

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: <a href="https://www.mutterkuh.ch/en/natura-beef">https://www.mutterkuh.ch/en/natura-beef</a>
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 $\geq 2500$ Number of observations per herd*year $\geq 5$ Number of observations per grader $\geq 30$ Number of observations per slaughterhouse $\geq 30$
Is embryo transfer applied? How are ET animals been identified? <sup>1</sup> 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 <sup>2a</sup>	MT-BLUP-AM-FR
Environmental effects <sup>2b</sup>	(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 <sup>3</sup>	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 $\sigma$ 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: <a href="mailto:sophie.kunz@qualitasag.ch">sophie.kunz@qualitasag.ch</a> <a href="http://www.qualitasag.ch">http://www.qualitasag.ch</a></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: <a href="mailto:svenja.strasser@mutterkuh.ch">svenja.strasser@mutterkuh.ch</a> <a href="http://mutterkuh.ch/en/">http://mutterkuh.ch/en/</a></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 <sup>(1)</sup>	Definition	$h_d^2$	$h_m$	$rg(d,m)$	$c^2$	$\sigma_p^2$
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;  $\sigma_p^2$ : 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

