



Status as of: 2023-03-24

Form GENO

DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS

Country (or countries)	SLOVENIJA
Main trait group ^a . NOTE. Only one trait group per form!	LONGEVITY (dlo)
Breed(s)	BSW
Trait definition(s) and unit(s) of measurement Attach an appendix if needed	Direct longevity: length of productive life (number of days from 1st calving to the culling or to the moment of data collection or till the end of sixth lactation). At the end of sixth lactation we marked records as censored.
Source of genotypes (chips used)	Weatherbys Scientific Bovine VersaSNP 50K Illumina Bovine SNP50 BeadChip 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: $DPGM = mean + \sum genotypes * effects + poly + error$.
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	
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	<p>VanRaden, P.M. Efficient methods to compute genomic predictions. J. Dairy Sci. 91(11):4414–4423. 2008.</p> <p>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.</p> <p>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.</p>
Key organization: name, address, phone, fax, e-mail, web site	<p>University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Groblje 3, 1230 Domžale, Slovenija</p> <p>Tel. +386 1 3203 886 Fax: +386 1 7241 005</p> <p>Barbara.Lustrek@bf.uni-lj.si</p> <p>Web site: http://rodica.bf.uni-lj.si/govedo</p>

^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:	9
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 \neq 4 years, provide the reason.	
If applying an age cutoff for test bulls \neq (YYYY-8), provide the reason	To pass the test.



Appendix GENO

Parameters used in genetic/genomic evaluation

Country (or countries):		SLOVENIA			
Main trait group:		LONGEVITY			
Breed (repeat as necessary):		BSW			
Trait	Definition	ITB ^a	h ^{2b}	Genetic variance ^b	Official proof standardisation formula ^c
dlo	Direct Longevity	X	0.0700	0.022	a=0 b=0.0808 c=12 d=100

^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: $\text{StandEval} = ((\text{eval} - a) / b) * c + d$ 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.