

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)	DEA (DEU & AUT)
Main trait group¹	Health, workability
NOTE! Only one trait group per form!	
Breed(s)	SIM, BSW
Trait definition(s) and unit(s) of measurement² Attach an appendix if needed	a. SCS ($\log_2(\text{SCC}/100,000)+3$) from first three lactations b. Milking speed (Austria, Baden-Wuerttemberg); $\sqrt{\text{kg/min}}$ from lactation 1 c. Milking speed (Bavaria); $\sqrt{\text{kg/min}}$ from lactation 1 d. Milking speed (only in BSW in parts of Austria); subjectively scored on a scale from 1 (very slow) to 6 (very fast) in lactation 1
Method of measuring and collecting data	a, c: from milk recording test plans (approved by ICAR) b: from milking speed recording (stop watch) d: At the same time as conformation traits are recorded; based on farmer's appraisal
Time period for data inclusion	All data since 1990
Age groups (e.g. parities) included	No weightings for lactations for SCS
Other criteria (data edits) for inclusion of records	SCS: 8 to 350 days in milk; Milking speed: 8 to 275 days in milk Age of calving (months): 1 st lact. 19-47; 2 nd lact. 29-64; 3 rd lact. 39-80
Criteria for extension of records (if applicable)	
Sire categories	All categories
Environmental effects³, pre-adjustments	No
Method (model) of genetic evaluation³	MT – ML – FR – TD – BLUP – AM
Environmental effects³ in the genetic evaluation model	F: herd test-day over lactations F: DIM nested within region * calving year * calving season * age at calving F: time of milking (trait c) R: PE of cow (traits a, c)
Adjustment for heterogeneous variance in evaluation model	No
Use of genetic groups and relationships	No
Blending of foreign/Interbull information in evaluation	No
Genetic parameters in the evaluation	See PART 2 for heritability/genetic variance estimates; for multiple-trait genetic evaluations, provide genetic correlation estimates between traits separately
System validation	Checks on data and results
Expression of genetic evaluations If standardised (e.g. RBV), give standardisation formula in the appendix	RBV for SCS (combination of EBVs from three lactations: 1:1:1) RBV for trait b (milking speed from Austria/ Baden-Wuerttemberg) RBVs have mean of 100 (base bulls) and s of 12; RBVs > 100 are desirable

FORM GE

Definition of genetic reference base	Bulls, 8 to 10 years old, with daughters in 10 or more herds; rolling base; changes every evaluation
Next base change	
Calculation of reliability	Approximation (Miształ-Wiggans approach)
Criteria for official publication of evaluations	Bulls: daughters in 10 or more herds
Number of evaluations / publications per year	Three
Use in total merit index⁴	Fractions of economic weights multiplied by genetic standard deviations are 9.7% for SCS (BSW: 10.0%) and 2.0% for milking speed, respectively
Anticipated changes in the near future	Application of a random-regression test-day model
Key reference on methodology applied	Sprengel et al. (2001): Proc. 2001 Interbull Meeting. Bull. No. 27.
Key organization: name, address, phone, fax, e-mail, web site	Institute of Animal Breeding; Bavarian State Research Center for Agriculture Prof.-Duerrwaechter-Platz 1, 85586 Grub, Germany phone: +49 89 99 141 140 ; fax: +49 89 99 141 199 e-mail: Joerg.Dodenhoff@lfl.bayern.de ; web site : www.lfl.bayern.de

1) Either: Production (e.g. milk, fat, protein), Conformation, Health (e.g. mastitis resistance, milk somatic cell, resistance to diseases other than mastitis), Longevity (e.g. direct longevity, combined 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 production traits as provided to Interbull

Country (or countries):

Main trait group: Production

Breed(s):

Trait	h^{2a}	genetic variance ^a	official proof standardisation formula ^b
Milk yield:			
Fat yield:			
Protein yield:			

^a If lactations, or part of lactations, are treated as separate traits, provide heritability estimates and genetic variances separately for each lactation, as well as for all lactations 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.

**Parameters for national genetic evaluations for conformation traits as provided to Interbull
(all breeds except Brown Swiss)**

Country (or countries):
Main trait group: Conformation
Breed(s):

Trait	Definition	h^{2a}	genetic variance ^a	official proof standardisation formula ^b
Stature				
Chest Width				
Body Depth				
Angularity				
Rump Angle				
Rump Width				
Rear Leg Set				
Rear Leg Rear View				
Foot Angle				
Fore Udder				
Rear Udder Height				
Udder Support				
Udder Depth				
Front Teat Placement				
Teat Length				
Rear Teat Placement				
Overall Conformation Score				
Overall Udder Score				
Overall Feet & Leg Score				

^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.

Parameters for national genetic evaluations for conformation traits as provided to Interbull

Country (or countries):

Main trait group:

Conformation

Breed:

Brown Swiss

Trait	Definition	h^{2a}	genetic variance ^a	official proof standardisation formula ^b
Stature				
Chest width				
Body depth				
Angularity				
Rump angle				
Rump Width				
Rear Leg Side View				
Pasterns/Foot Angle				
Deep Heel (Hoof Height)				
Fore Udder Attachment				
Rear Udder Attachment Height				
Rear Udder Attachment Width				
Udder Support				
Udder Depth				
Front Teat Placement				
Teat Length				
Rear Teat Placement				
Overall Conformation Score				
Overall Udder Score				
Overall Feet & Leg Score				

^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.

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

Country (or countries): DEA (DEU & AUT)
Main trait group: Health
Breed(s): BSW

Trait	h^{2a}	genetic variance ^a	official proof standardisation formula ^b
Milk Somatic Cell:	.20	2.006356	$RBV = -1 * 12 / \sqrt{2.006356} * (EBV_1 + EBV_2 + EBV_3) + 100$

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.

Parameters for national genetic evaluations for longevity traits as provided to Interbull

Country (or countries):

Main trait group: Longevity

Breed(s):

Trait	h^2	genetic variance	official proof standardisation formula ^a
Direct longevity:			
Combined longevity:			

^a 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.