Form GE

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)	SLOVENIJA
Main trait group[1] **NOTE!** Only one trait group per form!	HEALTH
Breed(s)	HOL, SIM, BSW
Trait definition(s) and unit(s) of measurement[2] Attach an appendix if needed	Somatic cell score (SCS) = $\log_2$(SCC), where SCC is somatic cells in ml.
Method of measuring and collecting data	ICAR Milk recording method to 29.2.2004 A4 method from 1.3.2004 AT4 method
Time period for data inclusion	Calving from 01.01.2004
Age groups (e.g. parities) included	1-5 parity
Other criteria (data edits) for inclusion of records	Days in milk >= 5 Number of herds >=3
Criteria for extension of records (if applicable)	
Sire categories	AI
Environmental effects[3], pre-adjustments	No
Method (model) of genetic evaluation[3]	ST Repeatability TD
Environmental effects[3] in the genetic evaluation model	F – calving season, parity R – herd*year, permanent environment FR – Ali, Schaeffer
Adjustment for heterogeneous variance in evaluation model	
Use of genetic groups and relationships	
Blending of foreign/Interbull information in evaluation	No
Genetic parameters in the evaluation	Use Appendix GE 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
System validation	Genetic trend validation – method 3
Expression of genetic evaluations If standardised (e.g. RBV), give standardisation formula in the appendix	BV12=((BV-a)/b)*12+100 a – mean of BV b – standard deviation of BV
Definition of genetic reference base	Population average
Next base change	Next evaluation
Calculation of reliability	Yes

Criteria for official publication of evaluations	reliability(sire) >= 0.5, reliability(dam) >= 0.4
Number of evaluations / publications per year	3
Use in total merit index[4]	HOL: SCS 6%
	BSW: SCS 8%
	SIM: SCS 2%
Anticipated changes in the near future	
Key reference on methodology applied	Web site: http://rodica.bf.uni-lj.si/govedo
Key organisation: name, address, phone, fax, e-mail, web site	University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Groblje 3, 1230 Domzale, Slovenija
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1) 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.

2) Indicate frequencies per category if the trait is categorical and specify transformation of data if practiced.

3) Use abbreviations for most common effects (see document with list of abbreviations at http://www-interbull.slu.se/service_documentation/General/list_of_abbreviations.rtf) and indicate random (R) or fixed (F).

4) Please give economic weights and indicate how they are expressed (preferably in genetic standard deviation units).

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

Country (or countries):   SLOVENIA
Main trait group: Health
Breed(s):   HOL

Trait	h^{2a}	genetic variance[a]	official proof standardisation formula[b]
Milk Somatic Cell	0.294	1.157	a=0 b=0.6693 c=12 d=100
Clinical Mastitis			

Country (or countries):   SLOVENIA
Main trait group: Health
Breed(s):   SIM

Trait	h^{2a}	genetic variance[a]	official proof standardisation formula[b]
Milk Somatic Cell	0.344	1.385	a=0 b=0.7240 c=12 d=100
Clinical Mastitis			

Country (or countries):   SLOVENIA
Main trait group: Health
Breed(s):   BSW

Trait	h^{2a}	genetic variance[a]	official proof standardisation formula[b]
Milk Somatic Cell	0.359	1.346	a=0 b=0.7149 c=12 d=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.