

## DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

<b>Country (or countries)</b>	SLOVENIJA
<b>Main trait group<sup>1</sup></b>	HEALTH
<b>NOTE!</b> Only one trait group per form!	
<b>Breed(s)</b>	HOL, SIM, BSW
<b>Trait definition(s) and unit(s) of measurement<sup>2</sup></b> Attach an appendix if needed	Somatic cell score (SCS) = $\log_2(\text{SCC})$ , where SCC is somatic cells in ml.
<b>Method of measuring and collecting data</b>	ICAR Milk recording method to 29.2.2004 A4 method from 1.3.2004 AT4 method
<b>Time period for data inclusion</b>	Calving from 01.01.2004
<b>Age groups (e.g. parities) included</b>	1-5 parity
<b>Other criteria (data edits) for inclusion of records</b>	Days in milk $\geq 5$ Number of herds $\geq 3$
<b>Criteria for extension of records (if applicable)</b>	
<b>Sire categories</b>	AI
<b>Environmental effects<sup>3</sup>, pre-adjustments</b>	No
<b>Method (model) of genetic evaluation<sup>3</sup></b>	ST Repeatability TD
<b>Environmental effects<sup>3</sup> in the genetic evaluation model</b>	F – calving season, parity R – herd*year, permanent environment FR – Ali, Schaeffer
<b>Adjustment for heterogeneous variance in evaluation model</b>	
<b>Use of genetic groups and relationships</b>	
<b>Blending of foreign/Interbull information in evaluation</b>	No
<b>Genetic parameters in the evaluation</b>	Use Appendix GE for heritability/genetic variance estimates; for multiple-trait genetic evaluations, provide genetic correlation estimates between traits separately. Use <b>also</b> appendices PR, CO, BCO, SM, LO, CA, as applicable, if you participate in the international genetic evaluations of Interbull
<b>System validation</b>	Genetic trend validation – method 3
<b>Expression of genetic evaluations</b> 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
<b>Definition of genetic reference base</b>	Mean of cows born in 2010
<b>Next base change</b>	2016
<b>Calculation of reliability</b>	Yes

<b>Criteria for official publication of evaluations</b>	reliability(sire) $\geq$ 0.5, reliability(dam) $\geq$ 0.4
<b>Number of evaluations / publications per year</b>	3
<b>Use in total merit index<sup>4</sup></b>	HOL: SCS 6% BSW: SCS 8% SIM: SCS 2%
<b>Anticipated changes in the near future</b>	Change of genetic base
<b>Key reference on methodology applied</b>	Web site: <a href="http://www.bf.uni-lj.si/zootehnika/struktura/katedre-in-enote/center-za-strokovno-delo-v-zivinoreji/govedo/">http://www.bf.uni-lj.si/zootehnika/struktura/katedre-in-enote/center-za-strokovno-delo-v-zivinoreji/govedo/</a>
<b>Key organisation: name, address, phone, fax, e-mail, web site</b>	University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Groblje 3, 1230 Domzale, Slovenija Tel. +386 1 3203 872 Fax: +386 1 7241 005 <a href="mailto:Jurij.Krsnik@bf.uni-lj.si">Jurij.Krsnik@bf.uni-lj.si</a> , <a href="mailto:Klemen.Potocnik@bf.uni-lj.si">Klemen.Potocnik@bf.uni-lj.si</a>

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](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 <sup>a</sup>	official proof standardisation formula <sup>b</sup>
Milk Somatic Cell	0.29	1.15204	$BV12=((BV-(0.0949))/0.6555)*-12+100$
Clinical Mastitis			

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

Trait	$h^{2a}$	genetic variance <sup>a</sup>	official proof standardisation formula <sup>b</sup>
Milk Somatic Cell	0.34	1.17619	$BV12=((BV-(0.0992))/0.7138)*-12+100$
Clinical Mastitis			

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

Trait	$h^{2a}$	genetic variance <sup>a</sup>	official proof standardisation formula <sup>b</sup>
Milk Somatic Cell	0.35	1.15204	$BV12=((BV-(0.0288))/0.7004)*-12+100$
Clinical Mastitis			

<sup>a</sup> 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.

<sup>b</sup> 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.