

Status as of: April 2021

Form BEEF

DESCRIPTION OF BEEF NATIONAL GENETIC EVALUATION SYSTEM

Country (or countries) Switzerland

Trait name: Carcass conformation, carcass fat, carcass weight

DATA COLLECTION

| | |
|-------------------------------------|--|
| Breed(s) | Angus, Aubrac, Braunvieh, Charolais, Limousin, Simmental |
| Trait definition | Carcass conformation for Natura-Beef label Carcass fat for Natura-Beef label Carcass weight for Natura-Beef label More information about Natura-Beef here: https://www.mutterkuh.ch/en/natura-beef |
| Method and frequency of measurement | Carcass conformation grade (CHTAX classification), carcass fat grade, carcass weight, slaughter date are recorded at the end of the slaughter chain. CHTAX classification for meat is scored as C to X by an expert [C (very good muscularity), H (good muscularity), T (average muscularity), A (poor muscularity), X (very poor muscularity)]. The phenotypes for carcass conformation are corresponding to these integer values: C = 7, H = 6, T+ = 5, T = 4, T- = 3, A = 2, X = 1. Carcass fat grade is scored on a scale of 1 to 5 by a classifier [5 (extremely fat), 4 (high fat coverage), 3 (regularly covered carcass), 2 (partially covered carcass), 1 (no fat coverage)] |
| Who does the performance recording? | Graders of Proviande (Proviande - the trade association of the Swiss meat industry) in slaughtering house. |
| Method of collecting data | Data are collected by Proviande and sent to Swiss Beef Cattle. |
| Which animals get recorded? | All slaughtered animals |
| Is birthday recorded? | Yes |
| Is day of recording available? | Yes |

| | |
|---|---|
| Are the data adjusted and/or selected? If yes please describe the methodology applied | Yes Carcass weight is measured in kilogram. In order to bring carcass weight to a similar scale as carcass conformation and carcass fat, carcass weight is transformed to deciton (1dt = 100kg). |
| Time period for inclusion of records | Since 1994 |
| Criteria (data edits) for inclusion of records | breed, sex, slaughtercategory, brandingprogram, grader, slaughterhouse, slaughter age should be available. Carcass conformation or carcass weight or carcass fat should be available. Carcass conformation and carcass fat has to have a variance in a herd. Number of observations per breed ≥ 2500 Number of observations per herd*year ≥ 5 Number of observations per grader ≥ 30 Number of observations per slaughterhouse ≥ 30 |
| Is embryo transfer applied? How are ET animals been identified? ¹ Is recipient mother ID recorded? | The technique is rarely applied. The performance data of ET animals are included. ET is appended to the animal's name. The recipient mother ID is recorded. |
| How do you treat incomplete data? | If the animal record doesn't fill the criteria for inclusion, the animal record is not considered for the genetic evaluation. |
| MODEL | |
| Model used for genetic evaluation ^{2a} | MT-BLUP-AM-FR |
| Environmental effects ^{2b} | (F) : sex, slaughterhouse, grader of Proviande for carcass conformation and carcass fat, year*season, breed combination. (R) : herd, animal. Covariate: fixed linear and quadratic regression on age at slaughter. |
| Use of genetic groups and relationships | genetic groups defined by breed, birth year and selection path |
| Genetic parameters in the model ³ | Appendix I BEEF |
| Adjustment for heterogeneous variance in evaluation model | No |
| System validation | Several data quality checks by Qualitas and Swiss beef cattle at different stages of the procedure, correlation between the previous and the current evaluation. |
| Definition of genetic reference base Next base change | Rolling base includes animals born 3 to 8 calendar years prior to current evaluation. Adjusted every year. |
| Assessment of index quality (computation of reliability, connection) | Reliabilities are computed by apax99. |

PUBLICATION

| | |
|---|---|
| Expression of genetic evaluations | Carcass conformation (F), carcass fat (FET) and carcass weight (SG) are calculated for Natura-Beef (NB). EBV standardized using RBV $=[(\text{Raw EBV} - \text{Base})/(\sigma)] * 12 + 100$, where σ is the genetic standard deviation and Base is the breeding value's mean of the rolling base. |
| Criteria per official publication of evaluations | EBVs are publishable for all animals included in the evaluation that belong to the breeds mentioned above |
| Number of evaluations / publications per year | 3 |
| Anticipated changes in the near future | |
| Key reference on methodology applied | |
| Key organization: Contact person, address, phone, fax, e-mail, website | <p>Evaluation Center: Qualitas AG Chamerstrasse 56, CH-6300 Zug, Switzerland Phone: +41 (0)41 768 92 60 e-mail: sophie.kunz@qualitasag.ch http://www.qualitasag.ch</p> <p>EBV's published by herdbook organisation: Swiss Beef Cattle Stapferstrasse 2, CH-5201 Brugg Phone: +41 (0)56 462 33 54 e-mail: svenja.strasser@mutterkuh.ch http://mutterkuh.ch/en/</p> |

- 1) Use Appendix II BEEF for sample ID of ET animals
- 2a) Use abbreviation listed in the attached list of abbreviation to define the type of model.
- 2b) Use abbreviation for most common effects as listed in the attached list of abbreviation indicating, also, if the effect is treated as random (R) or fixed (F).
- 3) Use Appendix I BEEF for heritability/genetic variance estimates.

Parameters used in genetic evaluation

Country:

Main trait group:

Breed: 2

| Trait ⁽¹⁾ | Definition | h_d^2 | h_m | $rg(d,m)$ | c^2 | σ_p^2 |
|----------------------|----------------------------------|---------|-------|-----------|-------|--------------|
| Fnb | Carcass conformation Natura-Beef | 0.42 | | | | |
| FETnb | Carcass fat Natura-Beef | 0.39 | | | | |
| SGnb | Carcass weight Natura-Beef | 0.55 | | | | |

h_d^2 : direct heritability; h_m^2 : maternal heritability; $rg(d,m)$: genetic correlation between direct and maternal effects; c^2 : repeatability of (maternal) permanent environmental effects; σ_p^2 : phenotypic variance.

1) If you have more than one trait provide the correlations between traits.

Heritability (diagonal) and genetic correlation (offdiagonal):

| h^2 diagonal, r_g offdiagonal | F_{NB} | FET_{NB} | SG_{NB} |
|--------------------------------------|----------|------------|-----------|
| F_{NB} | 0.42 | -0.06 | 0.45 |
| FET_{NB} | | 0.39 | 0.42 |
| SG_{NB} | | | 0.55 |

Genetic variance (diagonal) and covariance (offdiagonal)

| | F_{NB} | FET_{NB} | SG_{NB} |
|------------|----------|------------|-----------|
| F_{NB} | 0.198 | -0.012 | 0.042 |
| FET_{NB} | | 0.2 | 0.039 |
| SG_{NB} | | | 0.043 |

herd variance (diagonal) and covariance (offdiagonal)

| | F_{NB} | FET_{NB} | SG_{NB} |
|------------|----------|------------|-----------|
| F_{NB} | 0.032 | 0.037 | 0.02 |
| FET_{NB} | | 0.078 | 0.033 |
| SG_{NB} | | | 0.018 |

residual variance (diagonal) and covariance (offdiagonal)

| | F_{NB} | FET_{NB} | SG_{NB} |
|------------|----------|------------|-----------|
| F_{NB} | 0.244 | 0.001 | 0.026 |
| FET_{NB} | | 0.229 | 0.003 |
| SG_{NB} | | | 0.017 |

