NAV Nordisk Avlsværdi Vurdering
Nordic Cattle Genetic Evaluation

Development of a joint Nordic Beef × Dairy Genetic Evaluation

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1. Introduction

The strategy map for NAV - 2018 there had a path concerning beef cattle genetic evaluation. In August 2016 the NAV board decided to finance the development of NAV beef official evaluation including a part with beef × dairy crossbreds. The project documented in this report had as aim to develop modern joint official beef evaluations in NAV for AI beef bulls used in dairy herds based on phenotypes from dairy × beef offspring. The use of beef semen in dairy herds is increasingly important and efficient selection tools are needed for dairy farmers to choose the best AI beef bulls.

The outcome of the project, a ready-to-run NAV beef × dairy genetic evaluation, includes a separate evaluation for calving and carcass traits. The development of the Beef × dairy evaluation took place during 2017 and 2018. The first routine evaluation was carried out in December 2018. Seges (Ruth Davis) focused on developing the evaluation of calving traits and Växa Sverige (Freddy Fikse) on the evaluation of carcass traits. Traits definitions and models will be as similar as possible to the NAV Dairy evaluations for these trait groups.

Table 1.1. Abbreviations used for countries and breeds

Abbr	Abbreviations
DNK	Denmark, Danish
FIN	Finland, Finnish
SWE	Sweden, Swedish
HOL	Holstein
RDC	Red Dairy Cattle
JER	Jersey
AAN	Aberdeen Angus
BBL	Belgian Blue
BAQ	Blonde d'Aquitaine
BSH	British Shorthorn
BSM	Beef Simmental
CHA	Charolais
GLW	Galoway
HER	Hereford
HLA	Highland cattle
INR	INRA 95
LIM	Limousin
PIE	Piemontese
SAL	Salers
WAG	Wagyu
XXX	Crossbreds, Sometimes used for INRA 95

Table 1.2. Abbreviations used for traits

Abbr	Abbreviation
CSu	Calf survival
CE	Calving ease

CSi	Calf size
dgs/dgl	Daily carcass gain, short vs long fattening period
bcs	Carcass conformation score
fats	Carcass fat score

2. Design of workflow

At an early stage in the project, some time was spent on drafting a layout of the directory and file structure for the Beef × dairy evaluation; see Figure 2.1 and Appendix A. The directory structure follows that of other NAV evaluations in that there are separate directories per trait group. A directory "CMON" contains programs and files to create a dataset with beef × dairy crosses that qualify to be included in the evaluation, hereinafter referred to as the Common dataset. Wrapping up of an evaluation, i.e. combining breeding values from several trait groups, calculation of total merit indexes and implementation of publication rules is also done inside the "CMON" directory tree.

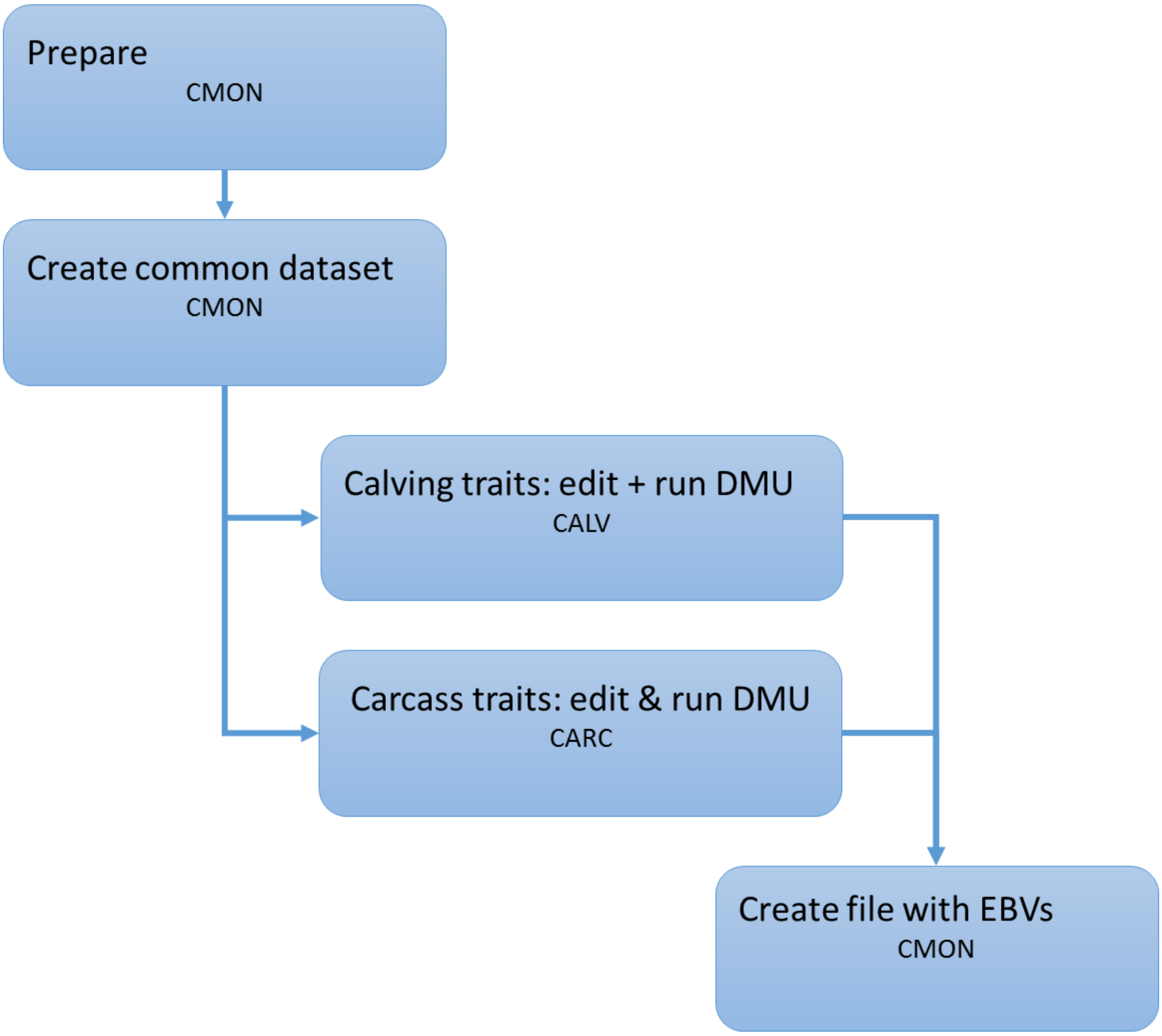

Figure 2.1. Schematic representation of the workflow.

3. Data used for the evaluation

3.1. Input data

There are, by-and-large, three data input sources for the Beef × dairy evaluation:

1) NAV pedigree
2) Files with calving data
3) Files with carcass data

Files for 2) and 3) have the same format as equivalent files used in the NAV Dairy evaluation. The only difference is that files used as input in the Beef × dairy evaluation include records for both purebred dairy as well as beef × dairy crossbred individuals. Date of creation of files with data used for the development of the Beef × dairy evaluation was late 2017 – early 2018 (Table 3.1).

The NAV pedigree used in the Beef × dairy evaluation is different from the NAV pedigree used for NAV Dairy evaluation in that it also includes records for beef × dairy crossbreds and beef sires from all three NAV countries.

Table 3.1. Data used for development of the Beef × dairy evaluation

	Calving traits	Carcass traits
Denmark	October 2017	October 2017
Finland	June 2017	December 2017
Sweden	June 2017	February 2018

Files for exchange of calving data contain information for three phenotypes: calf survival, calving ease and calf size (Denmark only). In addition, there was also info on birth herd, sex of the calf and parity of dam. Some calves (especially from Finland), did not have a record in the NAV pedigree file, and sire and dam information are retrieved from the file with calving data. Records for calving traits came in all sorts of shapes and size (Table 3.2) and have changed over time. Calf survival records were recoded for all countries such that 10 = dead and 11 = alive. Calving ease records were recoded for all countries into four categories, such that 1 was the category with the most difficult calving and 4 was the category with the easiest calvings. Exception to this were Swedish records pertaining to the old calving score system in use prior to May 2012, which only had two classes (treated separately in the heterogeneous variance adjustment; see Chapter 4.1). Calf size was only provided by Denmark, and only records with code 1-4 were considered. Interpretation of the calf size codes were as follows: 1 = small; 2 = below average; 3 = above average and 4 = large. See Pedersen et al. (2016) for more details on recording of calving traits.

Table 3.2. Details on recordings for calving traits

	Denmark	Finland	Sweden
Calf survival	7 classes (1-5,8-9)	O: 15 classes (0-9,E,J,K,P,V) N: 11 classes (1,3-4,8-9,21-26)	2 classes (1-2)
Calving ease	5 classes (1-5)	4 classes (1-4)	O: 2 classes (1-2)[2] N: 4 classes (11-12) + 14 more sporadically used classes
Calf size	5 classes (1-5)	-	-

[1] System `O´ was in use until 2002 and system `N´ has been used since 2002

[2] System `O´ was in use until May 2012 and system `N´ has been used since May 2012

Files for exchange of carcass data contain information for three phenotypes: (cold) slaughter weight, carcass conformation score, carcass fat score. In addition, there was also info on slaughter herd and date of slaughter. Recording of slaughter traits differed between countries for carcass fat score (Table 3.3). Swedish carcass fat scores were transformed to have similar scale as the other two countries.

Table 3.3. Details on recordings for slaughter traits

	Denmark	**Finland**	**Sweden**
Slaughter weight	Kg	Kg	Kg
Carcass conformation score	15 classes (1-15)	15 classes (1-15)	15 classes (1-15)
Carcass fat score	5 classes (1-5)	5 classes (1-5)	15 classes (1-15)

3.2. Data editing

Common data set

In the Beef × dairy evaluation, we include all crossbred calves born in the three countries from 2000 and onwards if they are; (i) after a purebred dairy dam of the breed RDC, Holstein or Jersey, (ii) after a purebred beef breed AI sire of one of the major beef breeds in our countries and (iii) born on a milk producing herd. The purpose of these edits was to ensure that data was included such that breeding values would reflect future commercial production circumstances for beef production by beef × dairy crossbreds. In particular, the edits avoid inclusion of data from herds switching from dairy to beef production.

For Denmark and Sweden, information about breed of dam is extracted from id_nor retrieved from the NAV pedigree. For Finland, breed of dam information is extracted from another source (fincr.fin_org).

Breed of sire information was extracted from id_nor of the sire retrieved from the NAV pedigree. For INRA bulls, the breed portion in id_nor is XXX (which means crossbred), and a special treatment of INRA bulls is done. As per November 2019, a list of bulls to be treated as INRA bulls is read (INRA_hb.txt). In some of the Nordic countries, the distinction between Fleckvieh and beef Simmental is not waterproof, and a hard-coded edit is done to exclude crossbreds with a Fleckvieh bull as sire. As per August 2020, this practice has been changed and crossbreds with a Fleckvieh bull as sire are also included.

Edit iii), requiring beef × dairy crossbreds to be born on a milk producing herd, is implemented such that beef × dairy crossbred calves only are included if there are 5 or more purebred calves born in the same herd-year.

The edit to include only beef × dairy crossbred offspring after AI sires was implemented by requiring crossbred offspring in 10 or more herds. For dairy bulls, information about status (AI vs other types) is in the so-called herdb_ascii file; at the time of development of the B×D genetic evaluation this information was not included for beef bulls, otherwise information from that file had been the natural criterion for removing offspring of non-AI beef sires.

Parity of dam was restricted to be at most 10, and beef × dairy crossbreds born from later parities were removed.

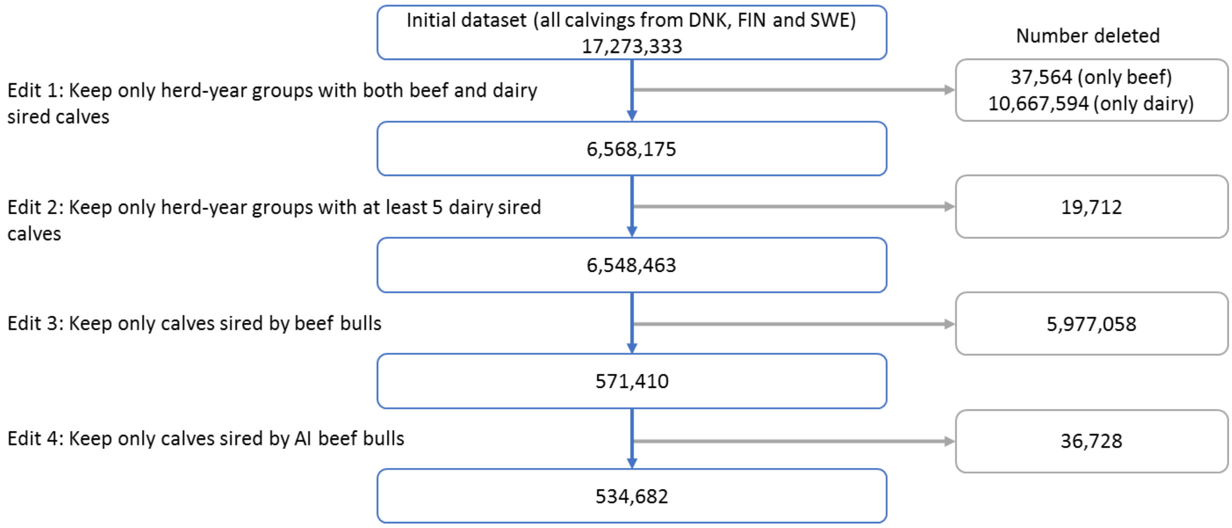

Figure 3.1. Illustration of the editing process to create the common dataset, including number of records deleted at each step.

Calving traits

The following edits were performed for calving traits:

- Records for twins and ET calves were discarded (around 3% of the records).
- Dam age at birth was required to be between 15 and 121 months.
- Finnish calving ease data from before 2003 was deleted.
- Records with deviating gestation length are excluded (Finland only).
- Calving ease records were recoded such that the higher the value, the easier was the calving. Codes 11 to 14 were used.
- Calf survival records were recoded such that 10 = dead and 11 = alive.

All these edits are performed the same way as in the Calving traits evaluation for dairy breeds (version of May 2018).

Carcass traits

The following edits were performed for carcass traits:

- Records were only considered for beef × dairy crossbreds slaughtered between 200 and 900 days of age.
- Dam age at birth was required to be at least 570 days and at most 110 months (9¼ years).
- Daily carcass gains larger than 1 kg/day were set to missing. (No lower limit was imposed).
- For Denmark, there is a requirement that the beef × dairy crossbred has been at least 90 days in the slaughter herd, for the slaughter record to be included in the genetic evaluation.

All these edits are performed the same way as in the Growth evaluation for dairy breeds (version of May 2018).

Mean age at slaughter by herd and birth year of the slaughtered beef × dairy crossbreds was calculated to assign slaughter records into short versus long fattening period. Mean slaughter age was calculated as the mean slaughter age for a herd and year (birth year of the slaughtered animal). For the three most recent years, the herd average four or five years prior to the evaluation date was substituted. For herd – year classes with only one slaughter individual, the herd average of slaughter age across the whole time period was substituted.

3.3. Data structure

There has been an increase in the use of beef semen in dairy herds in both Denmark, Finland and Sweden (Figure 3.2). However, the number of beef × dairy crossbred calves as well as the trend over years differs between countries. By tradition, Finland has used more beef semen in dairy herds than the other countries. The most rapid increase in the last decade has however been observed in Denmark. By August 2019, calving records from 714 380 beef × dairy crossbred calves were included. The corresponding number for the carcass traits was 273 417.

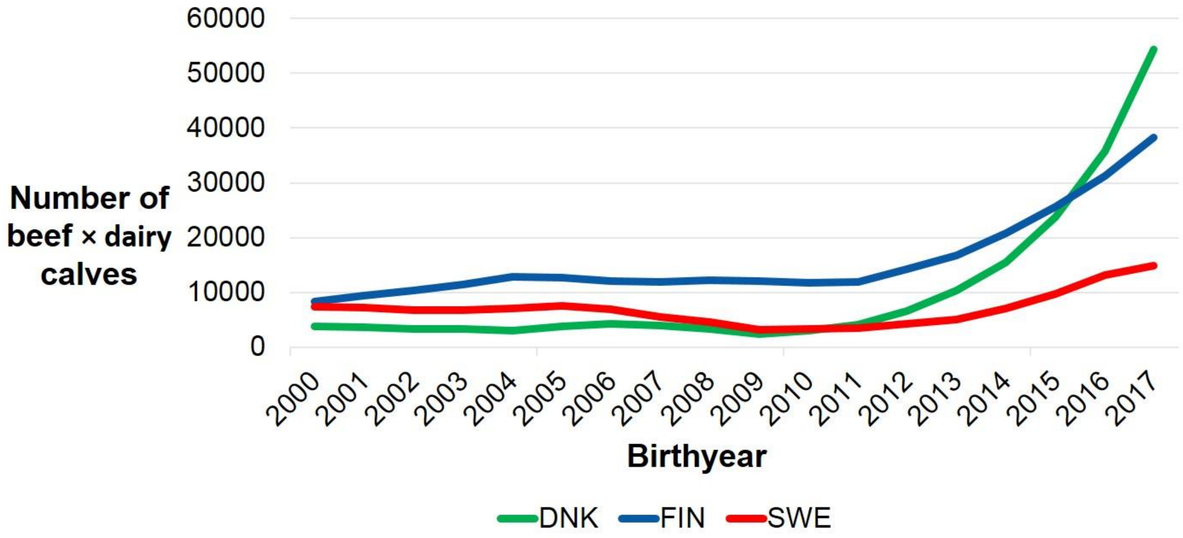

Figure 3.2. Number of beef × dairy crossbred calves born in Denmark, Finland and Sweden from year 2000 and onwards.

The distribution of sire breeds has varied much over time. Figure 3.3 displays the proportion of the crossbred calves, across all countries, after the major beef sire breeds. Considering crossbred calves born in 2018, the majority had either a BBL (41%) or BAQ (28%) sire. The remaining calves were more evenly distributed on the other sire breeds, and none of them exceeding 10%.

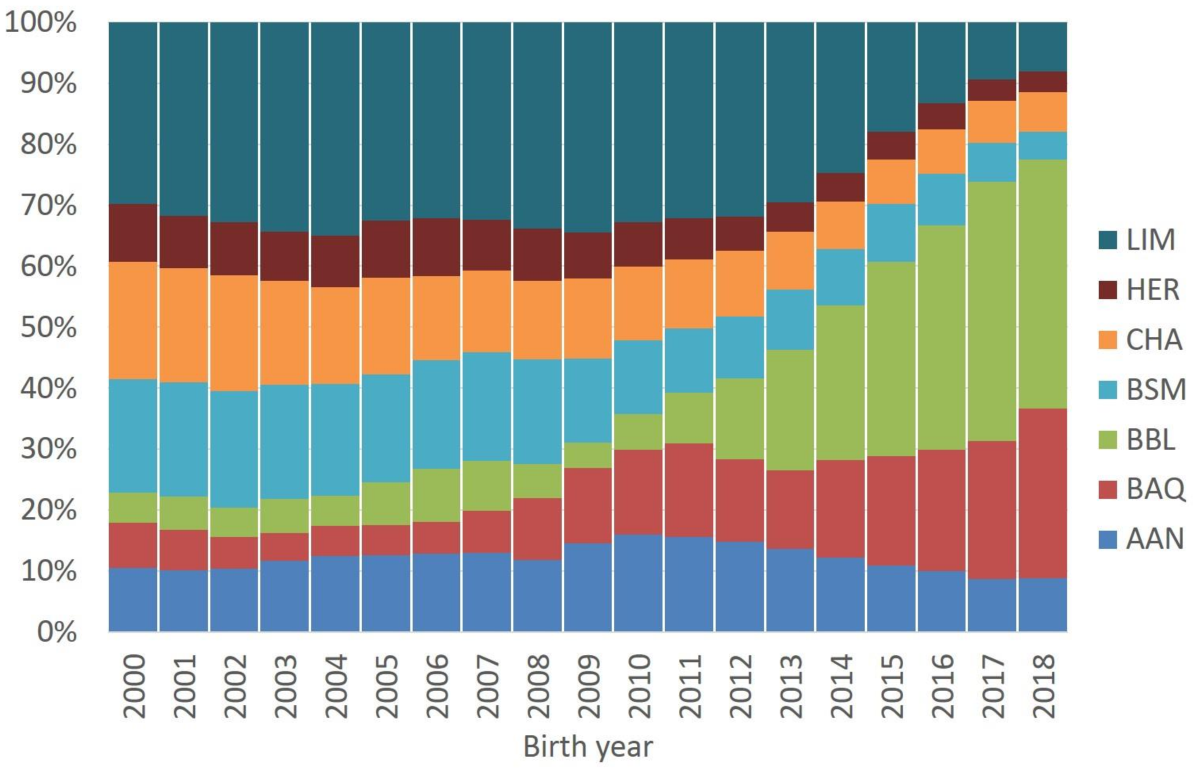

Figure 3.3. The distribution of seven largest beef sire breeds for beef × dairy crossbreds born between 2000 and 2018.

During the initial stage of the project emphasis was put on investigating and describing the structure of the data available for the Beef × dairy evaluation. As the aim was to compare beef sires from different beef breeds with each other, connectedness of beef breeds was investigated. Connections can be achieved in several ways, for example by beef sires that have been used in multiple herds, when several unrelated sires are used in the same herd. Aspects that were studied were:

- Connections between dams (through multiple offspring per dam, with sires from different breeds)
- Connections through herds (use of multiple sire breeds in the same herd – year class)

The conclusion of these investigations was that: The connection between sires, and sire breeds is good. The weakest data is for the first parity cows due to very few observations, and less sires used.

See Appendix C for a detailed account of the study of connectedness.

Mean slaughter age

New in the Beef × dairy evaluation (in comparison with the NAV Growth evaluation for dairy breeds) is the inclusion of slaughter records of females. It was therefore investigated whether or not the same cut-off (of 550 days) could be used for both males and females. For this purpose, the mean slaughter age was calculated for each herd – year – sex class. In Figure 3.4 and Figure 3.5, the distribution of herd average of slaughter age is shown separate by sex, for all herd – year classes and for ‘large’ herd – year – sex classes. In the second set of graphs (Figure 3.6 and Figure 3.7), the distribution of the difference in mean slaughter age within herd-year classes is illustrated, first for all herd-year classes and second for ‘large’ herd – year classes. The latter two graphs were based on herd-year classes that have sent both males and females to slaughter.

The herd average slaughter age in Denmark was below 500 days in nearly all cases, for both genders. Females were on average about 40 days older at slaughter compared to males. For Finland, on the other hand, females were slaughtered at a younger age than males, the difference being about 70 days. Looking at the distribution of slaughter age, most Finnish males are assigned to the long fattening period whereas nearly half of the females are assigned to the short fattening period if a cut-off of 550 days is used. In Sweden, females were slaughter at higher age than males, and the difference was more than 100 days. Nearly all females are assigned to the long fattening period if a cut-off of 550 days is used.

As a parenthesis, the distribution of slaughter age for beef × dairy crossbred males were fairly similar to that of pure bred dairy males.

Table 3.4. Mean slaughter age (days), by country and sex, for different subsets of herd – year – sex class sizes (all, at least 3 obs, at least 5 obs)

	All			Min 3 obs/hy			Min 5 obs/hy		
	M	F	Δ[1]	M	F	Δ[1]	M	F	Δ[1]
DNK	370	422	43	356	400	32	346	386	27
FIN	621	680	1	608	606	-69	600	575	-104
SWE	577	720	136	554	700	132	543	693	134

[1] Within-herd sex difference in slaughter age, calculated for herd-years that sent both males and females to slaughter, i.e. a subset of the herd-years used to calculate the statistics for the M and F column.

Table 3.5. Weighted mean slaughter age, by country and sex, for different subsets of herd – year – sex class sizes (all, at least 3 obs, at least 5 obs)

	All			Min 3 obs/hy			Min 5 obs/hy		
	M	F	Δ[1]	M	F	Δ[1]	M	F	Δ[1]
DNK	345	377		337	366		332	358	
FIN	600	521		597	510		593	503	
SWE	563	712		547	697		539	691	

[1] Not calculated

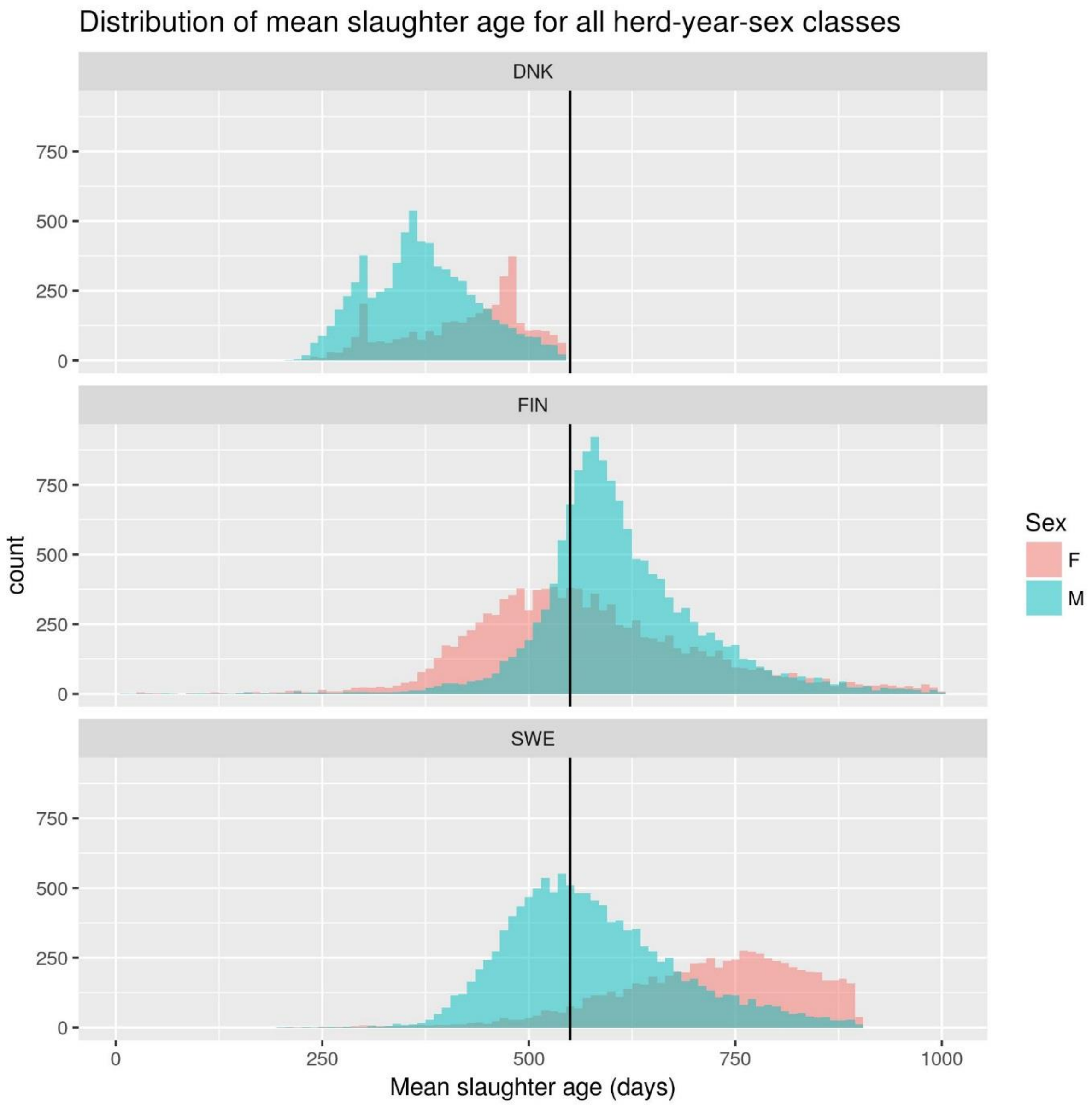

Figure 3.4. Distribution of mean slaughter age for males and females, by country; all herd – year – sex classes.

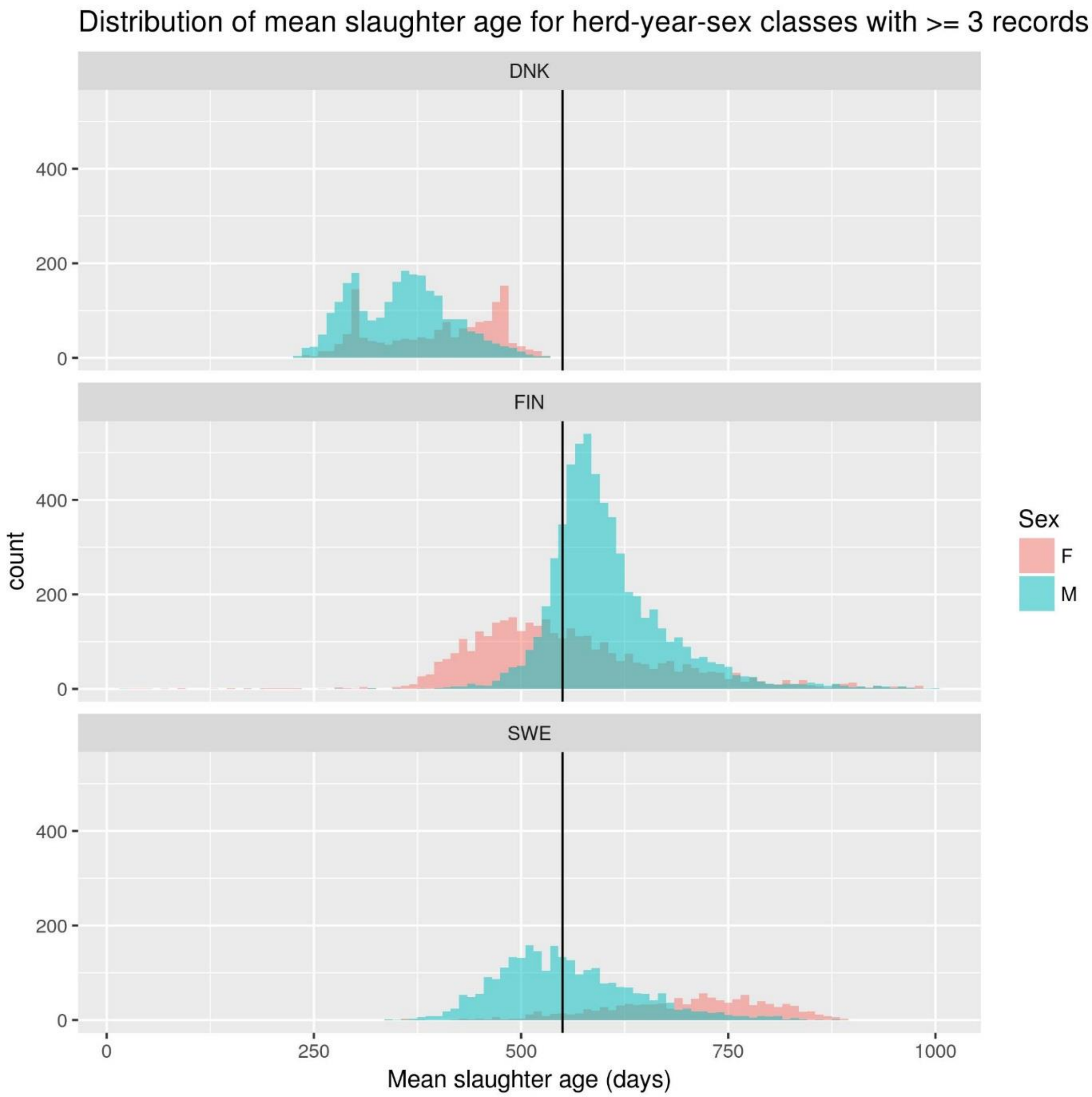

Figure 3.5. Distribution of mean slaughter age for males and females, by country; herd – year – sex classes with at least three slaughtered animals.

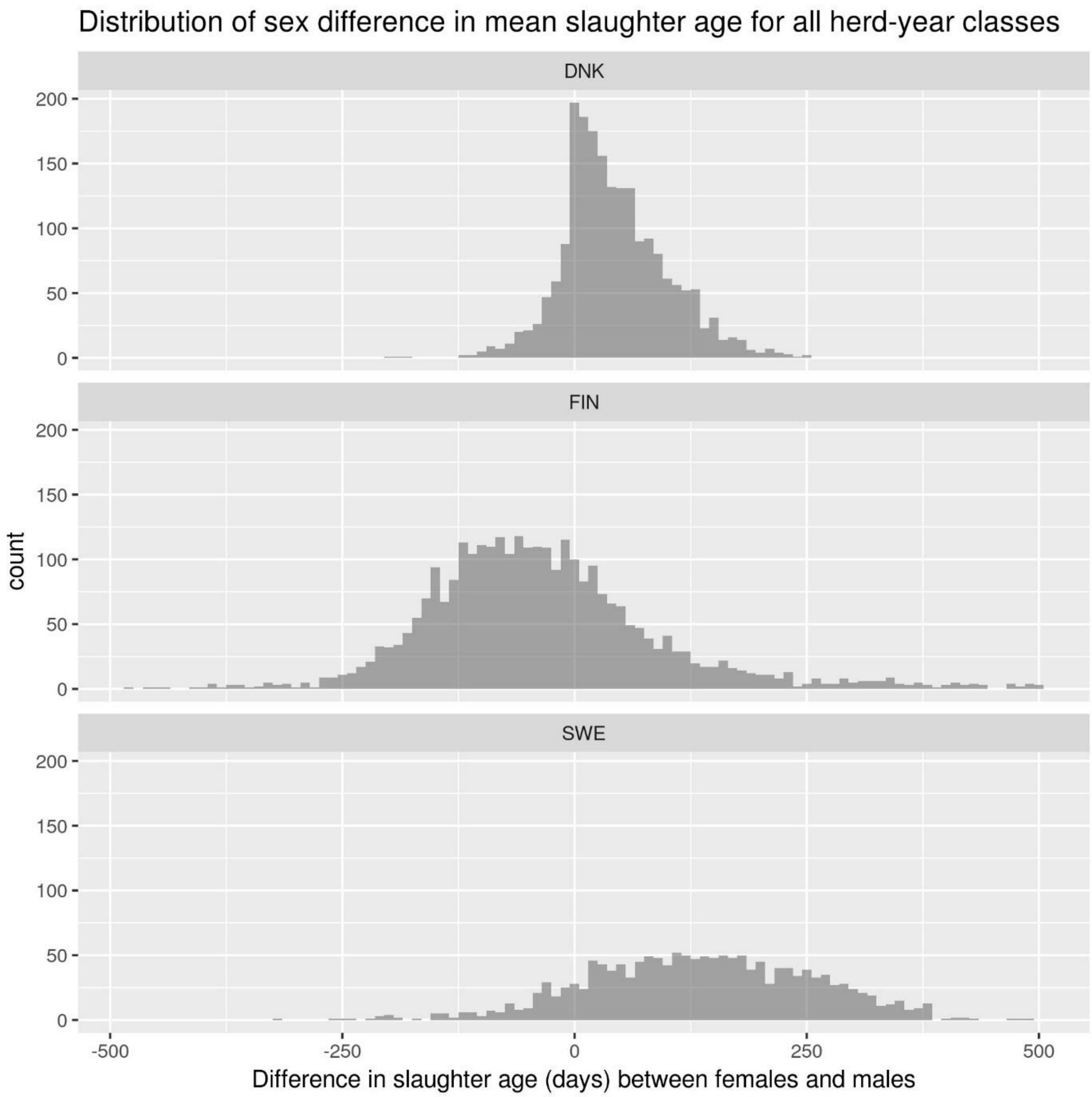

Figure 3.6. Difference in slaughter age between males and females for herd-years sending slaughtering both males and females; all herd-years.

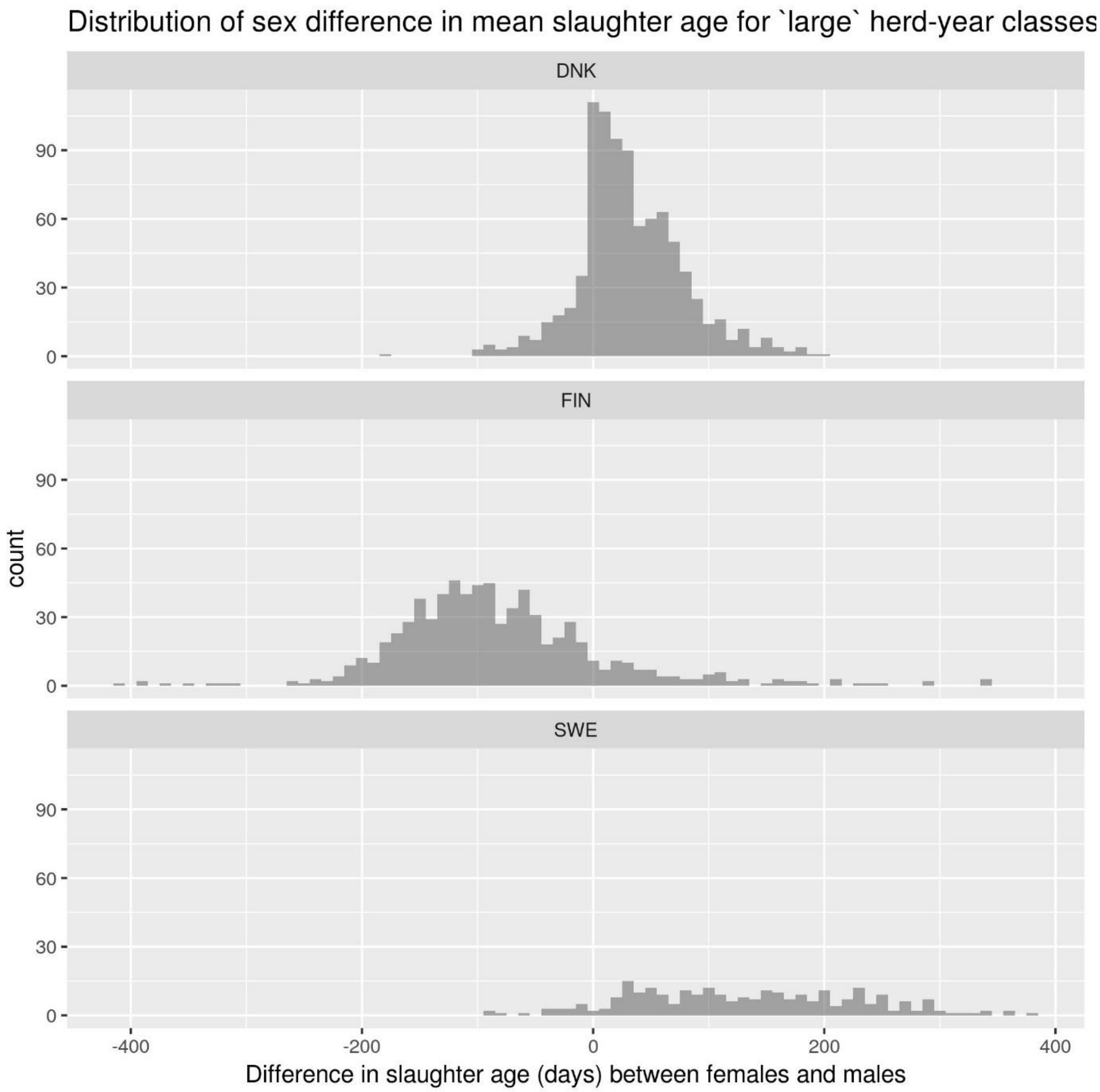

Figure 3.7. Difference in slaughter age between males and females for herd – years sending slaughtering both males and females; herd – years with at least 3 slaughtered males and 3 slaughtered females.

4. Genetic evaluation

4.1. Heterogeneous variance adjustments

Calving traits

Average levels of calf survival and calving ease differ by country and year (e.g., Appendix G), and variances are thus expected to be heterogeneous due the binomial/multinomial nature of these phenotypes. Hence, a simple phenotypic variance adjustment was implemented. Records are adjusted for differences in phenotypic variance within subclasses of country – calving year (cohorts of 5 years) – dam breed, and the adjustment is performed separately for each trait. For Sweden, variances for calving ease were adjusted separately due for the old and new recording system (see Chapter 3.1)

The formula for the adjustment was:

$$y_{ijk_{adj}} = \mu_{ijk} + \sigma_{desired} \cdot (y_{ijk} - \mu_{ijk})/\sigma_{ijk}$$

Where: y_{ijk} and $y_{ijk,adj}$ are an original and adjusted observation in the *ijk*th country – birth year cohort – breed of dam subclass, and μ_{ijk} and σ_{ijk}, are the corresponding mean and standard deviation. $\sigma_{desired}$ is the desired standard deviation, i.e. the standard deviation of the adjusted observations.

Carcass traits

Preliminary investigations showed that variances were heterogeneous across country, year of slaughter, sex, sire and dam breed. Overall, the Gini coefficient (calculated as in Urioste *et al.*, 2001) ranged from 0.16 (dgl) to 0.23 (fats), indicating moderate/mild heteroskedasticity. Sources of difference in phenotypic variances were further investigated by calculating the phenotypic variance within each country – year of slaughter – sex – length of fattening period – sire breed – dam breed subclasses, and by analyzing these with a log-linear model. This model included the effects of country, year, sex, length of fattening period, sire breed and dam breed. Significance of each factor is tabulated in Table 4.1.

Table 4.1. Significance of factors affecting phenotypic SD of observations for four carcass traits

	Daily carcass gain, short	Daily carcass gain, long	Carcass conformation score	Carcass fat score
Country	***	***	***	***
Year	*	**	***	***
”short” vs ”long”			***	***
Sex	***	***	***	***
Sire breed	***	***	***	***
Dam breed	***	NS	***	NS

* : $P < 0.05$; ** : $P < 0.01$; *** : $P < 0.001$

The phenotypic SD for carcass fat score, and to a lesser extent carcass conformation score, declined over time (Figure 4.1). The phenotypic SD for daily carcass gain appeared to be increasing slightly in the more recent years.

Phenotypic SD differed significant between sire breeds (Table 4.1), but a clear pattern (e.g. British breeds vs Continental breeds) was not easily identified (Figure 4.2). Since part of the difference in phenotypic SD may relate to genetic effects, which shall be reflected in breeding values, it was decided not to adjust for differences in phenotypic SD between sire breeds.

Phenotypic SD differed significant between dam breeds (Table 4.1) and was smaller for Jersey for all traits besides fat score (Figure 4.3). Since the use of sire breeds on dam breeds was not balanced, adjusting for differences in phenotypic SD due to dam breed is important.

Implementation

Differences in phenotypic SD within country – year – sex – dam breed subclasses were adjusted for. The adjustment was of the same type as for calving traits.

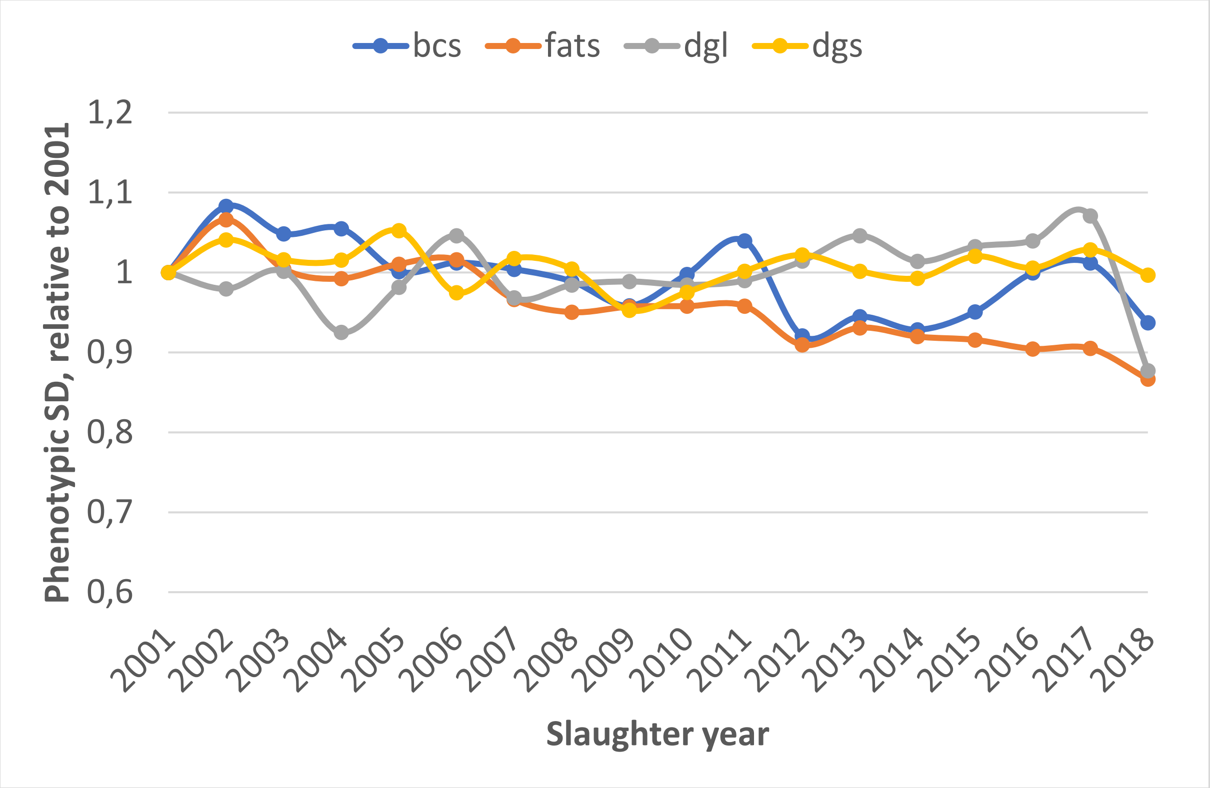

Figure 4.1. Phenotypic SD per slaughter year (relative to 2001) for four carcass traits.

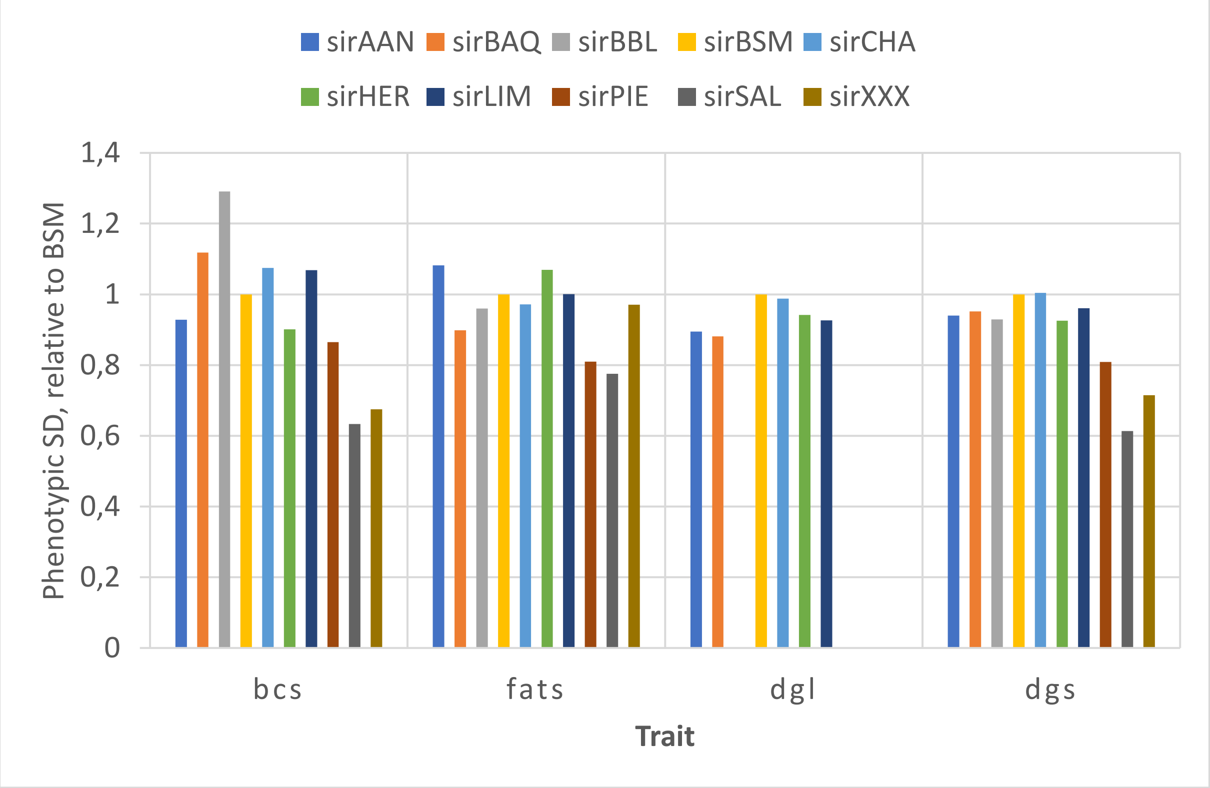

Figure 4.2. Phenotypic SD per sire breed (relative to Beef Simmental [BSM]) for four carcass traits.

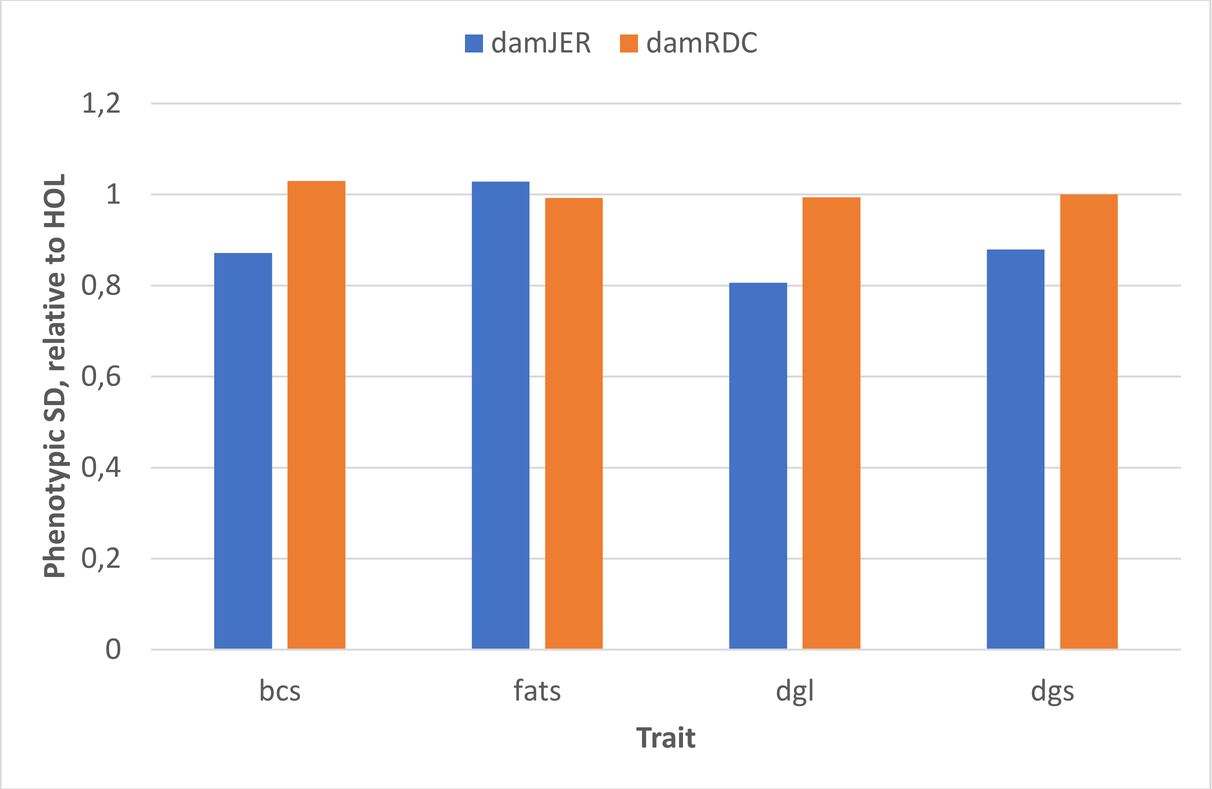

Figure 4.3. Phenotypic SD per dam breed (relative to HOL) for four carcass traits.

4.2. Statistical model

Observations for calving traits are influenced by the genetic value of the calf, and for calving traits also the environment provided by the dam of the calf, which in part is heritable. The genetic value of the calf is determined by the genetic merit of the sire and the dam and is also affected by heterosis as observations are recorded on beef × dairy crossbreds. Choice of statistical model for the genetic evaluation was preceded by a discussion how to consider the contributions of genetic merit, including genetic progress made in the dairy breeds, and heterosis, to the observations made on beef × dairy crossbreds (documented in Appendix A). The discussion landed in adopting a sire model, including a fixed effect of sire breed to adjust for systematic differences between beef sire breeds and a fixed effect of breed and birth year of dam to adjust for the genetic trend in the dairy breeds.

To ensure that sire breed effects could be estimated with some precision, records for crossbreds with a sire from a beef breed with few offspring in dairy herds were deleted. The cutoff point (lower limit) was 50 beef × dairy offspring per beef breed.

A relationship matrix is built for the beef sires that have beef × dairy crossbred offspring with data. Five generations of pedigree are traced back. The pedigree file contains sire and maternal grandsire of beef bulls. A pedigree file is constructed separately by evaluation group (calving vs carcass traits).

Calving traits

Calving traits were analyzed with the following model:

$$Y_{ijklmno} = CHY_i + CYM_j + CYS_k + Age_l + DBrY_m + SBr_n + s_o + e_{ijklmno} \quad \mathbf{(1a)}$$

Here:

CHY_i	country – herd – year of birth of calf
CYM_j	country – year – month of birth of calf
CYS_k	country – year – sex of calf of calf
Age_l	country – age of dam
$DBrY_m$	breed – year of birth of dam
SBr_n	breed of (beef) sire
s_o	sire
$e_{ijklmno}$	residual

The sire and residual effects are random effects; all other effects are fixed effects. Choice of systematic environmental effects to be included in the model was inspired by the NAV Dairy evaluation for calving traits. All traits were analysed with a linear model instead of threshold models, even if records for calving traits follow bi-/multinomial distributions.

Small country – herd – year classes were grouped by herd to achieve a minimum of three records per class. If there were fewer than three beef × dairy crossbreds over the whole time period, then the records of that herd were deleted. This procedure is done separately for first versus later parity records. This edit caused that 7712 first and 10,714 later parity records were discarded, i.e. 3.7% of the records.

Small breed – birth year of dam classes were grouped using the same procedure as for country – herd – year classes. The lower limit for class size was 50.

For primiparous cows, 21 age of dam classes were created: < 18 mo, 18, 19, …, 35, 36, > 36 mo. For multiparous calvings, parity number was used to define of dam age classes. Records with parity number exceed 6 were grouped together with sixth parity records.

The genetic evaluation employs a multiple-trait model with six traits: calving ease, calf survival and calf size for primiparous and multiparous cows. Genetic parameters are shown in Section 4.3.

Definition of contemporary group

It is critical in the statistical modelling of the data to ensure that an animal's performance is compared with other animals that have been subject to more or less the same environment and conditions (contemporaries). In the NAV Dairy evaluation for calving traits, this is achieved by including a fixed effect of country – herd – 5-year period and random effect of country – herd – year. For the calving traits this option was contemplated yet discarded because too many herd – 5-year groups would be too small due to the sparsity of data in the early period of included data (early 2000-ands). Hence, the approach of grouping country – herd – year classes within herd was implemented. See Appendix E for a detailed account of the investigation that was done.

Carcass traits

Carcass traits were analysed with the following model:

$$Y_{ijklmn} = CHY_i + +CYM_j + CCA_k + DBrY_l + SBr_m + s_n + e_{ijklmn} \quad (\mathbf{1b})$$

Here:

CHY_i country – slaughter herd – year of birth of crossbred

CYM_j country – year – month of slaughter of crossbred

CCA_l country – age of dam of crossbred

$DBrY_m$ breed – year of birth of dam

SBr_n breed of (beef) sire

s_o sire

e_{ijklmn} residual

The sire and residual effects were random effects; all other effects were fixed effects. Choice of systematic environmental effects to be included in the model was inspired by the NAV Dairy evaluation for carcass traits.

The definition of contemporary groups differed slightly between countries:

- Denmark: slaughter herd.
- Finland: slaughter herd – slaughterhouse (i.e. considering an interaction between slaughter herd and slaughterhouse).
- Sweden: slaughter herd – slaughterhouse (i.e. considering an interaction between slaughter herd and slaughterhouse).

Small country – herd – year classes, small country – year – month classes, small country – age of dam classes and small breed – birth year of dam classes were grouped as described above for calving traits. The minimum group size was 3 for country – herd – year, and 25 for all other factors.

The genetic evaluation employed a multiple-trait model with eight traits: daily carcass gain – short fattening period, daily carcass gain – long fattening period, carcass conformation score and carcass fat score for males and females. Genetic parameters are in shown Section 4.3.

Definition of contemporary groups

Data structure with respect to contemporary groups was tabulated, as was done for calving, albeit not as exhaustive. Round and about 20% of Danish and Finnish records were in herd – year groups with size less than three, and the corresponding figure for Sweden was 50% (Table 4.2). Grouping within consecutive years per herd reduced the occurrence of small contemporary groups by a half, but for Sweden a considerable portion of the data would be in herd – 5-year period groups with size less than three.

Hence, the procedure to group adjacent herd – year classes until the group size is at least three was applied for the carcass traits as well. Considerably more records could be kept, even after imposing a minimum group size of three.

Table 4.2. Number of slaughter records (ALL) and number of records in small contemporary groups, for two contemporary group definitions

	DNK	FIN	SWE		DNK	FIN	SWE
Males	**Number of obs / CH1Y**				**Number of obs / CH5Y**		
ALL	29579	55419	24890		29579	55419	24890
1	3342	5691	6937		1482	1652	3321

2	2464	5200	4688		1260	1606	2672
Females							
ALL	17109	50545	12296		17109	50545	12296
1	1538	6440	4772		816	2508	2782
2	1242	4184	2498		648	2270	1826

Table 4.3. Number of slaughter records (ALL) and number of records in small contemporary groups, after merging adjacent herd – year levels

	DNK	FIN	SWE
Males			
All	29579	55419	24890
≥3	27781	53003	20304
Females			
All	17109	50545	12296
≥3	15940	46744	8447

4.3. Genetic parameters

Calving traits

The genetic parameters were estimated based on all data from all countries, with a multiple-trait model including all six traits using DMUAI. The estimated heritabilities (Table 4.4) were in line with those used in the dairy evaluation (Table 4.5). The genetic correlations were in line with or higher than those from the dairy evaluation (Table 4.5).

Table 4.4. Estimated genetic parameters for calving traits[1]: heritability on the diagonal and genetic correlations above the diagonal and residual correlations on the below the diagonal; standard errors of estimates are in subscript

	CSu1	CSu2+	CE1	CE2+	CSi1	CSi2+
CSu1	**0.05** $_{0.003}$	0.88 $_{0.104}$	0.70 $_{0.120}$	0.67 $_{0.120}$	-0.80 $_{0.248}$	-0.50 $_{0.173}$
CSu2+		**0.01** $_{0.000}$	0.61 $_{0.098}$	0.62 $_{0.054}$	-0.53 $_{0.177}$	-0.43 $_{0.092}$
CE1	0.29 $_{0.008}$		**0.11** $_{0.005}$	0.97 $_{0.056}$	-0.89 $_{0.159}$	-0.93 $_{0.112}$
CE2+		0.28 $_{0.002}$		**0.05** $_{0.001}$	-0.80 $_{0.130}$	-0.84 $_{0.037}$
CSi1	-0.09 $_{0.017}$		-0.32 $_{0.016}$		**0.17** $_{0.013}$	0.83 $_{0.120}$
CSi2+		-0.03 $_{0.003}$		-0.21 $_{0.003}$		**0.09** $_{0.003}$

[1] CSu1 = for calf survival in first parity; CSu2+ = calf survival in later parities; CE1 = calving ease first parity; CE2+ = calving ease later parities; CS1 = calf size in first parity; CSi2+ = calf size in later parities (CSi2+)

Table 4.5. Genetic correlations (above diagonal) and heritabilities (diagonal) used in the dairy evaluation for calving traits[1]

	CSu1	CSu2+	CE1	CE2+	CSi1	CSi2+
CSu1	**0.035**	0.7	0.7	0.5	-0.4	-0.4
CSu2+		**0.01**	0.5	0.6	-0.4	-0.4
CE1			**0.06**	0.7	-0.7	-0.7
CE2+				**0.03**	-0.8	-0.7
CSi1					**0.2**	-0.8

CSi2+						**0.2**

[1] Source: NAV (2020)

Estimates of variance components are in Table 4.6. Note that these variance components relate to observations that have adjusted for heterogeneous variances. Variances (and heritabilities) for the calving traits are also influenced by the categorical nature of the observations, and as such are frequency dependent.

Table 4.6. Estimated sire and residual variances for calving traits; standard errors of estimates are in subscript

	VarS	**VarE**
CSu1	0.000834 $_{0.000224}$	0.067177 $_{0.000729}$
CSu+	0.000109 $_{0.000014}$	0.034129 $_{0.000076}$
CE1	0.011187 $_{0.002208}$	0.379859 $_{0.004689}$
CE2+	0.003138 $_{0.000283}$	0.254067 $_{0.000678}$
CSi1	0.019383 $_{0.006175}$	0.432992 $_{0.011067}$
CSi2+	0.007688 $_{0.000890}$	0.331712 $_{0.001305}$

Carcass traits

Genetic parameters were estimated with an 8-variate model using all data. The eight traits were Daily carcass gain – short fattening period, Daily carcass gain – long fattening period, Carcass conformation score and Carcass fat score, for males and females, respectively. The statistical model included fixed effects of country – dam age, country – birth month – birth year, herd – year, dam breed – dam year of birth and sire breed, and a random sire effect. Pedigree was traced back five generations for sires of the beef bulls with crossbred offspring and two generations for maternal grandsires of the beef bulls with crossbred offspring.

Table 4.7. Estimated genetic parameters for carcass traits[1]: heritability on the diagonal and genetic correlations above the diagonal and residual correlations on the below the diagonal; standard errors of estimates are in subscript

	dgs,♂	**dgl,♂**	**bcs,♂**	**fats,♂**	**dgs,♀**	**dgl,♀**	**bcs,♀**	**fats,♀**
dgs, ♂	**0.19** $_{0.017}$	0.97 $_{0.019}$	0.30 $_{0.055}$	-0.21 $_{0.061}$	0.83 $_{0.034}$	0.86 $_{0.035}$	0.22 $_{0.061}$	-0.27 $_{0.064}$
dgl, ♂		**0.21** $_{0.020}$	0.34 $_{0.056}$	-0.10 $_{0.063}$	0.85 $_{0.030}$	0.86 $_{0.031}$	0.25 $_{0.063}$	-0.21 $_{0.065}$
bcs, ♂	0.45 $_{0.004}$	0.45 $_{0.004}$	**0.32** $_{0.022}$	-0.17 $_{0.055}$	0.31 $_{0.058}$	0.24 $_{0.063}$	0.92 $_{0.015}$	-0.12 $_{0.060}$
fats, ♂	0.14 $_{0.005}$	0.18 $_{0.004}$	0.08 $_{0.003}$	**0.23** $_{0.018}$	-0.20 $_{0.063}$	-0.13 $_{0.066}$	-0.19 $_{0.058}$	0.88 $_{0.021}$
dgs, ♀					**0.33** $_{0.030}$	0.97 $_{0.015}$	0.35 $_{0.057}$	-0.30 $_{0.065}$
dgl, ♀						**0.32** $_{0.032}$	0.25 $_{0.065}$	-0.22 $_{0.069}$
bcs, ♀					0.37 $_{0.005}$	0.31 $_{0.006}$	**0.35** $_{0.028}$	-0.18 $_{0.062}$
fats, ♀					0.23 $_{0.005}$	0.24 $_{0.006}$	0.19 $_{0.004}$	**0.25** $_{0.022}$

[1] dgs = daily carcass gain, short fattening period; dgl = daily carcass gain, long fattening period; bcs = carcass conformation score; fats = carcass fat score. ♂ denotes trait on males and ♀ denotes trait on females.

Heritabilities ranged from 0.19 for Daily carcass gain, short fattening period, males to 0.26 for Carcass conformation score, females (Table 4.7). The heritabilities for both conformation and fat scores were similar for beef × dairy crossbreds compared to the NAV growth evaluation for dairy breeds. For both daily carcass gain traits, the heritabilities were somewhat lower for beef × dairy crossbreds compared to the NAV growth evaluation for dairy breeds.

Daily carcass gain for short and long fattening period was genetically highly correlated for both genders (Table 4.7). The genetic correlation between sex for the same trait ranged from 0.83 for Daily carcass gain, short fattening period to 0.92 for Carcass conformation score. The size of the genetic correlations among traits was very similar to that of dairy breeds, except for Carcass fat score.

Table 4.8. Genetic parameters used in the NAV growth evaluation for dairy breeds[1]; heritabilities on the diagonal, genetic correlation above the diagonal and residual correlations below the diagonal

	dgs	dgl	bcs	fats
RDC				
dgs	**0.28**	0.98	0.41	0.17
dgl	0	**0.31**	0.36	0.17
bcs	0.44	0.44	**0.29**	0.35
fats	0.29	0.34	0.24	**0.18**
HOL				
dgs	**0.36**	0.97	0.34	-0.14
dgl	0	**0.29**	0.32	-0.12
bcs	0.44	0.44	**0.29**	0.15
fats	0.26	0.29	0.23	**0.23**

[1] Source: NAV (2020)

Estimated variance components are in Table 4.9. Note that these variance components relate to observations that have been adjusted for heterogeneous variances.

Table 4.9. Estimated sire and residual variances for carcass traits; standard errors of estimates are in subscript

	VarS	VarE
dgs, ♂	$0.000169_{0.000016}$	$0.003328_{0.000024}$
dgl, ♂	$0.000148_{0.000015}$	$0.002625_{0.000017}$
bcs, ♂	$0.054530_{0.004204}$	$0.636957_{0.003074}$
fats, ♂	$0.010890_{0.000897}$	$0.175265_{0.000846}$
dgs, ♀	$0.000231_{0.000023}$	$0.002563_{0.000020}$
dgl, ♀	$0.000151_{0.000016}$	$0.001713_{0.000016}$
bcs, ♀	$0.055994_{0.004793}$	$0.575699_{0.003416}$
fats, ♀	$0.010288_{0.000966}$	$0.152418_{0.000904}$

4.4. Solving mixed model equations

DMU 5.3 software was used for the breeding value predictions. Mixed model equations were solved directly using the fspak option in the DMU4 module. This option calculates solutions as well as standard errors (of prediction).

4.5. Reliabilities of breeding values

Exact reliabilities were calculated as:

$$REL = 1 - SEP^2/\sigma_s^2$$

where SEP is the standard error of prediction (calculated by DMU4) and σ_S^2 is the sire variance.

Exact reliabilities could be calculated since the size of the mixed model equations is relatively small because a sire model is used. These exact reliabilities consider contemporary group size, distribution of sires of contemporary groups and number of sires per breed (c.f. uncertainty of the estimated breed effect).

Calving traits

Reliabilities were generally highest for calving ease and lowest for Calf survival (Table 4.10). Distribution of reliabilities was skewed, as is evident from comparing the mean (by breed) in Table 4.10 with the median in Table 4.11 for calving ease – multiparous cows. Correlations between reliabilities for the various traits included in the calving evaluation were generally very high (Table 4.12). Correlations with reliability for Calf size were lowest, probably because only part of the beef × dairy crossbreds had observations for Calf size (Denmark only) and because of the genetic correlation structure.

Table 4.10. Average reliability of breeding values for calving traits for all beef sires with beef × dairy offspring, by beef sire breed

	CSu1	CSu2+	CE1	CE2+	CSi1	CSi2+
AAN	0.48	0.46	0.61	0.61	0.49	0.51
BAQ	0.43	0.48	0.60	0.61	0.44	0.51
BBL	0.51	0.56	0.79	0.76	0.61	0.79
BSH	0.05	0.04	0.09	0.08	0.08	0.09
BSM	0.33	0.34	0.50	0.50	0.36	0.41
CHA	0.38	0.43	0.57	0.58	0.40	0.46
GLW	0.00	0.00	0.00	0.00	0.00	0.00
HER	0.38	0.37	0.50	0.50	0.38	0.40
HLA	0.09	0.09	0.15	0.15	0.10	0.11
INR	0.27	0.26	0.49	0.46	0.38	0.49
LIM	0.48	0.50	0.65	0.64	0.50	0.56
PIE	0.14	0.13	0.28	0.26	0.22	0.28

Table 4.11. Statistics for reliabilities breeding values for Calf survival – multiparous cows for all beef sires with beef × dairy offspring, by beef sire breed

	Min	5th pct	Median	95th pct	Max	Nr of sires
AAN	0.00	0.08	0.45	0.82	0.85	79
BAQ	0.00	0.13	0.44	0.85	0.89	68
BBL	0.12	0.20	0.58	0.83	0.95	101
BSH	0.04	0.04	0.04	0.04	0.04	2
BSM	0.00	0.09	0.31	0.72	0.84	222
CHA	0.04	0.06	0.44	0.80	0.86	109
GLW	0.00	0.00	0.00	0.00	0.00	1
HER	0.00	0.05	0.36	0.80	0.81	76
HLA	0.03	0.04	0.07	0.18	0.21	11
INR	0.19	0.19	0.25	0.36	0.38	5

LIM	0.04	0.12	0.49	0.87	0.90	136
PIE	0.08	0.09	0.13	0.18	0.19	7

Table 4.12. Correlation between reliabilities of breeding values for calving traits for all beef sires with beef × dairy offspring

	CSU2+	**CE1**	**CE2+**	**CSi1**	**CSi2+**
CSu1	0.98	0.94	0.95	0.92	0.84
CSu2+		0.90	0.93	0.86	0.79
CE1			0.99	0.98	0.96
CE2+				0.96	0.92
CSi1					0.98

Carcass traits

As expected, reliabilities increased with increasing number of beef × dairy offspring (Figure 4.4). Notable deviations from the general pattern for sires belonging to the INRA breed. The sire breed effect was estimated with less precision due to the low number of sires for this breed, and this uncertainty was reflected in the reliability.

Reliabilities for different traits were highly correlated; the lowest correlation was 0.97 (Carcass conformation score – males with Daily carcass gain – females). Reliabilities were somewhat lower for the female traits than for the male traits (Table 4.13 and Figure 4.6). This is probably due to the higher number of observations for male beef × dairy crossbred, as compared to female crossbreds.

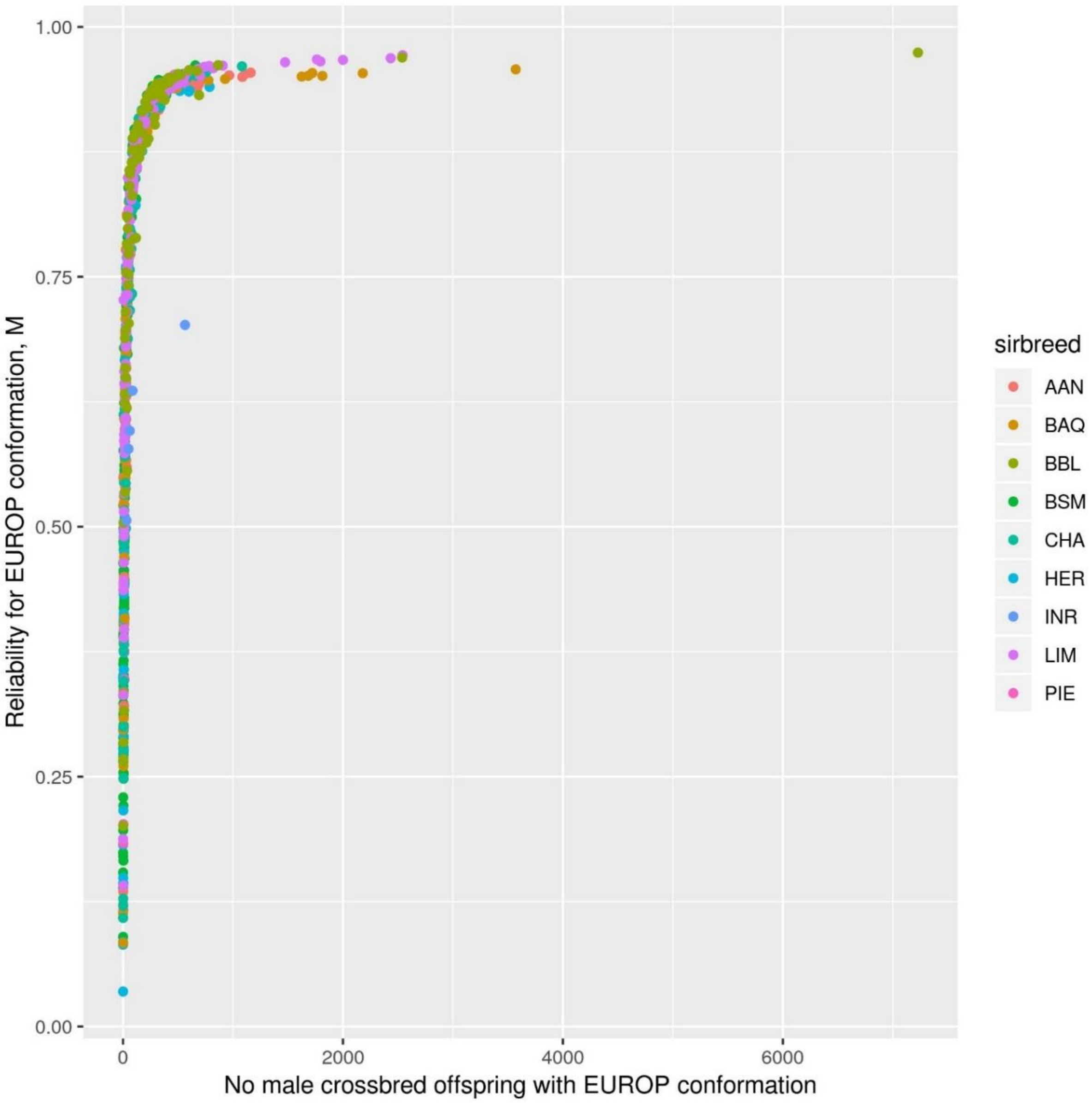

Figure 4.4. Number of male B×D offspring with carcass conformation observations and reliability of breeding value for Carcass conformation, males, for all beef sires with B×D offspring.

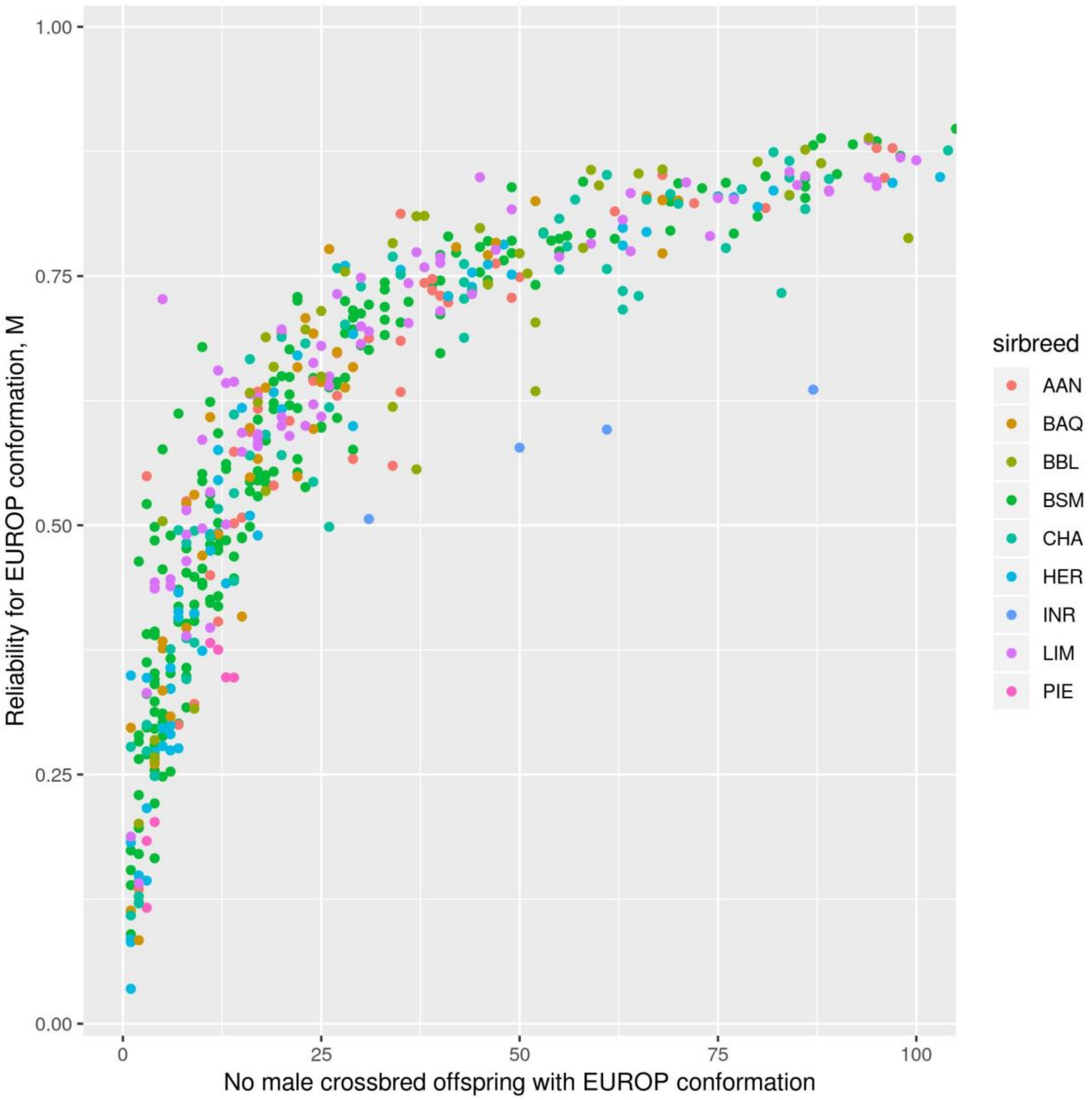

Figure 4.5. Number of male B×D offspring with carcass conformation observations and reliability of breeding value for Carcass conformation, males, for beef sires with less than 105 B×D offspring.

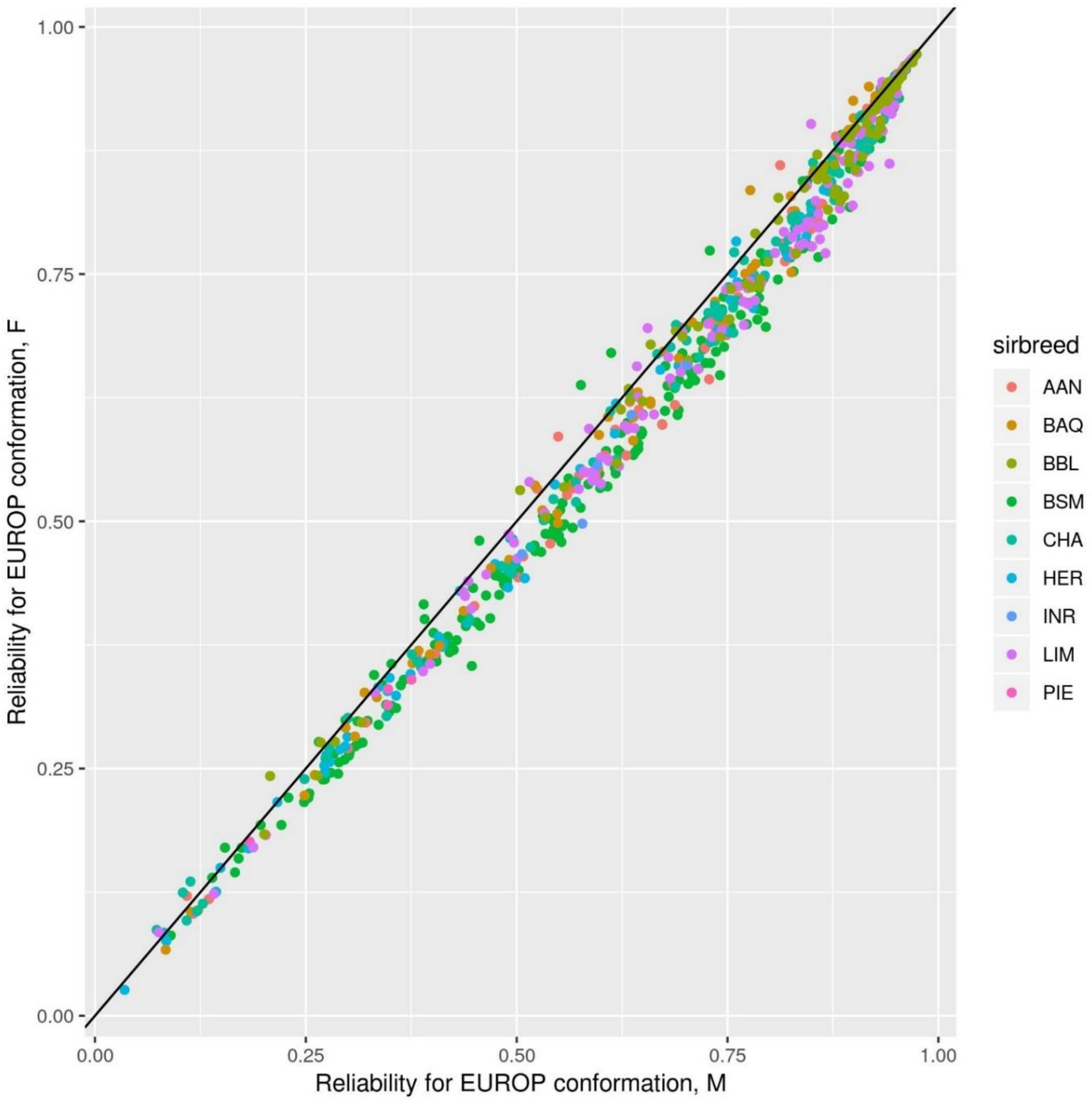

Figure 4.6. Number of male B×D offspring with carcass conformation observations and reliability of breeding value for Carcass conformation, males, for all beef sires with B×D offspring.

Table 4.13. Average reliability of breeding values for carcass traits for all beef sires with beef × dairy offspring, by beef sire breed

	dgs, ♂	dgl, ♂	bcs, ♂	fats, ♂	dgs, ♀	dgl, ♀	bcs, ♀	fats, ♀
AAN	0.68	0.68	0.75	0.71	0.66	0.66	0.73	0.68
BAQ	0.61	0.61	0.68	0.63	0.60	0.60	0.66	0.62
BBL	0.76	0.74	0.82	0.78	0.76	0.74	0.80	0.76
BSM	0.53	0.52	0.61	0.56	0.48	0.48	0.57	0.51
CHA	0.65	0.64	0.71	0.67	0.62	0.62	0.69	0.64
HER	0.52	0.51	0.59	0.54	0.48	0.49	0.57	0.51
INR	0.53	0.51	0.60	0.56	0.46	0.46	0.56	0.50
LIM	0.70	0.69	0.76	0.72	0.66	0.66	0.73	0.68
PIE	0.21	0.19	0.28	0.23	0.18	0.18	0.26	0.21

Table 4.14. Statistics for reliabilities breeding values for Carcass conformation score[1] for all beef sires with beef × dairy offspring, by beef sire breed

	Min	5th pct	Median	95th pct	Max	Nr sires
AAN	0.109	0.36	0.82	0.95	0.95	71
BAQ	0.084	0.25	0.73	0.95	0.96	65
BBL	0.201	0.30	0.89	0.95	0.97	91
BSM	0.090	0.25	0.63	0.94	0.96	217
CHA	0.073	0.13	0.80	0.95	0.96	100
HER	0.035	0.15	0.63	0.93	0.94	70
INR	0.506	0.52	0.60	0.69	0.70	5
LIM	0.076	0.44	0.83	0.96	0.97	125
PIE	0.116	0.14	0.35	0.38	0.38	7

[1] Calculated as the mean of reliability for male and female carcass conformation score

Sires with low reliability

Reliability for INRA sires was low despite their large number of offspring, noticeable in Figure 4.5 where INRA sires have lower reliability than sires of other breeds with the similar number of offspring. Relevant for the B×D genetic evaluation in this context is the inclusion of a fixed sire breed effect in the model (Chapter 4.2), and this effect is added back to the EBVs that are calculated (Chapter 5.1). There were few sires of the INRA breed (5 included in the Calving traits evaluation), which resulted in low precision (high SE) of the sire breed effect for INRA and subsequently the EBVs for INRA bulls, and this is reflected in the reliability. A more detailed investigation is summarized with the following points:

- The INRA sire with most offspring in the Calving evaluation had 1938 offspring in 289 herds
- His reliability for CSu2+ was 0.38.
- Assuming the heritability for CSu2+ (1.27%), an optimistic quick-and-dirty reliability (calculated as n/(n+k) was 0.86 (n = 1938) and a conservative reliability was 0.48 (n = 289).
- Reliability of a model without sire breed effect was 0.75.
- Considering that EBVs are calculated as K'b + M'u, both extracting relevant off-diagonals from the MME in DMU as well as a Gibbs sampling approach (keeping variance components fixed) confirmed the cost (i.e. lower precision of EBVs) of estimating the fixed sire breed effect for the INRA breed.

5. Calculation and expression of breeding values

5.1. Breeding Value = fixed sire breed effect + random sire effect

Breeding values of beef sires were calculated as the sum of the fixed breed effect and the random sire effect. The solution of the fixed breed effect needs to be added to ensure that breeding values are comparable across breeds.

The breed effect for daily carcass gain – long fattening period was not estimable for Belgian Blue and INRA, since these two sire breeds have only been used in Denmark and all Danish daily carcass gain records are realized with a short fattening period.

To solve this issue, these two missing breed effects were calculated with a regression model. Here, the estimated breed effects for daily carcass gain – long fattening period was the explanatory variable and the estimated breed effects for daily carcass gain – short fattening period was the outcome variable. The regression coefficients were estimated based on breeds with beef × dairy offspring for both short and long fattening period, and then applied to calculate breed effects for Belgian Blue and INRA.

This approach was motivated by the high genetic correlation between daily carcass gain short and long fattening period (Table 4.7), the high correlation between sire solutions for daily carcass gain short versus long period (Table 5.1 and Table 5.2), and the high R^2 of the regression model (Figure 5.1 and Figure 5.2).

Table 5.1. Correlation between sire solutions for daily carcass gain short and long fattening period, for the male and female daily carcass gain traits

	Male	Female
All beef sires	0.990	0.990
Beef sires > 100 offspring	0.998	0.998

Table 5.2. Correlation between sire solution for daily carcass gain short and long fattening period, for the male and female daily carcass gain traits, by breed and for beef sires with more than 100 offspring

	Male	Female
AAN	0.983	0.980
BSM	0.992	0.986
BAQ	0.993	0.992
CHA	0.986	0.989
HER	0.980	0.996
LIM	0.989	0.989

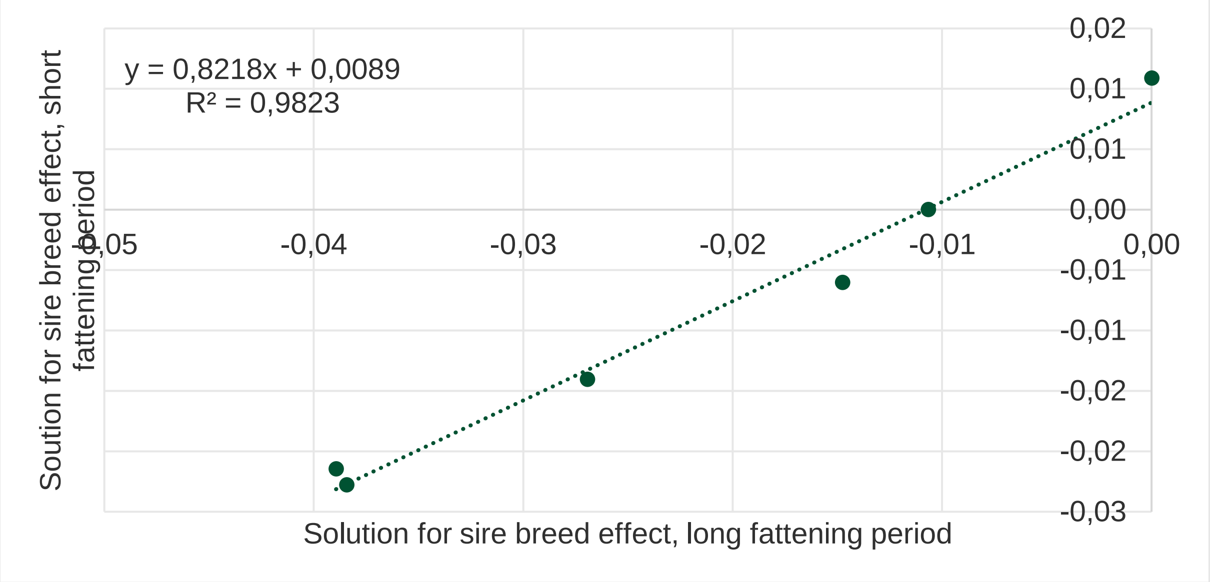

Figure 5.1. Solutions for sire breed short and long fattening period, for female daily carcass gain.

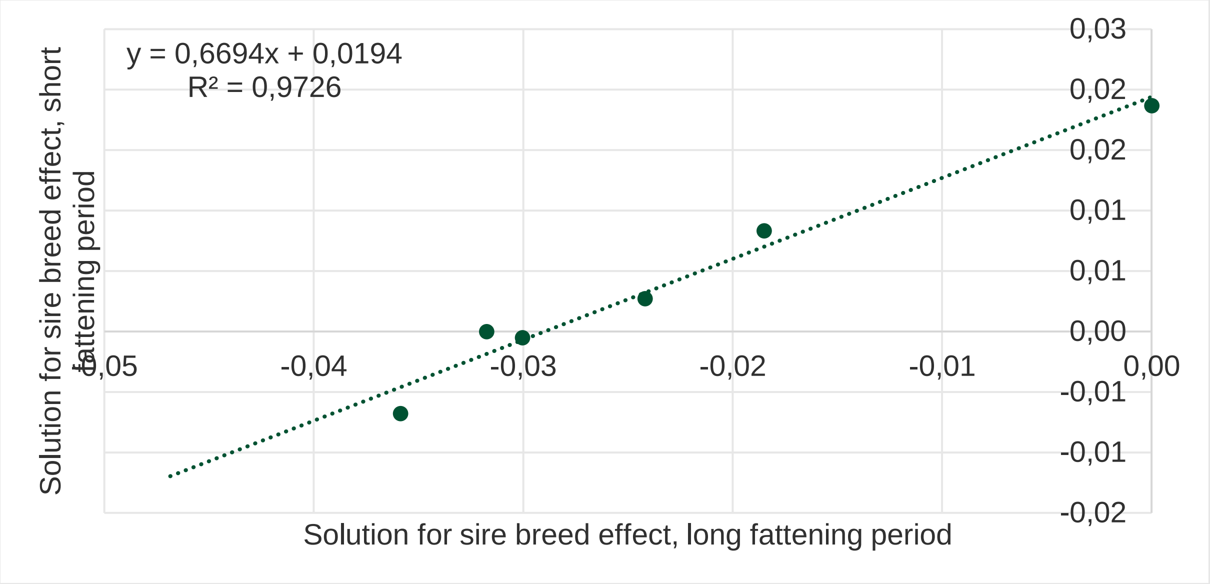

Figure 5.2. Solutions for sire breed effect short and long fattening period, for male daily carcass gain.

The performance of the beef × dairy crossbreds is affected by heterosis. However, a heterosis effect was not included in the model as the data structure (only F1) did not enable separating additive effects from heterosis effects. Thus, the breeding values did include (part of) the heterosis effects. The primary purpose of the Beef × dairy evaluation was to choose beef sires such to get the best possible beef × dairy crossbred offspring, meaning that heterosis will be expressed in the future offspring as well. Hence, not accounting for heterosis has probably limited effect when selecting beef bulls for producing beef × dairy crossbred offspring.

5.2. Standardization

Point of departure in standardization of breeding values was to institute an approach that resembled standardization of breeding values in the NAV Dairy evaluation, as both breeding values are targeted for dairy farmers. That is, relative EBVs were calculated with a mean of 100 and a standard deviation of 10. The crux was to define which exact group of animals should have relative EBVs with the desired mean and standard deviation. One requirement and challenge was to define the base such that relative EBVs remain stable in case no new information is added.

Mean of relative EBVs

An important condition for the definition of the genetic base is that a relative breeding value of 100 reflects the genetic level of actual selection candidates. Hence, the genetic base should be a rolling base, updated at each evaluation. The approach used today in the NAV Dairy evaluations, where cows 3-5 years old at the time of the evaluation have a mean relative breeding values of 100, was not feasible as animal models are used in the NAV Dairy evaluation but the Beef × dairy evaluation employs a sire model. Two options for establishing the base were considered:

1. At the time sire models were used for some traits in the NAV Dairy evaluation, a rolling base was constructed using the pedigree index of cows 3-5 years old. Along these lines, the genetic base in the Beef × dairy evaluation could be defined as the average of the sire EBVs for all beef × dairy crossbreds born within a given time window – e.g. 2-5 years before publication date.
2. The genetic base for the Danish X-index for beef sires used to produce beef × dairy crossbreeds included all beef sires with more than 10 offspring (the idea was to have a rolling but too few bulls fulfill the criteria and so far all beef sires are considered). Along these lines, the genetic

base in the Beef × dairy evaluation could be defined as the average EBV of all beef sires with an official EBV and born within a given time window – e.g. 3-13 years before publication date.

The first option was pursued, as the number of beef sires was relatively small, which would introduce a bit more instability in a genetic base according to option 2. Crossbreds were considered to define the genetic base if born 2-5 years before date of establishment of the base (more specifically: Jul 2013 – Sep 2016). There were approximately 165 thousand (CALV) and 91 thousand (CARC) beef × dairy crossbreds born in that time window.

NB: starting February 2020, the definition of the genetic base (mean) has been changed such to include only offspring of beef sires that can be marketed in all three Nordic countries; i.e. essentially excluding beef × diary offspring with a BBL sire from the base.

Standard deviation of relative EBVs

Important conditions for the setting the standard deviation were that sire EBVs have a clear spread within breed and at the same time avoid too sensitive EBVs (very extreme EBVs or large changes when small amount of data is added). While the genetic base for the mean of relative EBVs is rolling, the standard deviation of the relative EBVs should remain constant from one evaluation to the next, to ease interpretation of the EBVs.

Three options were considered:

1. Across-breeds average of within-breed SD for sires meeting certain criteria (birth years and reliability/number of offspring).
2. Across-breed SD for sires meeting certain criteria (birth years and reliability/number of offspring).
3. Define, using the genetic SD used in the genetic evaluation, the base such that a SD of 10 is equivalent to reliability of, say, 80%.

Options 1 and 2 would be based on actual breeding values for a group of beef sires that meet certain criteria. Such criteria are preferably strict to ensure that changes in the standardization of EBVs are small in the event of a future revision of the evaluation. On the other hand, strict criteria mean that fewer beef sires meet the criteria, and the small number of individuals in the group implies more instability, especially in the case of beef × dairy where relatively few sires have been used so far. An additional disadvantage with option 2 is that it is influenced by the number of bulls per breed, which might create additional instability in the event of a future revision of the evaluation.

The challenge with option 3 might be that the EBV to be published are a weighted combination of several traits (e.g. like for daily carcass gain with 4 traits), and the genetic SD is not straightforward to calculate for the combined index.

Alternative 1 to 3 might, if constructed carefully, end up with about the same results.

Options 1 and 2 differ in how they depend on between-breed differences, and the effect of between-breed differences varied greatly between traits (Table 5.3). Breed differences were especially large for carcass conformation score, as indicated by the large ratio in Table 5.3. The numbers in (Table 5.3) were based on some 170 beef sires from the Charolais, Limousin and Simmental breed, born 1995-2004 and with a reliability more than 50% (reliability approximated as n/(n+k), with n being the number of beef × dairy crossbreds and k being the sire variance ratio).

Table 5.3. (Ratio of) across-breed and pooled with-in breed standard deviations of breeding values[1]

	Across-breed SD	Pooled within-breed SD	Ratio
Daily carcass gain	1.09	0.77	1.41
Carcass conformation score	1.22	0.71	1.72
Carcass fat score	0.78	0.72	1.08

[1] Breeding values were expressed in units σ_s, i.e. breeding values on the original scale (same scale as phenotypes) were divided by the sire standard deviation

The distribution of breeding values for daily gain (expressed in units σ_s) for beef sires with crossbred offspring for three breeds in Figure F.1 illustrates the extent of breed differences for the calf survival – primiparous cows. For calving traits, the difference between the most extreme (and sufficiently large) breeds was 1.3 units σ_s for calf survival, primiparous cows (BBL vs HER; Figure F.1), 1.2 units σ_s for calf survival, multiparous cows (BBL vs HER; Figure F.2), 2.2 units σ_s for calving, primiparous cows (BBL vs AAN; Figure F.3) and 2.2 units σ_s for calving, multiparous cows (AAN vs BAQ; Figure F.4).

The distribution of breeding values for daily carcass gain (expressed in units σ_s) for beef sires with crossbred offspring for three breeds in Figure F.5 illustrates the extent of breed differences for the daily gain index. The peaks for Hereford and Charolais were two and a half units σ_s apart. The difference between the most extreme (and sufficiently large) breeds was just over 5 units σ_s for carcass conformation (BBL vs HER; Figure F.6) and around 5.9 units σ_s for carcass fat (BBL vs HER; Figure F.7).

Adopting option 1 or 3 for standard deviation, and considering the most extreme case, i.e. where bulls with a 100% reliability have a standard deviation of 10, would results in a difference of 25 index points between the mean EBV for Hereford and Charolais for daily carcass gain. Standardizing the breeding values such that bulls with a 80% reliability have a standard deviation of 10 would result in a difference of 28 index points (the sire standard deviation on the standardized scale is $10/\sqrt{0.80} = 11.18$, and multiplying this by 2.5 gives 27.9).

Option 3 was in the end chosen for standardizing breeding values, and such that bulls with a 100% reliability would have a standard deviation of 10. The reason for 100% reliability as reference point was that spread of breeding values for some traits (c.f. carcass conformation score and carcass fat score) would become extreme large if a lower value (e.g. 80%) be chosen. The reason for favoring option 3 over 1 was the relative instability of option 1 because of the low number of bulls that would have a very high reliability (close to 100%).

Statistics for relative breeding values

There is a negative genetic correlation between calving and carcass traits (e.g. Eriksson *et al.*, 2004). Comparing breeds, this was also observed where breeds good for carcass traits generally were not as good for calving traits (Table 5.4 – Table 5.10). It was apparent that lighter breeds, such as AAN, had higher average breeding values for Calf survival and Calving ease, compared to the heavier breeds, such as BBL. There was also a large variation within breed for the calving traits, for example illustrated by the difference between the 5th and 95th percentile of breeding values that on average was about 20 for Calf survival and just below 25 for Calving ease.

For carcass traits the opposite of the calving traits is apparent, where heavier breeds, such as CHA and BBL, on average have higher breeding values compared to lighter breeds (Table 5.8 – Table 5.10). Breed differences were much larger for carcass traits than for calving traits. There was large variation within all sire breeds for carcass traits; the difference between the 5th and 95th percentile was about 28 for Daily carcass gain and Carcass fat score, and about 30 for Carcass conformation score.

Table 5.4. Statistics for relative EBVs for Calf survival, primiparous cows, for beef sires with higher than 50% reliability for Calf survival, multiparous cows

	Min	5th pct	Median	95th pct	Max	N
AAN	85	96	106	116	117	36
BAQ	94	99	106	111	121	29
BBL	75	80	94	107	109	63
BSM	78	85	103	108	111	46
CHA	81	85	102	113	116	47
HER	88	92	106	112	117	27
LIM	82	90	101	112	114	66

Table 5.5. Statistics for relative EBVs for Calf survival, multiparous cows, for beef sires with higher than 50% reliability for Calf survival, multiparous cows

	Min	5th pct	Median	95th pct	Max	N
AAN	80	93	103	112	114	36
BAQ	89	95	104	109	118	29
BBL	76	81	96	109	111	63
BSM	77	87	102	110	114	46
CHA	72	83	100	113	114	47
HER	84	93	107	112	115	27
LIM	81	92	102	113	118	66

Table 5.6. Statistics for relative EBVs for Calving ease, primiparous cows, for beef sires with higher than 50% reliability for Calf survival, multiparous cows

	Min	5th pct	Median	95th pct	Max	N
AAN	94	103	116	122	124	36
BAQ	88	90	103	114	121	29
BBL	74	79	94	109	118	63
BSM	70	80	97	109	111	46
CHA	78	86	102	114	117	47
HER	101	102	108	115	121	27
LIM	74	82	99	110	114	66

Table 5.7. Statistics for relative EBVs for Calving ease, multiparous cows, for beef sires with higher than 50% reliability for Calf survival, multiparous cows

	Min	5th pct	Median	95th pct	Max	N
AAN	95	105	117	123	125	36
BAQ	85	88	101	110	118	29
BBL	75	80	98	112	120	63
BSM	69	80	97	108	109	46
CHA	70	81	95	107	110	47
HER	100	101	106	113	119	27
LIM	76	84	101	111	116	66

Table 5.8. Statistics for relative EBVs for Daily carcass gain for beef sires with higher than 50% reliability for Carcass conformation score

	Min	5th pct	Median	95th pct	Max	N
AAN	67	73	90	103	111	65
BAQ	76	82	102	111	115	49
BBL	84	95	108	123	129	85
BSM	78	92	105	118	122	142
CHA	88	97	112	125	139	80
HER	67	75	86	102	103	41
INR	70	72	84	99	103	5
LIM	75	79	94	110	113	112

Table 5.9. Statistics for relative EBVs for Carcass conformation score for beef sires with higher than 50% reliability for Carcass conformation score

	Min	5th pct	Median	95th pct	Max	N
AAN	52	60	70	81	83	65
BAQ	78	80	94	118	126	49
BBL	100	103	121	144	160	85
BSM	50	64	78	90	97	142
CHA	68	78	90	111	127	80
HER	55	58	67	79	83	41
INR	71	80	119	125	126	5
LIM	82	88	98	110	117	112

Table 5.10. Statistics for relative EBVs for Carcass fat score for beef sires with higher than 50% reliability for Carcass conformation score

	Min	5th pct	Median	95th pct	Max	N
AAN	116	122	137	154	169	65
BAQ	68	72	83	98	99	49
BBL	64	67	82	92	108	85
BSM	82	87	103	117	137	142
CHA	87	91	105	119	133	80
HER	127	129	141	155	161	41
INR	84	84	106	114	116	5
LIM	91	96	108	119	125	112

5.3. Publication of breeding values

Calving traits

The calving evaluation results in six breeding values per beef sire (Table 5.11). Calf size data is only available from Denmark and is included as indictor trait in the evaluation. All four remaining breeding values are published for beef sires that meet the publication criterion. Criteria to publish breeding values for a beef sire was that the its reliability for Calf survival – multiparous cows should exceed 50%, or that the bull had more than 500 offspring for Calf survival – multiparous cows.

Motivation for choosing Calf survival – multiparous cows as reference for publication criterion was that this trait is recorded in all countries, and that most beef × dairy crossbreds are borne by multiparous cows. Recording of calf survival is mandatory in EU countries, whereas recording of calving ease is voluntarily and not as widespread in Finland compared to the other two countries.

The genetic correlation between traits expressed by primiparous versus multiparous cows was only 0.6-0.7 (Table 4.4), which motivated publication of breeding values for primiparous traits.

Inclusion of a fixed effect of sire breed in the model had as consequence that (exact) reliabilities were low for some beef sires belonging to sire breeds with few sires, notably the INRA breed. Only very few sires from that breed had a reliability larger than 50%, despite larger amounts of offspring, and was the reason for the additional limit that breeding values could be published for sires that had been used a lot (i.e. more than 500 beef × dairy offspring for Calf survival – multiparous cows).

NB: starting November 2019, the publication criteria have been relaxed for calving traits, such that breeding values are also published when the reliability for Calving ease – multiparous cows exceeds 50%.

Carcass traits

The carcass evaluation results in eight breeding values per beef sire (Table 5.11). Because of the high genetic correlation between traits expressed in males versus females (Table 4.7), the breeding values are combined as a simple average (Table 5.11). Similarly, growth in short and long fattening period were genetically highly correlated, and breeding values for those traits were also combined as a simple average (Table 5.11).

Publication criterion for breeding values for carcass traits was like that for calving traits: the limit for publication was reliability of 50% for the breeding value for carcass conformation score, or at least 500 beef × dairy offspring for that trait.

Table 5.11. Calculated and published breeding values for calving and carcass traits

Trait group	Calculated EBVs	Published EBV
Calving	Calf survival, primiparous cows	Calf survival, primiparous cows
	Calf survival, multiparous cows	Calf survival, multiparous cows
	Calving ease, primiparous cows	Calving ease, primiparous cows
	Calving ease, multiparous cows	Calving ease, multiparous cows
	Calf size, primiparous cows	
	Calf size, multiparous cows	
Carcass	Daily carcass gain, bulls, short fattening period	Combined daily carcass gain [1]
	Daily carcass gain, bulls, long fattening period	
	Daily carcass gain, heifers, short fattening period	
	Daily carcass gain, heifers, long fattening period	
	Carcass conformation score, bulls	Combined carcass conformation score [2]
	Carcass conformation score, heifers	
	Carcass fat score, bulls	Combined carcass fat score [2]
	Carcass fat score, heifers	

[1] All four ingoing breeding values are weighted equally, i.e. with 25%

[2] Both ingoing breeding values are weighted equally, i.e. with 50%

5.4. Validation of breeding values

Size of the data and nature of the population and model limited the opportunities for validation and common approaches for validation (Interbull Methods I-IV) were not applicable. During the development of the Beef × dairy evaluation, consistency of the breeding values was assessed in several different ways:

- Consistency of EBVs from part-whole analyses. For example, by comparing EBVs from an analysis with only HOL dams and EBVs from an analysis with dams from all three dairy breeds.
- Consistency of EBVs from analyses with different (mutually exclusive) data sets. For example, by comparing EBVs from an analysis with only HOL dams and EBVs from an analysis with only RDC dams.
- Comparison of EBVs with simple phenotypic means of beef × dairy offspring per sire.
- Comparison of EBVs with national results (X-index in Denmark and SAP in Sweden).

5.4.1. Comparison with phenotypic means

The correlation between EBVs and phenotypic means (calculated per sire) is expected to be high if a sire model is used, which becomes evident from the breeding values into the information sources. A sire’s breeding values is a weighted combination of information on ancestors and progeny, where the latter receives most weight for the sizes of progeny groups in the Beef × dairy evaluation. The offspring contribution is the (weighted) combination of phenotypes adjusted for environmental (fixed) effects. The variation explained by environmental effects is higher for carcass traits than for calving traits (Chapter 6.1). The effect of adjustment for environmental effects on correlations between EBVs and sire phenotypic means is limited, since the data structure is not extremely unbalanced.

Specifying a “tolerance” value below which a correlation between EBVs and sire phenotypic mean would be considered worrying is difficult. It is though expected that the correlation increases with progeny group size, and this pattern is sought for when calculating the correlation for beef sires classified by progeny group size (e.g., Table H.1).

Result of comparison of EBVs with phenotypic means are in Appendix H, Appendix I, and Appendix K.

5.4.2. Comparison of EBVs from different analyses

In judging the correlation between EBVs for the same trait but from two different analyses two different cases can occur: there is overlap in the records, or there is no overlap in records used for both analyses. When there is no overlap in records included in the genetic evaluation, the correlation between EBVs is influenced by the reliability of the EBVs: the lower the reliability, the lower the EBVs. Specifically, the correlation is reduced by the factor (Blanchard *et al.*, 1983):

$$\frac{\sum REL_i \, REL'_i}{\sqrt{(\sum REL_i)(\sum REL'_i)}}$$

Where REL_i and REL'_i are the reliabilities of animal *i* for EBV1 and EBV2. This factor ranges between 0 and 1 (Figure 5.3).

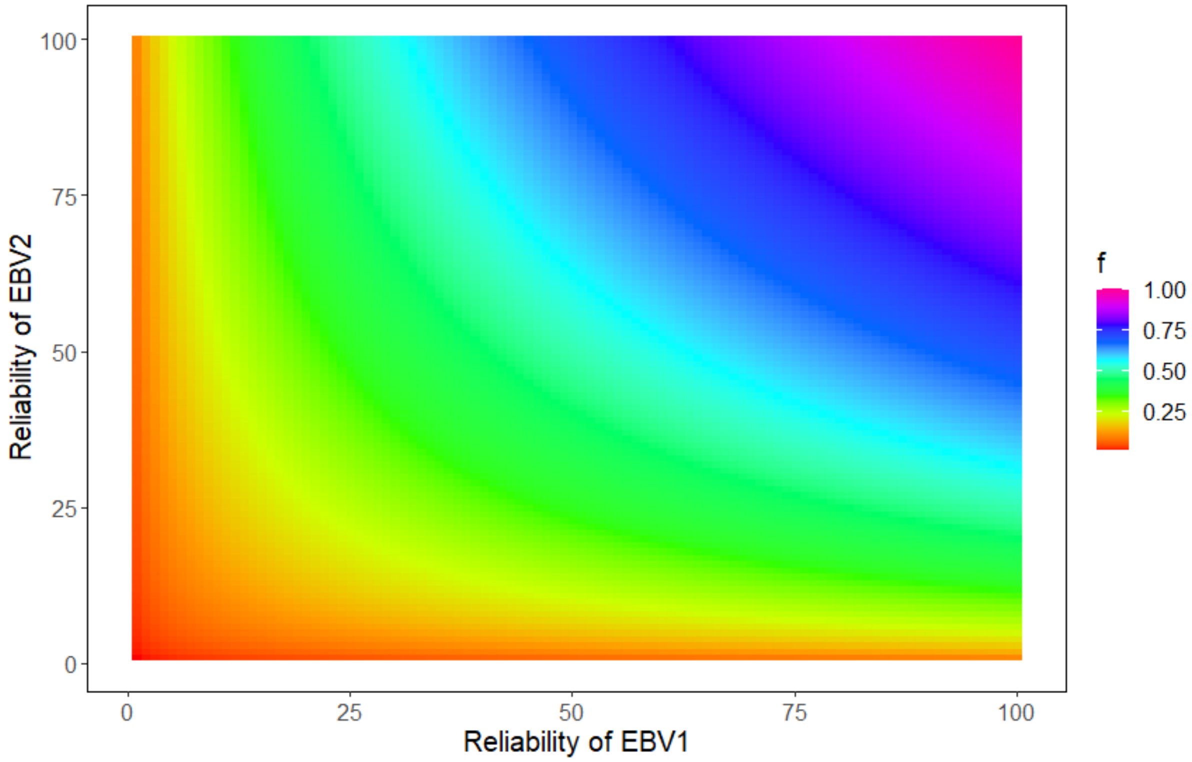

Figure 5.3. Reduction of correlation between two EBVs (EBV1 and EBV2) as a function of their reliabilities; data used to estimate EBV1 and EBV2 are assumed to be non-overlapping.

When there is overlap in data used to estimate both sets of EBVs, the correlation between EBVs is also influenced by the reliability of EBVs, but in a different way: the more different the reliability of both EBVs, the lower the correlation. Specifically, the correlation is calculated as (Reverter *et al.*, 1993):

$$\sqrt{\frac{\sum REL_i}{\sum REL'_i}}$$

When EBV1 and EBV2 are based on nearly the same data then the correlation is high, and when the EBV2 is based on much more data than EBV1 then the correlation gets lower (Figure 5.4).

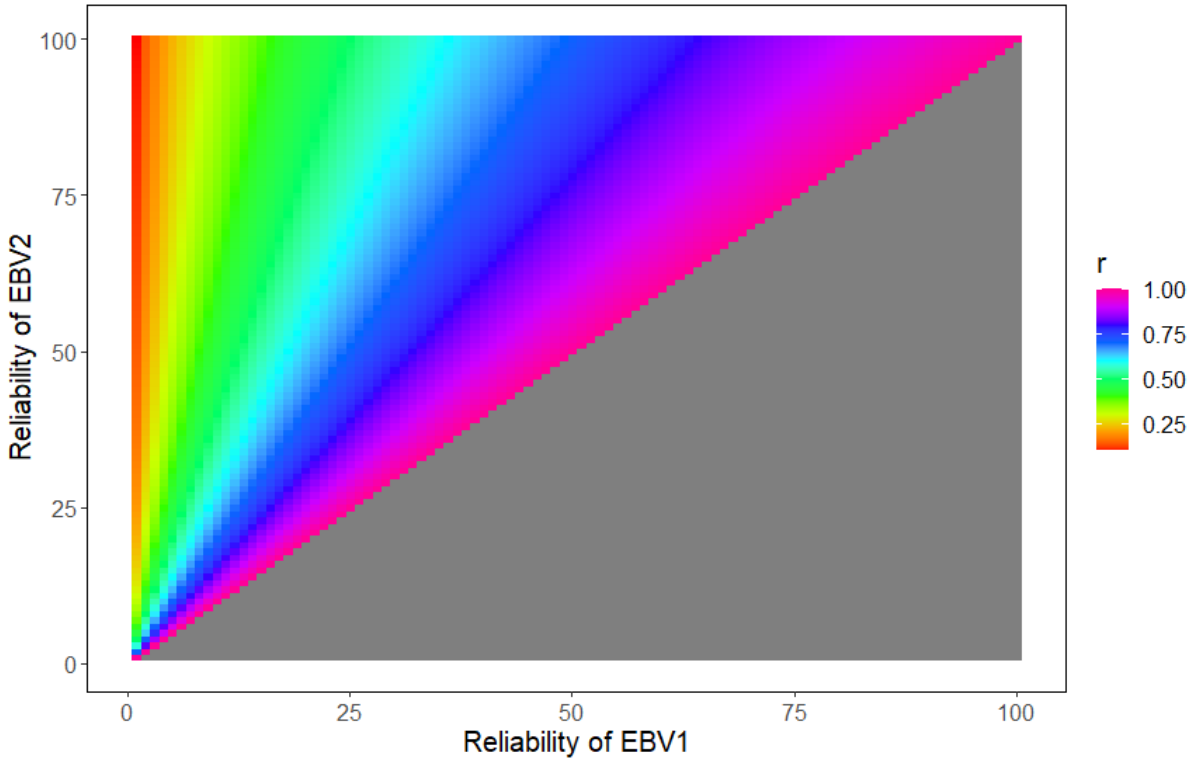

Figure 5.4. Expected correlation between two EBVs based on partly the same data.

Results of comparison of EBVs are in Appendix H and Appendix J.

5.4.3. Comparison with national evaluations

Danish X-index

The B×D EBVs were calculated with a more complex model than the X-index. This resulted in some re-ranking of the breeds. The sires included in the two different evaluations also varied. All sire breeds and sires were included in the Beef × dairy genetic evaluation, the only requirement was that the sires had been used in at least 10 milk-producing herds. Table 5.12 shows the number of sires in each evaluation is shown. Four of the sires that had an X-index did not receive an EBV from the Beef × dairy genetic evaluation. The reasons why these four sires only had an X-index was investigated and summarized in Table 5.13.

Table 5.12. The number of beef sires included in the different evaluations

	N
X-index	167
B×D evaluation (only DNK sires)	312
Both indexes	164
Only X-index	4
Only B×D evaluation	148

Table 5.13. The four 4 sires that only received an X-index, and the reason they did not receive EBVs from the Beef × dairy evaluation

Herdbook number	Breed	Name	Reason for deletion in the B×D evaluation
75784	LIM	ECHO	Harder editing
75665	LIM	DALHIA	Many beef cross dams

50665	SIM	BFG Resolut	Fleckvieh sire – should be deleted
78331	BBL	Indice	Not used in >10 herds

In calculation of the Danish X-index, phenotypes of calves born by crossbred dams were also included. The crossbred dams could be dairy cross, beef × dairy cross or dams with unknown sires. Calves born by crossbred dams were not included in the Beef × dairy genetic evaluation. Another difference was that breeding values from the X-index were calculated with correlated information from purebred calves. To see how much information sires in the X-index receive from crossbred dams and purebred offspring, the offspring in the evaluation for LIM and CHA sires was investigated.

From Table 5.14 it is apparent that on average the beef sires have more beef × dairy calves then purebred calves. For LIM sires, approx. 40 % of the total number of calves were purebred, whilst only approx. 35 % of the CHA offspring were purebred. This means that the X-index breeding values of the LIM sires were slightly more affected by correlated information from the purebred calves than for the CHA sires.

Table 5.14. Number of sires, purebred beef calves, beef × dairy crossbred calves and the proportion of beef × dairy crossbred calves for LIM and CHA sires in the Danish X-index evaluation

Sire breed	Nr sires	Nr purebred beef calves	Nr B×D calves	Proportion B×D calves
LIM	55	35,432	55,675	61%
CHA	11	5,754	11,017	66%

Especially calves with LIM sires had a large percentage of the dams are crossbred, nearly 50 % (Table 5.15). For calves with CHA sires, only approx. 40 % had a crossbred dam. Another difference was that a very large percentage of the crossbred dams of calves from LIM sires had an unknown beef sire. This can have quite a large influence on the breeding values, as calves from crossbred dams, especially dams with a large proportion of beef breeds, perform quite differently compared to calves from purebred dairy dams. As offspring from crossbred dams were excluded from the B×D genetic evaluation, only 50 % for LIM and 60 % for CHA of the calves were the same in the two evaluations. Therefore, it was expected that the breeding values from the two evaluations will not align completely, and especially for LIM a larger deviation was be expected.

Table 5.15. Percent calves from dairy crossbred dams, other crossbred dams, and total % calves from crossbred dams and purebred dairy dams in the Danish X-index evaluation

Sire breed	% dairy crossbred dam	% other crossbred dam	% total crossbred dams	% purebred dairy dams
LIM	5%	43%	47%	53 %
CHA	12%	25%	37%	63 %

Calf survival

For calf survival, there was some re-ranking of breeds, comparing the Danish X-index and the B×D EBVs (Table 5.16). Most notably, AAN went from the bottom to the top, but as there were very few sires, the EBVs had low unreliability. Another large change was for BAQ: according to the Danish X-index they were the best breed, but according to the B×D EBVs they ranked fourth. Looking at the phenotypic mean for BAQ in the Beef × dairy genetic evaluation, they were the best breed after AAN, and the model adjusted for some underlying trends that were not reflected in the phenotypic mean.

Table 5.16. Breed differences and ranking of the beef sire breeds for breeding values for Calf survival from the Danish X-index and the Beef × dairy genetic evaluation, the phenotypic mean from the Beef × dairy genetic evaluation

		Calf survival X-index		Calf survival B×D EBV		Calf survival B×D mean	
	N Sires	Deviation from mean	Rank	Deviation from mean	Rank	Deviation from mean	Rank
BSM	28	-0.59	5	-0.0012	6	-0.13%	5
AAN	7	-0.78	6	0.0028	1	1.25%	1
BAQ	10	1.05	1	-0.0001	4	0.59%	2
CHA	12	0.49	2	0.0013	2	0.41%	4
LIM	30	0.40	3	-0.0001	5	0.42%	3
BBL	77	-0.08	4	0.0000	3	-0.37%	6

For calf survival, the correlation to the B×D EBVs for all sires was 0.60 for the weighted X-index. In Table 5.17 correlations between then X-index and the B×D breeding values and phenotypic means are shown. The correlations for the small breeds (AAN, BAQ and CHA) were very low, but for the larger breeds, correlations were moderate.

Table 5.17. Correlations between the Danish X-index and the B×D breeding values and phenotypic mean for Calf survival, by sire breed

Sire breed	N sires	B×D EBV	B×D mean
BSM	28	0.75	0.69
AAN	7	0.17	0.77
BAQ	10	0.16	0.37
CHA	12	0.13	0.07
LIM	30	0.58	0.69
BBL	77	0.77	0.79

Calving ease

For calving ease, there was also some re-ranking: BSM went from the top to the bottom of the list, despite having a lot of sires (Table 5.18). For calving ease, the correlation between the B×D EBVs and the Danish X-index was 0.58. In general, the correlations between the two indexes were higher compared to calf survival, also for the smaller breeds (Table 5.19).

Table 5.18. Breed differences and ranking of the beef sire breeds for breeding values for calving ease from the Danish X-index and the B×D genetic evaluation, the phenotypic mean from the B×D genetic evaluation

	N Sires	Calving ease X-index		Calving ease B×D EBV		Calving ease B×D mean	
		Deviation from mean	Rank	Deviation from mean	Rank	Deviation from mean	Rank
BSM	28	0.092	1	-0.04255	6	-0.08872	6

AAN	7	-0.015	3	0.10861	1	0.14822	1
BAQ	10	-0.051	6	0.00818	3	0.01718	2
CHA	12	-0.025	5	-0.03238	5	0.01159	4
LIM	30	-0.009	2	0.01836	2	0.01558	3
BBL	77	-0.018	4	0.00243	4	0.00867	5

Table 5.19. Correlations between the Danish X-index and the B×D breeding values and phenotypic mean for calving ease, by sire breed

Sire breed	N sires	B×D EBV	B×D mean
BSM	28	0.80	0.86
AAN	7	0.12	0.38
BAQ	10	0.77	0.80
CHA	12	0.03	0.63
LIM	30	0.70	0.75
BBL	77	0.55	0.88

Conclusion

There are some inconsistencies between the X-index and the B×D breeding values both for calf survival and calving ease. The ranking within breed seemed to be consistent for the large breeds, but the ranking of breeds differed.

Carcass traits

Correlations between Danish X-index and the B×D breeding values for carcass traits were generally strong, but somewhat lower for Limousin (Table 5.20). Using only Danish data in the Beef × dairy genetic evaluation, correlations among breeding values went up especially for Limousin, but the correlations were still not at the same level as for the other beef sire breeds (Table 5.21). The number of bulls per sire breed with both a Danish X-index and a B×D breeding value for carcass traits based on more than 100 beef × dairy offspring was low (Table 5.20). Excluding two Limousin outliers, the correlation between the Danish X-index and the B×D breeding values increase considerably (Table 5.22). One of these two LIM sires had considerably more offspring included in the Beef × dairy genetic evaluation (compared to the Danish X-index; probably due to offspring from Finland or Sweden), and the other LIM sire had considerably less offspring in the Beef × dairy genetic evaluation (due to different data edits).

Table 5.20. Correlation between Danish X-index and the B×D breeding values for some carcass traits, by sire breed and for sires with more than 100 beef × dairy offspring in the Beef × dairy genetic evaluation

	dgs, ♂	dgl, ♀	bcs, ♂	bcs, ♀
BBL (n=53)	0.89	0.85	0.96	0.95
BSM (n=6)	0.83	0.86	0.95	0.92
LIM (n=19)	0.64	0.71	0.63	0.64
BAQ (n=3)	0.98	0.70	0.97	0.95
CHA (n=3)	0.98	0.99	0.90	0.99

Table 5.21. Correlation between Danish X-index and the B×D breeding values for some carcass traits, by sire breed and for sires with more than 100 beef × dairy offspring in the Beef × dairy genetic evaluation and using only Danish data in the B×D genetic evaluation

	dgs, ♂	dgl, ♀	bcs, ♂	bcs, ♀
BBL	0.89	0.85	0.96	0.95
BSM	0.84	0.87	0.97	0.97
LIM	0.69	0.75	0.66	0.67
BAQ	0.96	0.84	0.97	0.94
CHA	0.98	0.99	0.98	1.00

Table 5.22. Correlation between Danish X-index and with B×D Daily gain index, by sire breed and for different selection of bulls

	All bulls	Minus 2 LIM outliers	$rel_{dgl} > 0.50$	$rel_{dgl} > 0.50$ Minus 2 LIM outliers
BBL	0.83	0.83	0.85	0.86
BSM	0.66	0.66	0.68	0.68
LIM	0.68	0.78	0.66	0.76
BAQ	0.47	0.47	0.70	0.70
CHA	0.78	0.78	0.78	0.78

Swedish SAP (seminavelsprogrammet) breeding values

In Sweden, beef sires have had breeding values for calving traits for a long time through SAP (seminavelsprogrammet). The SAP breeding values were based on more data than the B×D breeding values.

The correlation between SAP and B×D breeding values were generally high (Table 5.23), somewhat lower for calving ease than for calf survival. The magnitude of deviation of the correlations from one has two reasons: selection of data and method for genetic evaluation. For the B×D genetic evaluation, records from milk producing herds, made since 2000 and for B×D crossbred calves with a purebred dairy dam (see Chapter 3.2). SAP breeding values, on the other hand, were based on data from a longer period and included offspring from crossbred dams. The other difference was the methodology, where SAP breeding values have been calculated with a selection index approach (BLP) and the B×D breeding values with BLUP. An important advantage of applying BLUP is better within-herd comparisons of beef × dairy crossbred calves with sires from different breeds.

Table 5.23. Correlation between Swedish SAP breeding values and B×D breeding values for four calving traits, by beef sire breed; SAP breeding values from a special evaluation including B×D offspring from dairy cows only

Breed	N	CSu1	CSu2+	CE1	CE2+
Simmental	45	0.42	0.44	0.63	0.79
Highland	4	0.89	0.73	0.88	0.98
Angus	18	0.57	0.55	0.61	0.64
Hereford	33	0.31	0.46	0.65	0.73
Blonde d’Aq	6	0.41	0.48	0.73	0.80
Charolais	45	0.48	0.68	0.66	0.71

Limousin	25	0.63	0.65	0.75	0.64

5.4.4. Stability when adding new data

In order to investigate the stability of breeding values after adding new data, an evaluation was run based on data extracted from national databases around June-August 2018. This means that roughly one year of data was added compared to Table 3.1. Data, analysis and EBVs relating to the data in Table 5.24 will be referred to as “current evaluation”, and data, analysis and EBVs relating to the data in Table 3.1 as “previous evaluation”.

Table 5.24. Data used to test stability of EBVs from the Beef × dairy evaluation

	Calving traits	Carcass traits
Denmark	June 2018	June 2019
Finland	July 2018	June 2018
Sweden	August 2018	July 2018

Calving traits

Updating the data yielded records for 80 thousand additional beef × dairy crossbreds, an increase of about 16% (Table 5.25). Finland was the country with most new records. Breed-wise, the increase was largest for Blonde d’Aquitaine (mostly from Finland), followed by Belgian Blue and Limousin (Table 5.26). Pattern of use of beef sires appeared to have been somewhat unsystematic, in that distribution of number of records by birth year of sires is wavering (Figure 5.5). Also, more recently born beef sires were expected to have more new offspring with adding data or more recent calvings, and the peak around 1999 was unexpected.

Table 5.25. Number of beef × dairy calves in current and previous evaluation by country

	Nr calves previous	Nr calves current	Difference	% increase
Denmark	166,377	188,208	21,831	13.1 %
Finland	217,597	261,373	43,776	20.1 %
Sweden	107,870	122,805	14,935	13.8 %
ALL	*491,844*	*572,386*	*80,542*	*16.4 %*

Table 5.26. Number of beef × dairy offspring in current and previous evaluation by beef sire breed for the seven largest breeds

	Nr calves previous	Nr calves current	Difference	% increase
AAN	50,601	58,375	7,774	15.4 %
BAQ	52,661	77,818	25,157	47.8 %
BBL	117,465	135,841	18,376	15.6 %
BSM	61,795	67,013	5,218	8.4 %
CHA	57,990	62,691	4,701	8.1 %
HER	30,366	33,709	3,343	11.0 %
LIM	117,257	132,823	15,566	13.3 %

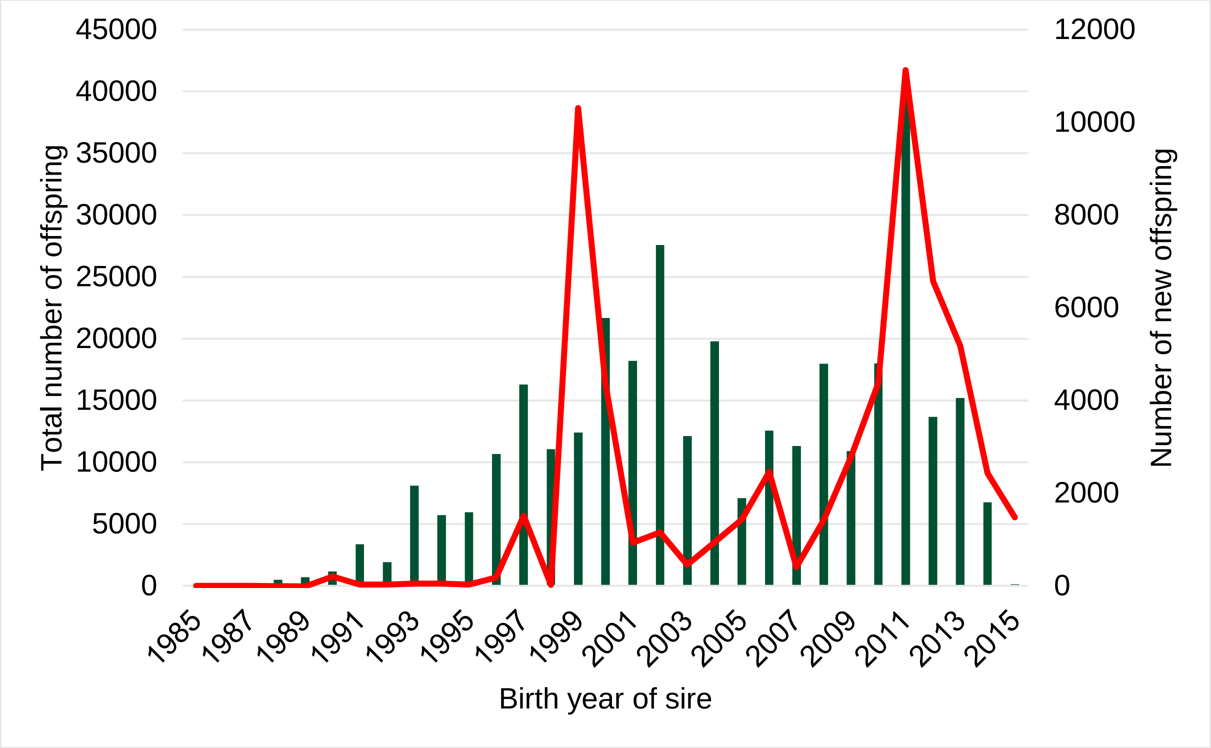

Figure 5.5. Number of beef × dairy offspring in previous evaluation (green bars, left y-axis) and number of new offspring in current evaluation (red line, right y-axis) by birth year of beef sire for calving traits.

An increase of number of sires for the most common breeds was observed with the update of the data (Table 5.27). The update of the data was accommodated by an update of the pedigree file. Both the additional data on beef × dairy crossbreds and the updated pedigree resulted in drastically increased genetic links between countries (Table 5.27).

Table 5.27. Number of sires per beef sire breed in previous and current evaluation; all sires and sires with 100 or more beef × dairy offspring

	All sires			**Sires with ≥ 100 offspring**		
	Previous	**Current**	**New sires**	**Previous**	**Current**	**New sires**
AAN	71	79	8	49	55	6
BAQ	60	68	8	41	49	8
BBL	94	101	7	86	90	4
BSH	2	2	0	1	1	0
BSM	214	222	8	108	112	4
CHA	103	109	6	73	74	1
GLW	1	1	0	0		0
HER	72	76	4	42	44	2
HLA	11	11	0	0		0
INR	5	5	0	5	5	0
LIM	126	136	10	90	97	7
PIE	7	7	0	1	1	0
SAL	1	1	0	0		0
WAG	1	1	0	0	1	1
Total	*768*	*819*	*51*	*496*	*529*	*33*

Table 5.28. Number of beef sires in pairs of countries in previous and current evaluation, by beef sire breeds

	Denmark - Finland			Denmark - Sweden			Finland - Sweden		
	Previous	**Current**	**New**	**Previous**	**Current**	**New**	**Previous**	**Current**	**New**
AAN	2	3	1	0	2	2	0	4	4
BAQ	5	9	4	2	2	0	0	6	6
BSM	2	3	1	0	8	8	0	5	5
CHA	4	4	0				0	1	1
HER				0	1	1			
HLA	1	1	0						
LIM	2	2	2	0	9	9	0	5	5
PIE	1	1	0						
Total	*17*	*23*	*6*	*2*	*22*	*20*	*0*	*21*	*21*

Correlations between breeding values were higher for the later parity traits than for the first parity traits, and higher for Calving ease than for Calf survival (Table 5.29). Lower correlations for first parity traits were expected as the amount of data for the first parity traits was rather limited and larger changes can therefore be seen when more data is added.

Correlations were higher for a subset of beef sires with more than 100 beef × dairy offspring in the previous evaluation. Split per breed (Table 5.30), it was observed that correlations were highest for BBL and lowest for HER, however, differences between breeds were small. As expected, the lower the number of offspring underlying the previous breeding value and the higher the number of additional offspring, the lower was the correlation between current and previous breeding values (Table 5.31).

Table 5.29. Correlation between current and previous breeding values from the calving evaluation by number of beef × dairy offspring in the previous evaluation

	All sires	Sires with ≥ 100 offspring
CSu1	0.92	0.94
CSu2+	0.93	0.96
CE1	0.96	0.97
CE2+	0.97	0.98
CSi1	0.94	0.95
CSi2+	0.99	0.98

Table 5.30. Correlation between current and previous breeding values from the calving evaluation by sire breed and number of beef × dairy offspring in the previous evaluation

	Sires	CSu1	CSu2+	CE1	CE2+	CSi1	CSi2+
AAN	All sires	0.93	0.94	0.92	0.91	0.92	0.90
	>100 offspring	0.95	0.95	0.94	0.94	0.95	0.93
BAQ	All sires	0.90	0.87	0.95	0.95	0.95	0.94
	>100 offspring	0.88	0.82	0.96	0.96	0.95	0.95
BBL	All sires	0.98	0.97	0.99	0.99	0.98	0.98

	>100 offspring	0.98	0.98	0.99	0.99	0.99	0.99
BSM	All sires	0.95	0.95	0.96	0.96	0.96	0.96
	>100 offspring	0.97	0.97	0.97	0.97	0.98	0.97
CHA	All sires	0.95	0.95	0.96	0.96	0.96	0.96
	>100 offspring	0.95	0.95	0.97	0.97	0.96	0.97
HER	All sires	0.91	0.92	0.91	0.91	0.92	0.91
	>100 offspring	0.93	0.94	0.92	0.92	0.92	0.92
LIM	All sires	0.95	0.94	0.96	0.96	0.96	0.95
	>100 offspring	0.97	0.96	0.97	0.97	0.98	0.97

Table 5.31. Correlation between current and previous breeding values from the calving evaluation by number of beef × dairy offspring in the previous evaluation and the number of additional offspring in the current evaluation

Nr offspring previous	Addition offspring current	Nr sires	CSu1	CSu2+	CE1	CE2+	CSi1	CSi2+
> 100	> 100	79	0.87	0.87	0.95	0.97	0.95	0.98
< 100		6	0.53	0.60	0.64	0.68	0.50	0.93
> 100	< 100	287	0.94	0.97	0.97	0.98	0.95	0.98
< 100		125	0.90	0.79	0.94	0.94	0.90	0.98
> 100	< 10	280	0.95	0.98	0.97	0.98	0.96	0.99
< 100		265	0.90	0.93	0.95	0.96	0.93	0.99
> 100	0	41	0.95	0.98	0.98	0.98	0.96	0.99
< 100		101	0.91	0.98	0.96	0.97	0.96	0.99

In conclusion, with correlations of >0,9 for all traits and all sire breeds it seems that the EBVs were stable when a large amount of additional information was added to the evaluation. A substantial number of new sires were added and surprisingly it seems that more sires had been used in multiple countries, which has improved the link between the three countries for the largest breeds.

Carcass traits

Updating the data yielded records for 60 thousand additional beef × dairy crossbreds, an increase of about 35%. Distribution of number of records by birth year of sires (Table 5.4) followed a similar unsystematic pattern as for calving traits (Figure 5.5).

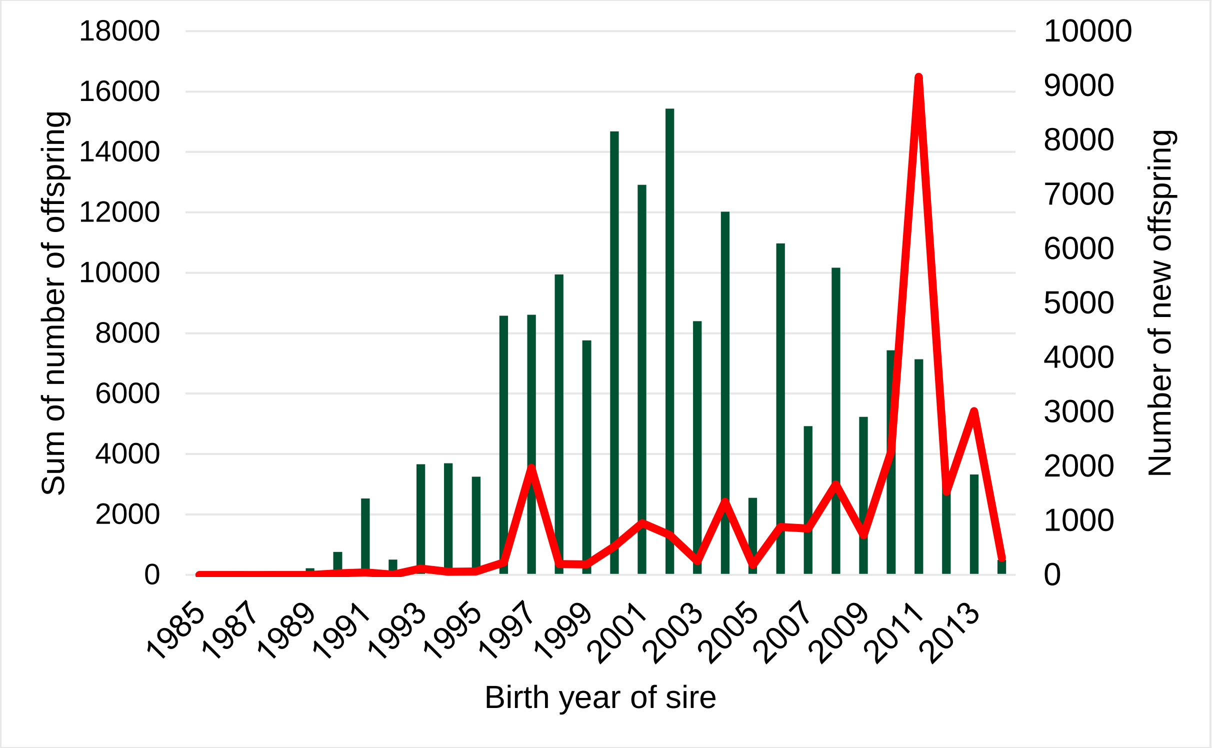

Figure 5.6. Number of beef × dairy offspring in previous evaluation (green bars, left y-axis) and number of new offspring in current evaluation (red line, right y-axis) by birth year of beef sire for carcass traits.

Correlations between current and previous breeding values were generally high for old beef sires and decreased for more recently born beef sires (Figure 5.7). Lower correlations for the more recent years were expect, as the bulk of additional data included in 'current' is from recently born beef × dairy crossbreds. Figure 5.6 illustrates that some older beef sires also had more beef × dairy offspring included in the current evaluation, explaining the "bumps" for the some of the earlier years. Limiting to a subset of beef sires with high reliability in 'previous' and few additional information in 'current', the correlations were near one (Figure 5.8).

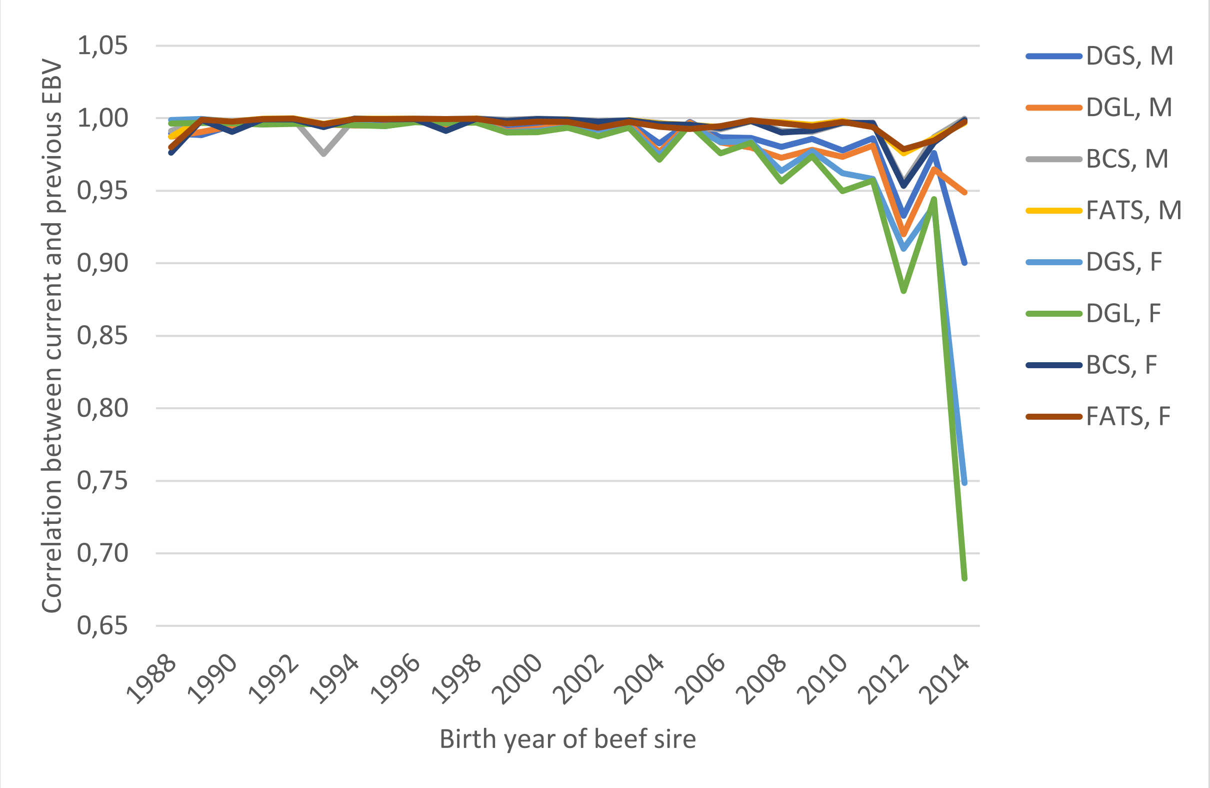

Figure 5.7. Correlations between EBVs for beef sires with offspring.

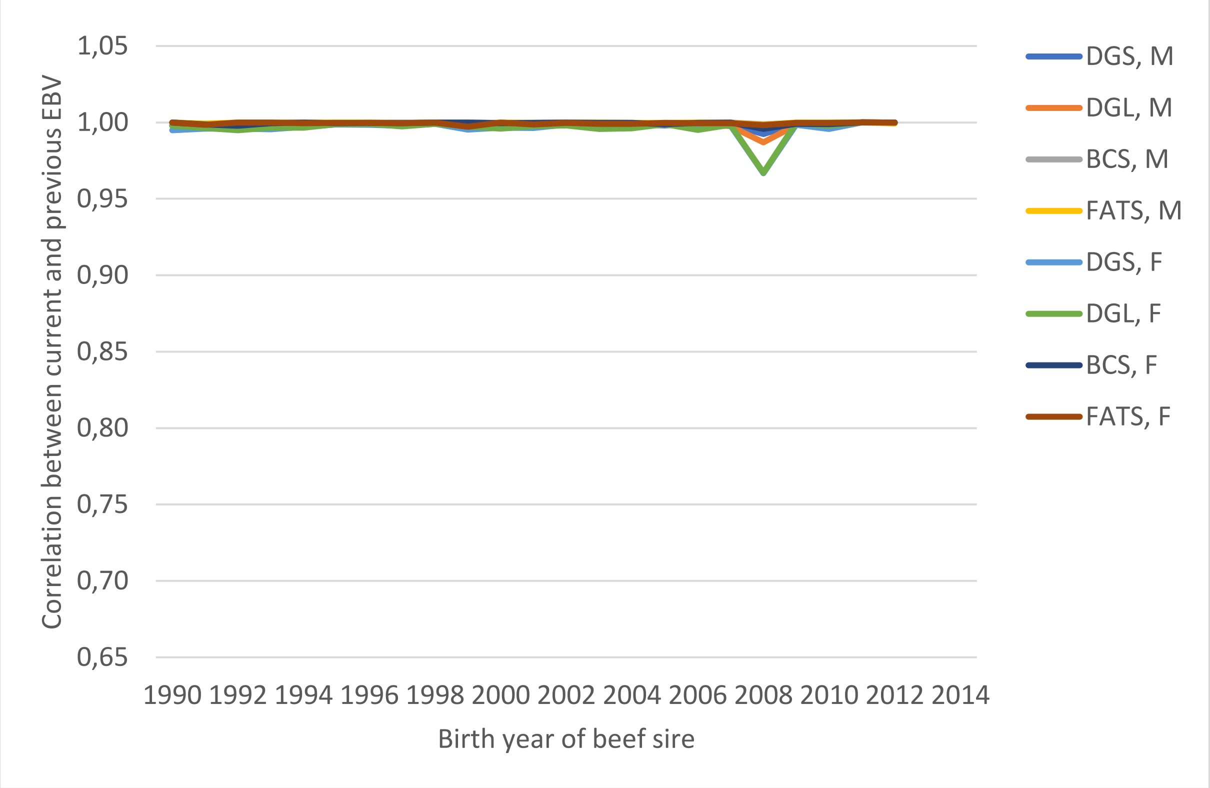

Figure 5.8. Correlation between EBVs for bulls with >50 offspring and <10 new offspring.

5.5. Interpretation of breeding values

Following the release of the NAV Beef × dairy evaluations, a request was put forward to clarify the relation between relative EBVs and the original phenotypes. This was documented in a note, included as Appendix G; values pertain to the NAV evaluation of August 2019.

6. Other results from the Beef × dairy genetic evaluation

6.1. Variation explained

Comparison of the variance of observations and the phenotypic variance provides a (rather) quick-and-dirty impression of how much variance is explained by the fixed effects in the model. For calving traits, fixed effects in the model explained least variation for Calf survival and most for Calf size (Table 6.1). Table 6.2 indicates that fixed effects generally explained more than 50% of the variance of observations for carcass traits.

Table 6.1. Variance of observations (V_y), phenotypic variance (σ_p^2) and the ratio $\left(V_y - \sigma_p^2\right)/V_y$ for calving traits

	Variance of observations	Phenotypic variance	Ratio
CSu1	0.0700	0.0680	0.03
CSu2+	0.0347	0.0342	0.01
CE1	0.4727	0.3910	0.17
CE2+	0.2984	0.2572	0.14
CSi1	0.6164	0.4524	0.27
CSi2+	0.4797	0.3394	0.29

Table 6.2. Variance of observations (V_y), phenotypic variance (σ_p^2) and their ratio $\left(V_y - \sigma_p^2\right)/V_y$ for carcass traits

	Variance of observations	Phenotypic variance	Ratio
dgs, ♂	0.0071	0.0035	0.51
dgl, ♂	0.0069	0.0028	0.60
bcs, ♂	1.1006	0.6915	0.37
fats, ♂	0.3079	0.1862	0.40
dgs, ♀	0.0089	0.0028	0.68
dgl, ♀	0.0066	0.0019	0.72
bcs, ♀	1.2036	0.6317	0.48
fats, ♀	0.3141	0.1627	0.48

6.2. Solutions for breed – birth year of dam effect

Calving traits

Solutions for the effect of breed – birth year of dam effect (Figure 6.1 - Figure 6.6) showed considerable (genetic) trend for the majority of calving traits, and elucidated presence of breed differences among dairy breeds with respect to calving performance. Differences among across years were however larger than differences between dam breeds.

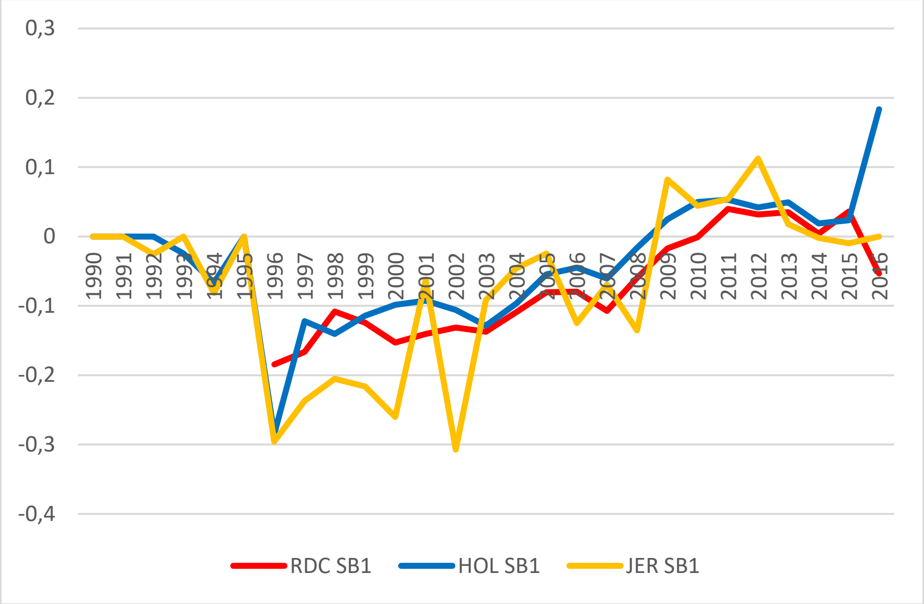

Figure 6.1. Solutions for breed – birth year of dam effect for CSu1.

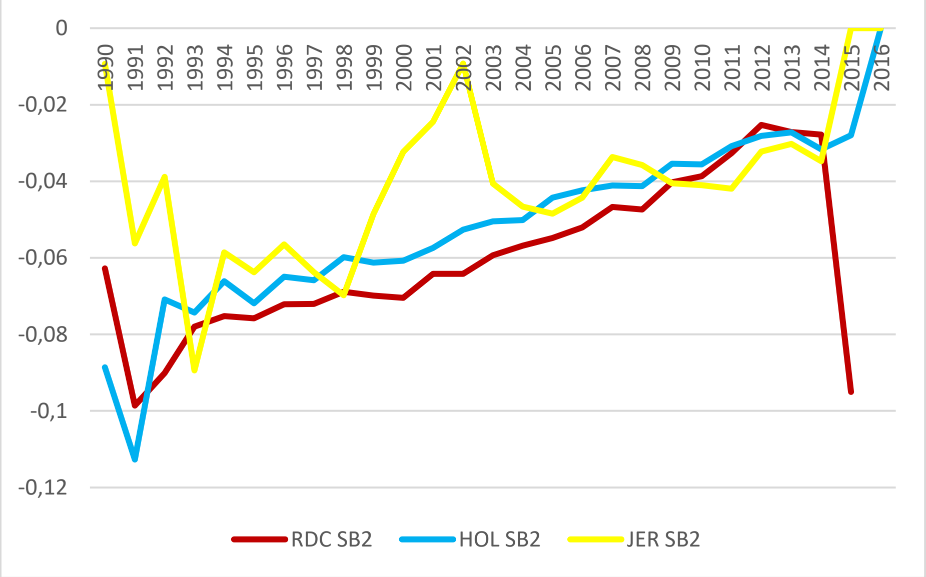

Figure 6.2. Solutions for breed – birth year of dam effect for CSi2+.

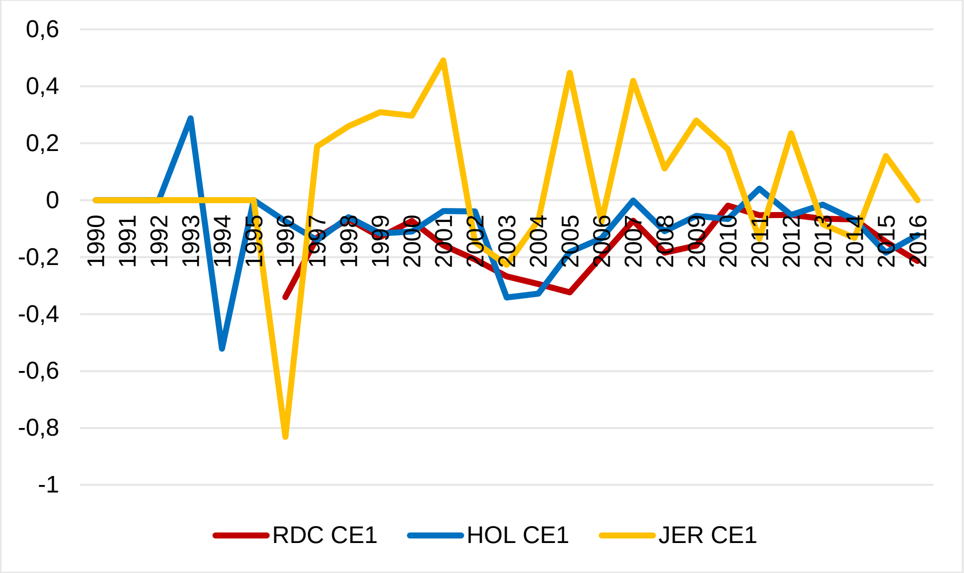

Figure 6.3. Solutions for breed – birth year of dam effect for CE1.

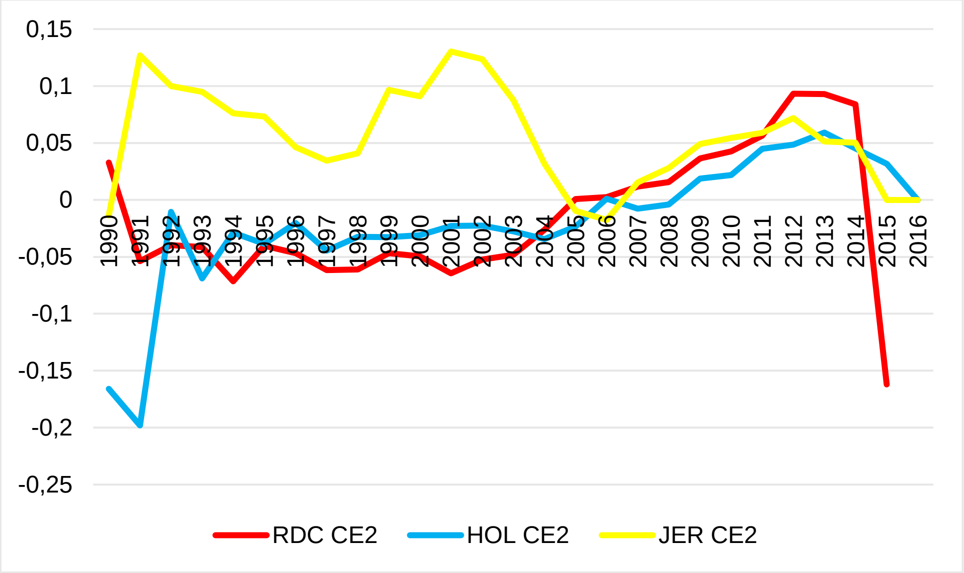

Figure 6.4. Solutions for breed – birth year of dam effect for Ce2+.

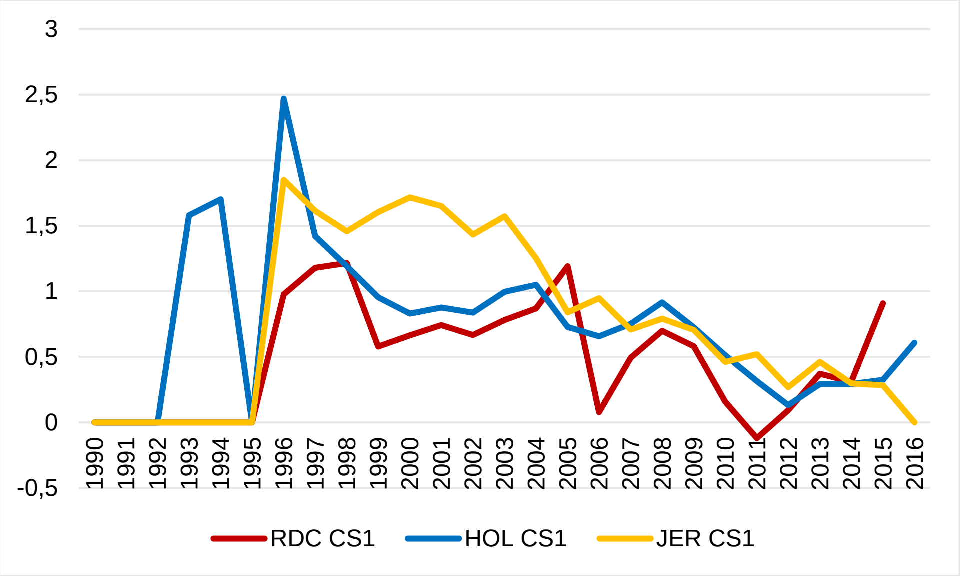

Figure 6.5. Solutions for breed – birth year of dam effect for CSi1.

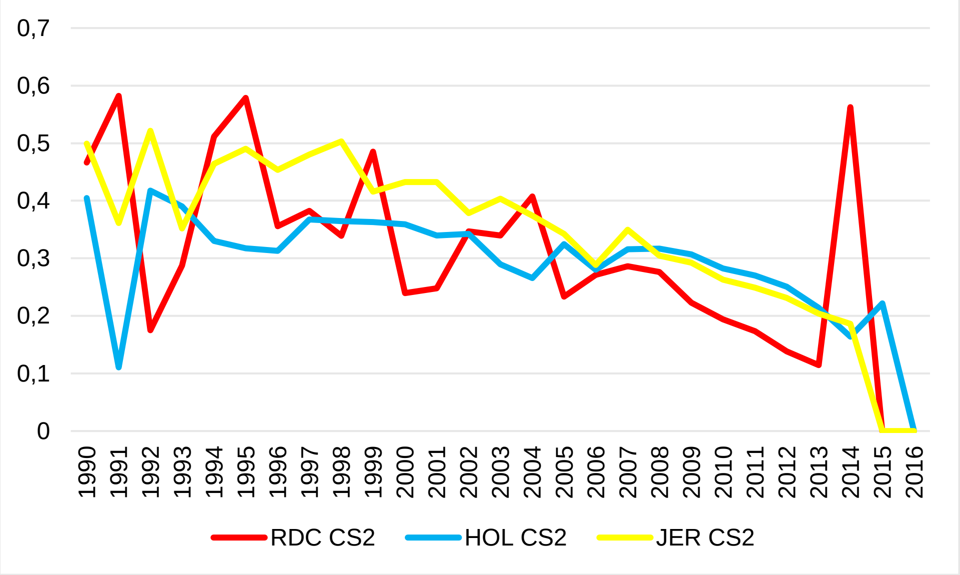

Figure 6.6. Solutions for breed – birth year of dam effect for CSi2+.

Carcass traits

Solutions for the effect of breed – birth year of dam effect (Figure 6.7 - Figure 6.10) showed a (genetic) trend for some of the carcass traits, and elucidated presence of breed differences among dairy breeds with respect to carcass traits. Differences among dam breeds appeared to be larger than differences among years.

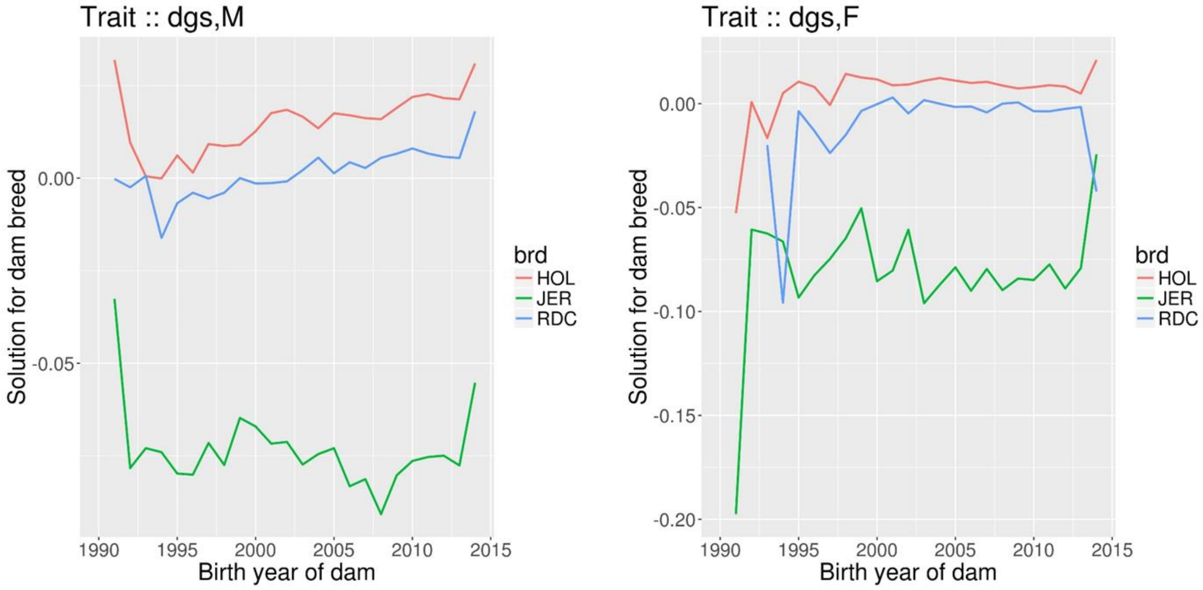

Figure 6.7. Solutions for breed – birth year of dam effect for Daily carcass gain – short fattening period, male and female trait.

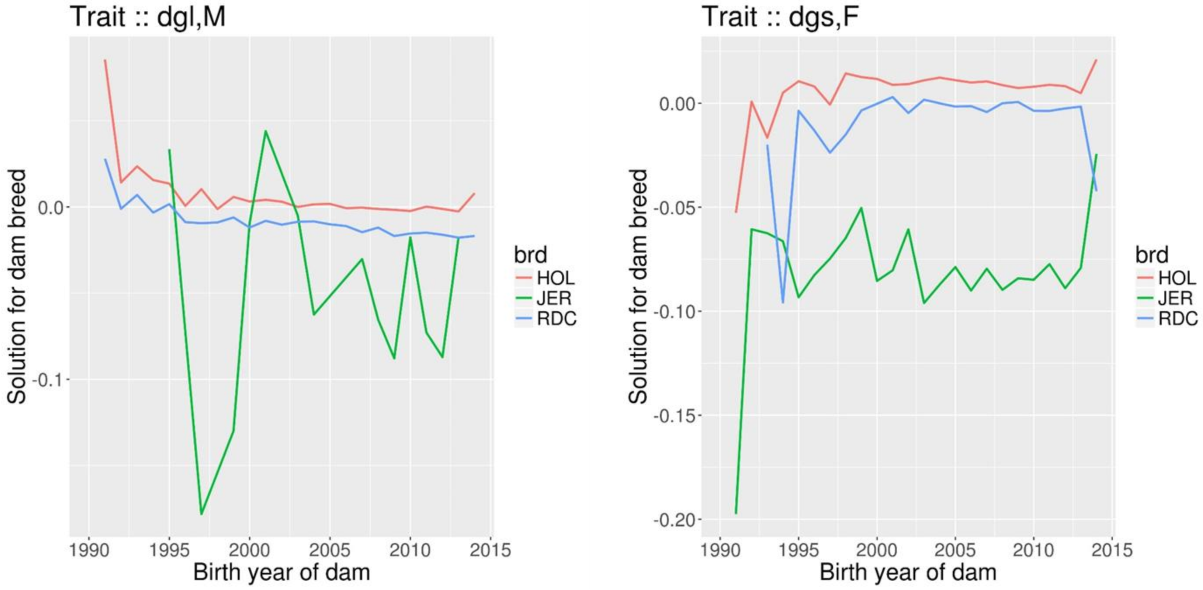

Figure 6.8. Solutions for breed – birth year of dam effect for Daily carcass gain – long fattening period, male and female trait.

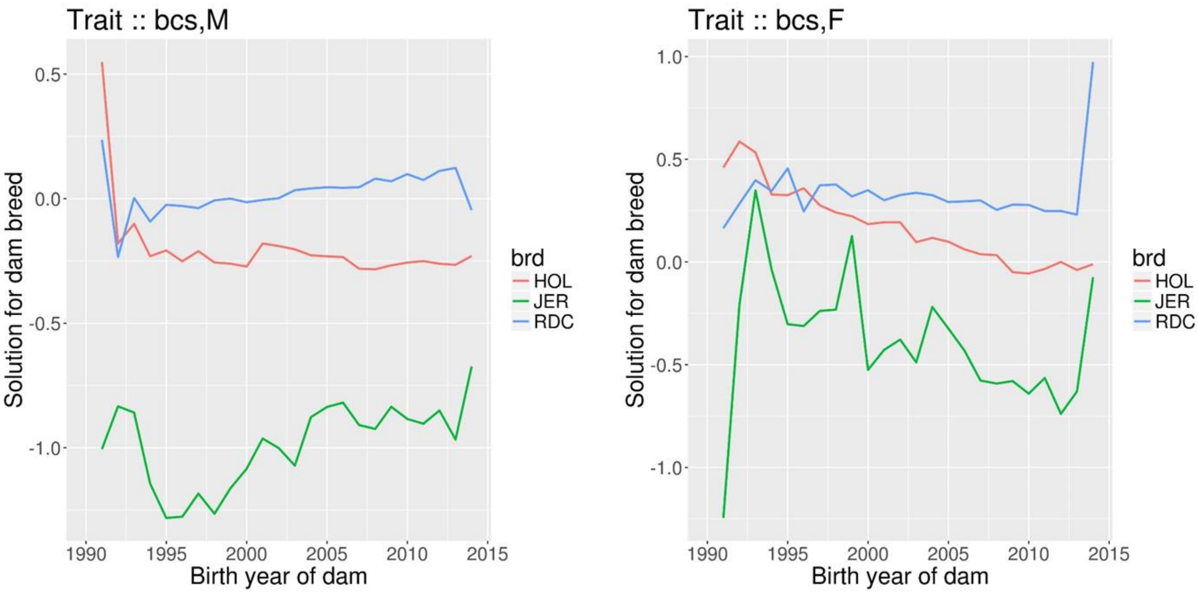

Figure 6.9. Solutions for breed – birth year of dam effect for Carcass conformation score, male and female trait.

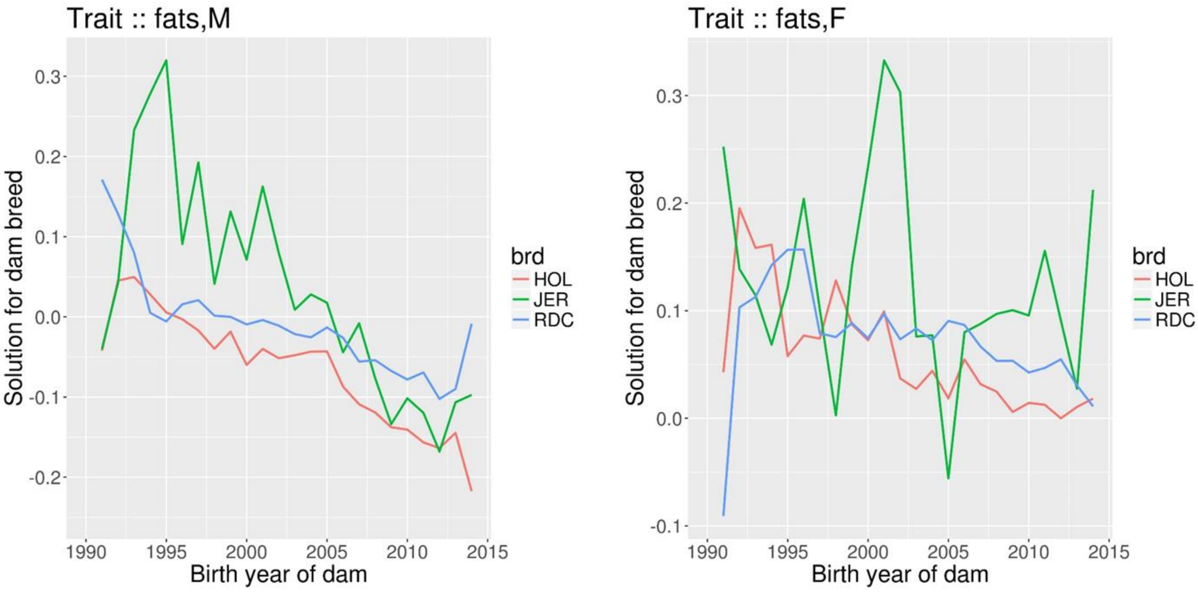

Figure 6.10. Solutions for breed – birth year of dam effect for Carcass fat score, male and female trait.

7. Verification

7.1. Input data

Genetic evaluation workflow *in brief*

The workflow for the Beef × dairy evaluation has three branches: CMON, CALV and CARC (Figure 2.1 and Appendix A). The CMON branches creates a common dataset with all beef × dairy crossbreds that qualify for inclusion in the Beef × dairy evaluation. In the CALV and CARC branches, the genetic evaluation for calving resp. carcass traits are done.

Input data for the CMON and CARC branches are files prepared by NAV owner organizations. The CALV branch builds further on data sets created in the CMON branch.

Checking input data

The following checks are done for CMON input data (i.e. calving files including purebred dairy calves; hereafter referred to as INP), separately for each country:

1. Identification of animals that disappeared from the current evaluation compared to the previous evaluation. *All animals (i.e. including purebred dairy).*
2. Comparison of number of animals by birth year and sex in current and previous evaluation. Unexpected deviations are marked. *All animals (i.e. including purebred dairy).*
3. Comparison of info on birth year, herd, sex, parity number and dam ID. *All animals (i.e. including purebred dairy)*. Unexpected deviations are listed.

The following checks are done for the common dataset (hereafter referred to as CMON):

1. Identification of animals that disappeared from the current evaluation compared to the previous evaluation.
2. Comparison of number of animals by birth year in current and previous evaluation. Unexpected deviations are marked.
3. Comparison of info on sire & dam breed, parity number and sire ID in current and previous evaluation. Unexpected deviations are listed.

The following checks are done for CALV input data, separately per country:

1. Identification of animals that disappeared from the current evaluation compared to the previous evaluation.
2. Comparison of number of animals by birth year in current and previous evaluation. Unexpected deviations are marked.
3. Comparison of info on herd, sex, birth date of dam and sire ID in current and previous evaluation. Unexpected deviations are listed.
4. Comparison of mean and standard deviation (by year and sex) for stillbirth and calving ease.

The following checks are done for CARC input data, separately per country:

1. Comparison of number of observations per year and gender in current and previous evaluation.
2. Comparison of number of animals by birth year and sex in current and previous evaluation. Unexpected deviations are marked.
3. Comparison of info on herd, slaughterhouse, date of slaughter, animal type (male, female), birth date of dam and sire ID in current and previous evaluation. Unexpected deviations are listed.
4. Comparison of mean and standard deviation (by year and sex) for slaughter weight, EUROP conformation, EUROP fat and age at slaughter. Unexpected deviations are listed.

7.2. Sire breeding values

The following checks are performed on the EBVs:

- Identification of beef sires that disappeared from the current evaluation compared to the previous evaluation.
- Change and standardized change in EBVs: distribution of bulls over classes of size change (e.g. # sires with a change of 2-3 units).
- List individual sires with large changes in EBV, no of beef × dairy offspring or reliability.
- Correlation between EBVs from current and previous evaluation (by year and by sire breed).

8. Future improvements

Improving the adjustment for heterogeneous variance for calving traits to handle frequency differences between countries and years.

More detailed modelling of (maternal) effect of dam on both calving and carcass traits.

9. References

Blanchard *et al.*, 1983. Estimation of genetic trends and correlations for Jersey cattle. *J Dairy Sci*, 66, 1947-1954.

Eriksson *et al*., 2004. Genetic relationships between calving and carcass traits for Charolais and Hereford cattle in Sweden. *J Anim Sci*, 82, 2269-2276.

NAV, 2019. NAV routine genetic evaluation of dairy cattle – data and genetic models. https://www.nordicebv.info/wp-content/uploads/2020/08/NAV-routine-genetic-evaluation_saved-feed-in-NTM-16062020.pdf.

Pedersen *et al*., 2016. NAV evaluation of calving traits. 23 pp.

Reverter *et al.*, 1993. Technical note: Detection of bias in genetic predictions. *J Anim Sci*, 72, 34-37.

Urioste *et al*., 2001. Evaluation of extent and amount of heterogeneous variance for milk yield in Uruguayan Holsteins. *Anim Sci*, 72, 259-268.

Appendix A. Considerations about the workflow for the Beef × dairy evaluation system

Directory structure

The directory structure follows that of other NAV evaluations in that there are separate directories per trait group. The directory “CMON” contains programs and files to create a dataset with beef × dairy crosses that qualify to be included in the evaluation. Trait-specific editing is done in the “edit” subdirectories for each trait group. Intermediate datasets are stored in the “datasets” subdirectories. Calculation (with DMU) and post-processing of breeding values and reliabilities are done in the “run” subdirectories. Wrapping up of an evaluation, i.e. combining breeding values from several trait groups, calculation of total merit indexes and implementation of publication rules are done in the “run” subdirectory under “CMON”. The file with publishable breeding values is put in the “datasets” subdirectory under “CMON”.

```
/nav/nav/BxD/
|--Lastrun
|   |--include
|   |--CMON
|   |   |--datasets
|   |   |--edit
|   |   `--run
|   |--CALV
|   |   |--datasets
|   |   |--edit
|   |   `--run
|   `--CARC
|       |--datasets
|       |--edit
|       `--run
|--Run-2018-05
```

Settings

The Lastrun directory contains two files with settings: “file_locations.inc” and “global_settings.inc” that are included (%include) in all SAS program files. SAS program files are written such that only these two files need to be edited from one evaluation to the next. SAS and other program files are also written such that only these two files need to be edited in dependent of if the evaluation is run in a routine environment or in a test environment.

Re-use of code

Code that is re-used can be stored in the directory “include”. For example, the workflow for all trait groups involves tracing of pedigree: the code is most efficiently maintained and stored in one place, and sourced (%include) by SAS programs in the subdirectory for each trait group. Code that is re-used tends to suffer from fewer bugs, and software that builds on macros that are re-used code tends to be easier to maintain; adoption of structured programming is for these reasons encouraged.

Repository

The latest version of the routine evaluation software (files with settings, program files, directive files, etc.) is stored in a repository. Each evaluation starts with making a copy of the whole repository in the directory where the evaluation is to be performed (below /nav/nav/BxD for a NAV routine evaluation, or another location for test evaluations). For now, the repository is in /nav/nav/BxD/repos. For the future, it is recommended to use version control software (e.g. Git or Mercurial) for maintaining routine evaluation software.

Abbreviations

Communication, both internal and external, is eased by a common vocabulary. Names, descriptions and codes related to the Beef × dairy evaluation are listed below, and are to be used as much as possible; e.g. in official documentation of the evaluation, in variable names in programs and datasets, etc.

The following four-letter codes are used for trait groups:

Code	Trait group
CALV	Calving traits
CARC	Carcass traits

Workflow – template

See attached Excel file for an example from the revised General Health evaluation (introduced in November 2017). The workflow conveys several pieces of information:

- Input used by each program
- Output generated by each program
- Command use to run each program
- Dependencies of components of the workflow
    - If the output of one program is used as input for another, this creates a dependency.

Microsoft Excel
97-2003-kalkylblad

Appendix B. Editing of the common dataset

The following variables are included in the common dataset:

- Calf ID (nav_id)
- Birthdate for calf
- Birth herd
- Dam ID (nav_did)
- Birthdate of dam
- Parity of dam
- Sire ID (nav_sid)
- Dam breed code
- Sire breed code
- Twin (0 = single birth, 1 = twin)
- ET calf (0 = normal, 1 = ET calf)

Step 1 – Assigning a breed code to INRA bulls

The INRA breed is a composite breed developed in France, with influx from, amongst others, Blonde d'Aquitaine, Belgium Blue, Charolais and Limousin. The breed proportions can vary greatly, and it is therefore not identified as a conventional breed. In Denmark it is denoted with XXX, as a crossbred. To evaluate INRA bulls in the Beef × dairy evaluation, it was therefore necessary to assign a breed name and code to identify these bulls. As INRA semen (to our knowledge) has only been used in Denmark, the Danish herd book numbers can be used to identify INRA bulls, since all INRA bulls are herd booked in the series from 88000-88100. However, other beef breed sires with double muscling, such as CHA or LIM, can also be registered in this number series. There is no way to differentiate these bulls from the INRA bulls, but they have not been used to a great extent and will presumably be deleted during the editing.

All sires with a herd book number from 88000-88100 are therefore assigned the breed abbreviation INR and the breed code 79. To ensure that no dairy sires have been incorrectly registered in this number series, the parents of the sires are checked to ensure that they are also beef breeds.

Step 2 – Numeric breed codes are assigned to all breeds

The breed abbreviations have been standardized to meet Interbull standards in the new NAV pedigree file. However, numeric breed codes vary between all three Nordic countries and have not been standardized. To facilitate programming, numeric breed codes were therefore assigned to each breed. Table B.5 contains a list of the abbreviations and the breed codes.

Only beef × dairy offspring of sires in the interval 50-81 will be used, as these codes are all beef breeds. Codes in the range 1-49 pertain to dairy breeds, and the range 81-90 pertains to *Bos indicus* breeds or breeds of other species that are not *Bos Taurus,* except for 85 (MAR) that is also a beef breed and offspring of which will be included in the dataset.

Step 3 – All herds must have both have dairy and beef × dairy calves

To avoid including data from small hobby farms with only a few beef × dairy crossbred animals, it was decided to only include farms that both have purebred dairy calves and beef × dairy crossbred calves. The edit was done at herd – year level, instead herd, to avoid deleting all data from farms that at some point switched from one production form to another. This edit resulted in a large reduction in the number of qualified animals (Edit 1 in Figure 3.1).

Step 4 – Avoid small hobby farms

To avoid including small hobby farms, which do not deliver milk, a minimum number of dairy calves was required. As the production systems between the three countries varies the average number of calves also varies. In Table B.1 the average number of calves per herd – year group is shown for each country.

Table B.1. Average number of calves born per year, for herds with both dairy and beef × dairy calves and for herds with only dairy calves

	DNK		FIN		SWE	
Herd type	**Mean**	**Median**	**Mean**	**Median**	**Mean**	**Median**
Beef × dairy and dairy calves	236	184	47	34	100	68
Only dairy calves	153	119	28	21	71	86

The average herd size was much greater in Denmark compared to both Sweden and Finland. The average herd size was higher for the herds that had beef × dairy and dairy calves, compared to those that only had dairy calves. The effect of different minimum limits per herd – year was tested for the three countries (Table B.2).

Table B.2. Number of deleted calves and % of total at different minimum limits of number of dairy calves per herd – year

Minimum number of dairy calves per herd – year	**Denmark**		**Finland**		**Sweden**	
	Nr calves deleted	**% of total**	**Nr calves deleted**	**% of total**	**Nr calves deleted**	**% of total**
1	4624	0.05	3244	0.08	3888	0.09
2	9332	0.10	9042	0.23	9570	0.22
3	14,066	0.16	17,724	0.45	17,157	0.40
4	18,678	0.21	30,452	0.78	26,193	0.61
5	23,713	0.26	48,007	1.23	37,993	0.89
6	28,957	0.32	71,755	1.83	51,919	1.22
7	34,837	0.38	103,500	2.64	67,725	1.59
8	41,053	0.45	144,556	3.69	86,565	2.03
9	47,767	0.53	195,964	5.00	108,066	2.53
10	55,197	0.61	256,764	6.56	131,536	3.09

When the minimum limit was set to 10 dairy calves, 6.5 % of the Finnish data was deleted. This limit seemed to be too strict. When the limit was instead set at five, only 1.2 % of the Finnish data was deleted, and less than 1 % of the Swedish and Danish data was deleted. Therefore, this limit was adopted.

Step 5 – Include only calves with beef breed sire

As it is only the beef breed sires we wish to evaluate, all dairy and indigenous cattle are deleted.

Step 6 – Exclude non-AI bulls

To avoid including non-AI bulls in the dataset, it was decided to exclude all sires that had only been used in a single herd. As is it quite possible some bulls could have been used in several herds without being an AI bull, the effect of excluding bulls that had only been used in 1, < 5 and < 10 herds was investigated (Table B.3).

Table B.3. Number and percentage of deleted sires and calves, at different editing levels for minimum number of herds/sire

	Sires kept	Sires deleted		Calves kept	Calves deleted	
	Nr	Nr	% of total	Nr	Nr	% of total
All sires	5632			571,410		
1 herd	1509	4132	73.2%	545,253	26,157	4.6%
< 5 herds	879	4762	84.4%	537,692	33,718	5.9%
< 10 herds	762	4879	86.5%	534,682	36,728	6.4%

In total, there were 5632 different beef sires. Over 70 % of the bulls were only used in a single herd. However, when calves from these sires were deleted, it only corresponded to 4.6 % of the total number of observations. The difference between sires used in at least 5 or 10 herds was very small. Only 0.5 % more observations were deleted when a minimum of 10 herds was required compared to 5. By using a cutoff point of at least 10 herds, nearly 90 % of the sires and 6.4 % of the observations from the original dataset were deleted.

It was decided to use the cutoff point of 10 herds in the final editing of the common dataset.

Progeny group sizes in the common dataset (after editing)

The average number of offspring and the number of sires for each breed are shown in Table B.4. The smaller breeds with few sires (WAG, SAL, PIE, HLA, GLW, BSH) had a lower average number of offspring, except for INRA that has been used quite intensively. The larger breeds with many sires (AAN, BAQ, BBL, LIM) had a high average number of offspring, especially BBL, where a single sire, Golden had over 25,000 offspring in Denmark. BSM, CHA, HER have not been used quite as intensively as the other breeds; there were many sires for those breeds, but each with fewer offspring.

Table B.4. Number of sires and statistics for number of offspring per sire for each beef breed

	N	Mean	Median	25 % Q	75 % Q
AAN	73	790	309	97	1147
BAQ	67	960	189	84	859
BBL	90	1293	677,5	255	1397
BSM	206	315	118	53	271
CHA	99	597	286	86	676
GLW	1	24	24	24	24
HER	68	478	197	41,5	505
HLA	10	39	29	26	37
INR	7	1057	270	195	2096
LIM	133	988	267	107	1107
PIE	6	71	68,5	19	96
SAL	1	56	56	56	56
WAG	1	109	109	109	109

Table B.5. List of breed abbreviations and codes

Abbreviation	Breed code
RDC	1
HOL	2
JER	3
RED	4
BSW	19
NOR	23
GRO	24
LAV	25
SRB	26
MON	27
FLE	28
BRU	29
FIC	35
AGK	45
JYK	46
GKR	48
LTR	49
NFB	49
RIN	49
SKB	49
TEL	49
VÄN	49
BSM	50
PIN	51
GRA	53
HLA	54
GVH	55
DXT	56
SAL	57
AAN	58
GLW	59
HWD	61
HER	63
LON	64
WPC	66
PIE	67
BAQ	68
BSH	69
CHA	70
CIA	72
ROM	73
LIM	75
WAG	77
BBL	78

INR	79
MGR	80
ZEB	83
MAR	85
XXX	90

Appendix C. Data structure and connectedness

How many observations for each sire breed?

In Denmark, nearly 2/3 of all beef × dairy calves were sired by a BBL sire (Table C.1). The second largest breed was LIM with 12.9 % of the calves. All other breeds constituted less than 5 % of the total amount of calves. In Finland, nearly 40 % of the calves were sired by LIM, followed by BAQ and AAN with 23 and 17 % respectively. In Sweden, the beef breeds were used more equally; BSM and CHA were largest with 7 % and 26 % of the calves each followed by HER and LIM. It is interesting to note that the use of beef breeds varies greatly between the three countries.

Table C.1. Number of calves for each sire breed by country

	DNK		FIN		SWE	
Sire breed	**N**	**%**	**N**	**%**	**N**	**%**
AAN	3231	1.9	41517	16.9	12924	11.3
BAQ	5583	3.2	56202	22.8	2530	2.2
BBL	116404	66.9	0	0	0	0
BSM	11401	6.5	22544	9.2	30983	27.1
CHA	6337	3.6	22646	9.2	30140	26.4
GLW	24	0.0	0	0	0	0
HER	1001	0.6	10450	4.2	21060	18.4
HLA	43	0.0	119	0.0	224	0.2
INR	7396	4.2	0	0	0	0
LIM	22098	12.7	92865	37.7	16371	14.3
PIE	415	0.2	9	0.0	0	0
SAL	56	0.0	0	0	0	0
WAG	109	0.1	0	0	0	0
Total	*174098*		*246352*		*114232*	

How many observations for each dam breed?

The use of dairy breeds also varied between the three countries (Table C.2). Jersey was mainly used in Denmark, whilst RDC and HOL were used in all three countries. In SWE, the distribution was nearly half to each breed, whilst in FIN the majority of calves had a RDC dam and in DNK the majority had a HOL dam.

Table C.2. Number of calves from each dam breed by country

	DNK		FIN		SWE	
Dam breed	**N**	**%**	**N**	**%**	**N**	**%**
HOL	125882	72.3	69655	28.3	49836	43.6
JER	32105	18.4	241	0.1	415	0.4
RDC	16112	9.3	176456	71.6	63981	56.0
Total	*174099*		*246352*		*114232*	

How many cows in each parity by country?

Not only is the use of dam and sire breed different, the amount of beef semen used in different parities also varied (Table C.3). In DNK and FIN less than 5 % of the beef × dairy calves were borne by first parity cows, but in Sweden more than double as many of the dams were first parity cows. Apart from the first parity, frequencies of parity number were quite similar for all three countries.

Table C.3. Distribution of the dam's parity number by country

Calving number	DNK		FIN		SWE	
	N	%	N	%	N	%
1	7382	4.2	10965	4.5	13184	11.5
2	46970	27.0	57475	23.3	31696	27.7
3	51148	29.3	68762	27.9	30265	26.5
4	34396	19.8	53023	21.5	20057	17.6
5	19605	11.3	30983	12.6	10968	9.6
6	9384	5.4	15597	6.3	5268	4.6
7	3944	2.3	7068	2.9	2166	1.9
8	1157	0.7	2342	1.0	596	0.5
9	103	0.1	136	0.1	32	0.0
10	6	0.0	-	-	-	-
11	3	0.0	-	-	-	-
12	-	-	1	0.00	-	-
Total	*174098*		*246352*		*114232*	

How many dams have multiple beef × dairy offspring?

Nearly 78 % of the dams had only one beef × dairy offspring (Table C.4), leaving only 22 % with multiple beef × dairy offspring. About 17 % of the dams had two beef × dairy offspring, and about 5 % had more than two.

Table C.4. Distribution of number of beef × dairy offspring per dam

Number of beef × dairy offspring per dam	Nr of dams	% of total
1	321986	77.9
2	69531	16.8
3	16465	4.0
4	4106	1.0
>4	1282	0.3
Total	*413370*	

How many dams have offspring from multiple beef breeds?

Of the dams that had multiple offspring (91,384), only 38 % had beef × dairy offspring with sires from different beef breeds (Table C.5); this corresponds to around 8 % of all dams with beef × dairy offspring. These dams are very valuable to enable accurate comparison of beef sires across beef breeds.

Table C.5. Number of dams with offspring from different sire breeds

Nr of different sire breeds	Nr of dams	% of dams with multiple offspring	% of total
1	56995	62.4%	
2	31896	34.9%	7.7%
3	2373	2.6%	0.6%
4	117	0.1%	0.0%
5	3	0.0%	0.0%
Total	*91384*		

How many bulls have been used with multiple dam breeds?

The majority of beef sires have been used on all three dam breeds (Table C.6); only 2 sires have been used on a single dam breed.

Table C.6. Number of dam breeds the beef sires have been used on

Nr of dam breeds	Nr of sires	% of total
1	2	0.3
2	278	36.5
3	482	63.2
Total	*762*	

How many herds have used multiple beef breeds?

It is important that multiple breeds have been used in the same herd – year group so that breed effects can be estimated precisely. As the calving evaluation is split into first versus later parities, the connection within herd – year group within parity group is also important.

Nearly 70 % of all herds have used multiple beef breeds throughout the whole time period (2000-2017; Table C.7). Only 31 % of the herds have used the same beef breed for all years.

Table C.7. Distribution number of different beef sire breeds per herd

Nr of breeds per herd	Nr of herds	% of total
1	7566	30.8
2	5590	22.7
3	4415	17.9
4	3429	13.9
5	2440	9.9
6	1096	4.5
7	51	0.2
8	10	0.0
10	3	0.0
Total	*24600*	

How many herds have used multiple beef breeds within the same year?

Surprisingly, a few herds used many different breeds within the same year (Table C.8). The majority (66.7 %) only used 1 beef breed during the same year. Nearly 30 % of the herds used 2-3 different beef breeds during a year.

Table C.8. Distribution of number of beef sire breeds per herd – year (HY) group

Nr of breeds per HY group	Nr of HY groups	% of total
1	92336	66.7
2	33005	23.8
3	9927	7.2
4	2618	1.9
5	483	0.3
6	68	0.0
7	1	0.0
8	1	0.0
Total	*138439*	

How many herds used multiple beef breeds within the same year by parity (first versus later)?

In over 90 % of the herd – year groups only a single beef breed had been used to inseminate the heifers (Table C.9). Only 6 % used 2 breeds. For later parities the distribution was better: in two-thirds of the herd – year groups one breed had been used, whilst two breeds had been used in nearly 25 % of the herd – year groups, and three breeds in 7 % of the herd – year groups.

Table C.9. Distribution of number of beef sire breeds per herd – year group for first and later parities

Nr of breeds per HY group	1st parity		>1 parity	
	Nr of HY groups	% of total	Nr of HY groups	% of total
1	9962	93.7	82340	67.2
2	619	5.8	29416	24.0
3	43	0.4	8378	6.8
4	4	0.0	2072	1.7
5			338	0.3
6			43	0.0
7			1	0.0
8			1	0.0
Total	*10628*		*122589*	

How many herds used multiple beef breeds within the same year, by parity (first versus later) and country?

As shown previously, the number of heifers inseminated with beef semen was greatest in Sweden. The average number of beef × dairy crossbred calves per herd was lowest in Finland, were there were many small farms. In Sweden the average number of beef × dairy crossbred calves per herd was higher, but not at high as Denmark. This should be considered when looking at results in Table C.9.

For the heifers, most herds only use a single beef breed (Table C.10). In Denmark and Sweden slightly more herds used multiple breeds compared to Finland.

Table C.10. Distribution of number of beef sire breeds used on heifers per herd – year group, by country

Nr of breeds per HY group	DNK		FIN		SWE	
	Nr of HY groups	% of total	Nr of HY groups	% of total	Nr of HY groups	% of total
1	2090	92.7	4151	96.3	3721	91.6
2	148	6.6	154	3.6	317	7.8
3	15	0.7	7	0.2	21	0.5
4	1	0.0	0	0.0	3	0.1
Total	*2254*		*4312*		*4062*	

For later parity cows a larger variety of beef breeds has been used within herd – year groups (Table C.11). This was especially the case for Finland, where over 35 % used multiple beef breeds. In Sweden, nearly 30 % used multiple breeds, whilst in Denmark only around 20 % inseminated with multiple beef breeds. This is probably due to the intensive use of BBL (Table C.1).

Table C.11. Distribution of number of beef sire breeds used on cows per herd – year group, by country

Nr of breeds per HY group	DNK		FIN		SWE	
	Nr of HY groups	% of total	Nr of HY groups	% of total	Nr of HY groups	% of total
1	13172	78.5	47368	63.1	21800	70.9
2	2844	17.0	19777	26.4	6795	22.1
3	604	3.6	6106	8.1	1668	5.4
4	126	0.8	1516	2.0	430	1.4
5	20	0.1	247	0.3	71	0.2
6	5	0.0	33	0.0	5	0.0
7	0	0.0	1	0.0	0	0.0
8	1	0.0	0	0.0	0	0.0
Total	*16772*		*75048*		*30769*	

How many common observations between sire breeds by herd – year?

To investigate how many herd – year groups had beef × dairy offspring from different beef sire breeds, a cross table of common herd – year groups for all combinations of sire breeds was constructed. Cross table were made for all parities (Table C.12), first parities (Table C.13) and later parity (Table C.14).

The link between the large breeds seems to be quite good. Especially LIM had a high number of observations in herd – year groups common with the other larger breeds. The connection in later parities was good between the large breeds. The number of first parity cows was much lower, however the breeds still shared some common herd – year groups.

Table C.12. Cross table with number of common herd – year groups for each combination of sire breed for all parities

	BAQ	BBL	BSM	CHA	GLW	HER	HLA	INR	LIM	PIE	SAL	WAG

AAN	5432	309	4325	3810	5	3273	55	55	10117	0	1	2
BAQ		414	3669	3661	0	1510	29	73	9220	22	9	5
BBL			688	463	4	103	14	285	1571	39	11	20
BSM				5163	2	3145	61	88	8409	14	10	5
CHA					1	3030	73	100	7772	10	2	6
GLW						2	2	0	4	0	0	0
HER							65	7	4286	3	2	1
HLA								1	84	1	2	0
INR									99	2	1	3
LIM										29	9	9
PIE											3	1
SAL												0

Table C.13. Cross table with number of common herd – year groups for each combination of sire breed for first parity

	BAQ	**BBL**	**BSM**	**CHA**	**GLW**	**HER**	**HLA**	**INR**	**LIM**	**PIE**	**SAL**	**WAG**
AAN	103	31	156	42	0	387	12	6	425	0	0	0
BAQ		21	33	13	0	15	0	3	62	3	2	1
BBL			26	8	1	14	0	9	88	2	2	2
BSM				51	0	102	0	4	167	3	1	0
CHA					0	36	1	0	56	0	0	0
GLW						0	0	0	1	0	0	0
HER							9	0	178	1	1	1
HLA								0	4	0	0	0
INR									7	0	0	0
LIM										3	1	1
PIE											1	1
SAL												0

Table C.14. Cross table with number of common herd – year groups for each combination of sire breed for later parities

	BAQ	**BBL**	**BSM**	**CHA**	**GLW**	**HER**	**HLA**	**INR**	**LIM**	**PIE**	**SAL**	**WAG**
AAN	4673	162	3393	2967	3	2583	32	33	8446	0	1	1
BAQ		387	3589	3602	0	1423	25	67	8996	19	6	2
BBL			623	444	3	55	10	267	1302	35	8	15
BSM				5028	1	2679	40	86	7936	11	7	5
CHA					1	2643	53	97	7414	9	2	6
GLW						1	1	0	2	0	0	0
HER							46	6	3852	3	1	0
HLA								1	64	1	2	0
INR									88	2	1	3
LIM										19	7	9
PIE											2	1
SAL												0

How many sires have been used within the same herd – year group

To evaluate sires, it is important that multiple sires have been used within the same herd – year group. If only a single sire is used for a whole herd – year group, then it is hard to distinguish the herd – year effect from the sire effect.

There were 128,345 different herd – year groups in total. More than half of these were from Finland (Table C.15). About 40 % of the Danish herds have only used a single sire, compared to nearly 50 % of the Swedish herds. It is positive to see that over 50 % of the herd – year groups had used multiple sires. Some herds used more than 10 different sires within the same year. Especially in Denmark many different sires have been used within the same year.

Table C.15. Distribution of number of sires per herd – year group

Nr of sires per herd – year	DNK		FIN		SWE	
	N	%	N	%	N	%
1	7348	40.5	35098	45.2	15854	48.6
2	3723	20.5	20458	26.4	7746	23.8
3	2258	12.4	11006	14.18	3979	12.2
4	1446	8.0	5511	7.1	2272	7.0
5	936	5.2	2718	3.5	1177	3.6
6	673	3.7	1395	1.8	667	2.0
7	488	2.7	697	0.9	387	1.2
8	349	1.9	327	0.4	219	0.7
9	260	1.4	182	0.2	113	0.3
10	212	1.2	94	0.1	64	0.2
>10	461	2.5	114	0.1	113	0.3
Total	*18154*		*77600*		*32591*	

Connection between first and later parities

For the first parity cows over 90 % of the herds only used a single beef breed (Table C.9). The connection between herd – year groups for sire breeds was not so strong, especially for first parity cows. The connection between first and later parities was therefore further investigated, since calvings by primiparous and multiparous cows will be treated as genetically different, but correlated traits.

In DNK and FIN less than 5 % of the beef × dairy calves were borne by primiparous cows, but in Sweden more than twice as many of the dams were primiparous cows. In total, there were 31,531 beef × dairy crossbred calves borne by primiparous cows. Of these, 6546 (20.7 %) had a beef × dairy calf in a later parity as well.

How many sires used in first and later parities?

Some sires are predominantly used for heifers, and others on cows. To see how strong the link was between parities, the number of sires from each sire breed with beef × dairy offspring borne by first versus later parity dams was investigated. If all sires were considered, then 91 % of all sires have been used to inseminate heifers. However, this also includes sires that have only sired a single calf. Only 68 % of the sires had at least 5 offspring from heifers (Table C.16). A larger percentage of sires from breeds such as AAN, HER and LIM, were used on heifers compared to breeds such BAQ, BBL and CHA. If the limit was set to 10 offspring, the picture was the same as for 5 offspring, but more extreme as only 50

% of the sires had more than 10 offspring born by heifers. All the sires used in the first parity were also used in later parities.

Table C.16. The number of sires used on heifers, by sire breed

		≥ 5 offspring		≥ 10 offspring	
Sire breed	**All sires**	Nr sires used on heifers	% of all sires	Nr sires used on heifers	% of all sires
AAN	73	69	95%	61	84%
BAQ	67	40	60%	27	40%
BBL	90	56	62%	37	41%
BSM	206	123	60%	74	36%
CHA	99	45	45%	27	27%
GAL	1	1	100%	0	0%
HER	68	56	82%	51	75%
HLA	10	6	60%	3	30%
INR	7	6	86%	5	71%
LIM	133	114	86%	96	72%
PIE	6	2	33%	1	17%
SAL	1	1	100%	1	100%
WAG	1	1	100%	1	100%
Total	*762*	*520*	*68%*	*384*	*50%*

In Table C.17 the amount of calves sired by each sire breed in either first parity or later is shown for all three countries. It is evident that breeds such as AAN, BSM and LIM have been used more on heifers, whilst breeds such as BAQ, BBL and CHA have been used predominantly on later parity cows. In Finland, 70 % of all calves borne by first parity cows were AAN. In Denmark LIM was the breed most used on heifers, whilst in Sweden AAN and HER were quite equal.

Table C.17. The number of calves sired by each beef breed for first and later parities, by country

	DNK				**FIN**				**SWE**			
	1st parity		**>1 parity**		**1st parity**		**>1 parity**		**1st parity**		**>1 parity**	
	N	**%**	**N**	**%**	**N**	**%**	**N**	**%**	**N**	**%**	**N**	**%**
AAN	891	12.1	2340	1.4	7628	69.6	33889	14.4	4575	34.7	8349	8.3
BAQ	175	2.4	5408	3.2	617	5.6	55585	23.6	115	0.9	2415	2.4
BBL	1557	21.9	114847	68.9								
BSM	851	11.5	10550	6.3	346	3.2	22198	9.4	1471	11.2	29512	29.2
CHA	76	1.0	6261	3.8	139	1.3	22507	9.6	566	4.3	29574	29.3
GLW	9	0.1	15	0.0								
HER	282	3.8	719	0.4	584	5.3	9866	4.2	4113	31.2	16947	16.8
HLA	9	0.1	34	0.0	15	0.1	104	0.0	65	0.5	159	0.2
INR	460	6.2	6936	4.2								
LIM	3000	40.6	19098	11.5	1635	14.9	91230	38.8	2279	17.3	14092	14.0
PIE	26	0.4	389	0.2	1	0.0	8	0.0				
SAL	16	0.2	40	0.0								
WAG	30	0.4	79	0.1								
Total	*7382*		*166716*		*10965*		*235387*		*13184*		*101048*	

The connection between first and later parities is not so strong, as there were very few first parity cows, especially from Denmark and Finland. However, just over 20 % of the dams that had a beef × dairy calf in their first parity also had a beef × dairy calf in a later parity. 50 % of the sires were used on heifers, and they all had more than 10 offspring in later parities. So, despite fairly weak connections for the dams, the sires seemed to be quite strongly connected across parities.

Conclusion

It seems that the data structure is not as weak as feared. The connection between sires and sire breeds is good. The weakest data is for the first parity cows due to the low number of observations, and lower number of sires that have been used to cover heifers.

- **Dams**
  - Nearly 35 % of the dams have multiple offspring
    - Off these nearly 40 % where from multiple sire breeds
      - This constitutes over 8 % of all dams that have multiple offspring from different sire breeds

- **Sires**
  - Only 2 out of 762 sires were only used on a single dam breed
    - Over 60 % sire offspring with all three dam breeds, strengthening the connection between dam breeds
  - The connection between sire breeds within herd * year groups was strong
    - Especially for later parities
      - First parity has very few observations
  - Many herd – year groups in common for all of the main beef breeds
  - Over 50 % of the herds used different sires within the same year, ensuring good links between sires

- **Herd – year**
  - 1/3 of all herds use multiple beef breeds within the same year
    - Under 10 % of the herds use multiple beef breeds for the heifers

- **Parity**
  - All sires were used in later parities
    - 50 % of the sires were not used on first parity cows
      - Especially BAQ, BBL, BSM and CHA
  - The sires create a good connection between first and later parities

Appendix D. Considerations about the statistical model for the genetic evaluation of beef × dairy crossbred for calving traits

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Background

The increased use of beef semen in dairy herds has created a demand for breeding values for beef sires to better plan matings of beef sires with dairy cows. A principal goal of the genetic evaluation for beef × dairy crossbreds is to allow comparisons of beef sires across the breeds.

The phenotype for calving traits is affected by two individuals: the calf itself, and its mother, and genetic effects influence both these components. These so-called direct and maternal genetic effects are not very strongly correlated (sometimes even negatively correlated). Hence, most genetic evaluations for calving traits include the direct and maternal genetic effects as separate effects.

The structure of the data to be included in the beef × dairy crossbred evaluation is special in the sense that there are only beef sires and dairy dams. Hence, there is no information for maternal traits for the beef sires, and there is much scarcer information (as compared to the dairy evaluation) for direct traits for dairy sires.

The purpose of this document is to describe options, their pros and cons, for the statistical model for the genetic evaluation of calving traits.

Options

Direct and maternal effects will be the focus of this document. The model will contain a number of (fixed/random) systematic environmental effects (like herd and year), which will be denoted as "syst env". Color coding in the models is such that gold relates to effects of the calf, and purple relates to the effects of the mother. Effects in *italics* are random effects, and effects in normal/roman are fixed effects.

AMDMP

Animal model with random direct and maternal genetic effects, as well as a random permanent environmental effect of dam (pe_{dam}); the random permanent environment effect can only be included if a dam can have more than one observation.

$$y = \text{syst env} + animal + dam + pe_{dam} + e$$

AMDM

Animal model with random direct and maternal genetic effects, without a random permanent environmental effect of dam. This model is used in the calving trait evaluation for dairy breeds.

$$y = \text{syst env} + animal + dam + e$$

AMDP

Animal model with random direct and maternal genetic effects, as well as a random permanent environmental effect of dam (pe_{dam}); the random permanent environment effect can only be included if a dam can have more than one observation.

$$y = \text{syst env} + animal + pe_{dam} + e$$

AMD

Animal model with random genetic effects of animal, without a random permanent environmental effect of dam. This model was used in the Danish pilot project on calving trait evaluation for beef × dairy breeds.

$$y = \text{syst env} + animal + e$$

Variations of AMDP wrt modeling of maternal effects

AMDPBY

Animal model with random genetic effects of animal, a fixed effect of dam breed – year, with a random permanent environmental effect of dam.

$$y = \text{syst env} + \text{breed}_{\text{dam}} - \text{year} + animal + pe_{dam} + e$$

AMDBY

Animal model with random genetic effects of animal, a fixed effect of dam breed – year, without a random permanent environmental effect of dam.

$$y = \text{syst env} + \text{breed}_{\text{dam}} - \text{year} + animal + e$$

Variations of AMDMP wrt modeling of direct effects

SMDMP

Sire-dam model with a random genetic effect of sire and dam, with a random permanent environmental effect of dam.

$$y = \text{syst env} + sire + dam + pe_{dam} + e$$

Other variations

SMDM

Sire-dam model with a random genetic effect of sire and dam, without a random permanent environmental effect of dam.

$$y = \text{syst env} + sire + dam + e$$

SMDPBY

Sire model with a random genetic effect of sire, a fixed effect of dam breed – year, with a random permanent environmental effect of dam.

$$y = \text{syst env} + \text{breed}_{\text{dam}} - \text{year} + sire + pe_{dam} + e$$

SMDBY

Sire model with a random genetic effect of sire, a fixed effect of dam breed – year, without a random permanent environmental effect of dam.

$$y = \text{syst env} + \text{breed}_{\text{dam}} - \text{year} + sire + e$$

Pros and Cons

Phenotypes for calving traits are affected by both the calf and the dam, and genetically the direct and maternal effects are not the same traits. One of the simplest models of all, AM, does not achieve this. Breeding values for beef sire from this model only describe the direct genetic effect whereas the breeding values for dairy sires from this model are affected by both direct and maternal genetic components. Assuming a unity correlation, the same heritability, etc. in a simple animal model is undesirable. Hence, the model of choice preferably separates the genetic contribution of both individuals (calf and dam).

Modelling of the maternal (genetic) effects can be achieved in several ways, by including

- Random maternal genetic effect and permanent environmental effect
- Random maternal genetic effect
- Random permanent environmental effect
- Fixed effect of dam breed – year and a random permanent environment effect
- Fixed effect of dam breed – year

The purpose of the evaluation is to calculate breeding values for direct genetic effects of beef sires, and the sole purpose of modelling of maternal (genetic) effects is to reduce noise in the breeding values of beef sires. Thus, models based on the first two options (with a random maternal genetic effect; AMDMP, AMDM) are probably too complex in relation to the data structure and the purpose of the genetic evaluation.

Including a fixed effect of dam breed – year appears to be the simplest solution of all, as it avoids the estimation of an effect for each dam, but accounts for (some of the) differences in genetic level for maternal traits. The disadvantage of this approach is that it ignores information if there are dams with multiple offspring. Those are treated as independent observations, where they in reality can provide links between beef sire breeds (if the same dam has multiple offspring with sires from different beef breeds).

Including a random permanent environment effect has the advantage of exploiting that dams can provide links between beef breed (creating more stable across breed comparisons). It also considers difference between dams more accurately. The disadvantage is that many effects need to be estimated.

Modeling of the direct genetic effects can be achieved in several ways, by including:

- Random direct genetic effect
- Random sire genetic effect

The purpose of the evaluation is to calculate breeding values for direct genetic effects of beef sires and including a random sire genetic effects suffices for that purpose. This approach also has the advantage of having fewer parameters (breeding values) to estimate, and that the trait and breeding values are clean from maternal effects.

Including a direct genetic effect by means of an animal model results in more parameters (breeding values) to estimate, for individuals that are not very interesting as selection candidates. More importantly, employing an animal model puts extra demands on the modeling of the maternal effects, to ensure that the trait and breeding values are as little affected by maternal effects as possible. (Some of the variation due to maternal effects will end up in the breeding values of dairy bulls if only a fixed effect of dam breed – year is included in the model).

Use of Pedigree information

All models contain a direct genetic effect (either via an animal effect or via a sire effect), and it makes good sense to use knowledge about relationships among individuals. For animal models, the pedigree information would include sire and dam of the individual, traced back for a number of generations. In case of sire models, there are a number of options, two of which are listed here: 1) full pedigree, i.e. for each beef sire we use info on the sire and dam of the beef sire (and trace the pedigree for a few generation), and 2) “male” pedigree, i.e. for each beef sire we use info on the sire and mgs for the beef sire (and trace the pedigree for a few generations). In practice the differences between these two options will be very small, as one can expect there to be sparse information about the beef bull dams. The advantage of “male” pedigree (in comparison to “full” pedigree) is a smaller pedigree relationship matrix and fewer breeding values to solve, which normally reduces the time to run the genetic evaluation.

Handling systematic breed differences

With respect to systematic differences between beef breeds, there are two options: phantom parent groups versus including beef sire breed as a fixed effect. The advantage of phantom parent groups is that systematical breed differences are automatically incorporated into the breeding values, whereas they need to be explicitly added to breeding values of beef sire breed is included as fixed effect (in order to make breeding values comparable across breeds). Phantom parent groups are fairly distant from the data (that is, if we trace back the pedigree for, say, five generations, then the phg describe those “historical” differences), whereas a fixed effect of beef breed describe the actual/current breed differences. In addition, inclusion of phantom parent groups requires rules to assign phantom parents to groups, which is not as straightforward as including a fixed effect of sire breed in the model. The latter two arguments result in a slight preference towards considering systematic breed differences by means of a fixed effect of sire breed in the model. It is then important to remember to add these breed differences to the breeding values.

Appendix E. Contemporary group definition for calving traits

Non-informative herd – year groups

The question regarding the amount of informative herd – year (HY) groups was raised. If a HY group only has used a single sire, or only a single calf has been born, they are in practice not informative with regards to the evaluation. Therefore, this was investigated.

In the NAV Dairy evaluation for calving traits, a fixed effect of herd – 5-year and a random effect of herd – year is included in the model. The fixed herd – 5-year effect takes the trend into account, and describes the deviation between years, whilst the random effect of HY models the deviation from the fixed effect and describes the deviation within herd. From a theoretical standpoint it is an advantage to include HY as a random effect especially when there are many small HY groups. In this way, the information is not lost, as would be the case if HY were included as a fixed effect. Including a fixed herd – 5-year effect ensures that the overall trend does not suffer much from bias, which would not be the case if only a random effect was included (i.e. the phenotypic trend would be regressed towards zero).

The challenge with the beef × dairy data is that there are much less observations, especially in the first years of the dataset (2000-2012). This has made it difficult to form HY groups that are large enough, as many of the groups only have a single observation, or only a single sire has been used. Even when the first 10 years were pooled into two 5-year groups, the number of small herd – 5-year groups was very high, especially for first parity cows. Different possibilities to handle were put forward, listed below.

Possible ways of handling small HY groups

The first years of the dataset contain a small amount of observations from 2000-2012.

- Pooling the years with few observations
  - 2, 5 or 10 year groups
    - Arbitrary which group size to choose
      - A tradeoff between accuracy and precision
    - The longer period of time that the years are pooled over, the more noise will be introduced, as many different things could have happened in that time period.
    - If all the “small” years are pooled together the HY groups would presumably be larger, but the variance would also be big between the years.
- Instead of pooling the years, the first years could be deleted
  - This would reduce the amount of data available, but if the data does not contribute with much information, this might not be a problem.
    - A downside is that pedigree relatedness is lost
- Include data on purebred dairy calves
  - To make the HY groups larger and more informative (i.e., better estimation of the mean of the HY group), data from purebred dairy calves could be included
    - HY group size would be increased

  - More observations would mean that the evaluation becomes computationally heavier.
  - Sire effects for dairy breeds needs to be modelled
  - More dams with multiple calvings, which will increase the connectedness in the data

- Include herd effects from the dairy evaluation
  - Estimated herd effects from the dairy evaluation could be included in order to predict the HY groups more accurately.

In the following different methods of handling this problem and their consequences have been investigated.

Number of observations in herd – year groups

Figure E.1 visualizes the percentage of herd – year (HY) groups with up to 5 calves borne by 1st parity cows. The columns with the bold colour are for all HY groups, and the lighter colours are the percentage of HY groups when the first 10 years are pooled into two 5-year groups. A large percentage of all HY groups had only a single observation: 61 %, 71 % and 59 % for DNK, FIN and SWE respectively. For all three countries, below 2 % of the HY groups contain more than 10 calves. This is due to very few calves being borne by 1st parity cows. By pooling the first 10 years (the light columns), the percentage of HY groups with only a single observation was reduced, especially for the Finnish HY groups, and a larger percentage of the HY groups had >1 calf. However, only 1.2, 1.8 and 2.9 % of the HY groups for Finland, Denmark and Sweden respectively had more than 10 calves.

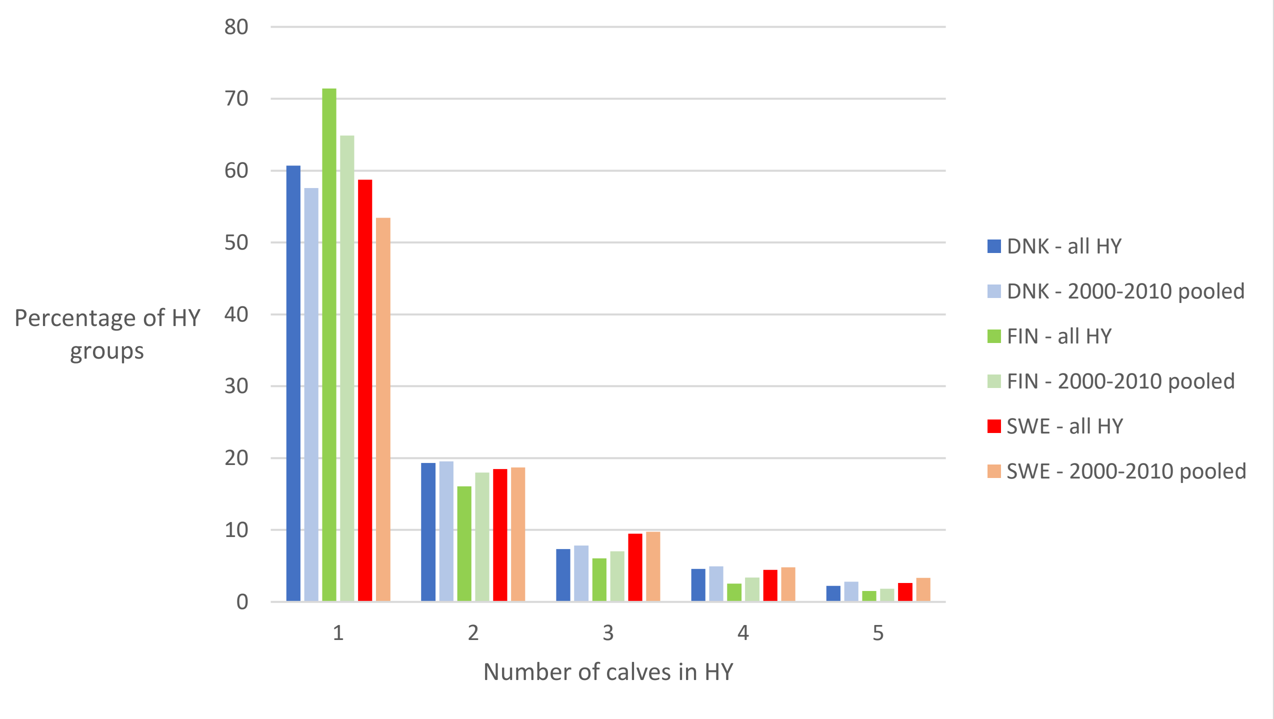

Figure E.1. Percentage of HY groups with up to 5 calves borne by 1st parity cows.

The majority of calves were borne by later parity cows, and therefore the percentage of HY groups with only a single observation was much lower than for the 1st parity cows: 29, 39, 41.5 % of the HY groups only had a single observation for DNK, FIN and SWE respectively (Figure E.2). If the first 10 years were pooled the percentage was further reduced to 22, 25 and 30 % for DNK, FIN and SWE respectively. However, there was still a large proportion of the HY groups that have less than 10 observations: 77, 96 and 95 % for DNK, FIN and SWE respectively. After pooling the percentage was 70, 89 and 88 % respectively.

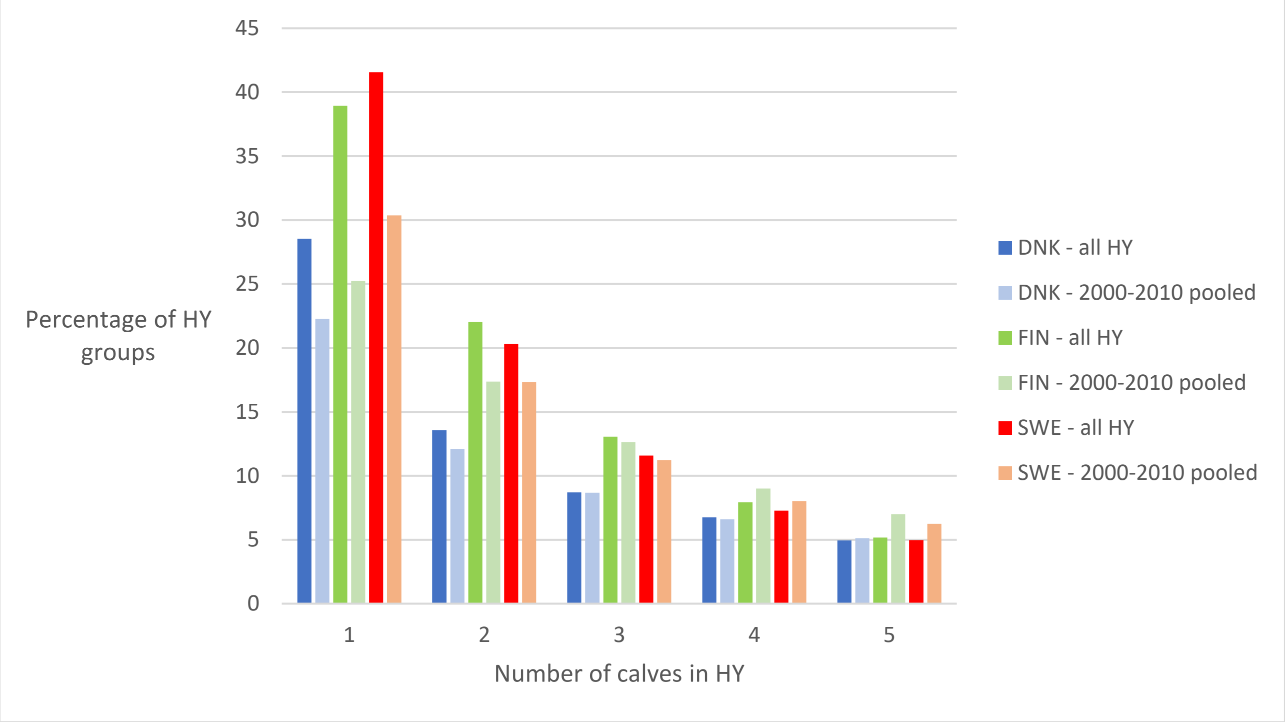

Figure E.2. Percentage of HY groups with up to 5 calves borne by later parity cows.

Different minimum levels were investigated for eliminating the non-informative HY groups. In Table E.1 three different cut off levels are shown ≤ 2, ≤ 5 and ≤ 10 calves for both first and later parities. As seen above, the amount of calves borne by 1st parity cows was very low, and as a result of this, there were also few animals in the HY groups. By pooling the data from 2000-2010 into two 5-year groups, this was slightly improved, but all countries had more than 70 % of the HY groups with only 2 or less observations; for Finland over 80 % of the HY groups were in this category. This makes it very difficult to edit the data for the 1st parity cows, as the majority of data would be lost at the lowest limit. With regards to later parities the data structure was better as there were more observations. However, at the minimum level nearly 50 % of the Swedish HY groups would be deleted.

Table E.1. Percentage of HY groups with ≤ 2, ≤ 5 and ≤ 10 calves, for all and pooled HY

		DNK		FIN		SWE	
		All HY	**pooled HY**	**All HY**	**pooled HY**	**All HY**	**pooled HY**
1st parity	**≤ 2**	80.0	77.1	87.5	82.9	77.2	72.2
	≤ 5	94.2	92.7	97.6	95.1	93.7	90.1
	≤ 10	98.6	98.2	99.7	98.8	98.6	97.1
Later parities	**≤ 2**	42.1	34.4	61.0	42.6	61.9	47.7
	≤ 5	62.5	54.8	87.1	71.3	85.7	73.2
	≤ 10	76.7	70.3	96.3	88.6	95.3	88.0

The amount of HY groups that would be deleted is very large, especially for the 1st parity cows, but the number of calves it corresponds to is shown in Table E.2. For the first parity, approximately 90 % (97 % for Finland) of the calves are in HY groups with 10 or less calves. When the first years were pooled, the percentage of calves in herds with more than 10 calves increased. This was the same for ≤ 2 and ≤ 5. For later parities Denmark varied greatly from both Finland and Sweden. Only 21.5 % of the Danish calves were in HY groups with ≤ 10 calves compared to over 50 % of the calves from FIN and SWE.

Table E.2. Percentage of calves in HY groups with ≤ 2, ≤ 5 and ≤ 10 calves, for all and pooled HY

		DNK		FIN		SWE	
		All HY	**pooled HY**	**All HY**	**pooled HY**	**All HY**	**pooled HY**
1st parity	**≤ 2**	48.7	43.3	65.2	53.5	45.2	35.3
	≤ 5	74.0	69.0	87.8	76.7	73.3	60.6
	≤ 10	90.0	87.4	97.1	90.5	90.0	80.7
Later parities	**≤ 2**	6.1	4.1	26.6	11.8	25.3	12.6
	≤ 5	14.6	11.0	57.6	33.3	52.5	31.4
	≤ 10	26.5	21.5	79.3	59.1	74.3	53.3

Conclusion

Nearly all the HY groups had 10 or less calves for 1st parity cows for all three countries. For later parities, the HY groups were slightly larger especially for Denmark. It seems that a lot of data would be lost if a minimum number of observations in each HY is demanded, despite pooling the first years. The percentage of calves for the different cut-off levels was slightly lower when the first 10 years were pooled into two 5-year groups. The majority of calves from 1st parity cows were in HY groups with 10 or less calves for all three countries. For calves from later parity cows, the percentage of calves that are in HY groups with 10 or less calves was lower, especially for Denmark. It does not seem feasible to restrict the size of the HY groups, as a very large percentage of the observations would be lost, especially for 1st parity cows, where the amount of observations was very low.

Consequences of edit on HY group size

It was investigated how much data would be lost by reducing the dataset, such that all HY had more than two beef × dairy crossbred calves, and what influence such edit would have on the sires. The analysis was done for first and later parities separately.

First parity

The number of calves borne by first parity cows from 2012-2016 was 14,012. In total, 433 different sires had offspring. In Table E.3, the number of sires with different numbers of offspring are shown, both for the full and the reduced dataset (>2 beef × dairy crossbreds per HY group). Of the 433 sires, 400 had less than 100 offspring borne by first parity cows. This corresponds to over 92 % of the sires. Only two sires had more than 500 offspring. By reducing the dataset (setting a minimum limit for number of calves per herd – year), over 20 % of the sires no longer had calves borne by first parity cows. In the reduced dataset only 340 bulls had sired offspring. Of these, 319 had less than 100 offspring, and none had over 300 offspring.

Table E.3. Number of sires in each offspring group for both the full and the reduced dataset for first parity cows

	Full		Reduced	
Nr offspring	**Nr sires**	**% of total**	**Nr sires**	**% of total**

< 100	400	92.4%	319	93.8%
100-200	17	3.9%	14	4.1%
200-300	8	1.8%	7	2.1%
300-400	3	0.7%	0	0.0%
400-500	3	0.7%	0	0.0%
> 500	2	0,5%	0	0,0%
Total	*433*		*340*	

For the sires with less than 100 offspring over 55 % had 10 or less offspring, and when the dataset was reduced it was over 60 % (Table E.4). The number of calves per sire was very low both in the full and reduced dataset. It could be argued that sires need to have more than 100 offspring for breeding values to be published. Requiring more than 100 offspring to publish breeding values, as is done in Denmark at present, only 33 sires would be published when all data was used and 21 sires when data was reduced. This means that 12 bulls would not be published if data is reduced.

Table E.4. Number of sires in each offspring group for both the full and the reduced dataset for first parity cows

	Full		Reduced	
Nr offspring	Nr sires	% of total	Nr sires	% of total
1	66	15.2%	50	14.7%
≤ 5	171	39.5%	156	45.9%
≤ 10	242	55.9%	215	63.2%
≤ 50	366	84.5%	303	89.1%
≤ 100	400	92.4%	319	93.8%

Later parities

For the later parities, there were 264,180 calves sired by 574 different bulls. By reducing the dataset to only contain HY groups with at least two beef × dairy calves, 3 % of the sires had no longer any offspring in the data. Approx. 50 % of the sires had less than 100 offspring, both for the full and the reduced dataset. Over 20 % of the sires had more than 500 offspring for both the full and reduced dataset (Table E.5).

Table E.5. Number of sires in each offspring group for both the full and the reduced dataset, for later parities

	Full		Reduced	
Nr offspring	Nr sires	% of total	Nr sires	% of total
< 100	280	48.8%	280	50.4%
100-200	69	12.0%	71	12.8%
200-300	53	9.2%	46	8.3%
300-400	26	4.5%	24	4.3%
400-500	19	3.3%	14	2.5%
> 500	127	22.1%	121	21.8%
Total	*574*		*556*	

Below 10 % of the sires had a single offspring, and the number was decreased when the dataset was reduced (Table E.6). 20 % of the sires had less than 10 offspring. It seems that by requiring at least two offspring in a HY groups, the sires with few offspring were deleted.

Table E.6. Number of sires in each offspring group for both the full and the reduced dataset, for later parities

	Full		Reduced	
Nr offspring	**Nr sires**	**% of total**	**Nr sires**	**% of total**
1	39	6.8%	31	5.6%
≤ 5	84	14.6%	78	14.0%
≤ 10	112	19.5%	107	19.2%
≤ 50	224	39.0%	214	38.5%
≤ 100	280	48.8%	280	50.4%

Considering the limit for publishing breeding values of 100 offspring per sire, 294 sires would be published when all data are used and 276 sires if data is reduced. This means that only 18 bulls would not be published if data is reduced.

Later parities 2014-2016

When use of beef semen for dairy became more intense in Denmark, many beef bulls were only used very limited, because beef breed organizations “cleaned up” their inventories. To see if the use of sires has been more intense in the most recent years 2014-2016, the same analysis was run for this period. In total, 212,513 crossbred calves were born in this time period. The picture (Table E.7 and Table E.8) is nearly the same as for 2012-2016, but there are slightly fewer beef sires with many offspring as there are fewer years.

Table E.7. Number of sires in each offspring group for both the full and the reduced dataset, for later parities.

	Full		Reduced	
Nr offspring	**Nr sires**	**% of total**	**Nr sires**	**% of total**
< 100	288	54.6%	287	55.5%
100-200	59	11.2%	62	12.0%
200-300	41	7.8%	39	7.5%
300-400	28	5.3%	22	4.3%
400-500	7	1.3%	6	1.2%
> 500	104	19.7%	101	19.5%
Total	*527*		*517*	

Table E.8. Number of sires in each offspring group for both the full and the reduced dataset, for later parities

	Full		Reduced	
Nr offspring	**Nr sires**	**% of total**	**Nr sires**	**% of total**
≤ 5	94	17.8%	90	17.4%
≤ 10	126	23.9%	127	24.6%
≤ 50	234	44.4%	233	45.1%
≤ 100	288	54.6%	287	55.5%

Conclusion

If a minimum limit is set to the number of offspring in a HY groups, then some sires will be edited out of the dataset or lose a significant amount of data. In the following section different editing criteria will be analysed.

Number of herd-year groups with calves from only a single sire

Over 70 % of the HY groups used only a single sire for their first parity cows; nearly 80 % of the Finnish HY groups used only a single sire (Table E.9). For the later parity cows, just below half of the HY groups used only a single sire; for the later parity cows most Swedish HY groups used only a single sire. When the HY groups from 2000-2010 were pooled in two 5-year groups, 5 % fewer HY groups had only a single sire for 1st parity cows and nearly 13 % fewer for later parity cows; the situation for especially the Finnish data improved substantially.

Table E.9. Number and percentage of HY groups with only a single sire, by parity and country, when treating HY as-is and when the first 10 years are pooled into 5-year groups

	First parity			**Later parities**		
	1 sire	**>1 sires**	**% total**	**1 sire**	**>1 sires**	**% total**
	HY as-is					
DNK	2548	982	72.2%	6807	9981	40.5%
FIN	5475	1507	78.4%	35012	41116	46.0%
SWE	4331	1871	69.8%	15664	15360	50.5%
Total	*12354*	*4360*	*73.9%*	*57483*	*66457*	*46.4%*
	First 10 years pooled in 5-year groups					
DNK	2217	1009	68.7%	4521	8956	33.5%
FIN	4213	1669	71.6%	14564	32123	31.2%
SWE	3265	1828	64.1%	7636	11933	39.0%
Total	*9695*	*4506*	*68.3%*	*26721*	*53012*	*33.5%*

Table E.10. Number and percentage of calves assigned to HY groups with only a single sire, by parity and country, when treating HY as-is and when the first 10 years are pooled into 5-year groups

	First parity			**Later parities**		
	1 sire	**>1 sires**	**% total**	**1 sire**	**>1 sires**	**% total**
	HY as-is					
DNK	3414	3787	47.4%	16803	136500	11.0%
FIN	6198	4896	55.9%	43531	193712	18.3%
SWE	5532	7592	42.2%	21565	79353	21.4%
Total	*15144*	*16275*	*48.2%*	*81899*	*409565*	*16.7%*
	First 10 years pooled in 5-year groups					
DNK	3023	4178	42.0%	12729	140574	8.3%
FIN	4814	6280	43.4%	19698	217545	8.3%
SWE	4260	8864	32.5%	11768	89150	11.7%
Total	*12097*	*19322*	*38.5%*	*44195*	*447269*	*9.0%*

Nearly 50 % of the calves were born in HY groups that only used a single sire for 1st parity cows, compared to only 16.7 % of the calves borne from later parity cows (Table E.10). The largest proportion of calves from herds that used only a single sire were from Finnish 1st parity cows, and for later parities it was the Swedish calves. When all HY groups from 2000-2010 were pooled in two 5-year groups, 10 % fewer calves borne by 1st parity cows were in HY that had only a single sire. For later parity cows the amount of calves was nearly halved to only 9 % of the calves.

Conclusion

By restricting the number of HY groups to only those that used more than one sire, for calves borne by 1st parity cows nearly 75 % of the HY groups and 50 % of the calves would be deleted if the first 10 years are not pooled. If the first 10 years are pooled into two groups, nearly 70 % of the HY groups would still be deleted, and nearly 40 % of the calves. This seems to be a quite drastic edit, but if the observations are essentially non-informative in the statistical model for genetic evaluation, then removing that many observations might not have a large effect on the results.

Investigation of the data from 2000-2012

As the contemporary group structure was found to be poor, further analyses were conducted. The structure of the data from 2000-2012, with few observations each year, was investigated. Three approaches were used: 1) all HY groups were counted separately, 2) the HY groups were pooled into two 6-year groups from 2000-2006 and 2006-2012, and 2) all 12 years were pooled together.

Percentage of HY groups

Table E.11 shows the percentage of HY groups with ≤2, ≤5 and ≤10 calves, by country, for the three approaches. Expectedly, when all the herd – years were pooled into a single HY group, the groups were larger than when all herd – years were separate. However, the increase in HY size was not very large for the 1st parity cows. For later parity cows around 80 % of all HY groups were ≤10 and around 40 % were ≤2.

Table E.11. Percentage of HY groups with ≤ 2, ≤ 5 and ≤ 10 calves (for calves born 2000-2012)

	DNK			FIN			SWE		
	All HY	**6-yrs**	**12-yrs**	**All HY**	**6-yrs**	**12-yrs**	**All HY**	**6-yrs**	**12-yrs**
				1st parity					
≤2	82.4	76.1	74.7	89.7	81.8	79.5	79.4	70.4	68.8
≤5	94.4	91.3	90.2	98.5	94.5	93.3	95.2	89.0	87.9
≤10	98.6	97.6	97.0	99.8	98.5	97.9	99.0	96.3	96.0
				>1 parity					
≤2	56.9	45.7	43.6	67.5	39.3	36.8	66.3	44.9	42.0
≤5	78.3	67.9	66.1	92.0	67.3	63.0	89.1	70.0	66.9
≤10	90.4	81.8	79.7	98.5	86.0	81.6	97.0	85.8	83.6

Percentage of calves in HY groups

Table E.12 shows the percentage of calves in HY groups with ≤2, ≤5 and ≤10 calves. As for the percentage of HY groups, the number of calves in small HY groups were reduced by pooling. The reduction was larger as there are many more calves borne by later parity cows compared to first parity cows.

Table E.12. Percentage of calves in HY groups with ≤ 2, ≤ 5 and ≤ 10 calves (for calves born 2000-2012)

DNK	FIN	SWE

	All HY	6-yrs	12-yrs	All HY	6-yrs	12-yrs	All HY	6-yrs	12-yrs
	1st parity								
≤2	51.5	39.4	36.7	70.4	50.3	45.1	49.7	50.3	45.1
≤5	73.6	62.8	58.9	91.3	73.1	68.3	78.6	73.1	68.3
≤10	89.6	82.6	79.5	97.6	87.9	83.9	92.4	87.9	83.9
	>1 parity								
≤2	16.2	8.0	6.8	36.4	9.7	7.4	31.2	10.6	8.8
≤5	33.9	19.0	16.9	72.3	28.3	21.8	61.1	27.0	23.3
≤10	53.9	32.8	29.1	90.9	53.2	42.1	81.6	47.8	42.8

Conclusion

Even when all years were pooled together, the number of HY groups with more than 10 calves was very low, especially for first parity cows. For later parity cows the improvement was much larger, but the amount of 'noise' pooling so many years together could be quite problematic.

Investigation of data from 2012-2016

Table E.13 shows how many calves were born from 2012-2016. Most calves are from the most recent years for all three countries. Finland has had a high level of beef × dairy calves for longer than Sweden and Denmark. But the increase in use of beef semen has been largest in the latter two countries.

Table E.13. Number of calves born 2012-2016 by country

Year	ALL		DNK		FIN		SWE	
	Nr calves	%	Nr calves	%	Nr calves	%	Nr calves	%
2012	24453	8.8	6065	5.00	14207	12.67	4181	9.3
2013	31299	11.3	9565	7.9	16675	14.9	5059	11.3
2014	42150	15.2	14320	11.8	20864	18.6	6966	15.6
2015	57283	20.6	21993	18.1	25682	22.9	9608	21.5
2016	123007	44.2	69467	57.2	34568	30.9	18972	42.4
Total	*278192*		*121410*		*111996*		*44786*	

In practice, it is only in Sweden that heifers are routinely inseminated with beef semen. In Denmark and Finland only 3 and 4 % of the calvings from 2012-2016 are heifer calvings. Only 5 % of all the calves are from heifer calvings. The majority of calves are borne by dams in their 2, 3 or 4 calving (Table E.14). The very small number of calvings by primiparous cows also resulted in very few observations per HY group, especially for Denmark and Finland (Table E.15).

Table E.14. Number of calves by parity number of the dam (for calves born 2012-2016)

Dam parity number	DNK		FIN		SWE	
	Nr calves	%	Nr calves	%	Nr calves	%
1	3519	2.9	4708	4.2	5785	12.9
2	31885	26.3	26944	24.1	12847	28.7
3	36654	30.2	32704	29.2	12023	26.9
4	24854	20.5	24344	21.7	7554	16.9
5	14253	11.7	13530	12.1	3891	8.7
6	6667	5.5	6319	5.6	1799	4.0
7	2722	2.2	2649	2.4	714	1.6

8	778	0.6	776	0.7	167	0.4
9	70	0.1	22	0.0	6	0.0
10	5	0.0				
11	3	0.0				

Table E.15. Number of HY groups and calves borne by primiparous cows in HY groups with ≤ 2, ≤ 5 and ≤ 10 calves (for calves born 2012-2016)

	DNK		FIN		SWE	
	Nr HY	Nr Calves	Nr HY	Nr Calves	Nr HY	Nr Calves
≤2	77.3	46.5	83.5	56.6	74.1	39.7
≤5	94.2	75.9	95.9	81.4	91.5	66.2
≤10	98.8	91.8	99.5	95.7	98.1	86.7

In Table E.16 the number of calves, HY groups and the average number of calves in each HY group is shown for calves borne by 1st parity cows. The number of calves each year was low for all three countries, but surprisingly most calves were most in Finland. The percentage of calves borne by 1st parity cows in Sweden was much higher than Finland, but the total number of calves was higher in Finland compared to Sweden. The average number of calves in a HY group was only approximately 2 for all three countries, slightly higher for Sweden and lower for Finland.

Table E.16. Number of calves, HY groups and the average number of calves per HY for primiparous cows (for calves born 2012-2016)

Year	DNK			FIN			SWE		
	Nr calves	Nr HY	calves/ HY	Nr calves	Nr HY	calves/ HY	Nr calves	Nr HY	calves/ HY
2012	469	255	1.8	872	516	1.7	516	267	1.9
2013	611	283	2.2	1029	616	1.7	588	287	2.0
2014	618	282	2.2	1279	673	1.9	928	382	2.4
2015	677	317	2.1	1403	718	2.0	1233	482	2.6
2016	1144	517	2.2	125	99	1.3	2520	1024	2.5
Average			*2.1*			*1.7*			*2.3*

There were many more calves borne by later parity cows compared to 1st parity for all countries. This was also reflected in Table E.17, which shows the number of HY groups and calves borne by later parity cows in HY groups with ≤2, ≤5 and ≤10 calves. In Denmark over 80 % of the calves were in HY groups with more than 10 calves, whilst for Finland and Sweden it was only approximately 40 % of the calves. The percentage of HY groups with more than 10 calves was still low, especially for Finland and Sweden.

Table E.17. Number of HY groups and calves borne by multiparous cows in HY groups with ≤ 2, ≤ 5 and ≤ 10 calves (for calves born 2012-2016)

	DNK		FIN		SWE	
	Nr HY	Nr Calves	Nr HY	Nr Calves	Nr HY	Nr Calves
≤2	27.3	2.8	43.3	13.0	50.2	15.4
≤5	47.0	8.5	73.9	37.5	76.7	38.1
≤10	63.6	18.0	90.4	63.8	90.7	62.0

Comparison of three time periods

To evaluate how to treat the data in a future evaluation, three time periods 2000-2016, 2000-2012 and 2012-2016 were compared. In Table E.18 the number of HY groups borne by later parity cows in HY groups with ≤2, ≤5 and ≤10 calves for the three scenarios are shown. It is evident that the number of beef × dairy crossbred calves has greatly increased in later years (2012-2016). This has resulted in more calves being born within each HY group. In the early years (2000-2012) only few calves were born in each HY. For Finland and Sweden, the differences were not as large as for Denmark; this is also due to a higher average herd size in Denmark compared to the other countries.

Table E.18. Number of HY groups for calves borne by primiparous cows in HY groups with ≤2, ≤5 and ≤10 for three time periods

	DNK			FIN			SWE		
	2000-2016	**2000-2012**	**2012-2016**	**2000-2016**	**2000-2012**	**2012-2016**	**2000-2016**	**2000-2012**	**2012-2016**
≤2	42.1	56.9	27.3	61.0	67.5	43.3	61.9	66.3	50.2
≤5	62.5	78.3	47.0	87.1	92.0	73.9	85.7	89.1	76.7
≤10	76.7	90.4	63.6	96.3	98.5	90.4	95.3	97.0	90.7

Not only the average HY group size that has increased over time. Also the percentage of calves in HY groups with more than 10 calves has increased drastically from 2000-2012 to 2012-2016, the increase was 36, 27 and 20 % for Denmark, Finland and Sweden respectively (Table E.19).

Table E.19. Number calves borne by multiparous cows in HY groups with ≤2, ≤5 and ≤10, for three time periods

	DNK			FIN			SWE		
	2000-2016	**2000-2012**	**2012-2016**	**2000-2016**	**2000-2012**	**2012-2016**	**2000-2016**	**2000-2012**	**2012-2016**
≤2	6.1	16.2	2.8	26.6	36.4	13.0	25.3	31.2	15.4
≤5	14.6	33.9	8.47	57.6	72.3	37.5	52.5	61.1	38.1
≤10	26.5	53.9	17.97	79.3	90.9	63.8	74.3	81.6	62.0

Conclusion

The quality of the data from the most recent years was much better than from 2000-2012. Nevertheless, it does not seem like a good option to delete small HY groups. Therefore, an alternative approach was initiated.

Grouping of HY groups

As the HY groups are very small, especially for the first years of the data, and for 1st parity cows, it was decided to pool some of the herd – year groups. It was decided that HY groups should be pooled together within the same herd, until they had at least 3 observations. Not all herds had multiple observations, so some HY groups will still only consist of one or two observations. The pooling was done starting from the earliest year, going forwards to the most recent years. If the last HY had fewer than three observations, it was pooled with a previous HY groups, until there were at least three observations.

First parity

Before the pooling there were 18,122 herd – year groups. After the pooling over nearly 40 % of the HY groups were merged, leaving 11,207 different HY groups. Table E.20 shows the number of HY groups that have up to 10 observations, and the percentage of the total number of HY groups for each level. Before pooling 68 % of the HY groups only had a single observation, whilst after pooling this number was nearly halved to just under 40 %. After pooling the number of HY groups with more than three observations is significantly increased. The number of HY groups is halved.

Table E.20. Number of HY groups by group size (Nr obs) before and after pooling HY for calvings after primiparous cows

	Before pooling		After pooling	
Nr Obs	Nr HY	% of total	Nr HY	% of total
1	12299	67.9%	4065	36.3%
2	3029	16.7%	1818	16.2%
3	1261	7.0%	2316	20.7%
4	595	3.3%	1314	11.7%
5	318	1.8%	724	6.5%
6	187	1.0%	346	3.1%
7	123	0.7%	214	1.9%
8	91	0.5%	126	1.1%
9	46	0.3%	74	0.7%
10	40	0.2%	51	0.5%

Later parities

For calves borne by later parity cows, the number of calves in each HY group was not as low as for the first parity cows. Before pooling over 40 % of the HY groups however only had a single observation (Table E.21). This was severely decreased to only 4 % after pooling. The number of HY groups with only two observations also decreased greatly from 20.7 % to only 4.3 %.

Table E.21. Number of HY groups by group size (Nr obs) before and after pooling HY for calvings after multiparous cows

	Before pooling		After pooling	
Nr Obs	Nr HY	% of total	Nr HY	% of total
1	59230	42.4%	3188	3.9%
2	28932	20.7%	3557	4.3%
3	16278	11.7%	25562	31.0%
4	9687	6.9%	16395	19.9%
5	6096	4.4%	9914	12.0%
6	4145	3.0%	6145	7.5%
7	2978	2.1%	3963	4.8%
8	2106	1.5%	2679	3.2%
9	1526	1.1%	1819	2.2%
10	1247	0.9%	1405	1.7%

Conclusion

By pooling the HY groups into groups with at least three observations, the contemporary group structure is greatly improved. This seems like a good solution to the HY problems. However, it should be kept in mind that this method of pooling is quite a rough approach. Some HY groups could be pooled across many years, and a lot of management changes could have happened during this time period. This will introduce more “noise” in the model. This increased “noise” is however compensated by the great improvement in number of informative HY groups. It was decided that all HY groups with less than three observations should be deleted.

Appendix F. Distribution of (standardized) breeding values

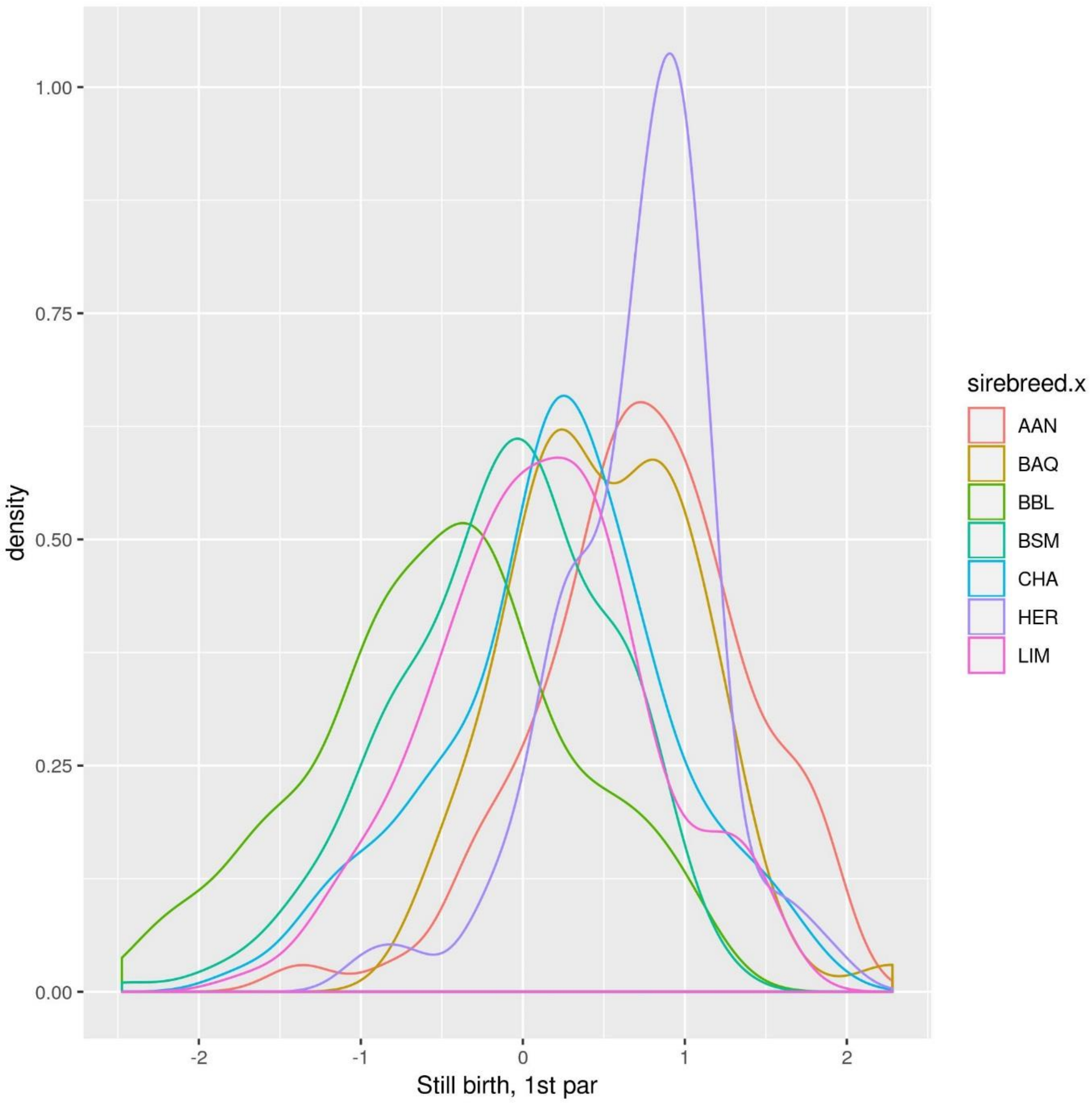

Figure F.1. Distribution of breeding values for still birth, primiparous cows (1st par), expressed in units σ_s, for beef sires with crossbred offspring from the 7 most used beef breeds.

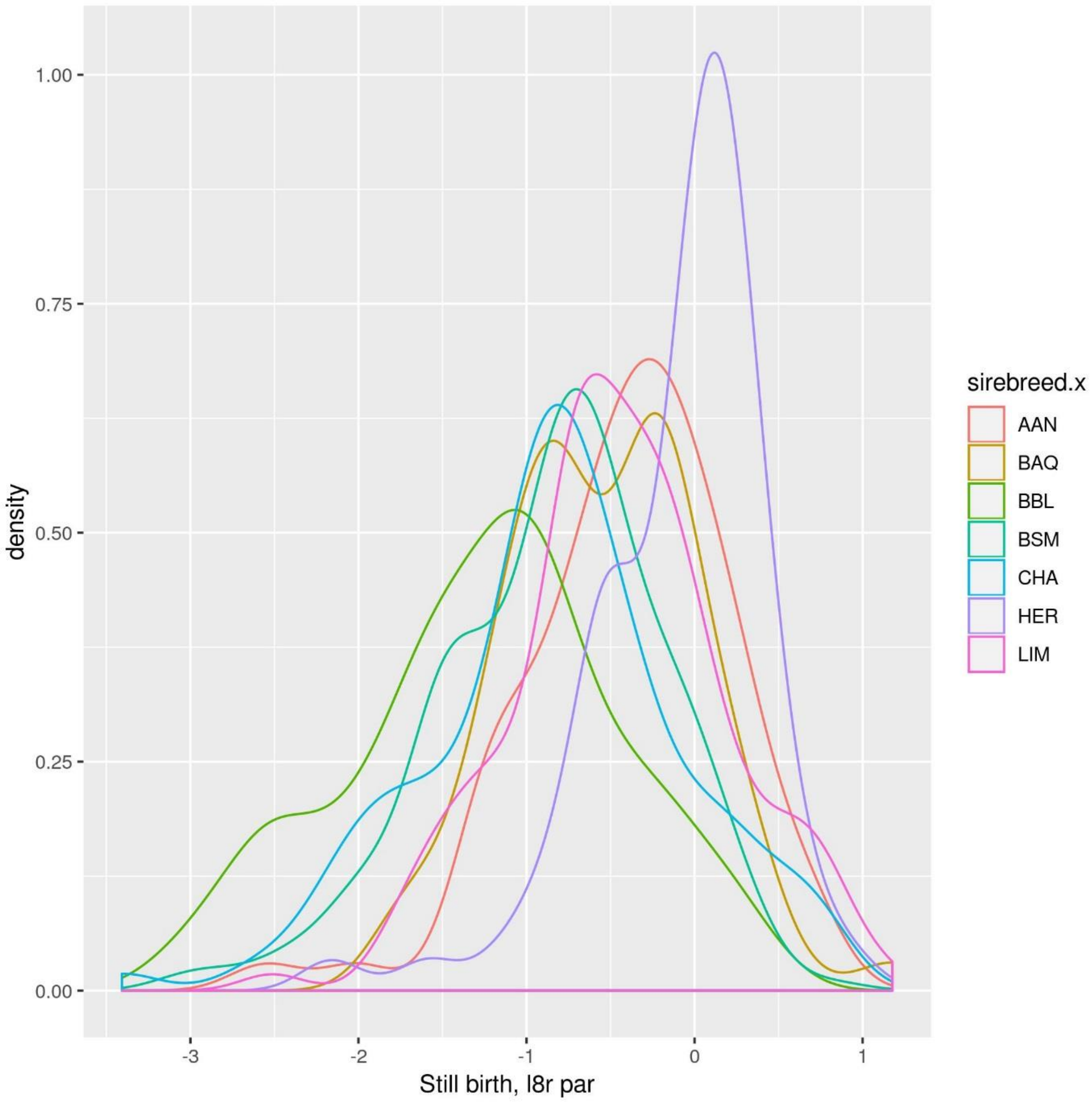

Figure F.2. Distribution of breeding values for stillbirth, multiparous cows (l8r par), expressed in units σ_s, for beef sires with crossbred offspring from the 7 most used beef breeds.

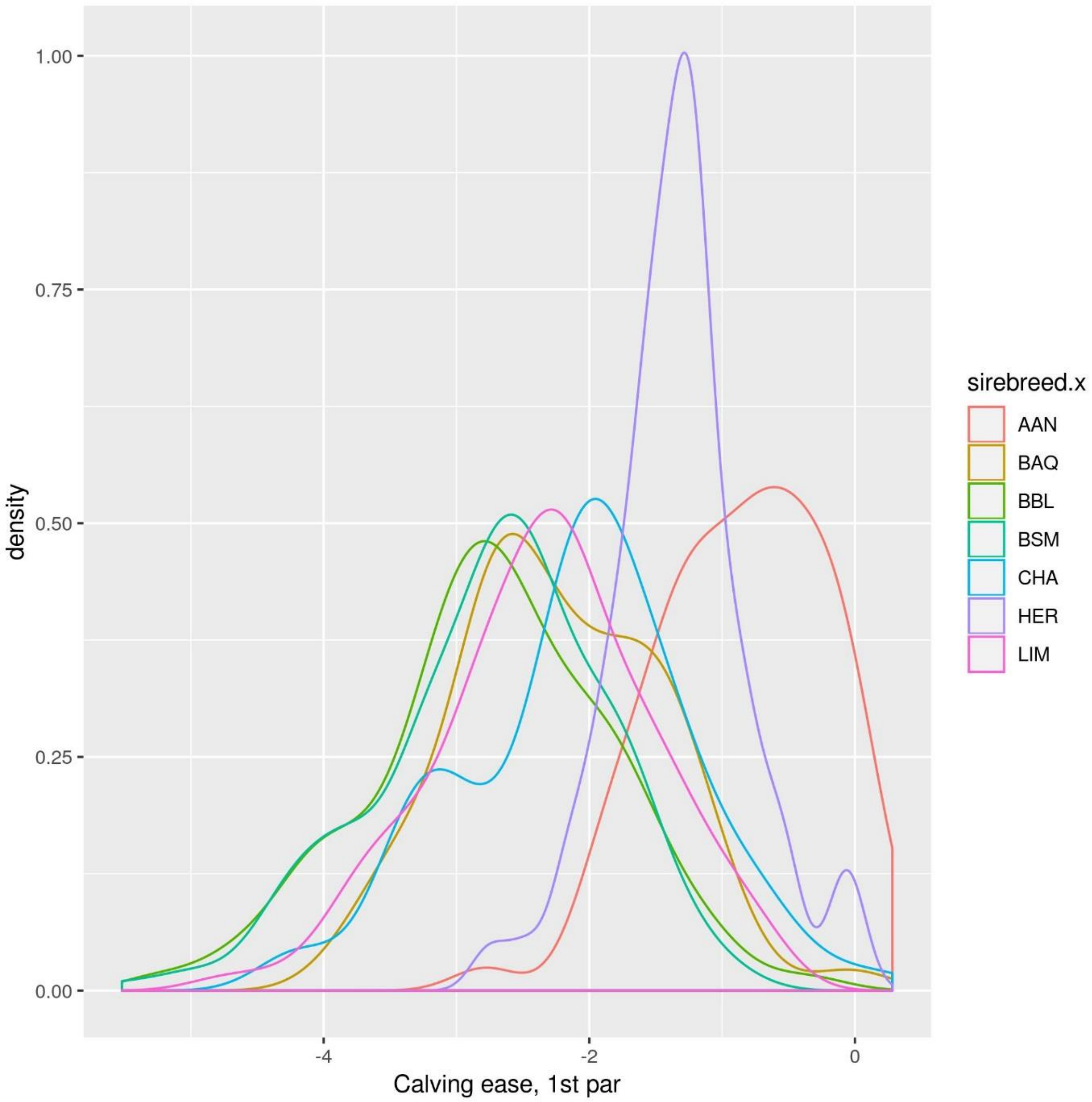

Figure F.3. Distribution of breeding values for calving ease, primiparous cows (1st par), expressed in units σₛ, for beef sires with crossbred offspring from the 7 most used beef breeds.

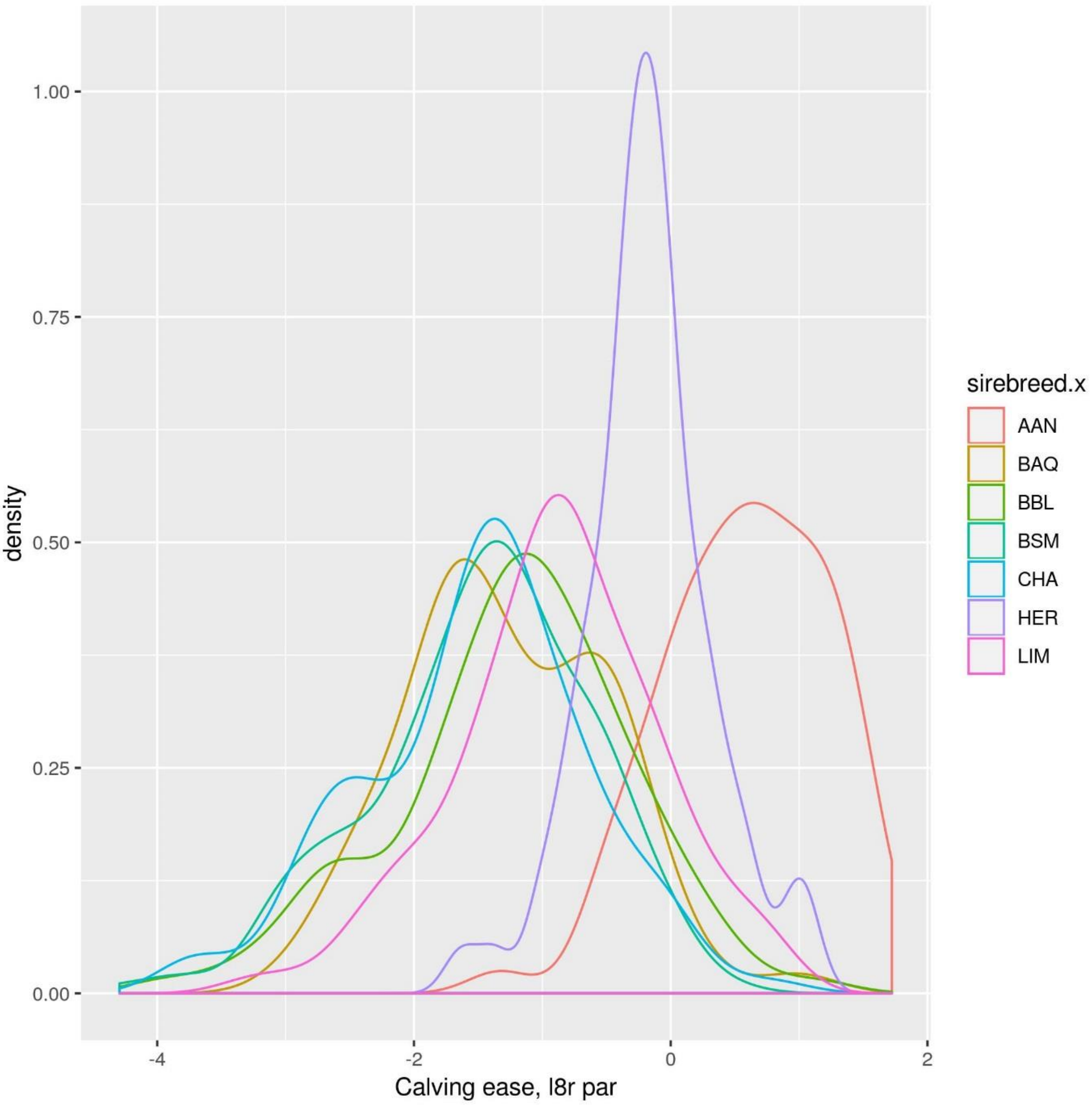

Figure F.4. Distribution of breeding values for calving ease, multiparous cows (l8r par), expressed in units σ_s, for beef sires with crossbred offspring from the 7 most used beef breeds.

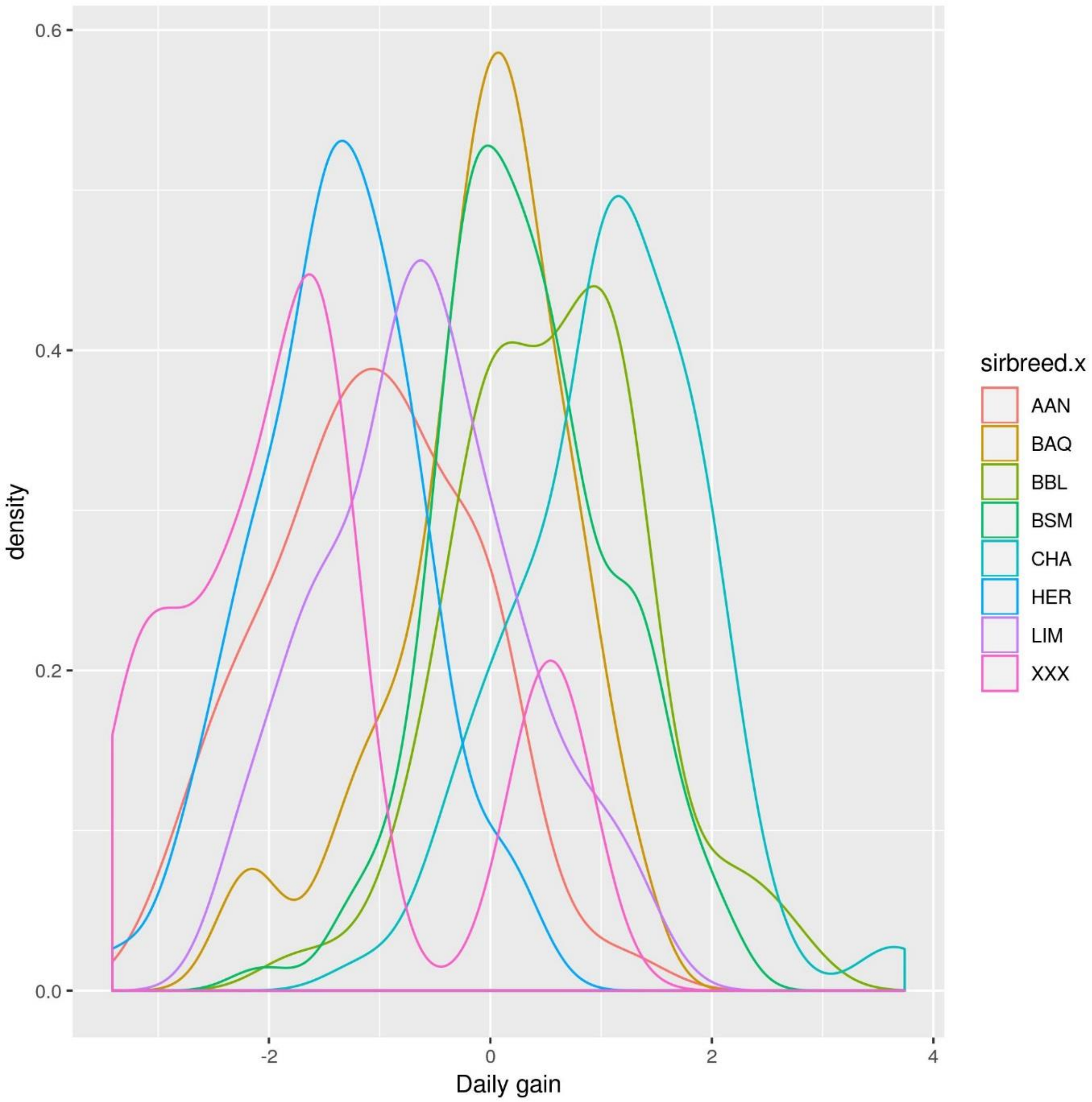

Figure F.5. Distribution of breeding values for daily carcass gain index, expressed in units σ_s, for beef sires with crossbred offspring from the 8 most used beef breeds.

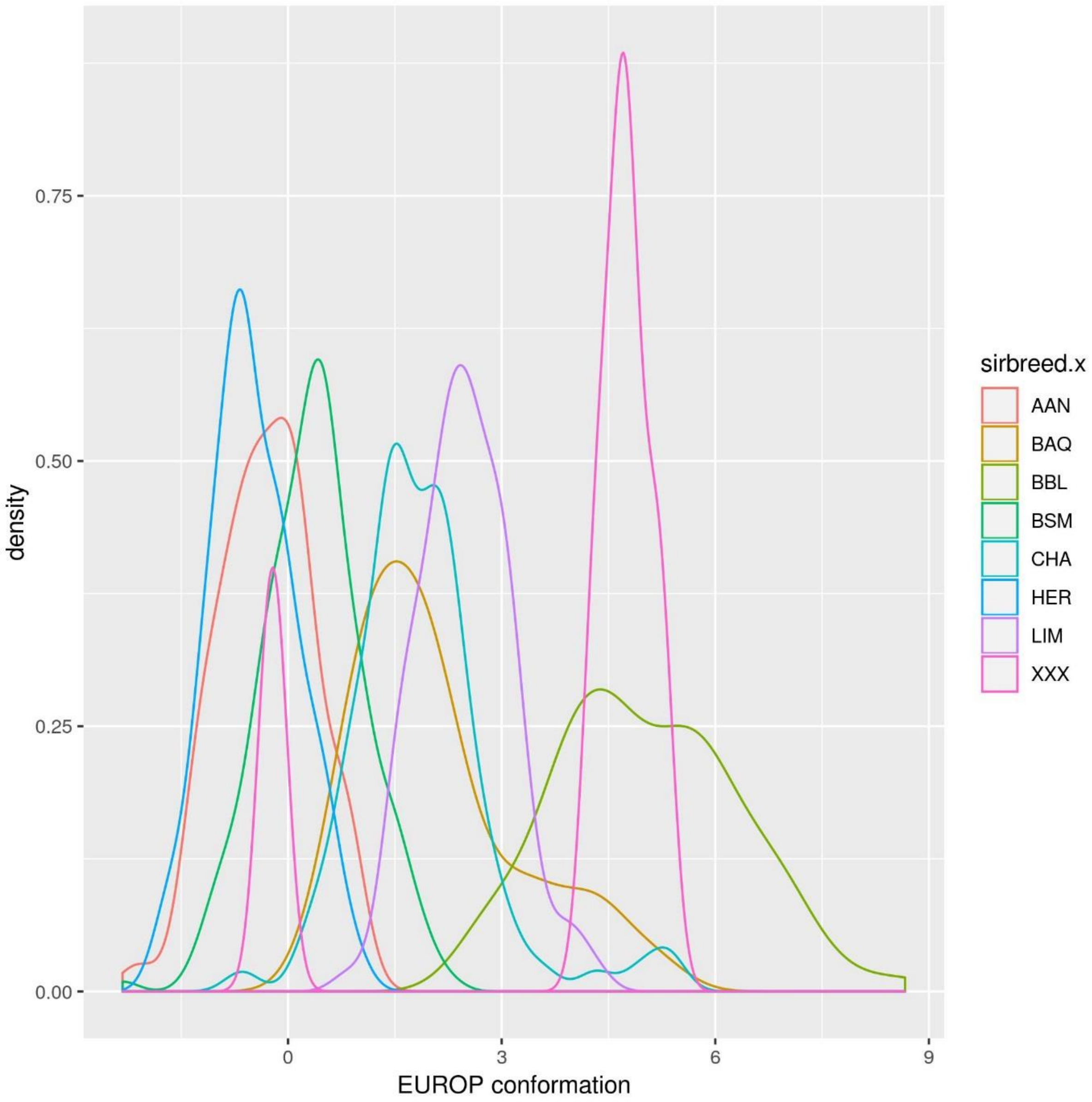

Figure F.6. Distribution of breeding values for carcass conformation index, expressed in units σ_s, for beef sires with crossbred offspring from the 8 most used beef breeds.

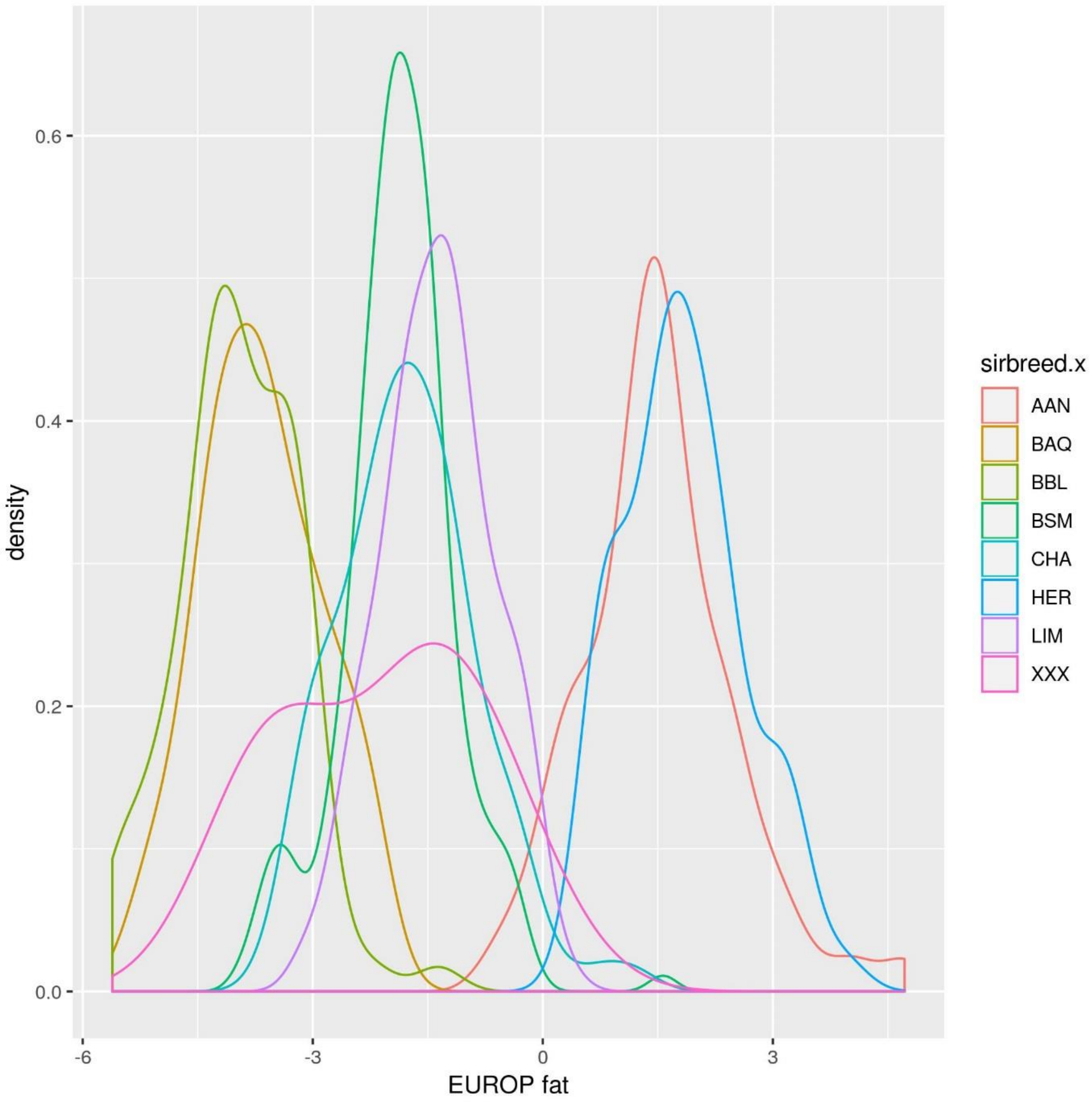

Figure F.7. Distribution of breeding values for carcass fat index, expressed in units σ_s, for beef sires with crossbred offspring from the 8 most used beef breeds.

Appendix G. Relation between index units and original phenotypes for the B×D genetic evaluation

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Background

Breeding values from the NAV B×D genetic evaluation are expressed as relative breeding with a mean of 100 and a standardization of 10. Occasionally it is helpful to be able to translate the breeding values to the original scale. This document outlines which translation factors to use, and how they have been obtained.

Under the hood of the B×D genetic evaluation

Standardization (or transformation) is done at two places in the B×D genetic evaluation (both CALV and CARC):

Here, y_{org} are the original records. Note that these standardizations are done for each of the traits separately. The type of standardization done at both places is a linear regression of the form: $\mu_{new} + \sigma_{new} \cdot (x - \mu_{old})/\sigma_{old}$, where the factors μ_{new}, μ_{old}, σ_{new} and σ_{old} determine the standardization.

The purpose of the translation factors is to translate differences in EBVs to expected differences at phenotypic level (the y_{org}). Hence, the difference in μ and σ for both standardizations needs to be considered.

The differences in μ are in the present document handled by calculating the mean of y_{org} and EBV for (nearly) the same group of animals: crossbred calves used to define the mean of the base for EBVs. Differences in σ are handled by a set of multiplication factors, exemplified below.

Males and females are treated as genetically different traits in the carcass evaluation. Hence, the effect of one index unit can be different for the female compared to the male trait. This is most notably the case for carcass daily gain.

The trait calving ease is special in the sense that it is recorded as a categorical trait with multiple categories. Hence, an attempt is made to convert values to % easy calving.

Principle of calculations

Calving traits

Standardization of breeding values is done such that solutions (from DMU) are divided by the sire standard deviation (σ_s, half the genetic standard deviation) and multiplied by 10.

Hence, to back transform from EBVs to the y_{adj} scale, a multiplication by $\sigma_s/10$ needs to be done.

The adjustment for heterogeneity of variance for carcass traits is a simple one as outlined above where deviations from the mean are scale to the desired variance. The variance of observations before and after HV adjustment are not necessarily the same, and the difference thus need to be considered in the translation.

Hence, to back transform from the y_{adj} to the y_{org} scale, a multiplication by $sd(y_{org})/sd(y_{adj})$ needs to be done. The values for $sd(y_{org})$ and $sd(y_{adj})$ are calculated based on (roughly) the same crossbreds that determine the EBV base of 100.

Taken together, a one unit change in EBV relates to a change of $\sigma_s/10 \times sd(y_{org})/sd(y_{adj})$ on the original scale, *expressed in the crossbred offspring*. The latter is because a sire model is used in the B×D CARC evaluation. The values are tabulated below.

Table: Effect of 1 index unit larger EBV for a beef bull on phenotypic performance of B×D crossbred progeny: calving traits

Country	Phenotype			
	Calf survival, 1st lactation (0-1)	Calf survival, later lactations (0-1)	Calving ease, 1st lactation (point)	Calving ease, later lactations (point)
Denmark	0.003075	0.001045	0.01117	0.005514
Finland	0.003032	0.001204	0.01085	0.006126
Sweden	0.002434	0.000977	0.00840	0.004618

For Calf survival, the change on the phenotypic scale can be directly translated into percentage survival of the crossbred offspring. This is however not the case for Calving ease, as it recorded on a scale with more than two categories. The change on the phenotypic scale was therefore translated to the change to % easy calvings.

For the current frequency distribution of the classes the threshold between the classes on an underlying scale is determined. By increasing the mean of the underlying distribution value with a small increment, a new frequency distribution is obtained given these thresholds; after that, a new mean of scores (phenotypic scale for Calving ease) can be calculated. A grid search was done to determine how large increment was needed to obtain the desired mean of scores.

As an example, the current frequency distribution for later parities in Sweden is 90.5%, 6.6%, 2.3% and 0.6% for the categories easy calving without help, easy calving with help, difficult calving and difficult calving with veterinary assistance. Compared to a bull with EBV=100, offspring of a bull with EBV=110 are expected to have a mean of 3.87 on the phenotypic scale (i.e. an improvement of 0.046; NB phenotypic scale is reversed in the genetic evaluation, with 1=difficult calving with veterinary assistance and 4=easy without calving). This corresponds to 93.7% easy calving without help, i.e. an improvement of 3.2%. The table below list expected percentage easy calvings for more cases.

Table: Expected percentage easy calving without help in later lactations when a bull with EBV 90, 100 or 110 is used

	Bull EBV = 90	Bull EBV = 100	Bull EBV = 110
Denmark	77.7	81.5	85.4
Finland	70.9	75.3	79.8
Sweden	87.5	90.5	93.7

Carcass traits

Standardization of breeding values is done such that solutions (from DMU) are divided by the sire standard deviation (σ_s, half the genetic standard deviation) and multiplied by 10. Indexes are calculated by taking the average of the male and female trait, and in addition to that, for carcass daily gain, by taking the average of the short and long period. The averaging as such does not affect the translation.

Hence, to back transform from EBVs to the y_{adj} scale, a multiplication by $\sigma_s/10$ needs to be done.

The adjustment for heterogeneity of variance for carcass traits is a simple one as outlined above where deviations from the mean are scale to the desired variance. The variance of observations before and after HV adjustment are not necessarily the same, and the difference thus need to be considered in the translation.

Hence, to back transform from the y_{adj} to the y_{org} scale, a multiplication by $sd(y_{org})/sd(y_{adj})$ needs to be done. The values for $sd(y_{org})$ and $sd(y_{adj})$ are calculated based on (roughly) the same crossbreds that determine the EBV base of 100.

Taken together, a one unit change in EBV relates to a change of $\sigma_s/10 \times sd(y_{org})/sd(y_{adj})$ on the original scale, *expressed in the crossbred offspring*. The latter is because a sire model is used in the B×D CARC evaluation. The values are tabulated below.

Table: Effect of 1 index unit larger EBV for a beef bull on phenotypic performance of B×D crossbred progeny: carcass traits

Gender	Country	Phenotype			
		Carcass daily gain, short (kg/day)	Carcass daily gain, long (kg/day)	Carcass conformation score (1-15)	Carcass fat score (1-5)
Female	Sweden	0.0015	0.0010	0.029	0.010
Female	Denmark	0.0015		0.035	0.010
Female	Finland	0.0014	0.0013	0.029	0.017
Male	Sweden	0.0014	0.0015	0.031	0.010
Male	Denmark	0.0014		0.041	0.010
Male	Finland	0.0014	0.0014	0.037	0.014

Examples

How to calculate a bull's effect on the offspring:
EBV deviation from mean * value for 1 EBV unit (from the table – in the example we use a value of 0.0015 for carcass daily gain, female, for Denmark)

- Example: Bull with EBV for carcass daily gain 110: (110 – 100) * 0.0015 = 0.015 kg/day = 15 g/day. That is, female crossbred offspring is expected to grow 15 g/day faster than female crossbred offspring from a bull with 100 as EBV.

How to calculate expected performance of bull's average offspring:
Bulls effect + breed average (from the table – in the example we use a value of 0,06)

- Example: Bull with EBV for carcass daily gain 110: 0.554 + 0.015 = 0.569 kg/day = 569 g/day for female crossbred offspring. (NB 0.554 is the mean value of carcass daily gain, female, short period, Denmark for the crossbreds that determine the EBV base of 100.)

Appendix H. Validation of breeding values through data increments

To evaluate the model for calving traits, several validation steps were conducted. At each step more information was added, either in the form of more dam breeds, sire breeds or countries. The genetic evaluation was a single-trait evaluation of CSu2+.

The sires were classified in three different categories: <50, 50-300 or >300 offspring. Correlations were calculated between the phenotypic mean of the sires' offspring, and the estimated EBV. The note contains different methods of validation for the beef × dairy breeding values. This includes comparisons to the phenotypic mean, between different groups of animals and to the current national beef × dairy indexes.

Step 1-3 (Addition of dam breeds)

In step 1-3 the dam breeds were added one by one. The Pearson correlation between the EBV and the phenotypic mean of the sire for Calf survival – multiparous cows was calculated for each validation step.

In the first test evaluation, only records for beef × dairy crossbred by Danish BBL sires and HOL dams were included. This was expected to be the largest and most homogenous group, as over 70 % of the Danish calves were in this group and the BBL sires have been used very intensively.

For step 1, there were only 3 sires with <50 offspring and therefore the results for that group were very unreliable. For the group of sires with >300 offspring, the correlation was 0.75.

In step 2 information is added for beef × dairy crossbreds that had Danish BBL sire and an RDC dam. The correlation for the sires in the group from >50-300 increased slightly as more offspring were added, whilst the correlation for the sires with many offspring >300 was unchanged, as expected.

In step 3 information was added for beef × dairy crossbreds that had Danish BBL sire and a JER dam. The JER and HOL breeds are quite different from each other, however, the correlations nevertheless increased for both the >50-300 and >300 groups of sires after adding the beef × JER offspring.

Table H.1. Correlation between sire phenotypic mean and EBV for CSu2+ from three different evaluations (validation steps 1-3) for three groups of sires (number of sires per group in parenthesis)

Validation step	**1**	**2**	**3**
Country	**DNK**	**DNK**	**DNK**
Sire breeds	**BBL**	**BBL**	**BBL**
Dam breeds	**HOL**	**HOL,RDC**	**ALL**
< 50	0.91 (3)	0.95 (3)	0.94 (3)
50-300	0.61 (28)	0.64 (28)	0.74 (26)
> 300	0.75 (62)	0.75 (62)	0.80 (64)

As there are not that many calves with a JER dam, the extra information provided by BBL × JER crossbreds is diluted by the BBL × HOL crossbreds. To see if the BBL sires were ranked in the same way, the correlation between the EBVs of BBL sires only evaluated on information from calves with HOL dams and EBV's of BBL sires only evaluated on information from calves with JER dams was calculated. Only 16 BBL sires had >300 offspring with JER dams, which made the results unreliable. The Pearson correlation was 0.54, which was quite low. This indicates that BBL sires would not rank in the same way between HOL and JER dams, but as the correlation was based on few sires and offspring, the results shall be interpreted with caution.

The EBV from step 1 (with only information from Holstein dams and Danish BBL sires) were compared to the EBV from step 3 (with all dam breeds and Danish BBL sires). All sires had been used with all three dam breeds. The Pearson correlation between both EBVs was 0.93. A high correlation was expected, because a large proportion of the BBL × dairy calves had HOL dams and they contributed with much more information to the EBVs from step 3 than RDC and JER dams.

Step 4-6 (Addition of sire breeds)

Records for beef × dairy crossbred from other sire breeds were subsequently added. In step 4, records for crossbred calves with a LIM sire were added. In step 5, beef × dairy offspring from the major sire breeds were added, and in step 6 all Danish beef × dairy offspring were included in the genetic evaluation.

The correlation between the phenotypic mean and the EBVs were at the same level after adding information from beef × dairy crossbreds with a LIM sire, compared to including only BBL × dairy offspring (Table H.2).

The correlation between the EBVs from step 3 and 4 across all three groups of sires was over 0.95. If instead the comparison was conducted between EBVs calculated using only LIM × dairy and EBVs from step 4 (based on both BBL × dairy and LIM × dairy crossbreds), the correlation between the EBVs was above 0.95 for sires with >300 offspring and 0.92 for sires with 50-300 offspring. This indicates very little reranking of the sires within breed when BBL and LIM were evaluated together.

Looking at BBL and LIM sires with >300 offspring, the correlation between EBVs calculated in step 4 and 5 were also above 0.95 for sires. So, the EBVs remained stable despite adding more sire breeds to the genetic evaluation. This was also the case when all sire breeds were included, looking at sires with >300 offspring for all the major beef breeds. The reason that the correlations were lower for sires with few offspring, is that the less information there is for a sire, the more its EBV is regressed towards the sire breed mean.

In step 6 records for all Danish beef × dairy crossbreds were included. That is, also breeds with under 10 sires were included, which made the results more uncertain, and therefore the correlation for the sires with few offspring was low. For sires with over 300 sires, the correlation was still high.

Table H.2. Correlation between sire phenotypic mean and EBV for CSu2+ from three different evaluations (validation steps 3-6) for three groups of sires (number of sires per group in parenthesis)

Validation step	3	4	5	6
Country	**DNK**	**DNK**	**DNK**	**DNK**
Sire breeds	**BBL**	**BBL,LIM**	**Major**	**ALL**
Dam breeds	**ALL**	**ALL**	**ALL**	**ALL**
< 50	0.94 (3)	0.91 (7)	0.53 (29)	0.34 (48)
50-300	0.74 (26)	0.75 (57)	0.67 (139)	0.45 (155)

> 300	0.80 (64)	0.77 (86)	0.79 (117)	0.80 (120)

In a supplementary validation step, EBVs were calculated for all sire breeds separately, and the correlation between EBVs from these sire breed-specific genetic evaluations and those calculated in step 5 and 6 were compared. The correlations were generally high (Table H.3), despite a low number of sires in some of the groups.

Table H.3. Correlation between EBVs calculated in step 5 and 6 and EBVs from sire breed-specific genetic evaluations

		BBL		**LIM**		**CHA**		**BSM**		**BAQ**	
		N	**Corr**	**N**	**Corr**	**N**	**Corr**	**N**	**Corr**	**N**	**Corr**
Step 5	**< 50**	3	1.00	4	0.94	6	0.83	12	0.86	6	0.77
	50-300	26	0.98	35	0.88	12	0.79	41	0.90	18	0.69
	> 300	64	0.99	18	0.91	8	0.94	10	0.81	3	0.98
Step 6	**< 50**	3	1.00	4	0.98	6	0.88	12	0.85	6	0.90
	50-300	26	0.97	35	0.88	12	0.82	41	0.91	18	0.69
	> 300	64	0.99	18	0.92	8	0.89	10	0.86	3	1.00

Step 7 (Addition of countries)

In step 7 information from all countries was included. This decreased the correlation between the phenotypic mean and EBVs of the sires that had >300 offspring (Table H.4), which was surprising, as the correlation for sires with few offspring is increased.

Table H.4. Correlation between the sire phenotypic mean and EBV for CSu2+ from two different evaluations (validation steps 6-7) for three groups of sires (number of sires per group in parenthesis)

Validation step	**6**	**7**
Country	**DNK**	**ALL**
Sire breeds	**ALL**	**ALL**
Dam breeds	**ALL**	**ALL**
< 50	0.34 (48)	0.42 (131)
50-300	0.45 (155)	0.48 (321)
> 300	0.80 (120)	0.59 (316)

To investigate if the decrease in correlation was a consequence of differences in phenotypic level between the countries, the EBVs were also estimated for each country separately. The correlations between EBVs from within-country and across-country estimated EBVs were high > 0.9 for looking at sires with over 300 offspring, and lower for sires with fewer offspring (Table H.5).

Table H.5. Correlation between EBVs calculated in step 7 and EBVs from country-specific genetic evaluations for three groups of sires

Number of offspring	Correlation
< 50	0.848
50-300	0.785
> 300	0.930

Next, in Table H.6, EBVs from Danish sires are compared, i.e. EBVs from a model with only Danish records and EBVs from a model with records from all three countries. As only few sires had offspring in multiple countries, it is expected that the correlation should be high. This was also the case: for sires with over 300 beef × dairy offspring the correlation was very close to 1.

Table H.6. Correlation between EBVs calculated in step 7 and EBVs from Danish genetic evaluation for three groups of sires

Number of offspring	Correlation
< 50	0.773
50-300	0.962
> 300	0.995

Using EBVs from the supplementary validation step described above (where EBVs were calculated for all sire breeds separately), the correlation between EBVs from these sire breed-specific genetic evaluations and those calculated in step 7 were compared. The correlations were generally high (Table H.7), despite a low number of sires in some of the groups.

Table H.7. Correlation between EBVs calculated in step 7 and EBVs from sire breed-specific genetic evaluations

		BBL		LIM		CHA		BSM		BAQ	
		N	**Corr**	**N**	**Corr**	**N**	**Corr**	**N**	**Corr**	**N**	**Corr**
Step 7	**< 50**	3	1.00	4	0.98	6	0.83	12	0.84	6	0.77
	50-300	26	0.97	35	0.86	12	0.80	41	0.91	18	0.68
	> 300	64	0.99	18	0.91	8	0.90	10	0.86	3	0.99

The use of beef breeds varied greatly between the three countries. To correctly estimate the country levels it is essential that there are genetic links between countries, either due sires having been used in multiple countries or due to related sires having been used in multiple countries. If genetic links are weak, the genetic level of the sires can be difficult to disentangle from the country effect (confounding). Table H.8, showing the number of common sires, sires of sires and grandsires of sires, indicates that only DNK and FIN have used some of the same sires. SWE has no common sires with the other two countries. However, all three countries have common sires of sires and grandsires of sires.

Table H.8. The number of common sires, sires of sires and grandsires of sires between countries

Common sires

	DNK	FIN	SWE
DNK	321	18	0
FIN	18	200	0
SWE	0	0	263
Common sires of sires			
	DNK	**FIN**	**SWE**
DNK	274	22	7
FIN	22	149	6
SWE	7	6	237
Common grandsires of sires			
	DNK	**FIN**	**SWE**
DNK	238	27	9
FIN	27	135	13
SWE	9	13	215

Investigation of the fixed effect of sire breed

To evaluate if the sire breeds are evaluated correctly in a model with information from all three countries, solutions for the fixed effect of sire breed were investigated. The assumption of the model is that differences between breeds are similar in different countries. Limousin is used broadly across all three countries and was taken as reference (its effect was set to 0), and the level of the other sire breeds was compared to that of Limousin. The estimated fixed effects from evaluations where each country was run separately, and an evaluation of all countries together is shown in Figure H.1.

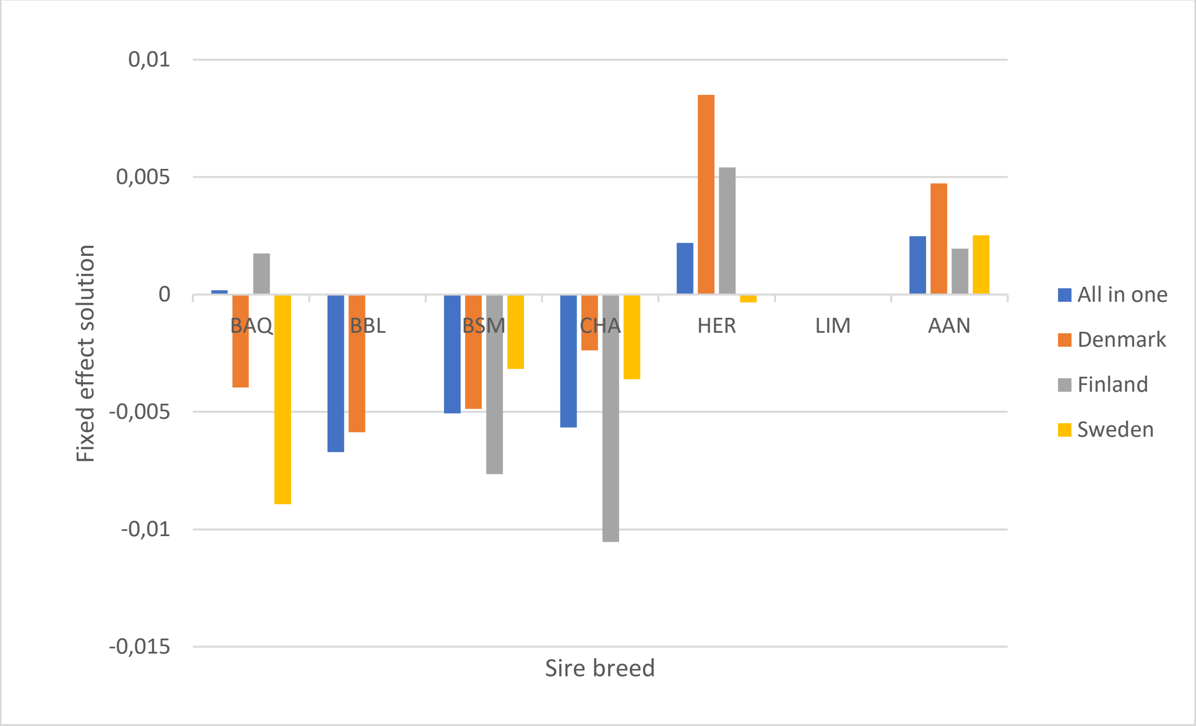

Figure H.1. Solutions for fixed effects of sire breed from models where each country was evaluated separately and a model where all countries were evaluated together.

For some of the smaller breeds such as BAQ and HER, there was more variation between countries. However, for the larger breeds such as BSM, the level between countries was more similar. Also for the evaluation where information from all three countries was included it seemed that the fixed effect solutions followed the overall (country-specific) ranking of the sire breeds fairly well.

Conclusion

Correlations between breeding values and the sires phenotypic mean were moderate and tended to be higher for sires with larger number of offspring. As expected, correlations were slightly lower when breeding values were estimated across countries compared to country-wise estimation of breeding values.

Appendix I. Comparison of the B×D breeding values and the phenotypic mean

Calf survival, later parities – BBL and BSM

An inconsistency in the ranking of the sire breeds on the phenotypic means and on the breeding values was found and investigated. BBL and BSM switched ranking, so they were the first breeds to be investigated. To ensure that there was no interference of any of the effects in the genetic model, a "naked" model that only included a fixed effect of sire breed and no pedigree was used.

The results are shown in Table I.1. Phenotypes are expressed as the survival rate. When all sires were included, BBL sires were best phenotypically but worst genetically. However, if the comparison was made for sires with over 100 offspring, then BBL were worst both phenotypically and genetically.

This is an effect of variation in use of sires. BSM have been used much less intensively than BBL and many BSM sires had only sires a small number of offspring, whilst for BBL the average number of offspring was nearly 10 times greater (Table I.2). This makes the reliability of the breeding values for BSM much lower than for BBL, and therefore the breeding values are regressed more towards 0 compared to BBL.

Table I.1. Number of sires, sire phenotypic mean, fixed effect of sire breed, EBV + fixed effect of sire breed, EBV, and differences to the mean for BBL and BSM sire, for EBV for CSu2+ from a "naked" model for all sires and sires with > 100 offspring

	N	Sire mean		Fixed effect		EBV+Fixed effect		EBV	
	All sires								
All	154	95.27%		95.92%		95.50%		-0.00141	
BBL	93	95.42%	0.14%	95.45%	-0.47%	95.45%	-0.05%	-0.00161	-0.000203
BSM	61	95.05%	-0.22%	95.58%	-0.34%	95.58%	0.08%	-0.00110	0.000309
	Sires with > 100 offspring								
ALL	108	95.52%		95.92%		95.51%		0.000343	
BBL	83	95.42%	-0.10%	95.45%	-0.47%	95.46%	-0.05%	0.000104	-0.00024
BSM	25	95.84%	0.33%	95.58%	-0.34%	95.69%	0.18%	0.001136	0.000793

Table I.2. Number of offspring, sires, average and range of number of offspring per sire for BSM and BBL

	BSM	BBL
No. offspring	7032	85748
No. sires	61	93
Average no. offspring	115	922
Range	(11-494)	(11-21,724)

All sire breeds - "naked" model

Looking at all sire breeds and results from a "naked" model, it is also apparent that there was some re-ranking (Table I.3). When the comparison was done between sires with >100 offspring (Table I.4), the ranking between the phenotype and the EBVs was consistent.

Table I.3. Number of offspring, number of sires, sire phenotypic mean, fixed effect of sire breed, EBV + fixed effect of sire breed, EBV, differences to the mean and rank for six sire beef breeds, for EBV for CSu2+ from a "naked" model for all sires

	N off	N sire	Sire mean		Rank	Fixed effect		Rank	EBV + Fixed effect		Rank
All	112,414	275	95.55%			95.55%			95.86%		
AAN	763	18	94.97%	-0.58%	6	96.46%	0.91%	1	96.46%	0.60%	1
BAQ	4,138	23	95.98%	0.43%	3	96.29%	0.74%	3	96.29%	0.43%	3
BBL	85,748	93	95.42%	-0.13%	4	95.45%	-0.10%	6	95.45%	-0.41%	6
BSM	7,032	61	95.05%	-0.50%	5	95.58%	0.03%	5	95.58%	-0.28%	5
CHA	4,119	25	96.02%	0.46%	2	96.18%	0.63%	4	96.21%	0.35%	4
LIM	10,614	55	96.13%	0.58%	1	96.34%	0.79%	2	96.34%	0.48%	2

Table I.4. Number of offspring, number of sires, sire phenotypic mean, fixed effect of sire breed, EBV + fixed effect of sire breed, EBV, differences to the mean and rank for six sire beef breeds, for EBV for CSu2+ from a "naked" model for sires with > 100 offspring

	N off	N sire	Sire mean		Rank	Fixed effect		Rank	EBV + Fixed effect		Rank
All	106,697	152	95.84%			95.55%			95.79%		
AAN	292	1	98.57%	2.73%		96.46%	0.91%		97.39%	1.60%	
BAQ	3,463	10	96.86%	1.02%	1	96.29%	0.74%	2	96.51%	0.71%	1
BBL	85,225	83	95.42%	-0.42%	5	95.45%	-0.10%	5	95.46%	-0.33%	5
BSM	5,354	25	95.84%	0.00%	4	95.58%	0.03%	4	95.69%	-0.10%	4
CHA	3,487	10	96.45%	0.61%	3	96.18%	0.63%	3	96.30%	0.51%	3
LIM	8,876	23	96.53%	0.69%	2	96.34%	0.79%	1	96.47%	0.68%	2

All sire breeds – full model

When the evaluation was run for the full model that included pedigree and all fixed effects, and statistics for calculated for sires with >100 offspring, some re-ranking occurred (Table I.5). This re-ranking most probably was due to adjustment of the fixed effects.

Table I.5. Number of offspring, number of sires, sire phenotypic mean, fixed effect of sire breed, EBV + fixed effect of sire breed, EBV, differences to the mean and rank for six sire beef breeds, for EBV for CSu2+ from the full model for sires with > 100 offspring

	N off	N sire	Sire mean		Rank	Fixed effect		Rank	EBV + Fixed effect		Rank
All	106697	152	95.84%			95.55%			100.24%		
AAN	292	1	98.57%	2.73%		100.90%	5.35%		101.42%	1.17%	
BAQ	3463	10	96.86%	1.02%	1	100.40%	4.85%	3	100.55%	0.31%	2
BBL	85225	83	95.42%	-0.42%	5	99.96%	4.41%	5	99.96%	-0.29%	5
BSM	5354	25	95.84%	0.00%	4	100.59%	5.04%	2	100.50%	0.26%	3
CHA	3487	10	96.45%	0.61%	3	100.01%	4.46%	4	100.09%	-0.15%	4
LIM	8876	23	96.53%	0.69%	2	100.88%	5.33%	1	100.89%	0.65%	1

Calving ease

For calving ease, there was also some inconsistency when the evaluation was run with the full model and using all sires (Table I.6). When the evaluation was run for sires with >100 offspring, with the full model, only CHA and LIM switched rank (Table I.7).

Table I.6. Number of offspring, number of sires, sire phenotypic mean, fixed effect of sire breed, EBV + fixed effect of sire breed, EBV, differences to the mean and rank for six sire beef breeds, for EBV for Ce2+ from the full model for all sires

	N off	N sire	Sire mean		Rank	Fixed effect		Rank	EBV + Fixed effect		Rank
All	102723	275	3,62						3,11		
AAN	696	18	3,66	0,04	3	3,22		1	3,22	0,11	1
BAQ	3792	23	3,56	-0,06	5	3,10		5	3,10	-0,01	5
BBL	79116	93	3,67	0,05	1	3,11		3	3,11	0,01	3
BSM	5971	61	3,55	-0,07	6	3,06		6	3,06	-0,05	6
CHA	3714	25	3,66	0,04	2	3,11		4	3,11	0,00	4
LIM	9434	55	3,62	0,00	4	3,13		2	3,13	0,02	2

Table I.7. Number of offspring, number of sires, sire phenotypic mean, fixed effect of sire breed, EBV + fixed effect of sire breed, EBV, differences to the mean and rank for six sire beef breeds, for EBV for Ce2+ from the full model for sire with > 100 offspring

	N off	N sire	Sire mean		Rank	Fixed effect		Rank	EBV + Fixed effect		Rank
All	96959	143	3,66						3,11		
AAN	282	1	3,83	0,17		3,22		1			
BAQ	3032	8	3,72	0,06	2	3,10		5	3,13	0,0176	2
BBL	78394	80	3,67	0,01	3	3,11		3	3,11	0,0034	3
BSM	4352	23	3,57	-0,09	5	3,06		6	3,06	-0,0474	5
CHA	3055	9	3,72	0,06	1	3,11		4	3,11	-0,0024	4
LIM	7844	22	3,66	0,00	4	3,13		2	3,13	0,0247	1

Conclusion

When comparing to the phenotypic mean, it is important to look at sires with a significant amount of offspring, especially for stillbirth, where one dead calf can change the mean greatly. It seemed that the ranking of the sire breeds by the model was acceptable.

Appendix J. Comparison between EBVs calculated with a single-trait and a multiple-trait model

All sires, all dam breeds, all countries

Breeding values calculated with a multiple-trait model with all 6 calving traits were compared to breeding values calculated with a single-trait model for each trait. The correlations have been calculated among breeding values that were estimated using phenotypic records from all sire breeds, all dam breeds and for all three countries. It is expected that the correlation is not 1, as correlated information between the traits is used in the multiple-trait model.

For the later parity traits, correlations were all above 0.9, and correlations were lower for first parity traits (Table J.1). There is only limited number of phenotypes for first parity traits, so the correlated information had a larger effect on these traits compared to the later parity traits.

Table J.1. Correlation between EBVs estimated with a single-trait and a multiple-trait model, for all countries together and by country (of most offspring)

	CSu1	CSu2+	CE1	CE2+	CSi1	CSi2+
All	0.84	0.94	0.73	0.97	0.83	0.95
DNK	0.89	0.96	0.76	0.95	0.86	0.99
FIN	0.61	0.95	0.73	0.99	0.82	0.92
SWE	0.62	0.91	0.63	0.98	0.80	0.92

The correlation between the breeding values was also calculated within sire breed (Table J.2). The correlations for the first parity traits were low for all sire breeds and traits. For the later parity traits, the correlations were higher, except for calf size for which correlations ranged from 0.4-0.98.

Table J.2. Correlation between EBVs estimated with a single-trait and a multiple-trait model, by sire breed

Sire breed	CSu1	CSu2+	CE1	CE2+	CSi1	CSi2+
AAN	0.77	0.84	0.71	0.90	0.38	0.40
BAQ	0.37	0.87	0.09	0.96	0.33	0.67
BBL	0.35	0.96	0.41	0.96	0.40	0.98
BSM	0.41	0.86	0.39	0.96	0.38	0.60
CHA	0.29	0.93	0.17	0.97	0.24	0.64
HER	0.72	0.90	0.58	0.79	0.44	0.64
LIM	0.51	0.92	0.58	0.91	0.52	0.76

To see if there was concordance with the phenotypic mean, correlations between the breeding values from the single-trait and multiple-trait models were compared to the phenotypic mean per sire. For the first parity traits the correlations were very low (Table J.3). This was probably due to the correlated information from the later parities that influenced the breeding values, and because data from all countries and dam breeds were included in the evaluation. For the later parity traits correlations were higher, but all still below 0.7. Comparing correlations for the ST and MT breeding values, there was a tendency that correlations with the sire phenotypic mean were higher when breeding values were estimated with a multiple-trait model compared to a single-trait model for first parity traits, but for later parity traits it was opposite. Within sire breed, the first parity traits also had lower correlations between the breeding values and the phenotypic mean, compared to the later parity traits (Table J.4).

Table J.3. Correlation between sire phenotypic mean and EBVs calculated with a single-trait (ST) or multiple-trait (MT) model, for all countries and by country (of most offspring)

		CSu1	CSu2+	CE1	CE2+	CSi1	CSi2+
All	**MT**	0.16	0.46	0.25	0.37	0.41	0.64
	ST	0.11	0.48	0.30	0.37	0.38	0.63
DNK	**MT**	0.14	0.46	0.25	0.66	0.41	0.64
	ST	0.07	0.48	0.29	0.67	0.38	0.63
FIN	**MT**	0.15	0.54	0.37	0.54	-	-
	ST	0.18	0.53	0.28	0.56	-	-
SWE	**MT**	0.21	0.50	0.19	0.60	-	-
	ST	0.30	0.58	0.32	0.62	-	-

Table J.4. Correlation between sire phenotypic mean and EBVs calculated with a single-trait (ST) or a multiple-trait (MT) model, by sire breed

		CSu1	CSu2+	CE1	CE2+	CSi1	CSi2+
AAN	**MT**	0.38	0.42	-0.09	-0.01	0.36	0.41
	ST	0.34	0.58	0.21	0.06	0.37	0.40
BAQ	**MT**	0.03	0.39	0.22	0.51	0.50	0.37
	ST	0.42	0.46	0.26	0.51	0.33	0.27
BBL	**MT**	0.16	0.67	0.10	0.58	0.27	0.59
	ST	0.33	0.70	0.37	0.54	0.43	0.57
BSM	**MT**	0.17	0.53	0.26	0.55	0.23	0.78
	ST	0.36	0.59	0.59	0.56	0.31	0.77
CHA	**MT**	0.13	0.57	0.12	0.50	0.35	0.76
	ST	0.56	0.60	0.37	0.47	0.54	0.78
HER	**MT**	0.15	0.28	0.14	0.11	0.37	0.56
	ST	0.09	0.35	-0.01	0.25	0.63	0.65
LIM	**MT**	0.20	0.52	0.47	0.39	0.47	0.75
	ST	0.38	0.54	0.37	0.44	0.45	0.72

Sires with >100 offspring, all dam breeds, all countries

To ensure that the breeding values were estimated with some reliability, sires with under 100 offspring were deleted from the comparison. Correlations for the first parity traits increased (Table J.5), but the results were based on a small number of sires. All correlations were above 0.8 for the first parity traits and above 0.9 for later parity traits.

Table J.5. Correlation between EBVs estimated with a single-trait and a multiple-trait model, for all countries together and by country (of most offspring), for sires with >100 offspring

	CSu1	CSu2+	CE1	CE2+	CSi1	CSi2+
All	0.81	0.93	0.90	0.98		
DNK	0.85	0.93	0.83	0.96	0.83	0.99
FIN	0.87	0.96	0.83	0.99		

SWE	0.81	0.92	0.92	0.98		

Within sire breed, only AAN, HER and LIM had sires with over 100 offspring, but not for calf size – first parity as this trait is only evaluated in Denmark where little beef semen is used on heifers. Correlations between breeding values from ST or MT models were all high (Table J.6).

Table J.6. Correlation between EBVs estimated with a single-trait and a multiple-trait model, by sire breed and for sires with >100 offspring

Sire breed	CSu1	CSu2+	CE1	CE2+	CSi1	CSi2+
AAN	0.86	0.86	0.84	0.93	-	0.91
BAQ	-	0.89	-	0.99	-	0.99
BBL	-	0.96	-	0.97	-	0.98
BSM	-	0.89	-	0.97	-	0.99
CHA	-	0.94	-	0.98	-	0.99
HER	0.79	0.94	0.93	0.86	-	-
LIM	0.84	0.92	0.65	0.95	-	0.98

Correlations between the phenotypic mean and the breeding values were low to moderate, but higher for the bulls with > 100 offspring compared to the correlations calculated for all sires (Table J.7 vs Table J.3). The correlation between the phenotypic mean and breeding values from the ST model were higher compared to breeding values from the MT model for nearly all traits.

Table J.7. Correlation between sire phenotypic mean and EBVs calculated with a single-trait (ST) or a multiple-trait (MT) model, for all countries and by country (of most offspring)

		CSu1	CSu2+	CE1	CE2+	CSi1	CSi2+
All	**MT**	0.35	0.59	0.02	0.37		
	ST	0.40	0.64	0.16	0.37		
DNK	**MT**	0.48	0.71	0.80	0.71	0.78	0.69
	ST	0.25	0.70	0.81	0.70	0.40	0.68
FIN	**MT**	0.76	0.82	0.82	0.65		
	ST	0.68	0.81	0.89	0.66		
SWE	**MT**	0.41	0.64	0.32	0.71		
	ST	0.56	0.74	0.48	0.73		

Correlations between the phenotypic mean and the breeding values calculated within sire breed were slightly higher for sires with > 100 offspring compared to all sires (Table J.8 vs Table J.4). For the smaller breeds such as AAN and HER, however, correlations were very low and not significant.

Table J.8. Correlation between sire phenotypic mean and EBVs calculated with a single-trait (ST) or a multiple-trait (MT) model, by sire breed

		CSu1	CSu2+	CE1	CE2+	CSi1	CSi2+
AAN	**MT**	0.37	0.50	-0.02	0.00		0.95
	ST	0.36	0.61	0.03	-0.01		0.92
BAQ	**MT**		0.40		0.47		0.66
	ST		0.47		0.48		0.67

BBL	**MT**		0.75		0.60		0.66
	ST		0.77		0.57		0.65
BSM	**MT**		0.69		0.49		0.87
	ST		0.77		0.46		0.87
CHA	**MT**		0.58		0.50		0.91
	ST		0.67		0.47		0.91
HER	**MT**	0.32	0.44	0.18	-0.02		
	ST	0.48	0.50	0.46	0.03		
LIM	**MT**	0.63	0.52	0.22	0.39		0.80
	ST	0.56	0.54	0.62	0.44		0.81

Conclusion

The results obtained in the MT model are in line with those found in the ST model. Correlations between breeding values calculated in the two models were high. This supports using the MT model in the B×D genetic evaluation.

Appendix K. Correlations between EBVs and sire phenotypic means

Correlations for Calving traits

In Table K.1 and Table K.2, the correlation between EBV and phenotypic mean is shown for all six calving traits. All the results are from single trait analyses. For the first parity traits, correlations for sires with <50 offspring were very low, for sires with 30-500 correlations were higher, but there are very few sires with >300, so these correlations were also low. In general, correlations were higher for calving ease compared to stillbirth. Correlations were higher when only the Danish data was included, compared to when data from all countries are included.

Table K.1. Correlation between the phenotypic mean and the calculated breeding values and number of beef sires available to calculate the correlation, for all traits and grouped by number of beef × dairy offspring per beef sire (<50, >50-300 and >300 offspring)

	CSu1	CSu2+	CE1	CE2+
	Correlation			
<50	0.135	0.423	0.295	0.305
>50-300	0.453	0.476	0.350	0.411
>300	0.342	0.590	-0.390	0.360
	Number of bulls			
<50	633	131	659	181
>50-300	111	321	92	325
>300	24	316	17	262

Table K.2. Correlation between the phenotypic mean and the calculated breeding values based only on Danish information and number of beef sires available to calculate the correlation, for all traits and grouped by number of beef × dairy offspring per beef sire (<50, >50-300 and >300 offspring)

	CSu1	CSu2+	CE1	CE2+	CS1	CS2+
	Correlation					
<50	0.120	0.341	0.347	0.584	0.383	0.644
>50-300	0.517	0.451	0.637	0.776	0.645	0.592
>300	0.729	0.797	-	0.653	-	0.710
	Number of bulls					
<50	269	48	295	70	296	81
>50-300	25	155	26	155	26	150
>300	4	120	2	98	1	92

Correlations for Carcass traits

Correlations between EBVs (calculated with a multiple-trait model) and sire phenotypic means were higher for carcass traits than for calving traits (Table K.1 vs Table K.3)**Table K.4**. This was expected because of the higher heritabilities for carcass traits, even though comparing sire phenotypic means with multiple-trait EBVs (carcass traits) would result in worse agreement than comparing sire phenotypic means with single-trait EBVs (calving traits). Agreement between EBVs and sire phenotypic means was better when only records on Danish beef × dairy crossbreds were used. This is expected as EBVs from the multi-country evaluation contains information from all three countries that is weighted together in the EBV whereas sire phenotypic means were calculated on a per-country basis.

Table K.3. Correlation between B×D breeding values and sire phenotypic means for some carcass traits, by sire breed and for sires with more than 100 beef × dairy offspring in the Beef × dairy genetic evaluation

	dgs, ♂	dgl, ♀	bcs, ♂	bcs, ♀
BBL (n=53)	0.52		0.82	0.81
BSM (n=6)	0.57	0.44	0.73	0.63
LIM (n=19)	0.50	0.48	0.54	0.44
BAQ (n=3)	0.49	0.58	0.68	0.69
CHA (n=3)	0.60	0.45	0.74	0.62
AAN	0.51	0.62	0.86	0.71
HER	0.79	0.70	0.83	0.62

Table K.4. Correlation between B×D breeding values and sire phenotypic means for some carcass traits, by sire breed and for sires with more than 100 beef × dairy offspring in the Beef × dairy genetic evaluation and using only Danish data in the B×D genetic evaluation

	dgs, ♂	dgl, ♀	bcs, ♂	bcs, ♀
BBL (n=53)	0.53		0.84	0.85
BSM (n=6)	0.66		0.27	0.36
LIM (n=19)	0.65		0.76	0.51
BAQ (n=3)	0.88		1.00	1.00
CHA (n=3)	0.18		0.90	0.68