DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)	SLOVENIJA
Main trait group[1] **NOTE!** Only one trait group per form!	CONFORMATION
Breed(s)	BSW
Trait definition(s) and unit(s) of measurement[2] Attach an appendix if needed	See appendix
Method of measuring and collecting data	Linear scoring from 1st lactation is included in genetic evaluation.
Time period for data inclusion	ofr, rle, thp, oru, ful, udb, bcs : Scoring from 01.01.2009 others : Scoring from 01.01.2004
Age groups (e.g. parities) included	1st parity
Other criteria (data edits) for inclusion of records	Classifier*year >= 20 scores (calving date - birth date) <= 1200 days 5 <= (scoring date - calving date) <= 365
Criteria for extension of records (if applicable)	
Sire categories	AI
Environmental effects[3], pre-adjustments	No
Method (model) of genetic evaluation[3]	MT – AM – BLUP sta, cwi, bde, ran, rls, fan, hde, ruh, ruw, ude, ftl, tpl, rle, hoq, tdi, tth, bcs: F1 + F2 + F3 + R ocs, ofl, rwi, ofr, thp, oru: F1 + F2 + F3 + linear regression(bcs) + R usu, ftp, rtp, ous, fua, ful, udb: F1 + F2 + F3 + F4 + R
Environmental effects[3] in the genetic evaluation model	F1 – classifier*year F2 – class(birth year)*class(scoring date - calving date) F3 – calving season*year F4 – class(time interval from milking) R – herd
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 >= 0.25
Number of evaluations / publications per year	3
Use in total merit index[4]	BSW: Stature 0.9%, Rear leg set 1.4%, Pasterns/Foot angle 1.2%, Deep heel 0.7%, Teat length 0.3%, Rump angle 0.7%, Fore udder attachment 0.7%, Rear udder height 0.7%, Rear udder width 0.7%, Udder depth 1.4%, Body depth 1.2%, Chest width 1.2%, Rump width 0.3%, Front teat placement 0.5%, Rear teat placement 0.3%, Udder support 1% Top line 0.1% Rump length0.3% Thurl position 0.3% Hock quality 0.1% Fore udder length 0.7% Teat direction 0.3% Teat thickness 0.2%
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 Tel. +386 1 3203 872 Fax: +386 1 7241 005 Jurij.Krsnik@bf.uni-lj.si, Klemen.Potocnik@bf.uni-lj.si

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 conformation traits as provided to Interbull

Country (or countries):   SLOVENIJA
Main trait group: Conformation
Breed: Brown Swiss

Trait	Definition	h^{2a}	genetic variance[a]	official proof standardisation formula[b]
Stature	cm	0.458	7.721	a=0 b=1.8540 c=12 d=100
Chest Width	Scale 1-9	0.128	0.175	a=0 b=0.2178 c=12 d=100
Body Depth	Scale 1-9	0.171	0.283	a=0 b=0.2346 c=12 d=100
Angularity				
Rump Angle	Scale 1-9	0.243	0.447	a=0 b=0.3206 c=12 d=100
Rump Width	Scale 1-9	0.168	0.281	a=0 b=0.2320 c=12 d=100
Rear-Leg Set	Scale 1-9	0.162	0.288	a=0 b=0.2647 c=12 d=100
Foot Angle	Scale 1-9	0.135	0.240	a=0 b=0.2325 c=12 d=100
Heel Depth/Hoof Height	Scale 1-9	0.052	0.092	a=0 b=0.1292 c=12 d=100
Fore Udder Attachment	Scale 1-9	0.195	0.347	a=0 b=0.2969 c=12 d=100
Rear Udder Height	Scale 1-9	0.137	0.244	a=0 b=0.2839 c=12 d=100
Rear Udder Width	Scale 1-9	0.130	0.228	a=0 b=0.2890 c=12 d=100
Udder Support	Scale 1-9	0.158	0.275	a=0 b=0.2418 c=12 d=100
Udder Depth	Scale 1-9	0.250	0.464	a=0 b=0.3480 c=12 d=100
Front Teat Placement	Scale 1-9	0.275	0.503	a=0 b=0.4161 c=12 d=100
Front Teat Length	Scale 1-9	0.382	0.697	a=0 b=0.4942 c=12 d=100
Rear Teat Placement	Scale 1-9	0.347	0.634	a=0 b=0.4809 c=12 d=100
Overall Conformation Score	Points	0.173	0.534	a=0 b=0.3851 c=12 d=100
Overall Udder Score	Points	0.239	1.518	a=0 b=0.6467 c=12 d=100
Overall Feet/Legs Score	Points	0.076	0.888	a=0 b=0.4230 c=12 d=100
Locomotion				
Body Condition Score				
Overall Frame	Points	0.134	1.121	a=0 b=0.5553 c=12 d=100
Top Line	Scale 1-9	0.192	0.347	a=0 b=0.2868 c=12 d=100
Rump Length	Scale 1-9	0.159	0.281	a=0 b=0.2416 c=12 d=100
Thurl Position	Scale 1-9	0.031	0.055	a=0 b=0.0831 c=12 d=100
Overall Rump	Points	0.108	1.078	a=0 b=0.4579 c=12 d=100
Hock Quality	Scale 1-9	0.156	0.280	a=0 b=0.2604 c=12 d=100
Fore Udder Length	Scale 1-9	0.161	0.279	a=0 b=0.2826 c=12 d=100

Udder Balance	Scale 1-9	0.132	0.235	a=0 b=0.2189 c=12 d=100
Teat Direction	Scale 1-9	0.326	0.592	a=0 b=0.4684 c=12 d=100
Teat Thickness	Scale 1-9	0.227	0.409	a=0 b=0.3599 c=12 d=100

[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.