

Status as of: 2021-04-12
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## 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, from 201508 DFS participated in Interbeef as a joint country and sent data together from a joined unofficial model with common trait definition, data editing and genetic parameters.

The DFS trait definitions and model description is detailed below.

#### Trait name: Weaning weight

#### DATA COLLECTION

Breed(s)	Charolais , Limousin, Simmental, Aberdeen angus, Hereford
Trait definition	Weaning weight gain as weight gain at 200 days (see exact trait definition under data adjustment)
Method and frequency of measurement	Recorded by scale at an age between 140 to 260 days in D, 150 to 250 days in Finland and 140 to 250 in Sweden.
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	In D recording is done by farmer and sample of herds are also weighed by technician to evaluate farmer registration. In F recording is done by farmer or breeding advisor. In S recording is done by the farmers and supervised by assistants from the recording organization.
Which animals get recorded?	Only purebred animals in model.
Is birthday recorded?	Yes
Is day of recording available?	Yes
Are the data adjusted and/or selected? If yes please describe the methodology applied	$AWW=200*((ww-bw)/(days\ between\ ww\ and\ bw))$ where ww=weaning weight, bw= birth weight  Adjusted for heterogenous variance between birth years, countries (DFS) and gender (M/F).

Time period for inclusion of records	Records since 1980 from D and S, from 1985 from F.
Criteria (data edits) for inclusion of records	<p>Only purebred animals with known dam</p> <p>Observations that are recorded between 140-260 days of age of a weight from 50 up to 600 kilograms are included in the evaluation.</p> <p>Outliers are excluded based on the the <i>median absolute deviation</i> (MAD) which is calculated by country (DFS) and gender (M/F). Therefore, AWW is deleted if:</p> <p><math>AWW &lt; \max(0.001, \text{median} - 3.5*(\text{mad}*1.4528))</math>  <math>AWW &gt; \text{median} + 3.5*(\text{mad}*1.4528)</math></p>
Is embryo transfer applied? How are ET animals been identified? <sup>1</sup>	Records from ET animals are excluded so these animals get only pedigree indices.
Is recipient mother ID recorded?	<i>D, F and S: ET applied, and recipient mothers recorded.</i>
How do you treat incomplete data?	Deleted
MODEL	
Model used for genetic evaluation <sup>2a</sup>	<p>MT-BLUP-AM DAM MPE (direct and maternal effect)</p> <p>AWW in the official NAV Pure-bred Beef model is analyzed together with:</p> <p>BWT: Birth weight (includes records from DFS, breeding values from maternal (m) and direct effect (d))  PWG: Post-weaning weight gain (FS)  YW: Yearling weight (D, m and d)  CDG: Carcass daily gain (DFS)  CCO: Carcass conformation score (DFS)  CFA: Carcass fat score (DFS)</p>
Environmental effects <sup>2b</sup>	<p><math>HYS^1 (F) + ASEX^2 (F) + TWIN^3 (F) + AACA^4 (F) + SEAS^5 (F) + AAWG^6 (X) + AAWG2^7 (X)</math></p> <p><sup>1</sup>HYS: herd-birth year (from Nov-Oct)  <sup>2</sup>ASEX: country-sex  <sup>3</sup>TWIN: country-twin  <sup>4</sup>AACA: country-dam age-time  <sup>5</sup>SEAS: country-year-month  <sup>6</sup>AAWG: age at weighing (nested by ASEX)  <sup>7</sup>AAWG2: age at weighing x Age at weighing (nested by ASEX)</p>
Use of genetic groups and relationships	<p>Genetic phantom groups are used:</p> <p>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)</p>

	<p>before).</p> <p>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).</p> <p>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...</p> <p><b>1980:</b> year &lt; 1980 and year ≤ 1989;  <b>1990:</b> 1990 ≥ Year ≤ 1999;  Etc.</p> <p>Relationship matrix is used.</p>
Genetic parameters in the model	Estimated for CHA and HER and applied them within breed group (Continental and British). (See <b>Appendix I BEEF</b> )
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	<p>Trends and comparing successive evaluations (breeding value correlations, standard deviations and deviations/standardized changes.</p> <p>Validation using full and reduced models for model’s under-development.</p>
Definition of genetic reference base Next base change	<p>Animals in the base population:</p> <ul style="list-style-type: none"> <li>• Males and females</li> <li>• Birth year: 5 – 9 years of age at the publication date</li> <li>• 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.</li> </ul>
Assessment of index quality (computation of reliability, connection)	Approximate reliabilities of breeding values are calculated using the APAX99 software.
<b>PUBLICATION</b>	
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	Upon the finalization of the new NAV PbB model (June 2021), genetic correlations among the calving traits will be available
Key reference on methodology applied	<i>D: <a href="http://www.lr.dk/kvaeg/diverse/principles.pdf">www.lr.dk/kvaeg/diverse/principles.pdf</a> F: - S : <a href="http://www.vxa.se/Radgivning-service/Avel/Avel-pa-djupet1/Avelsvardering-for-kottraser/">http://www.vxa.se/Radgivning-service/Avel/Avel-pa-djupet1/Avelsvardering-for-kottraser/</a> + <i>Eriksson et al., 2007, Genetic Evaluation of Beef Cattle in Sweden, Eriksson et al. Interbull Technical Workshop Paris, France March 9-10, 2007</i> <i>Hans Stålhammar, 1997, Genetic Studies of Beef Characteristics in Swedish Cattle Breeds 1997, Acta Univ. Agr. Sueciae, Agraria 55</i></i>
Key organization: Contact person, address, phone, fax, e-mail, website	<b>DFS contact persons (also Swedish contact person):</b> Växa Sverige: Elisenda Rius-Vilarrasa, Box 7023, S-750 07 Uppsala, Sweden, Phone: +46- 10 471 06 19, <a href="mailto:Elisenda.rius-vilarrasa@vxa.se">Elisenda.rius-vilarrasa@vxa.se</a> , <a href="http://www.vxa.se">www.vxa.se</a>  <b>Danish contact person:</b> Seges: Anders Fogh, Agro Food Park 15, DK 8200 Aarhus N Denmark, Phone : +45 8740 5337, <a href="mailto:adf@seges.dk">adf@seges.dk</a> , <a href="http://www.seges.dk">www.seges.dk</a>  <b>Finnish contact person:</b> Faba: Kaisa Sirkko, Box 40, FI-01301 Vantaa, Finland, Phone : +358 20747 2052, <a href="mailto:kaisa.sirkko@faba.fi">kaisa.sirkko@faba.fi</a> , <a href="http://www.faba.fi">www.faba.fi</a>

- 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**

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: Adjusted weaning weight

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

	mBW <sup>1</sup>	dBW <sup>2</sup>	mWWG <sup>3</sup>	dWWG <sup>4</sup>	mYW <sup>5</sup>	dYW <sup>6</sup>	PWG <sup>7</sup>	SDG <sup>8</sup>	CCO <sup>9</sup>	CFA <sup>10</sup>
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

<sup>1</sup>Maternal birth weight, <sup>2</sup>Direct birth weight, <sup>3</sup>Maternal weaning weight gain, <sup>4</sup>Direct weaning weight gain, <sup>5</sup>Maternal yearling weight, <sup>6</sup>Direct yearling weight, <sup>7</sup>Post-weaning weight gain, <sup>8</sup>Slaughter daily gain, <sup>9</sup>Carcass conformation class and <sup>10</sup>Carcass fat class.

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

	mBW <sup>1</sup>	dBW <sup>2</sup>	mWWG <sup>3</sup>	dWWG <sup>4</sup>	mYW <sup>5</sup>	dYW <sup>6</sup>	PWG <sup>7</sup>	SDG <sup>8</sup>	CCO <sup>9</sup>	CFA <sup>10</sup>
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

<sup>1</sup>Maternal birth weight, <sup>2</sup>Direct birth weight, <sup>3</sup>Maternal weaning weight gain, <sup>4</sup>Direct weaning weight gain, <sup>5</sup>Maternal yearling weight, <sup>6</sup>Direct yearling weight, <sup>7</sup>Post-weaning weight gain, <sup>8</sup>Slaughter daily gain, <sup>9</sup>Carcass conformation class and <sup>10</sup>Carcass fat class.

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

	BW <sup>1</sup>	WWG <sup>2</sup>	YW <sup>3</sup>
BW	0.85		
WWG	5.34	188.74	
YW	6.21	192.10	205.58

<sup>1</sup>Birth weight, <sup>2</sup>Weaning weight gain and <sup>3</sup>Yearling weight.

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

	BW <sup>1</sup>	WWG <sup>2</sup>	YW <sup>3</sup>
BW	0.84		
WWG	3.12	104.60	
YW	4.51	100.53	111.85

<sup>1</sup>Birth weight, <sup>2</sup>Weaning weight gain and <sup>3</sup>Yearling weight.

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

	BW <sup>1</sup>	WWG <sup>2</sup>	YW <sup>3</sup>	PWG <sup>4</sup>	SDG <sup>5</sup>	CCO <sup>6</sup>	CFA <sup>7</sup>
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

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

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

	BW <sup>1</sup>	WWG <sup>2</sup>	YW <sup>3</sup>	PWG <sup>4</sup>	SDG <sup>5</sup>	CCO <sup>6</sup>	CFA <sup>7</sup>
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

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

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

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

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

Vp: phenotypic variance, c<sup>2</sup>: maternal permanent environmental; h<sub>d</sub><sup>2</sup>: direct heritability and h<sub>m</sub><sup>2</sup>: maternal heritability.

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

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

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

Vp: phenotypic variance, c<sup>2</sup>: maternal permanent environmental; h<sub>d</sub><sup>2</sup>: direct heritability and h<sub>m</sub><sup>2</sup>: maternal heritability.

