Status as of: 2013-02-07

**Form GENO**

**DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS**

|  |  |
| --- | --- |
| Country (or countries)  | Switzerland (CHR) |
| Main trait groupa. NOTE. Only one trait group per form!  | Conformation |
| Breed(s)  | HOL |
| Trait definition(s) and unit(s) of measurementAttach 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) |
| Source of genotypes (chips used)  | Illumina BovineSNP50 BeadChip (v1 and v2) |
| Imputation method for missing genotypes  | No imputation. Missing genotypes are treated as heterozygous. |
| Propagation of genomic information to non-genotyped descendants and ancestors  | No |
| Animals included in reference population (males, females, countries included, total number)  | HOL/RED, Swiss Fleckvieh and SIM males with a progeny proof of at least 65% reliability (domestic or MACE) |
| Source of phenotypic data (DYD, de-regressed proofs, national EBVs and/or MACE evaluations)  | Deregressed proofs, calculated from national EBVs and MACE evaluations |
| Other criteria (data edits) for inclusion of records  | Genomic data was included only if the call rate was at least 90% |
| Criteria for extension of records (if applicable)  |  |
| Sire categories  |  |
| Genomic model (linear, Bayesian, polygenic effect, genotypes or haplotypes)  | Bayesian model (Bayes C) using genotypes, without polygenic effect. |
| Blending of direct genomic value (DGV) with traditional EBV  | Yes, according to Sullivan's (2009) method. |
| Environmental effects in the genetic evaluation model  |  |
| Adjustment for heterogeneous variance in evaluation model  |  |
| Computation of genomic reliability  | DGV reliability is identical for all animals and is calculated according to the following formula applied to validation bulls:rel(DGV) = r2(DGV,EBV)Reliability of GEBV is computed and is at least the highest of DGV and EBV reliabilities |
| Blending of foreign/Interbull information in evaluation  | MACE evaluations are included in the SNP effect estimations |
| Genetic parameters in the evaluation  | Use Appendix GENO 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  |
| Expression of genetic evaluationsIf standardized (e.g. RBV), give standardization formula in the appendix  | DGV standardization is based on reference bulls so that their mean DGV is equal to their mean deregressed proof and the regression of DGV on deregressed proof is forced to 1. |
| Definition of genetic reference base  | Cows born in 1993 |
| Labeling of genomic evaluations  | G for animals with domestic proofGA for animals with parent averageGI for animals with international proof (MACE) |
| Criteria for official publication of evaluations  | All GEBVs are official. |
| Number of evaluations / publications per year  | 3 full releases (April, August, December)Immediate releases of newly genotyped animals |
| Use in total merit index  | GZW is calculated with genomic values |
| Anticipated changes in the near future  |  |
| Key reference on methodology applied  |  |
| Key organization: name, address, phone, fax, e-mail, web site  | Qualitas AGChamerstrasse 566300 ZugSwitzerlandPhone: +41 41 768 9292email: info@qualitasag.ch |

aEither: 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.

## System Validation

|  |  |
| --- | --- |
| Approximate number of test bulls for this trait group: | 190 |
| If including foreign reference bulls:4-yr old de-regressed MACE EBVs, ORCurrent de-regressed MACE EBVsIf including foreign test bulls (type of proof 21 or 22), provide the reason. | Inclusion of 4-yr old de-regressed MACE EBVs |
| If using a truncation ≠ 4 years, provide the reason. |  |
| If applying an age cutoff for test bulls ≠ (YYYY-8), provide the reason |  |

# Appendix GENO

## Parameters used in genetic/genomic evaluation

|  |  |
| --- | --- |
| Country (or countries):  | Switzerland (CHR) |
| Main trait group:  | Conformation |
| Breed (repeat as necessary):  | HOL |
| Trait  | Definition  | ITBa  | h2b  | Genetic varianceb  | Official proof standardisation formulac  |
| Stature | Height at withers, measured in cm | X | 0.45 | 5.45 | a= 0.0 b =2.336 c= 12 d= 100 |
| Chest Width | Distance between fore legs, at shoulder height | X | 0.20 | 0.22 | a= 0.0 b =0.472 c= 12 d= 100 |
| Body Depth | Depth of the last rib, side view | X | 0.36 | 0.39 | a= 0.0 b =0.626 c= 12 d= 100 |
| Angularity | not recorded |  |  |  |  |
| Rump Angle | Angle of the rump from hips to pins | X | 0.37 | 0.39 | a= 0.0 b =0.628 c= 12 d= 100 |
| Rump Width | Distance between pins | X | 0.24 | 0.25 | a= 0.0 b =0.497 c= 12 d= 100 |
| Rear Leg Set | Angle of the hock in the rear leg, side view | X | 0.27 | 0.23 | a= 0.0 b =0.476 c= 12 d= 100 |
| Rear Leg Rear View | Angle of rear legs | X | 0.21 | 0.31 | a= 0.0 b =0.554 c= 12 d= 100 |
| Foot Angle | Pasterns, side view | X | 0.22 | 0.18 | a= 0.0 b =0.423 c= 12 d= 100 |
| Fore Udder | Attachment between body and fore udder | X | 0.31 | 0.44 | a= 0.0 b =0.665 c= 12 d= 100 |
| Rear Udder Height | Rear udder attachment height | X | 0.36 | 0.39 | a= 0.0 b =0.621 c= 12 d= 100 |
| Udder Support | Visibility of the suspensory ligament, rear view | X | 0.34 | 0.39 | a= 0.0 b =0.628 c= 12 d= 100 |
| Udder Depth | Distance between hock and bottom of udder | X | 0.34 | 0.32 | a= 0.0 b =0.566 c= 12 d= 100 |
| Front Teat Placement | Placement of front teats, front view | X | 0.48 | 0.49 | a= 0.0 b =0.700 c= 12 d= 100 |
| Teat Length | Length of front teats, side view | X | 0.51 | 0.79 | a= 0.0 b =0.888 c= 12 d= 100 |
| Rear Teat Placement | not recorded |  |  |  |  |
| Overall Conformatin Score | Overall composite score | X | 0.34 | 1.87 | a= 0.0 b =1.366 c= 12 d= 100 |
| Overall Udder Score | Composite score for udder except teats | X | 0.37 | 5.19 | a= 0.0 b =2.278 c= 12 d= 100 |
| Overall Feet & Leg Score | Composite score for feet & legs | X | 0.22 | 3.03 | a= 0.0 b =1.741 c= 12 d= 100 |
| Locomotion | not recorded |  |  |  |  |
| Body Condition Score | not evaluated |  |  |  |  |

aIndicate, with X, traits that are submitted to Interbull for international genetic evaluations.

bIf 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.

cExpressed 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.