

## DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

<b>Country (or countries)</b>	Switzerland
<b>Main trait group<sup>1</sup></b> NOTE! Only one trait group per form!	Production
<b>Breed(s)</b>	Red Holstein, Simmental
<b>Trait definition(s) and unit(s) of measurement<sup>2</sup></b> Attach an appendix if needed	Milk, fat, and protein lactation yields (305-day) in kg
<b>Method of measuring and collecting data</b>	Until February 2004 all TD-records collected according to ICAR A4-method; now ~50% AT4
<b>Time period for data inclusion</b>	Cows which first calved since January 1, 1987, Pedigree is traced back 3 generations from that date
<b>Age groups (e.g. parities) included</b>	All parities
<b>Other criteria (data edits) for inclusion of records</b>	Includes all test day records between 5 and 365 days in milk (DIM). test day records are expressed as 24-hour yields.
<b>Criteria for extension of records (if applicable)</b>	No extension of records is required
<b>Sire categories</b>	All bulls
<b>Environmental effects<sup>3</sup>, pre-adjustments</b>	Heterogeneous herd-test day variance adjustment, adjustment factors are estimated every run
<b>Method (model) of genetic evaluation<sup>3</sup></b>	MT (milk yield, fat yield, protein yield, somatic cell score) – ML (1, 2, 3+) - RR – TD -BLUP– AM. Later lactations (4 and up) are considered to be genetically the same as third lactation, permanent environmental effects in lactation 6 and later are assumed to be the same as 5 <sup>th</sup> lactation
<b>Environmental effects<sup>3</sup> in the genetic evaluation model</b>	Fixed: Herd-test day Regression on DIM within Parity - Age of calving - Region - Time Period - Season combination (6th order polynomials). Random: Animal lactation curve, lactation curve for permanent environment (4th order polynomials).
<b>Adjustment for heterogeneous variance in evaluation model</b>	Yes, see pre-adjustments
<b>Use of genetic groups and relationships</b>	Phantom parent groups are defined based on ancestry, birth year, breed and selection pathway
<b>Blending of foreign/Interbull information in evaluation</b>	Blending of Interbull proofs (previous evaluation) of foreign proven bulls.
<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>	Method 3
<b>Expression of genetic evaluations</b> If standardised (e.g. RBV), give standardisation formula in the appendix	EBV in kgs (305- day yield) within each lactation then averaged across lactations.

<b>Definition of genetic reference base</b>	Rolling base yearly updated in May, defined by cows born 6 to 8 calendar years ago, that have test day records included in the genetic evaluation: e.g. April 2011: cows born 2003 to 2005
<b>Next base change</b>	
<b>Calculation of reliability</b>	Similar to the procedure used to calculate EDC's
<b>Criteria for official publication of evaluations</b>	AI-bulls: - 10 daughters with at least 3 TD-records each in 10 herds and 300 inseminations as sampling bulls (1st year) in official domestic progeny test program <b>or</b> - 20 daughters with at least 3 TD-records each in 20 herds and reliability (ebv protein) $\geq 65\%$ NS-bulls: -10 daughters with at least 3 TD-records each in 3 herds
<b>Number of evaluations / publications per year</b>	3
<b>Use in total merit index<sup>4</sup></b>	ILM (production index)= 26 % fat kg, 52 % protein kg, 5 % fat content, 17 % protein content GZW (TMI)= 50 % ILM, 10 % SCS, 15 % longevity, 5 % persistency of lactation, 20 % conformation
<b>Anticipated changes in the near future</b>	none
<b>Key reference on methodology applied</b>	Schaeffer, L. R., J. Jamrozik, G. J. Kistemaker, and B. J. Van Doormaal. 1999. Experience with a test day model. J. Dairy Sci. (Abstract & to be submitted for publication) Jamrozik, J., L. R. Schaeffer, and F. Grignola. 1998. Genetic parameters for production traits and somatic cell score of Canadian Holsteins with multiple trait random regression model 6WCGALP. 23:303-306. Jamrozik, J., L. R. Schaeffer, Z. Liu, and G. Jansen. 1997. Multiple trait random regression test day model for production traits. Interbull Bulletin No. 16:43.
<b>Key organisation: name, address, phone, fax, e-mail, web site</b>	Evaluation Center: Qualitas AG Chamerstrasse 56, CH-6300 Zug, Switzerland Phone: +41 (0)41 768 92 92 Fax: +41 (0)41 768 92 99 e-mail: zws@qualitasag.ch Internet: <a href="http://www.qualitasag.ch">http://www.qualitasag.ch</a>  EBV's published by herdbook organisation: swissherdbook cooperative Schützenstrasse 10, CH-3052 Zollikofen <a href="http://www.swissherdbook.ch">http://www.swissherdbook.ch</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 production traits as provided to Interbull

Country (or countries):	Switzerland
Main trait group:	Production
Breed(s):	Red Holstein, Simmental

Trait	$h^{2a}$	genetic variance <sup>a</sup>	official proof standardisation formula <sup>b</sup>
Milk yield:	.41	346830	$a = 237; c = 1; b = 1; d = 0$
Fat yield:	.36	589	$a = 11; c = 1; b = 1; d = 0$
Protein yield:	.36	260	$a = 6; c = 1; b = 1; d = 0$

<sup>a</sup> 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.

<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.

## Lactation heritabilities (diagonal), 305d PE correlations (above diagonal) and 305d genetic correlations (below diagonal) for Red &amp; White breed.

	M1	F1	P1	SCS 1	M2	F2	P2	SCS 2	M3	F3	P3	SCS 3
M1	<b>.41</b>	.90	.96	-.22	.52	.44	.54	-.05	.43	.35	.43	.02
F1	.65	<b>.35</b>	.93	-.18	.43	.53	.51	-.05	.35	.45	.41	.01
P1	.90	.73	<b>.35</b>	-.18	.51	.50	.59	-.04	.41	.40	.46	.03
SCS1	.20	.13	.16	<b>.24</b>	-.05	-.02	-.05	.35	-.03	-.01	-.01	.29
M2	<b>.75</b>	.45	.64	.12	<b>.43</b>	.88	.95	-.27	.52	.44	.52	-.05
F2	.43	.76	.49	.06	.67	<b>.40</b>	.92	-.29	.44	.56	.51	-.07
P2	.62	.53	.71	.10	.89	.76	<b>.40</b>	-.25	.53	.52	.59	-.04
SCS2	.15	.10	.14	.58	.01	-.04	-.01	<b>.29</b>	-.14	-.15	-.14	.52
M3	<b>.68</b>	.34	.56	.14	<b>.85</b>	.51	.73	.07	<b>.38</b>	.87	.95	-.20
F3	.36	.66	.40	.07	.52	.83	.60	.01	.65	<b>.33</b>	.91	-.22
P3	.52	.41	.59	.11	.72	.61	.81	.05	.87	.76	<b>.34</b>	-.17
SCS3	.16	.11	.13	.53	.03	-.03	-.02	.65	-.01	-.09	-.05	<b>.27</b>

Heritability, Genetic and permanent environmental variances  
(milk, fat, protein – 305d yield (kg<sup>2</sup>), SCS – average daily score).  
Combined values are submitted to Interbull

<b>Effect</b>	<b>Trait</b>	<b>Lactation</b>	<b>Variance</b>
<b>Genetic</b>	<b>Milk</b>	1	323,498
		2	444,157
		≥ 3	474,994
		Combine d	346,830
	<b>Fat</b>	1	477
		2	811
		≥ 3	851
		Combine d	589
	<b>Protein</b>	1	238
		2	361
		≥ 3	380
		Combine d	260
<b>SCS</b>	1	.378	
	2	.454	
	≥ 3	.598	
	Combine d	.343	
<b>Permanent Environment</b>	<b>Milk</b>	1	371,992
		2	494,173
		≥ 3	443,025
	<b>Fat</b>	1	600
		2	775
		≥ 3	749
	<b>Protein</b>	1	334
		2	448
		≥ 3	420
	<b>SCS</b>	1	.809
		2	.840
		≥ 3	.630
<b>Heritability</b>	<b>Milk</b>	Combine d	.41
	<b>Fat</b>	Combine d	.36
	<b>Protein</b>	Combine d	.36
	<b>SCS</b>	Combine d	.27

## DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

<b>Country (or countries)</b>	Switzerland
<b>Main trait group<sup>1</sup></b> NOTE! Only one trait group per form!	Conformation
<b>Breed(s)</b>	Red Holstein, Simmental
<b>Trait definition(s) and unit(s) of measurement<sup>2</sup></b> Attach an appendix if needed	3 measured body traits; 23 descriptive traits (7 body, 5 feet & legs, 7 udder, 4 teats); final score (body, feet & leg, udder, teats)
<b>Method of measuring and collecting data</b>	Data collection by Breeders' Federation experts on individual farm
<b>Time period for data inclusion</b>	June 1992
<b>Age groups (e.g. parities) included</b>	1st lactation
<b>Other criteria (data edits) for inclusion of records</b>	Exclusion of data from non-randomly selected scorings
<b>Criteria for extension of records (if applicable)</b>	
<b>Sire categories</b>	All
<b>Environmental effects<sup>3</sup>, pre-adjustments</b>	None
<b>Method (model) of genetic evaluation<sup>3</sup></b>	MT-BLUP-AM All traits are analyzed jointly. Overall score is calculated from the 4 estimated composite position scores
<b>Environmental effects<sup>3</sup> in the genetic evaluation model</b>	Herd-group * year * quarter year (F); classifier * year (F); calving age (F); stage of lactation (F); time of classification (F); pasture (F); housings system (F); PE effect of cow (R)
<b>Adjustment for heterogeneous variance in evaluation model</b>	None
<b>Use of genetic groups and relationships</b>	Yes
<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>	Interbull validation method III
<b>Expression of genetic evaluations</b> If standardised (e.g. RBV), give standardisation formula in the appendix	Standardized to a mean of 100 and standard deviation of 12 $RBV = 100 + ((BV - \text{mean BV of base animals}) / \text{genetic standard deviation}) * 12$
<b>Definition of genetic reference base</b>	reference base for Red Holstein calculated from the mean of cows born in 1993
<b>Next base change</b>	
<b>Calculation of reliability</b>	
<b>Criteria for official publication of</b>	Publication if at least 10 daughters with records in first lactation

<b>evaluations</b>	
<b>Number of evaluations / publications per year</b>	3
<b>Use in total merit index<sup>4</sup></b>	yes ( $0.20 * (.4 * \text{overall conformation} + .2 * \text{overall feet\&leg} + 0.3 * \text{overall udder} + .1 * \text{overall teats})$ ), standardized to a mean of 100 and standard deviation of 12
<b>Anticipated changes in the near future</b>	
<b>Key reference on methodology applied</b>	
<b>Key organisation: name, address, phone, fax, e-mail, web site</b>	<p>Evaluation Center:  Qualitas AG  Chamerstrasse 56, CH-6300 Zug, Switzerland  Phone: +41 (0)41 768 92 92  Fax: +41 (0)41 768 92 99  e-mail: zws@qualitasag.ch  Internet: <a href="http://www.qualitasag.ch">http://www.qualitasag.ch</a></p> <p>EBV's published by herdbook organisation:  swissherdbook cooperative  Schützenstrasse 10, CH-3052 Zollikofen  <a href="http://www.swissherdbook.ch">http://www.swissherdbook.ch</a></p>

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 conformation traits as provided to Interbull  
(all breeds except Brown Swiss)**

<b>Country (or countries):</b>	Switzerland
<b>Main trait group:</b>	Conformation
<b>Breed(s):</b>	Red Holstein

Trait	Definition	$h^{2a}$	genetic variance <sup>a</sup>	official proof standardisation formula <sup>b</sup>	
Stature	Height at withers, measured in cm	0.45	5.45	a= 0.0 c= 12	b =2.336 d= 100
Chest Width	Distance between fore legs, at shoulder height	0.20	0.22	a= 0.0 c= 12	b =0.472 d= 100
Body Depth	Depth of the last rib, side view	0.36	0.39	a= 0.0 c= 12	b =0.626 d= 100
Angularity	<i>not recorded</i>	--	--	--	--
Rump Angle	Angle of the rump from hips to pins	0.37	0.39	a= 0.0 c= 12	b =0.628 d= 100
Rump Width	Distance between pins	0.24	0.25	a= 0.0 c= 12	b =0.497 d= 100
Rear Leg Set	Angle of the hock in the rear leg, side view	0.27	0.23	a= 0.0 c= 12	b =0.476 d= 100
Rear Leg Rear View	Angle of rear legs	0.21	0.31	a= 0.0 c= 12	b =0.554 d= 100
Foot Angle	Pasterns, side view	0.22	0.18	a= 0.0 c= 12	b =0.423 d= 100
Fore Udder	Attachment between body and fore udder	0.31	0.44	a= 0.0 c= 12	b =0.665 d= 100
Rear Udder Height	Rear udder attachment height	0.36	0.39	a= 0.0 c= 12	b =0.621 d= 100
Udder Support	Visibility of the suspensory ligament, rear view	0.34	0.39	a= 0.0 c= 12	b =0.628 d= 100
Udder Depth	Distance between hock and bottom of udder	0.34	0.32	a= 0.0 c= 12	b =0.566 d= 100
Front Teat Placement	Placement of front teats, front view	0.48	0.49	a= 0.0 c= 12	b =0.700 d= 100
Teat Length	Length of front teats, side view	0.51	0.79	a= 0.0 c= 12	b =0.888 d= 100
Rear Teat Placement	<i>not recorded</i>				
Overall Conformation Score	Overall composite score	0.34	1.87	a= 0.0 c= 12	b =1.366 d= 100
Overall Udder Score	Composite score for udder except teats	0.37	5.19	a= 0.0 c= 12	b =2.278 d= 100
Overall Feet & Leg Score	Composite score for feet & legs	0.22	3.03	a= 0.0 c= 12	b =1.741 d= 100
Locomotion	<i>not recorded</i>				

Body Condition Score	<i>not evaluated</i>			
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- <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.



## DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

<b>Country (or countries)</b>	Switzerland
<b>Main trait group<sup>1</sup></b> NOTE! Only one trait group per form!	Health
<b>Breed(s)</b>	Red Holstein, Simmental
<b>Trait definition(s) and unit(s) of measurement<sup>2</sup></b> Attach an appendix if needed	Somatic cell score (log 2): expressed as average daily score
<b>Method of measuring and collecting data</b>	Until February 2004 all TD-records collected according to ICAR A4-method; now ~50% AT4
<b>Time period for data inclusion</b>	Cows which first calved since January 1, 1987, Pedigree is traced back 3 generations from that date
<b>Age groups (e.g. parities) included</b>	All parities
<b>Other criteria (data edits) for inclusion of records</b>	Includes all test day records between 5 and 365 days in milk (DIM).
<b>Criteria for extension of records (if applicable)</b>	No extension of records is required
<b>Sire categories</b>	All bulls
<b>Environmental effects<sup>3</sup>, pre-adjustments</b>	Heterogeneous herd-test day variance adjustment, adjustment factors are estimated every run
<b>Method (model) of genetic evaluation<sup>3</sup></b>	MT (milk yield, fat yield, protein yield, somatic cell score) – ML (1, 2, 3+) - RR – TD -BLUP– AM. Later lactations (4 and up) are considered to be genetically the same as third lactation, permanent environmental effects in lactation 6 and later are assumed to be the same as 5th lactation.
<b>Environmental effects<sup>3</sup> in the genetic evaluation model</b>	Fixed: Herd-test day Regression on DIM within Parity - Age of calving - Region - Time Period - Season combination (6th order polynomials). Random: Animal lactation curve, lactation curve for permanent environment (4th order polynomials).
<b>Adjustment for heterogeneous variance in evaluation model</b>	Yes, see pre-adjustments
<b>Use of genetic groups and relationships</b>	Phantom parent groups are defined based on ancestry, birth year, breed and selection pathway
<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>	Method 3
<b>Expression of genetic evaluations</b> If standardised (e.g. RBV), give standardisation formula in the appendix	RBV: EBVs for average score within each lactation are averaged across lactations and then standardized to a mean of 100 and a genetic standard deviation of 12. Sign is changed such that high RBVs are desirable: $RBV = 100 + (-12) * ((EBV - \text{mean EBV of base animals}) / \text{genetic standard deviation})$

<b>Definition of genetic reference base</b>	Rolling base yearly updated in May, defined by cows born 6 to 8 calendar years ago, that have test day records included in the genetic evaluation: e.g. April 2011: cows born 2003 to 2005
<b>Next base change</b>	
<b>Calculation of reliability</b>	Similar to the procedure used to calculate EDC's
<b>Criteria for official publication of evaluations</b>	All bulls: 65 % reliability of EBV for SCS and published proof for production traits.
<b>Number of evaluations / publications per year</b>	3
<b>Use in total merit index<sup>4</sup></b>	GZW (TMI)= 50 % ILM (production index), 10 % SCS, 15 % longevity, 5 % persistency of lactation, 20 % conformation
<b>Anticipated changes in the near future</b>	none
<b>Key reference on methodology applied</b>	Schaeffer, L. R., J. Jamrozik, G. J. Kistemaker, and B. J. Van Doormaal. 1999. Experience with a test day model. J. Dairy Sci. (Abstract & to be submitted for publication) Jamrozik, J., L. R. Schaeffer, and F. Grignola. 1998. Genetic parameters for production traits and somatic cell score of Canadian Holsteins with multiple trait random regression model. 6WCGALP. 23:303-306. Jamrozik, J., L. R. Schaeffer, Z. Liu, and G. Jansen. 1997. Multiple trait random regression test day model for production traits. Interbull Bulletin No. 16:43.
<b>Key organisation: name, address, phone, fax, e-mail, web site</b>	Evaluation Center: Qualitas AG Chamerstrasse 56, CH-6300 Zug, Switzerland Phone: +41 (0)41 768 92 92 Fax: +41 (0)41 768 92 99 e-mail: zws@qualitasag.ch Internet: <a href="http://www.qualitasag.ch">http://www.qualitasag.ch</a>  EBV's published by herdbook organisation: swissherdbook cooperative Schützenstrasse 10, CH-3052 Zollikofen <a href="http://www.swissherdbook.ch">http://www.swissherdbook.ch</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):	Switzerland
Main trait group:	Health
Breed(s):	Red Holstein, Simmental

Trait	$h^{2a}$	genetic variance <sup>a</sup>	official proof standardisation formula <sup>b</sup>
Milk Somatic Cell:	0.27	0.343	$a = 0; c = -12; b = 0.5857; d = 100$
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.

## Lactation heritabilities (diagonal), 305d PE correlations (above diagonal) and 305d genetic correlations (below diagonal) for Red &amp; White breed.

	M1	F1	P1	SCS 1	M2	F2	P2	SCS 2	M3	F3	P3	SCS 3
M1	<b>.41</b>	.90	.96	-.22	.52	.44	.54	-.05	.43	.35	.43	.02
F1	.65	<b>.35</b>	.93	-.18	.43	.53	.51	-.05	.35	.45	.41	.01
P1	.90	.73	<b>.35</b>	-.18	.51	.50	.59	-.04	.41	.40	.46	.03
SCS1	.20	.13	.16	<b>.24</b>	-.05	-.02	-.05	.35	-.03	-.01	-.01	.29
M2	<b>.75</b>	.45	.64	.12	<b>.43</b>	.88	.95	-.27	.52	.44	.52	-.05
F2	.43	.76	.49	.06	.67	<b>.40</b>	.92	-.29	.44	.56	.51	-.07
P2	.62	.53	.71	.10	.89	.76	<b>.40</b>	-.25	.53	.52	.59	-.04
SCS2	.15	.10	.14	.58	.01	-.04	-.01	<b>.29</b>	-.14	-.15	-.14	.52
M3	<b>.68</b>	.34	.56	.14	<b>.85</b>	.51	.73	.07	<b>.38</b>	.87	.95	-.20
F3	.36	.66	.40	.07	.52	.83	.60	.01	.65	<b>.33</b>	.91	-.22
P3	.52	.41	.59	.11	.72	.61	.81	.05	.87	.76	<b>.34</b>	-.17
SCS3	.16	.11	.13	.53	.03	-.03	-.02	.65	-.01	-.09	-.05	<b>.27</b>

Heritability, Genetic and permanent environmental variances (milk, fat, protein – 305d yield (kg<sup>2</sup>), SCS – average daily score). Combined values are submitted to Interbull

<b>Effect</b>	<b>Trait</b>	<b>Lactation</b>	<b>Variance</b>
<b>Genetic</b>	<b>Milk</b>	1	323,498
		2	444,157
		≥ 3	474,994
		Combine d	346,830
	<b>Fat</b>	1	477
		2	811
		≥ 3	851
		Combine d	589
	<b>Protein</b>	1	238
		2	361
		≥ 3	380
		Combine d	260
<b>SCS</b>	1	.378	
	2	.454	
	≥ 3	.598	
	Combine d	.343	
<b>Permanent Environment</b>	<b>Milk</b>	1	371,992
		2	494,173
		≥ 3	443,025
	<b>Fat</b>	1	600
		2	775
		≥ 3	749
	<b>Protein</b>	1	334
		2	448
		≥ 3	420
	<b>SCS</b>	1	.809
		2	.840
		≥ 3	.630
<b>Heritability</b>	<b>Milk</b>	Combine d	.41
	<b>Fat</b>	Combine d	.36
	<b>Protein</b>	Combine d	.36
	<b>SCS</b>	Combine d	.27

## DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

<b>Country (or countries)</b>	Switzerland (CHR)
<b>Main trait group<sup>1</sup></b> NOTE! Only one trait group per form!	Longevity
<b>Breed(s)</b>	Red Holstein, Simmental
<b>Trait definition(s) and unit(s) of measurement<sup>2</sup></b> Attach an appendix if needed	Productive life span of cow, days
<b>Method of measuring and collecting data</b>	The productive life span is calculated using data from the milk recording system: number of days between the first calving and the last test date. Information from the national animal tracing database is used to determine whether the cow was culled or sold to a non-herd book farm after the last recorded test date. In the latter case, the record of the cow is treated as right censored.
<b>Time period for data inclusion</b>	Lactations with calving date after January 1, 1980
<b>Age groups (e.g. parities) included</b>	Parities 1 to 6. Records of cows with more than 6 lactations are treated as right censored at the end of lactation 6.
<b>Other criteria (data edits) for inclusion of records</b>	Minimum number of daughters per sire : 6 Minimum number of (lactation) records per herd and year: 4 Cows that change herds (within herd book / milk recording scheme) are left truncated, i.e. only lactation records pertaining to the last herd of each cow are used to define environmental effects. If herd size changes by >50 % compared to the previous year, lactation records associated with the respective calving year are discarded. Consequently, records of productive life are treated as either right censored or left truncated.
<b>Criteria for extension of records (if applicable)</b>	
<b>Sire categories</b>	85% of data from AI-sires; 15% from NS-sires; all data (AI first and second crop and NS are used in the evaluations; 80 % of first calving cows are inseminated with young bulls; ~100 bulls are tested each year.
<b>Environmental effects<sup>3</sup>, pre-adjustments</b>	none
<b>Method (model) of genetic evaluation<sup>3</sup></b>	Direct longevity: ST S-MGS survival analysis model, applying a proportional hazards model with a piecewise Weibull baseline hazard distribution, stratified according to lactation stage (4 stages: 0-50, 51-200, 201-340 and >340 days after calving) within lactation number (1 to 6). Combined longevity: direct proofs are combined with 3 indicator traits (SCS, udder depth, overall feet & legs) using selection index theory.
<b>Environmental effects<sup>3</sup> in the genetic evaluation model</b>	<i>HYS</i> : 2 seasons are distinguished per year. This random class effect is time-dependent and changes when a cow is transferred, and on April 1 and October 1 of each year. It is assumed that the dispersion follows the loggamma distribution; <i>Age</i> : At first calving. This fixed effect is categorised in 7 levels with steps of

	<p>2 months (<math>\leq 26</math> / 27-28 / 29-30 / 31-32 / 33-34 / 35-36 / <math>\geq 37</math>)</p> <p><i>Alpine pasture</i>: fixed time dependent effect of alpine pasture (yes/no) * geographic zone (1-4) * calving season (2)</p> <p><i>Within Herd*year*parity-deviation for milk yield and combined fat &amp;protein content</i>: time-dependent effects of within-herd*year*parity (1 vs. 2-6) deviations for milk yield (5 classes: &lt; 80%, 80 - 94%, 95 - 104%, 105 - 120%, and &gt; 120% of the herd average) and sum of fat and protein content (5 classes: &lt; 94%, 94 - 97%, 98 - 101%, 102 - 106%, and &gt; 106% of the herd average) within parity (2 classes: 1, 2-6) and calving year, based on the age-adjusted 305d lactation records, with changes at each new calving. Cows without standard lactation records in the current lactation are assigned to the same production class as in the previous lactation.</p> <p><i>Herd size change</i>: fixed time-dependent effect of herd size change relative to the previous herd*year: 6 possible classes: -50 to -20 %, -20 to -10 %, -10 to 0 %, 0 to +10 %, +10 to +20 %, +20 to +50 % (first two currently not used)</p>
<b>Adjustment for heterogeneous variance in evaluation model</b>	no
<b>Use of genetic groups and relationships</b>	Unknown parents in the sire-MGS pedigree are grouped together according to country and year of birth.
<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>	check of input/output data, comparison with former evaluations
<b>Expression of genetic evaluations</b> If standardised (e.g. RBV), give standardisation formula in the appendix	RBV: sire solutions are standardized to a base mean of 100 and a genetic (sire) standard deviation of 12, the scale is inverted such that a high risk of culling results in a low RBV.
<b>Definition of genetic reference base</b> <b>Next base change</b>	Male rolling base, defined by bulls born 8 to 12 calendar years ago with a minimum reliability of 50 %, yearly updated with the spring-evaluation, e.g. 2011: bulls born 1999 to 2003
<b>Calculation of reliability</b>	Direct longevity see Yazdi et al., 2002, JDS 85:1563-1577 Combined longevity based on selection index theory
<b>Criteria for official publication of evaluations</b>	Reliability of 50% (combined longevity)
<b>Number of evaluations / publications per year</b>	3
<b>Use in total merit index<sup>4</sup></b>	Weight of 10 % in Total Merit Index.
<b>Anticipated changes in the near future</b>	none
<b>Key reference on methodology applied</b>	<b>Stricker, C., Sharifi, R., Schnyder, U. and Ducrocq, V.,</b> An improved model for the genetic evaluation for length productive life, Session 39, 58 <sup>th</sup> EAAP-Meeting, Dublin 2007
<b>Key organisation: name, address, phone, fax, e-mail, web site</b>	Evaluation Center: Qualitas AG Chamerstrasse 56, CH-6300 Zug, Switzerland

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swissherdbook cooperative

Schützenstrasse 10, CH-3052 Zollikofen

<http://www.swissherdbook.ch>

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 longevity traits as provided to Interbull

<b>Country (or countries):</b>	Switzerland (CHR)
<b>Main trait group:</b>	Longevity
<b>Breed(s):</b>	Holstein (Red&White)

Trait	$h^2$	genetic variance	official proof standardisation formula <sup>a</sup>
Direct longevity:	0.1126	0.03624	$a = -0.0274584; c = -12; b = 0.190368; d = 100$
Combined longevity:			

<sup>a</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.



## DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

<b>Country (or countries)</b>	Switzerland
<b>Main trait group<sup>1</sup></b> NOTE! Only one trait group per form!	Calving traits
<b>Breed(s)</b>	Red Holstein, Simmental
<b>Trait definition(s) and unit(s) of measurement<sup>2</sup></b> Attach an appendix if needed	1) gestation length, days 2) calving ease, 3 categories (3=no help, 2=easy pull, 1=heavy pull & caesarean) 3) calves born alive vs. stillbirth (binary) 4) birth weight of calf, kg category traits multiplied by 100 for GE to get a percentage scale
<b>Method of measuring and collecting data</b>	1) calculated from insemination and calving date 2) score reported by breeders at registration of calves via national animal traffic database 3) stillbirth reported by breeders via national animal traffic database (since November 2005) or directly to herdbook (April 2003 to April 2005) 4) estimated or weighted by breeder and reported at registration of calves via national animal traffic database
<b>Time period for data inclusion</b>	calving records since October 2002
<b>Age groups (e.g. parities) included</b>	All parities if at least one of the first two calvings of a cow is included
<b>Other criteria (data edits) for inclusion of records</b>	birth weight: missing or 20 kg birth weight 80 kg gestation length: 255 days gestation length 310 days age at calving: parity 1: 17 months age at calving 44 months parity 2: 31 months age at calving 60 months parity 3: 44 months age at calving 75 months parity 4: 57 months age at calving 168 months calvings sired by beef breeds (crosses) are excluded
<b>Criteria for extension of records (if applicable)</b>	No extension of records
<b>Sire categories</b>	85% of data from AI-sires; 15% from NS-sires; all data (AI first and second crop and NS are used in the evaluations; 80 % of first calving cows are inseminated with young bulls; ~100 bulls are tested each year.
<b>Environmental effects<sup>3</sup>, pre-adjustments</b>	none
<b>Method (model) of genetic evaluation<sup>3</sup></b>	MT-RP-BLUP-SM, correlated direct and maternal genetic effects (Sire-MGS)
<b>Environmental effects<sup>3</sup> in the genetic evaluation model</b>	HY (R): up to 3 consecutive years grouped for small herds parity * age at calving (F) year * season * economic zone (F) sex of calf (F): male, female or unknown (often for stillbirth) way of data collection (F): progeny test (yes/no) * directly to herd book vs. by way of animal traffic database
<b>Adjustment for heterogeneous variance in evaluation model</b>	no
<b>Use of genetic groups and relationships</b>	Sire-MGS pedigree, no genetic groups

<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>	
<b>Expression of genetic evaluations</b> If standardised (e.g. RBV), give standardisation formula in the appendix	RBV
<b>Definition of genetic reference base</b> <b>Next base change</b>	Rolling base, yearly updated with spring evaluation, defined by bulls born 8 to 10 calendar years ago, e.g. April 2011: bulls born 1999 to 2001 April 2012
<b>Calculation of reliability</b>	Reliabilities are approximated using program accf90 by I. Misztal and the “Sire only”-approach as described by Wiggans et al., 2008, J. Dairy Sci. 91:4058–4061
<b>Criteria for official publication of evaluations</b>	100 calvings (offspring of bull) for direct traits 100 calvings of bulls’ daughters for maternal traits gestation length & birth weight (both direct & maternal) not published
<b>Number of evaluations / publications per year</b>	3
<b>Use in total merit index<sup>4</sup></b>	No
<b>Anticipated changes in the near future</b>	None
<b>Key reference on methodology applied</b>	
<b>Key organisation: name, address, phone, fax, e-mail, web site</b>	Evaluation Center: Qualitas AG Chamerstrasse 56, CH-6300 Zug, Switzerland Phone: +41 (0)41 768 92 92 Fax: +41 (0)41 768 92 99 e-mail: zws@qualitasag.ch Internet: <a href="http://www.qualitasag.ch">http://www.qualitasag.ch</a>  EBV’s published by herdbook organisation: swissherdbook cooperative Schützenstrasse 10, CH-3052 Zollikofen <a href="http://www.swissherdbook.ch">http://www.swissherdbook.ch</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 used in genetic evaluation

<b>Country (or countries):</b>	Switzerland
<b>Main trait group:</b>	Calving traits
<b>Breed (repeat as necessary):</b>	Red Holstein, Simmental

Trait	Definition	ITB <sup>a</sup>	h <sup>2b</sup>	genetic variance <sup>b</sup>	official proof standardisation formula <sup>c</sup>
Direct gestation length	Days from successful insemination to calving		0.599	4.6896	
Direct calving ease	Calving ease score multiplied by 100	X	0.053	45.304	a = 0.0; c =12; b = 6.731; d = 100
Direct (inverse) stillbirth	Percentage of calves born alive	X	0.006	0.5472	a = 0.0; c =12; b = 0.740; d = 100
Direct birth weight	Weight of calf at birth, kg		0.149	1.4114	
Maternal gestation length	Days from successful insemination to calving		0.158	1.2365	
Maternal calving ease	Calving ease score multiplied by 100	X	0.041	34.843	a = 0.0; c =12; b = 5.903; d = 100
Maternal (inverse) stillbirth	Percentage of calves born alive	X	0.016	1.461	a = 0.0; c =12; b = 1.209; d = 100
Maternal birth weight	Weight of calf at birth, kg		0.039	0.3712	

<sup>a</sup> Indicate, with X, traits that are submitted to Interbull for international genetic evaluations.

<sup>b</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>c</sup> Expressed 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.



## DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

<b>Country (or countries)</b>	Switzerland
<b>Main trait group<sup>1</sup></b> NOTE! Only one trait group per form!	Female fertility
<b>Breed(s)</b>	Red Holstein and Holstein
<b>Trait definition(s) and unit(s) of measurement<sup>2</sup></b> Attach an appendix if needed	Non Return Rate after 56 Days (NRR), % (Trait 4) Interval from Calving to First Service (ICF), days (Trait 2)
<b>Method of measuring and collecting data</b>	Inseminations reported by AI-technicians via AI-companies (~95%) or directly by breeders (~5%), natural services reported by bull owners.
<b>Time period for data inclusion</b>	All AI and NS records since 1994
<b>Age groups (e.g. parities) included</b>	Records of cows from all lactations (no virgin heifers)
<b>Other criteria (data edits) for inclusion of records</b>	First service within lactation used if: 30 days ICF 200 days; Occurrence of a second service within 12 to 56 days after first service invokes a return event (Non Return Event = 0 or false)
<b>Criteria for extension of records (if applicable)</b>	
<b>Sire categories</b>	all sires
<b>Environmental effects<sup>3</sup>, pre-adjustments</b>	none
<b>Method (model) of genetic evaluation<sup>3</sup></b>	MT – BLUP – AM
<b>Environmental effects<sup>3</sup> in the genetic evaluation model</b>	Age*parity (both, F); sampling code (NRR, F); year*month of calving (ICF, F); year*month of service (NRR, F); herd*year (both, R); technician (NRR, R); service bull*batch of sperm collection (NRR, R); PE (both, R)
<b>Adjustment for heterogeneous variance in evaluation model</b>	none
<b>Use of genetic groups and relationships</b>	genetic groups are assigned to unknown parents according to birth year, sex and origin of the animal
<b>Blending of foreign/Interbull information in evaluation</b>	none
<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>	
<b>Expression of genetic evaluations</b> If standardised (e.g. RBV), give standardisation formula in the appendix	Standardized: days from calving- first inseminations Percentage of daughters not inseminated within 56 days after first insemination
<b>Definition of genetic reference base</b>	rolling base, cows born 2003-2005
<b>Next base change</b>	April 2012

<b>Calculation of reliability</b>	Reliabilities are approximated using the approach of Strabel et al. 2001, J.Anim. Sci. 79:833-839, implemented in program accf90 by I. Mistzal
<b>Criteria for official publication of evaluations</b>	For both traits (NRR and ICF): Reliability(ICF) 65 % EBVs' are published for bulls only
<b>Number of evaluations / publications per year</b>	4
<b>Use in total merit index<sup>4</sup></b>	no
<b>Anticipated changes in the near future</b>	none
<b>Key reference on methodology applied</b>	Schnyder U. & Stricker C., 2002, Interbull Bulletin No. 29, 138-141
<b>Key organisation: name, address, phone, fax, e-mail, web site</b>	<p>Evaluation Center:  Qualitas AG  Chamerstrasse 56, CH-6300 Zug, Switzerland  Phone: +41 (0)41 768 92 92  Fax: +41 (0)41 768 92 99  e-mail: zws@qualitasag.ch  Internet: <a href="http://www.qualitasag.ch">http://www.qualitasag.ch</a></p> <p>EBV's published by herdbook organisation:  swissherdbook cooperative  Schützenstrasse 10, CH-3052 Zollikofen  <a href="http://www.swissherdbook.ch">http://www.swissherdbook.ch</a></p>

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 used in genetic evaluation

<b>Country (or countries):</b>	Switzerland
<b>Main trait group:</b>	Female fertility
<b>Breed (repeat as necessary):</b>	Red Holstein

Trait	Definition	ITB <sup>a</sup>	h <sup>2b</sup>	genetic variance <sup>b</sup>	official proof standardisation formula <sup>c</sup>
Trait 1: Maiden heifer's ability to conceive					
Trait 2: Lactating cow's ability to start cycling	Number of days between calving and first service	x	0.04	31.52	b= 5.61, c = 12 d=100
Trait 3: Lactating cow's ability to conceive 1					
Trait 4: Lactating cow's ability to conceive 2	Proportion of non return events within 56 days after first service (%)	x	0.01	0.0022	b= .047, c = - 12, d=100
Trait 5: : Lactating cow's interval calving-conception					

<sup>a</sup> Indicate, with X, traits that are submitted to Interbull for international genetic evaluations.

<sup>b</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>c</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.

Genetic and residual covariances for countries with national multiple trait evaluations.

Genetic covariances on upper diagonals, residual covariances on lower diagonals.

Trait name	Trait 1:	Trait 2:	Trait 3:	Trait 4:	Trait 5:
Trait 1: Maiden heifer's ability to conceive					
Trait 2: Lactating cow's ability to start cycling				0.0011	
Trait 3: Lactating cow's ability to conceive 1					
Trait 4: Lactating cow's ability to conceive 2		-0.6393			
Trait 5: : Lactating cow's interval calving-conception					