 8 calendar years ago, that have test day records included in the genetic evaluation: e.g. April 2025: cows born 2017 to 2019 |
| Labeling of genomic evaluations  | G for animals with domestic proof(CH-label requirements for bulls; own phenotype for cows)GA for genotyped animals not fulfilling the CH requirementsGI for animals with international proof |
| Criteria for official publication of evaluations  | All GEBVs are published; though some restrictions apply for the bi-weekly predictions (related to AI sires in bi-weekly predictions) |
| Number of evaluations / publications per year  | 3 full releases (April, August, December)Bi-weekly releases for newly genotyped animals |
| Use in total merit index  | see PREP Database for conventional genetic evaluation |
| Anticipated changes in the near future  | none |
| Key reference on methodology applied  | Pitkänen, T. J., Koivula, M., Strandén, I., Aamand, G. P., & Mäntysaari, E. A. (2020). Integration of MACE breeding values into domestic multi-trait test-day model evaluations. In Proceedings of the 71st Annual Meeting of the European Federation of Animal Science (Vol. 31).Gao, H., Kudinov, A. A., Taskinen, M., Pitkänen, T. J., Lidauer, M. H., Mäntysaari, E. A., & Strandén, I. (2023). A computationally efficient method for approximating reliabilities in large-scale single-step genomic prediction. Genetics Selection Evolution, 55(1), 1.Kempe, R., Koivula, M., Pitkänen, T., Stephansen, R., Pösö, J., Nielsen, U., ... & Lidauer, M. (2024). Single-step genomic prediction models for metabolic body weight in Nordic Holstein, Red dairy cattle, and Jersey. Interbull Bulletin, (60), 92-96. |
| Key organization: name, address, phone, fax, e-mail, web site  | Qualitas AGChamerstrasse 566300 ZugSwitzerlandphone: +41 41 768 9292email: info@qualitasag.ch |

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: | 60 |
| 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. | 4-yr old de-regressed MACE EBVs have been used |
| If using a truncation ≠ 4 years, provide the reason. |  |
| If applying an age cutoff for test bulls ≠ (YYYY-8), provide the reason |  |

# Appendix GENO