Status as of: 2023-03-24

# Form GENO

## DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS

| | |
|---|---|
| Country (or countries) | SLOVENIJA |
| Main trait group[a].<br>NOTE. Only one trait group per form! | WORKABILITY (msp) |
| Breed(s) | BSW |
| Trait definition(s) and unit(s) of measurement<br>Attach an appendix if needed | Milking Speed: linear score 1 – 5. |
| Source of genotypes (chips used) | Weatherbys Scientific Bovine VersaSNP 50K<br>Illumina Bovine SNP50 BeadChip<br>GeneSeek Genomic Profiler v4 |
| Imputation method for missing genotypes | |
| Propagation of genomic information to non-genotyped descendants and ancestors | |
| Animals included in reference population (males, females, countries included, total number) | All genotyped animals with MACE. |
| Source of phenotypic data (DYD, de-regressed proofs, national EBVs and/or MACE evaluations) | De-regressed predicted genetic merit (DPGM) is calculated as: DPGM = EBV/REL. In the genomic model, DPGM are weighted by $REL_{dau} / (1 - REL_{dau})$ , where $REL_{dau}$ is reliability from daughters. |
| Other criteria (data edits) for inclusion of records | |
| Criteria for extension of records (if applicable) | |
| Sire categories | All |
| Genomic model (linear, Bayesian, polygenic effect, genotypes or haplotypes) | An iterative, nonlinear model with heavy-tailed prior for marker effects analogous to Bayes A is used. Base population allele frequencies are subtracted from genotypes, and a polygenic effect (poly) with 10% of additive variance is fit in the model: DPGM = mean + ∑genotypes*effects + poly + error. |
| Blending of direct genomic value (DGV) with traditional EBV | The evaluation model includes international (MACE) evaluation of ancestors, and consequently the foreign information for non-genotyped ancestors is included |
| Environmental effects in the genetic evaluation model | |

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| Adjustment for heterogeneous variance in evaluation model | |
| Computation of genomic reliability | Reliability of direct genomic value is computed from the traditional daughter equivalents plus the genomic daughter equivalents, which differ for each animal depending on its average genomic relationship to the reference population. Final reliability is computed by selection index using reliabilities of DGV, traditional PGM, and subset PGM. |
| Blending of foreign/Interbull information in evaluation | Calculation of DGV includes foreign information from a subset of the current Interbull evaluation for the genotyped animals. |
| Genetic parameters in the evaluation | Use Appendix GENO for heritability/genetic variance estimates; for multiple-trait genetic evaluations, provide genetic correlation estimates between traits separately. Use also appendices PR, CO, BCO, SM, LO, CA, as applicable, if you participate in the international genetic evaluations of Interbull |
| Expression of genetic evaluations If standardized (e.g. RBV), give standardization formula in the appendix | GEBV |
| Definition of genetic reference base | The same as used in the national genetic evaluation. |
| Labeling of genomic evaluations | |
| Criteria for official publication of evaluations | |
| Number of evaluations / publications per year | There will be 3 evaluations per year. The release dates would be two weeks after the official release of Interbull evaluations. |
| Use in total merit index | |
| Anticipated changes in the near future | |
| Key reference on methodology applied | VanRaden, P.M. Efficient methods to compute genomic predictions. J. Dairy Sci. 91(11):4414–4423. 2008. |
| | VanRaden, P.M., Van Tassell, C.P., Wiggans, G.R., Sonstegard, T.S., Schnabel, R.D., Taylor, J.F., and Schenkel, F.S. *Invited review:* Reliability of genomic predictions for North American Holstein bulls. J. Dairy Sci. 92(1):16–24. 2009. |
| | Wiggans, G.R., VanRaden, P.M., Bacheller, L.R., Tooker, M.E., Hutchison, J.L., Cooper, T.A., and Sonstegard, T.S. Selection and management of DNA markers for use in genomic evaluation . J. Dairy Sci. 93(5):2287-2292. 2010. |
| Key organization: name, address, phone, fax, e-mail, web site | University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Groblje 3, 1230 Domžale, Slovenija |
| | Tel. +386 1 3203 886 Fax: +386 1 7241 005 Barbara.Lustrek@bf.uni-lj.si Web site: http://rodica.bf.uni-lj.si/govedo |

[a]Either: 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: | 21 |
| If including foreign reference bulls: 4-yr old de-regressed MACE EBVs, OR Current de-regressed MACE EBVs If including foreign test bulls (type of proof 21 or 22), provide the reason. | Foreign reference bulls are included due to small number of domestic bulls. |
| If using a truncation ≠ 4 years, provide the reason. | |
| If applying an age cutoff for test bulls ≠ (YYYY-8), provide the reason | To pass the test. |

# Appendix GENO

## Parameters used in genetic/genomic evaluation

| Country (or countries): | SLOVENIA | | | | |
|---|---|---|---|---|---|
| Main trait group: | WORKABILITY | | | | |
| Breed (repeat as necessary): | BSW | | | | |
| Trait | Definition | ITB[a] | $h^{2b}$ | Genetic variance[b] | Official proof standardisation formula[c] |
| msp | Milking Speed | X | 0.0739 | 0.074 | a=0 b=0.0664 c=12 d=100 |

[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.