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Form BEEF

DESCRIPTION OF BEEF NATIONAL GENETIC EVALUATION SYSTEM

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

Comment: From 201508 DFS participate in Interbeef as one country and send data together from a joined unofficial model with common trait definition, editing and parameters. This DFS trait definition and model is described below. However, it is not identical to the national models that are still official in Denmark, Finland and Sweden, respectively. Also the data collection and official publication is so far done nationally. Some descriptions related to national models are kept in cursive.

Trait name: Weaning weight

DATA COLLECTION

Breed(s)	Charolais , Limousin
Trait definition	DFS: Weaning weight as weight 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 125 to 275 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?	DFS: Only purebred animals in model. <i>In D and S all purebred animals, in F recording includes purebred and crossbred animals.</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: $AWW=200*((ww-bw)/(days\ between\ ww\ and\ bw))$ where ww=weaning weight, bw= birth weight Also we adjust aww for heterogeneous variance between countries. <i>In D No adjustment, age at weighing is used as a fixed effect in national model. In F: Adjustment to weight at 200 d. In S: trait defined as in DFS model but no correction for het.gen var.</i>

Time period for inclusion of records	DFS: records since 1980 from D and S, from 1985 from F.
Criteria (data edits) for inclusion of records	<p>DFS: only purebred animals with known sire and dam</p> <p><i>D: Weight limits: 50-600 kg, animals moved to another herd in the period from birth to weighting deleted.</i></p> <p><i>F: Animal is connected to a herd which belongs to the beef cattle recording system, the breed of the animal is beef breed, the breed of the animal is same than the breed of the mother and the father (f1 crosses are excluded), animal has at least one measurement (birth weight, weaning weight, yearling weight, or slaughter weight), weaning weight has been weighed when animal has been 150-250 days, if animal has 2 or more weaning weights in database the weight which is weighed nearest 200 days is selected, weaning weight is between 100-550 kg.</i></p> <p><i>S: only purebred animals from 1980, with known sire and known birth weight, weaning weight between age 125-275 days and weight limits 50-600.</i></p>
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>D, F and S: ET applied and recipient mothers recorded.</i>
How do you treat incomplete data?	Deleted
MODEL	
Model used for genetic evaluation ^{2a}	<p>DFS: ST-BLUP-AM DAM MPE (direct and maternal effect)</p> <p><i>In national models for WW, MT-BLUP-AM are used.</i></p> <p><i>D: birth weight, weaning weight, yearling weight, net slaughter weight (purebred and crossbred) and growth on performance test station are included (some traits as both direct and maternal effects)</i></p> <p><i>F: birth weight, weaning weight, yearling weight and slaughter weight (direct and maternal effects on all traits)</i></p> <p><i>S: birth weight, weaning weight and yearling weight (direct and maternal effects on the two first)</i></p>
Environmental effects ^{2b}	<p>DFS: HYS¹ (F) + ASEX² (F) + TWIN² (F) + AACA² (F) + SEAS² (F)</p> <p>¹Defined as in the national evaluations (D:birth herd*birth year from nov-oct, F: weaning herd*weaning year, S: weaning herd*birth year from oct-sept) and turned into unique DFS serial number</p> <p>²Classes of fixed effects are country coded</p> <p><i>D, F and S: Same environmental effects as in DFS model, but somewhat different class definitions. Also D and F has correction for sex*age of animal (X or F, respectively)</i></p>
Use of genetic groups and relationships	DFS: No grouping, relationship matrix

	<i>D, F and S: Relationship matrix. In D four genetic groups (Danish_{old}, Danish_{new}, French, and Other countries) are used and in F genetic groups by year of birth and by origin – imported or domestic – are used. In S no genetic groups.</i>
Genetic parameters in the model ³	
Adjustment for heterogeneous variance in evaluation model	DFS: Yes, we adjust for heterogeneous variance across country in our joint DFS model. <i>D, F and S: No</i>
System validation	Trends and comparing successive evaluations
Definition of genetic reference base Next base change	DFS: The EBVs from joint DFS model are so far unofficial and will not be published but will only be used for validation of IB EBVs on DFS scale. The genetic base (for the mean) will be defined as DFS animals born 3-8 yr before evaluation and with aww record and RBV will be computed (fixed value for std of EBVs not decided). <i>In D, F and S there are rolling bases with animals born 3-7, 2-7 and 4-9 years, respectively, before current evaluation. In D the genetic base is animals with high reliability on EBV.</i>
Assessment of index quality (computation of reliability, connection)	DFS: No reliabilities calculated from joint DFS model. <i>In D and S reliability is calculated by an approximate selection index methodology (counting number of records on individual, progeny, sire, dam and their progeny). In F reliabilities are computed by MiX99 and ApaX99.</i>
	PUBLICATION
Expression of genetic evaluations	DFS: see under Definition of genetic reference base <i>In D: direct and maternal genetic effects are not published, but EBV for direct genetic effect is a part of the sub index for growth potential at weaning (called VÆKST) and EBV for maternal genetic effect is a part of the sub index for milking ability (called MÆLK). These EBVs are standardized in comparison with the reference base (mean 100 and SD 10). The sub-indices are used to construct a total merit index (S-indeks).</i> <i>In F: direct and maternal genetic effects are published as both EBV and RBV (mean 100 and SD 10). Weaning weight index is included in the total merit index for bulls and cows according to below: Bulls: -0,5*birth weight index (direct) + 0,3*weaning weight index (direct) + 1,0* yearling weight index (direct) Cows: -0,3*birth weight index (direct) + 0,3* weaning weight index (maternal)+ 1,0* yearling weight index (direct)</i> <i>In S: direct and maternal genetic effects are published as RBV (mean 100 and SD 10). The maternal RBV is included in a “Maternal” sub-index and also in total merit index for bulls and cows.</i>

Criteria per official publication of evaluations	<p>DFS: see under Definition of genetic reference base</p> <p><i>In D: MÆLK: reliability on MÆLK or S-indeks above 10% VÆKST: reliability on VÆKST or S-indeks above 10%</i></p> <p><i>In F: EBV is published when domestic animal has own weight record. If own weight record is missing, the requirements are: Domestic cows, 2 progeny results and Domestic bulls, 5 progeny results. The requirements for imported and ET animals are: Imported and ET cows, 2 progeny results and Imported and ET bulls, 10 progeny results.</i></p> <p><i>S: Own or offspring with phenotypic records.</i></p>
Number of evaluations / publications per year	<p>DFS: the joint unofficial DFS model will be run in connection to data delivery for the Interbeef evaluations.</p> <p><i>In D, F and S the national the number of official evaluations per year are 4, 5 and 3, respectively.</i></p>
Anticipated changes in the near future	No
Key reference on methodology applied	<p><i>D: www.lr.dk/kvaeg/diverse/principles.pdf</i></p> <p><i>F: -</i></p> <p><i>S : http://www.vxa.se/Radgivning-service/Avel/Avel-pa-djupet1/Avelsvardering-for-kottraser/</i></p> <p><i>+</i></p> <p><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></p> <p><i>Hans Stålhammar, 1997, Genetic Studies of Beef Characteristics in Swedish Cattle Breeds 1997, Acta Univ. Agr. Sueciae, Agraria 55</i></p>
Key organization: Contact person, address, phone, fax, e-mail, website	<p>DFS contact person (also Swedish contact person): Växa Sverige: Emma Carlén, Box 7023, S-750 07 Uppsala, Sweden, Phone: +46-10-4710614, emma.carlen@vxa.se, www.vxa.se</p> <p>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</p> <p>Finnish contact person: Faba: Kaisa Sirkko, Box 40, FI-01301 Vantaa, Finland, Phone : +358 20747 2052, kaisa.sirkko@faba.fi, www.faba.fi</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.

Form BEEF

Appendix I BEEF

Parameters used in genetic evaluation

Country: DFS

(below are parameters used in DFS ST unofficial model, which are currently the same as the national Swedish parameters for CHA and national Danish parameters for LIM).

Main trait group: Adjusted weaning weight

Breed: CHA

Trait ⁽¹⁾	Definition	h_d^2	h_m^2	$r_{g(d,m)}$	c^2	σ_p^2
AWW	200 days adjusted weaning weight	0,20	0,14	-0,14	?	850

Breed: LIM

Trait ⁽¹⁾	Definition	h_d^2	h_m^2	$r_{g(d,m)}$	c^2	σ_p^2
AWW	200 days adjusted weaning weight	0,27	0,12	-0,16	0,09	997

h_d^2 : direct heritability; h_m^2 : maternal heritability; $r_{g(d,m)}$: 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 (e.g. a.w.w. at 120d and 210d) provide the correlations between traits.

