

Status as of: 2018-10-15

Form BEEF

DESCRIPTION OF BEEF NATIONAL GENETIC EVALUATION SYSTEM

Country (or countries) DFS (Denmark, Finland and Sweden)

Comment: From 202104 DFS sends data to Interbeef from a joined official genetic evaluation for Pure-bred Beef with common trait definitions, data editing and genetic parameters. Official publication of breeding values from the new NAV model is expected for the first time on June 2021. Data recording is done nationally.

Previously, 20181015 DFS jointly sent carcass data to Interbeef to participate in research projects. However, the model and genetic parameters for carcass traits were from an unofficial NAV model.

The DFS trait definitions and model description is detailed below.

Trait name: Carcass weight (CWE), carcass daily gain (CDG), carcass conformation score (CCO), carcass fat (CFA)

DATA COLLECTION

Breed(s)	Charolais , Limousin, Simmental (BSM)
Trait definition	*CWE (kg) – This trait is not included in our join official evaluation. This trait is included in interbeef following the same data edits and model descriptions as for the rest of carcass traits. *CDG (g/d) – calculated as: CWE minus half breed average for birth wt (wt expressed in gram) and divided by age at slaughter in days *CCO (1-15) *CFA (1-5) (In Sweden and Finland scale from 1-15 is transform to a scale from 1-5) All the traits are corrected for heterogeneous variance in different countries. For CWE and CDG values are rounded to integers but for CCO and CFA we delivered values with 2 decimals. (see exact trait definition under data adjustment)
Method and frequency of measurement	Recorded at slaughterhouses in D, F and S

Who does the performance recording?	Responsible for the recording is Seges, Faba and Växa Sverige in D, F and S, respectively.
Method of collecting data	
Which animals get recorded?	DFS: Only purebred animals in the current model (and sent to Interbeef). <i>We will probably want to deliver carcass data from crossbreds in the future since this data is also recorded nationally but not yet available at a joint level.</i>
Is birthday recorded?	Yes
Is day of recording available?	Yes
Are the data adjusted and/or selected? If yes please describe the methodology applied	DFS: We adjust all 3 traits for heterogeneous variance between countries, gender and birth year.
Time period for inclusion of records	DFS: records since 1980 included from all countries. However, carcass data only available from later years. (D 1994-, F 2007-, S 1997-)
Criteria (data edits) for inclusion of records	DFS: in the joint DFS editing we only keep carcass records from purebred animals with known dam and if age of animal at time for slaughter is between 180 and 1200 days of age and weight within that period is over 56kg and below 1150kg. Outliers are excluded based on the the <i>median absolute deviation</i> (MAD) which is calculated by country (DFS) and gender (M/F). Therefore, CWE, CDG, CCO and CFA records are deleted if: [TRT]< max(0.001, median - 3.5*(mad*1.4528)) [TRT]> median + 3.5*(mad*1.4528))
Is embryo transfer applied? How are ET animals been identified? ¹	DFS: in joint model records from ET animals are excluded so these animals get only pedigree indices.
Is recipient mother ID recorded?	<i>604-files sent to Interbeef.</i>
How do you treat incomplete data?	All three carcass records (cdg, cco and cfa) are deleted if CDG is missing. (CWE we don't have this traits in the evaluation)
MODEL	
Model used for genetic evaluation ^{2a}	DFS: MT-BLUP-AM (only direct genetic effect) CDG, CCO and CFA are in the official NAV Pure-bred Beef model analyzed together with: BWT: Birth weight (includes records from DFS, breeding values from maternal (m) and direct effect (d)) AWW: Adjusted weaning weight gain (m,d) PWG: Post-weaning weight gain (FS,d) YW: Yearling weight (D, m and d)
Environmental effects ^{2b}	DFS: HY ¹ (F) + ASEX ² (F) + TWIN ² (F) + AACA ² (F) + SEAS ^{2,3}

	(F) + SAGE (X) + SAGE HYS¹ (F) + ASEX² (F) + TWIN³ (F) + AACA⁴ (F) + SEAS⁵ (F) + AAWG⁶ (X) + AAWG2⁷ (X) ¹HYS: herd-birth year (from Nov-Oct) ²ASEX: country-sex ³TWIN: country-twin ⁴AACA: country-dam age-time ⁵SEAS: country-year-month ⁶AAWG: age at weighing (nested by ASEX) ⁷AAWG2: age at weighing x Age at weighing (nested by ASEX)
Use of genetic groups and relationships	Genetic phantom groups are used: For AAN and CHA 6 different origins: Danish, Finish, Swedish, European, American and “rest” (rest: includes different breed from the breed of evaluation and other countries than the ones listed before). For SIM LIM and HER: 4 different origins Danish, Finish, Swedish and “rest” (rest: includes different breed from the breed of evaluation and other countries than the ones listed before). For all breeds and regardless of origin, groups are also defined depending on birth year of animal with unknown parents. Groups on birth year is divided in periods of 10 years from 1980 and onwards... 1980: year< 1980 and year <=1989; 1990: 1990>=Year<=1999; Etc. Relationship matrix is used.
Genetic parameters in the model	Estimated for CHA and HER and applied them within breed group (Continental and British). (See Appendix I BEEF)
Adjustment for heterogeneous variance in evaluation model	Phenotypic variance is adjusted by country (D, F or S), gender (M or F) and birth year class
System validation	Trends and comparing successive evaluations
Definition of genetic reference base Next base change	Animals in the base population: • Males and females • Birth year: 5 – 9 years of age at the publication date • Include animals having at least one observation in the trait group (i.e. for aww or post-weaning weight gain or yearling weight or carcass daily gain or carcass conformation score or carcass fat scores) or having at least having 5 offspring with observations.

Assessment of index quality (computation of reliability, connection)	Approximate reliabilities of breeding values are calculated using the APAX99 software.
PUBLICATION	
Expression of genetic evaluations	Direct and maternal breeding values are expressed relative to the animals in the base population. Animals in the base population are standardized to an average breeding value of 100 and a standard deviation of 10. Standard deviations for all traits are kept constant at every evaluation (changes to the standardized factors might be motivated from model or genetic parameter changes). For the mean, a rolling base is implemented and the mean of the animals in the base population changes at every consecutive evaluation.
Criteria per official publication of evaluations	<i>Since is a new model, publication criteria is yet to be decided (update this filed after June 2021)</i>
Number of evaluations / publications per year	Four/five times per year <i>In D, F and S the national the number of official evaluations per year are 4, 5 and 3, respectively.</i>
Anticipated changes in the near future	Yes – we will develop official joint DFS models for all beef traits within the coming years.
Key reference on methodology applied	<i>D: www.lr.dk/kvaeg/diverse/principles.pdf F: - S : http://www.vxa.se/Radgivning-service/Avel/Avel-pa-djupet1/Avelsvardering-for-kottraser/ + Eriksson et al., 2007, Genetic Evaluation of Beef Cattle in Sweden, Eriksson et al. Interbull Technical Workshop Paris, France March 9-10, 2007 Hans Stålhammar, 1997, Genetic Studies of Beef Characteristics in Swedish Cattle Breeds 1997, Acta Univ. Agr. Sueciae, Agraria 55</i>
Key organization: Contact person, address, phone, fax, e-mail, website	DFS contact persons (also Swedish contact person): Växa Sverige: Elisenda Rius-Vilarrasa, Box 7023, S-750 07 Uppsala, Sweden, Phone: +46- 10 471 06 19, Elisenda.rius-vilarrasa@vxa.se , www.vxa.se Danish contact person: Seges: Anders Fogh, Agro Food Park 15, DK 8200 Aarhus N Denmark, Phone : +45 8740 5337, adf@seges.dk , www.seges.dk Finnish contact person:

- 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.

Form BEEF

Appendix I BEEF

Parameters used in genetic evaluation

Country: DFS

Below are the genetic parameters used in NAV Pure-bred Beef evaluation official model for the prediction of breeding values for British (AAN and HER) and Continental breeds (SIM, CHA and LIM).

Main trait group: carcass traits

Table 0.1a. Genetic variances used in the breeding value prediction for breeds

	mBW ¹	dBW ²	mWWG ³	dWWG ⁴	mYW ⁵	dYW ⁶	PWG ⁷	SDG ⁸	CCO ⁹	CFA ¹⁰
mBW	2.26									
dBW	-0.97	9.64								
mWWG	4.44	-5.51	172.19							
dWWG	2.39	16.90	-26.79	163.28						
mYW	8.48	-8.89	202.71	-27.05	262.20					
dYW	5.00	46.68	-27.29	305.93	-69.31	806.98				
PWG	3.65	15.64	-3.34	94.10	-12.14	302.46	224.88			
SDG	18.36	28.73	401.57	319.57	482.93	824.82	378.44	2501.33		
CCO	-0.09	0.02	1.53	0.98	2.27	1.38	0.38	14.00	0.56	
CFA	0.00	-0.31	1.32	-0.55	1.53	-1.10	-0.33	2.86	0.03	0.12

¹Maternal birth weight, ²Direct birth weight, ³Maternal weaning weight gain, ⁴Direct weaning weight gain, ⁵Maternal yearling weight, ⁶Direct yearling weight, ⁷Post-weaning weight gain,

⁸Slaughter daily gain, ⁹Carcass conformation class and ¹⁰Carcass fat class.

Table 0.1b. Genetic variances used in the breeding value prediction for Continental breeds

	mBW ¹	dBW ²	mWWG ³	dWWG ⁴	mYW ⁵	dYW ⁶	PWG ⁷	SDG ⁸	CCO ⁹	CFA ¹⁰
mBW	1.70									
dBW	-0.68	6.31								
mWWG	1.90	-3.35	138.12							

dWWG	3.71	11.58	-24.98	176.99						
mYW	4.87	-5.93	148.91	-17.28	196.37					
dYW	8.08	37.07	-28.25	334.26	-64.30	927.46				
PWG	4.13	13.21	-33.37	85.43	-58.96	363.91	283.25			
SDG	12.12	20.09	308.23	332.26	366.71	900.88	322.88	2332.21		
CCO	0.01	0.18	1.19	0.78	1.62	3.99	2.09	16.98	0.69	
CFA	-0.04	-0.23	1.09	-0.02	1.37	-0.55	-0.12	2.46	-0.03	0.16

¹Maternal birth weight, ²Direct birth weight, ³Maternal weaning weight gain, ⁴Direct weaning weight gain, ⁵Maternal yearling weight, ⁶Direct yearling weight, ⁷Post-weaning weight gain,

⁸Slaughter daily gain, ⁹Carcass conformation class and ¹⁰Carcass fat class.

Table 0.2a. Maternal permanent environmental variances used in the breeding value prediction for British breeds

	BW ¹	WWG ²	YW ³
BW	0.85		
WWG	5.34	188.74	
YW	6.21	192.10	205.58

¹Birth weight, ²Weaning weight gain and ³Yearling weight.

Table 0.2b. Maternal permanent environmental variances used in the breeding value prediction for Continental breeds

	BW ¹	WWG ²	YW ³
BW	0.84		
WWG	3.12	104.60	
YW	4.51	100.53	111.85

¹Birth weight, ²Weaning weight gain and ³Yearling weight.

Table 0.3a. Residual variance used in the breeding value prediction for British breeds

	BW ¹	WWG ²	YW ³	PWG ⁴	SDG ⁵	CCO ⁶	CFA ⁷
BW	8.74						
WWG	4.73	570.98					
YW	20.88	592.64	1536.75				
PWG	5.82	-54.27	0.00	902.48			
SDG	12.65	651.14	1461.93	681.90	3000.17		
CCO	0.21	4.30	9.91	5.05	34.14	1.47	
CFA	0.04	2.03	4.83	2.43	13.08	0.16	0.28

¹Birth weight, ²Weaning weight gain, ³Yearling weight, ⁴Post-weaning weight gain, ⁵Slaughter daily gain, ⁶Carcass conformation class and ⁷Carcass fat class.

Table 0.3b. Residual variance used in the breeding value prediction for Continental breeds

	BW ¹	WWG ²	YW ³	PWG ⁴	SDG ⁵	CCO ⁶	CFA ⁷
BW	8.49						
WWG	3.76	662.49					
YW	17.23	685.88	1842.09				
PWG	1.73	-112.45	0.00	1119.69			
SDG	-0.35	826.58	2127.81	1070.09	4106.80		
CCO	0.17	4.81	15.73	9.85	41.17	1.58	
CFA	0.08	2.81	7.44	3.78	14.77	0.16	0.31

¹Birth weight, ²Weaning weight gain, ³Yearling weight, ⁴Post-weaning weight gain, ⁵Slaughter daily gain, ⁶Carcass conformation class and ⁷Carcass fat class.

Table 0.4. Phenotypic variance and variance ratios used in the breeding value prediction of British breeds

	Vp	c ²	h _d ²	h _m ²
BW ¹	20.524	0.041	0.470	0.110
WWG ²	1068.400	0.177	0.153	0.161
YW ³	2742.191	0.075	0.294	0.096
PWG ⁴	1127.363		0.199	
SDG ⁵	5501.503		0.455	
CCO ⁶	2.022		0.275	
CFA ⁷	0.406		0.302	

¹Birth weight, ²Weaning weight gain, ³Yearling weight, ⁴Post-weaning weight gain, ⁵Slaughter daily gain, ⁶Carcass conformation class and ⁷Carcass fat class.

Vp: phenotypic variance, c²: maternal permanent environmental; h_d²: direct heritability and h_m²: maternal heritability.

Table 0.5. Phenotypic variance and variance ratios used in the breeding value prediction of continental breeds

	Vp	c ²	h _d ²	h _m ²
BW ¹	16.648	0.050	0.379	0.102
WWG ²	1057.213	0.099	0.167	0.131
YW ³	3013.461	0.037	0.308	0.065
PWG ⁴	1402.936		0.202	
SDG ⁵	6439.014		0.362	
CCO ⁶	2.268		0.305	
CFA ⁷	0.468		0.343	

¹Birth weight, ²Weaning weight gain, ³Yearling weight, ⁴Post-weaning weight gain, ⁵Slaughter daily gain, ⁶Carcass conformation class and ⁷Carcass fat class.

Vp: phenotypic variance, c²: maternal permanent environmental; h_d²: direct heritability and h_m²: maternal heritability.

Form BEEF

Appendix II BEEF

Sample of ET animal IDs

Country:

Main trait group:

Breed:

ET animal ID
