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 un-official model with common trait definition, data editing and genetic parameters.

The DFS trait definitions and model description is detailed below.

Trait name: Birth weight, calving ease, still birth

DATA COLLECTION

Breed(s)	Charolais , Limousin, Simmental, Aberdeen angus, Hereford
Trait definition	**DFS:** BWT: Birth weight (in Sweden it can be measured at d 1-4, corrected for in model). CAE: Calving ease (score 1-4, in DNK there is also score 5 pooled to score 4) STB: Still birth (score 0-1) **All the traits are corrected for heterogeneous variance in different countries and therefore we do not have integers but use 1 decimal for BWT and 2 decimals for CAE and STB.** (see exact trait definition under data adjustment)
Method and frequency of measurement	Recorded by farmer at time for calving.
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 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	**DFS:** Two levels of heterogenous variance adjustment are applied on all three calving traits. The first one: to remove systematic differences between countries, gender of the calf and birth year. The second one is based on snell scores. This method was mainly to handle phenotypic differences in the Swedish data from a shift in the recording of calving difficulties.
Time period for inclusion of records	**DFS:** records since 1980 included from all countries (however, data used in national evaluations is a bit different, for Sweden for example data from 1986 is used).
Criteria (data edits) for inclusion of records	**DFS:** only purebred animals with known sire and dam Outliers are excluded based on the the *median absolute deviation* (MAD) which is calculated by country (DFS) and gender (M/F). Therefore, a calving trait [TRT] is 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] Is recipient mother ID recorded?	**DFS:** in joint model records from ET animals are excluded so these animals get only pedigree indices. *D, F and S: ET applied and recipient mothers recorded.*
How do you treat incomplete data?	Deleted
MODEL	
Model used for genetic evaluation[2a]	ST-BLUP-AM DAM MPE (direct and maternal effect) ***NOTE!*** *The official NAV PbB model will include correlations between three calving traits (BWT, CAE and STB). To date a final set of variance components are not ready and cannot be provided in this form. However, we welcome the opportunity to introduced correlations at any forthcoming test run.*
Environmental effects[2b]	HYS[1] (F) + ASEX[2] (F) + TWIN[3] (F) + AACA[4] (F) + SEAS[5] (F) [1]HYS: herd-birth year (from Nov-Oct) [2]ASEX: country-sex [3]TWIN: country-twin [4]AACA: country-dam age-time [5]SEAS: country-year-month
Use of genetic groups and	Genetic phantom groups are used:

relationships	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 [3]	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	Two levels of heterogenous variance adjustment are applied on all three calving traits. The first one: to remove systematic differences between countries, gender of the calf and birth year. The second one is based on snell scores. This method was mainly to handle phenotypic differences in the Swedish data from a shift in the recording of calving difficulties.
System validation	Trends and comparing successive evaluations (breeding value correlations, standard deviations and deviations/standardized changes. Validation using full and reduced models for model's under-development.
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	*Since is a new model, publication criteria is yet to be decided (update this filed after June 2021)*
Number of evaluations / publications per year	Four/five times per year *In D, F and S the national the number of official evaluations per year are 4, 5 and 3, respectively.*
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	*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*
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:** Faba: Kaisa Sirkko, Box 40, FI-01301 Vantaa, Finland,

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.
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Appendix I BEEF

Parameters used in genetic evaluation

Country: DFS
Below are parameters used in DFS official model estimated based on the current NAV model
Main trait group: Calving traits

Table 0.1a. Phenotypic variance and variance ratios used in the breeding value prediction of British breeds (AAN and HER)

	c^2	h_d^2	h_m^2	σ^2_p
BWT	0.041	0.4616	0.1101	24.61
CAE	0.034	0.0363	0.025	0.26
SBT	0.015	0.0165	0.0113	0.13

h_d^2 : direct heritability; h_m^2 : maternal heritability; c^2: repeatability of (maternal) permanent environmental effects; σ_P^2: phenotypic variance.

Table 0.1b. Phenotypic variance and variance ratios used in the breeding value prediction of continental breeds (CHA, LIM and SIM)

	c^2	h_d^2	h_m^2	σ^2_p
BWT	0.055	0.3846	0.104	22.8
CAE	0.032	0.0447	0.0229	0.26
SBT	0.028	0.0122	0.0095	0.13

h_d^2 : direct heritability; h_m^2 : maternal heritability; c^2: repeatability of (maternal) permanent environmental effects; σ_P^2: phenotypic variance.

NOTE! The official NAV PbB model will include correlations between three calving traits (BWT, CAE and STB). To date a final set of variance components are not ready and cannot be provided in this form. However, we welcome the opportunity to introduced correlations at any forthcoming test run.

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Sample of ET animal IDs

Country:
Main trait group:
Breed:

ET animal ID

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