NAV routine Beef x Dairy genetic evaluation
– data and genetic models

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Contents

1. Introduction

Beef semen is used intensively in dairy herds. Nordic breeding values for beef AI bulls used on dairy cattle are based on phenotypes from beef x dairy offspring in Denmark, Sweden, and Finland. The breeding values are calculated jointly by NAV (Nordic Cattle Genetic Evaluation), which is owned by SEGES, Växa Sverige and FABA Co-op.

This cooperation and joint evaluation make it possible to compare AI beef sires for use in dairy herds across beef breeds and countries. The genetic evaluation was introduced in December 2018. The traits are included in a Nordic Beef x Dairy Index (NBDI), which was introduced in November 2019. NBDI is a tool for the dairy farmer to select beef bulls that will give the most profitable crossbred calves.

The genetic evaluation system in NAV complies with international rules for registration, documentation, calculations, etc.

In this publication, we wish to describe the methods and models used in the joint Nordic Beef x Dairy genetic evaluation.

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2. NBDI - Nordic Beef x Dairy Index

The Nordic Beef x Dairy Index (NBDI) describes a beef bull's genetic potential for producing crossbred beef × dairy offspring that gives the farmers the best economy. It is composed of sub-indices for birth and growth. In the Nordic countries different fattening periods are used in practice. The length of the fattening period affects the economic values of the growth traits. Therefore, beef bulls get two indices for growth and two NBDI depending on fattening period short (age at slaughter < 550 days) or long (age at slaughter > 550 days).

Traits in NBDI

Economic values take into account differences in age at slaughter and consequently differences in carcass weight, but also differences in price models for EUROP form and fatness.

- **NBDI, long**, includes birth index, young stock survival and growth index, long
- **NBDI, short**, includes birth index, young stock survival and growth index, short

How the different breeding values are combined into NBDI is the result of thorough economic calculations and expectations on future production conditions and price relations.

Economic values in NBDI

The input for the calculation model is a set of economic and biological assumptions.
For the calculation of economic value of improving beef cattle traits a standard scenario was used. This is a conventional herd with a culling rate of 32%, 50% of replacement heifers born by sexed semen and 70–75% of the older cows inseminated with beef sires. The economic values are calculated in a modified version of the NTM model from 2018 – see https://www.nordicebv.info/wp-content/uploads/2018/11/2018.11.06-NTM-2018-report-Full.pdf.

The results are expressed per crossbred calf. The economic values presented are the effect of improving a trait of the beef sire with one unit. The effect is the value per crossbred calf born.

In Table 2.1 is the value of improving the traits of the beef sire traits with one phenotypic unit under different production circumstances.

Table 2.1. Value of improving phenotypic traits of beef sires used in dairy herds. Value per crossbred calf under different production circumstances. Average across dam breeds.

Economic values/unit	Short fattening period	Long fattening period
Daily carcass gain (€ per kg/day)	256.7	350.0
Carcass conformation score (€ per point)	3.3	10.1
Fat score (€ per point)	4.1	-6.6
Survival, later (€ per calf)[1]	205.0	205.0
Calving ease, later (€ per point)[1+2]	40.6	40.6
Young stock survival, early period (€ per calf)	216.6	216.6
Young stock survival, late period (€ per calf)	360.5	360.5

[1] Assumption that no beef × dairy crossbreds are born at 1st calving.
[2] Includes cost of cow mortality in early lactation due to difficult calving

Calculation of NBDI

NBDI is calculated by weighting the EBVs for each sub-index (explained above).

NBDI is calculated as shown in the formulas below. The weights used for each standardized sub-trait are shown in Table 2.2.

Beef AI sires:

$$NBDI = 0 + \sum_{i=1}^{n}(breeding\ value(i) - 100) \times weight\ factor(i)$$

were
- Breeding value$_i$ =   Breeding value of the ith trait
- Weight factor$_i$ =   The weight factor for the ith trait

NBDI is standardized to have an average of zero and a standard deviation of 10. The standardization of the indices in NBDI is described in the later chapter "Expression and standardization".

Table 2.2. NBDI weight factors.

	NBDI, short	NBDI, long
Birth	0.50	0.45
Young stock survival	0.73	0.66
Growth, long		0.79
Growth, short	0.55	

The main traits in NBDI, namely Birth and Growth index, are calculated as shown in the formulas below. The weights used for each standardized sub-trait are shown in Table 2.3.

$$Main\ traits = 100 + \sum_{i=1}^{n}(breeding\ value(i) - 100) \times weight\ factor(i)$$

NBDI is published if a bull has official indices for Birth, Growth and Youngstock survival.

Correlation between NBDI and sub-indices

The expected change for each sub-index when NBDI is selected for, is expressed as a percentage of the maximum change for that index and is shown in Table 2.3. Maximum change is obtained if selection is based solely on the trait in question.

Table 2.3. Expected change for each NBDI sub-trait represented by the (within-breed) correlation between NBDI and each sub-index.

	NBDI, short	NBDI, long
Birth	0.37	0.18
Youngstock survival	0.69	0.51
Growth, short	0.50	0.66
Growth, long	0.43	0.72

References

[Total Merit Index (NBDI) for beef sires used for dairy cattle](#)

[2019.10.14-TMI-of-beef-sires-used-for-dairy-crosses.pdf (nordicebv.info)](#)

[2018.11.06-NTM-2018-report-Full.pdf (nordicebv.info)](#)

3. Birth

The birth index includes two breeding values, calf survival and calving ease, both in later lactations, weighted together according to their economic value. The index for birth describes a bull's crossbred offspring's genetic potential to be born easily and alive. The breeding values are based on calving records from later lactations and correlated information from primiparous calving's.

Trait definitions

Records from the first to tenth calving are included and are referred to as first versus later calving's, respectively. Only direct effects are estimated for all traits.

The traits are calf survival (CSU) within the first 24 hours, calving ease (CE) and calf size (CSI). The definitions of the traits are shown in Table 3.1. Survival is registered as 0 or 1, calving ease is measured in 4 categories (2 categories in SWE up to 2012), and calf size is measured in 4 classes (only DNK data). Calf size is only used as an indicator trait.

Table 3.1. Abbreviations and definitions of traits included in evaluation of calving traits.

Abbreviation	Definition
CSU, 1st calving (CSU_1)/SU, $\geq 2^{nd}$ calving ($CSU_{\geq2}$)	Survival in the first 24 hours after birth for heifers and cows separately (recoded to 2 classes for all countries)
CE, 1st calving (CE_1)/CE, $\geq 2^{nd}$ calving ($CE_{\geq2}$)	Calving ease for heifers and cows separately (recoded to 4 classes for all countries)
CSI, 1st calving (CSI_1/)/CS, $\geq 2^{nd}$ calving ($CSI_{\geq2}$)	Size for heifers and cows separately (only DK; 4 classes)

Basic editing rules

For all traits a general editing is done. Calves are included if they are:
1. Born in Denmark, Sweden, or Finland 2000 and onwards
2. Born by a purebred dairy dam of the breed RDC, Holstein or Jersey
3. Sired by a beef AI sire
4. Born in a milk producing herd

The purpose of these edits is to ensure that data 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.

The general editing rules are followed by a specific editing for birth traits:
- Records for twin calves were deleted
- Records with dam age at birth lower than 15 months or above 121 months are deleted
- Finnish calving ease data from before 2003 was deleted.
- Records with deviating gestation length are excluded (Finland only).

Pre-adjustment

All traits were pre-adjusted for heterogeneous variance within subclasses of country – calving year (5-year periods)- dam breed.

Genetic evaluation

Model
A multitrait and multibreed sire model is used. Below are the effects in the model.:

- Country – herd – year of birth of calf   fixed
- Country – year – month of birth of calf   fixed
- Country – year – sex of calf   fixed
- Country – age of dam   fixed
- Breed – year of birth of dam   fixed
- Breed of (beef) sire   fixed
- Sire   Random
- Residual   Random

No heterosis effect is included in the model, and the EBV expresses the sum of additive effect and effect of heterosis that can be observed in beef × dairy crossbred offspring.

Genetic parameters
The parameters used in the genetic evaluation for calving traits are shown in Table 3.2.

Table 3.2. Estimated genetic parameters for calving traits[1]: heritability on the diagonal and genetic correlations above the diagonal.

	CSU_1	$CSU_{\geq 2}$	CE_1	$CE_{\geq 2}$	CSI_1	$CSI_{\geq 2}$
CSU_1	**0.05**	0.88	0.70	0.67	-0.80	-0.50
$CSU_{\geq 2}$		**0.01**	0.61	0.62	-0.53	-0.43
CE_1			**0.11**	0.97	-0.89	-0.93
$CE_{\geq 2}$				**0.05**	-0.80	-0.84
CSI_1					**0.17**	0.83
$CSI_{\geq 2}$						**0.09**

[1] CSU_1 = for calf survival in first parity; $CSU_{\geq 2}$ = calf survival in later parities; CE_1 = calving ease first parity; $CE_{\geq 2}$ = calving ease later parities; CSI_1 = calf size in first parity; $CSI_{\geq 2}$ = calf size in later parities

Index
Effect of "Breed of sire" from the genetic model is added to the EBV's for calf survival and calving ease before standardization. The standardization of the relative breeding values is described in the chapter "Expression and standardization".

The birth index includes standardized indices for calf survival and calving ease in later lactations, combined with weight factors (Table 3.3).

Table 3.3. Weights in calculation of birth index.

	Birth
$CSU_{\geq 2}$	0.58
$CE_{\geq 2}$	0.53

Index is published for a bull, if reliability for either $SU_{\geq 2}$ or $CE_{\geq 2}$ is above 50% or number of BxD offspring for $SU_{\geq 2}$ is at least 500.

Correlation between the birth index and underlying traits

The expected progress for each trait, when birth index is selected for, expressed as the proportion of maximum progress for that trait (Table 3.4). The maximum progress is obtained if selection is solely based on the trait in question. The results are based sires born 2007-2010.

Table 3.4. Correlations between index for birth index and breeding values for calf survival and calving ease.

Index	Correlation
CSU_1	0.96
CE_1	0.94
$CSU_{\geq 2}$	0.94
$CE_{\geq 2}$	0.96

Expected effect of the breeding values

The effect of the subindices in birth expressed on the original scale is shown in Table 3.5. It is expressed as the difference in performance of two progeny groups, where there is a difference of 1 index units in the sires.

Table 3.5. Effect of 1 index unit larger EBV for a beef bull on phenotypic performance of BxD crossbred progeny. Average in parentheses

Index	Scale	Denmark	Finland	Sweden	High values mean
CSU_1	%	0.26 (93.0)	0.28 (92.8)	0.21 (96.1)	Less stillborn calves
CE_1	Points	0.0082	0.0100	0.0072	Less difficult calvings
$CSU_{\geq 2}$	%	0.10 (96.8)	0.11 (95.8)	0.09 (97.5)	Less stillborn calves
$CE_{\geq 2}$	Points	0.0043	0.0053	0.0040	Less difficult calvings

References

BxD_final_report.pdf (nordicebv.info)

2019.10.14-TMI-of-beef-sires-used-for-dairy-crosses.pdf (nordicebv.info)

4. Growth

The growth index (short or long) includes three breeding values; daily carcass gain, carcass conformation score and carcass fat score, combined with economic weights.

The index for growth describes a bull's crossbred offspring's genetic potential for daily carcass gain, carcass conformation score and carcass fat score. The breeding values are based on slaughter results from male and female crossbred calves raised with either a long, extensive fattening period of at least 550 days or a short, intensive fattening period.

Trait definitions

Daily carcass gain is based on combining breeding values for bulls and heifers with short (CGS) and long (CGL) fattening period, respectively, with equal weights. Conformation (CCS) and fat (CFS) score are based on combing breeding values for bulls and heifers with equal weights. Carcass conformation score is recorded following the EUROP system in 15 ordered classes. All three countries use the same scale. Carcass fat score is recorded in 15 classes in Finland and Sweden and 5 classes in Denmark. The Swedish fat scores are divided by 3 to harmonize with the Danish and Finnish data. Trait abbreviations are shown in Table 4.1.

Table 4.1. Abbreviations and definitions of traits included in evaluation of growth.

Abbreviation	Definition
CGS	Daily carcass gain, Short fattening period, up to 550 days
CGL	Daily carcass gain, Long fattening period, more than 550 days
CCS	Carcass conformation score (15 classes)
CFS	Carcass fat score (FI and SE 15 classes, DK 5 classes)

Basic editing rules

For all traits a general editing is done. Calves are included if they are:
1. Born in Denmark, Sweden, or Finland 2000 and onwards
2. Born by a purebred dairy dam of the breed RDC, Holstein or Jersey
3. Sired by a purebred beef AI sire of one of the major beef breeds
4. Born in a milk producing herd

The purpose of these edits is to ensure that data 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.

The general editing rules are followed by a specific editing for carcass traits:
- Calves slaughtered younger than 200 days of age or older than 900 days of age are deleted
- Calves with a dam younger than 570 days or older than 3.370 days are deleted
- Daily carcass gains larger than 1 kg/day were set to missing
- For Denmark, calf's with less than 90 days in slaughter herd, slaughter data is set to missing.

Pre-adjustment
All traits were pre-adjusted for heterogeneous variance within subclasses of country – year – sex – dam breed.

Genetic evaluation

Model

A multitrait and multibreed sire model is used. Separate breeding values are estimated for males and females. Below are the effects in the model:

- Country – slaughter herd – year of birth of crossbred   fixed
- Country – year – month of slaughter of crossbred   fixed
- Country – parity of dam of crossbred   fixed
- Breed – year of birth of dam   fixed
- Breed of (beef) sire   fixed
- Sire   random
- Residual   random

No heterosis effect is included in the model, and the EBV expresses the sum of additive effect and effect of heterosis that can be observed in beef × dairy crossbred offspring.

Genetic parameters

The parameters used in the genetic evaluation for carcass traits are shown in Table 4.2.

Table 4.2. Estimated genetic parameters for carcass traits[1]: heritability on the diagonal and genetic correlations above the diagonal.

		Male traits				Female traits			
		CGS	CGL	CCS	CFS	CGS	CGL	CCS	CFS
Male	CGS	**0.19**	0.97	0.30	-0.21	0.83	0.86	0.22	-0.27
	CGL		**0.21**	0.34	-0.10	0.85	0.86	0.25	-0.21
	CCS			**0.32**	-0.17	0.31	0.24	0.92	-0.12
	CFS				**0.23**	-0.20	-0.13	-0.19	0.88
Female	CGS					**0.33**	0.97	0.35	-0.30
	CGL						**0.32**	0.25	-0.22
	CCS							**0.35**	-0.18
	CFS								**0.25**

[1] CGS = daily carcass gain, short fattening period; CGL = daily carcass gain, long fattening period; CCS = carcass conformation score; CFS = carcass fat score

Index

The growth index (short or long) includes three breeding values: daily carcass gain, carcass conformation score and carcass fat score, combined according to their economic weights. Index for daily carcass gain is calculated as average of short and long period for both sexes (4 traits). Index for carcass conformation score and index for carcass fat score are calculated as average of subindexes for both sexes. Effect of "Breed of sire" from the genetic model is added to the EBV's for the individual bulls before standardization. The standardization of the breeding values is described in the chapter "Expression and standardization".

The standardized EBVs for carcass gain, conformation score and fat score are combined by weight factors (Table 4.3).

Table 4.3. Weight factors in calculation of growth index (short and long)

	Growth, short	Growth, long
Daily carcass gain	0.95	0.71

Carcass conformation score	0.26	0.53
Carcass fat score	0.09	-0.12

Index is published for a bull, if reliability for CCS is above 50 % or number of BxD offspring for CCS is at least 500.

Correlation between the growth index and the underlying traits

The expected progress of each trait, when growth index is selected for, expressed as a proportion of maximum progress for that trait, is shown in Table 4.4. The maximum progress is obtained if selection is solely based on the trait in question.

Table 4.4. Correlation between the growth index and indices for carcass gain, classification score and fat score.

Index	Growth, short	Growth, long
CGS, male	0.95	0.81
CGS, female	0.96	0.84
CGL, male	0.96	0.81
CGL, female	0.95	0.79
CCS, male	0.44	0.72
CCS, female	0.42	0.70
CFS, male	-0.09	-0.33
CFS, female	-0.18	-0.37

Expected effect of the breeding values

The effect of subindices in growth expressed on the original scale is shown in Table 4.5. It is expressed as the difference in performance of two progeny groups, where there is a difference of 1 index units in the sires.

Table 4.5. Effect of 1 index unit larger EBV for a beef bull on phenotypic performance of BxD crossbred progeny. Average in parentheses.

Trait, sex and rearing period	Scale	Denmark	Finland	Sweden	High values mean
Daily carcass gain, males, short	g/day	1.4 (659)	1.5 (643)	1.3 (637)	Higher growth rate
Daily carcass gain, females, short	g/day	1.5 (559)	1.4 (487)	1.5 (485)	Higher growth rate
Daily carcass gain, males, long	g/day	-	1.4 (626)	1.5 (593)	Higher growth rate
Daily carcass gain, females, long	g/day	-	1.2 (454)	1.0 (413)	Higher growth rate
Carcass score, males	1-15	0.033 (6.3)	0.040 (7.7)	0.030 (6.7)	Higher classification
Carcass score, females	1-15	0.027 (6.0)	0.032 (6.3)	0.028 (6.4)	Higher classification
Fat score, males	1-5	0.010 (2.6)	0.012 (2.2)	0.009 (2.3)	Higher fat score
Fat score, females	1-5	0.007 (3.0)	0.015 (2.7)	0.010 (2.9)	Higher fat score

References

BxD_final_report.pdf (nordicebv.info)

2019.10.14-TMI-of-beef-sires-used-for-dairy-crosses.pdf (nordicebv.info)

5. Youngstock survival

The youngstock survival index includes two breeding values, young stock survival early period (day 1-30) and young stock survival late period (day 31-200), weighted together according to their economic value. The index for youngstock survival describes a bull's crossbred offspring's genetic potential to survive from birth to day 200 post-birth. The breeding values are based on animal entry-exit records routinely registered in compliance with EU regulations.

Trait definitions

In the evaluation of youngstock survival, two traits are considered (Table 5.1).

Table 5.1. Abbreviations and definitions of traits included in evaluation of growth.

Abbreviation	Definition
P1	Calf survival in the period: 1 to 30 days
P2	Calf survival in the period: 31 to 200 days

Records for P1 are set to missing in the following cases:
- If the crossbred calf is killed during day 1-7.
- If the crossbred calf is slaughtered, exported or otherwise lost during day 1-30
- If the crossbred calf is less than 30 days old at the date of data extraction

If the crossbred calf dies day 30 or before, the P1 variable is set to 0, otherwise it is 1.

Records for P2 are set to missing in the following cases.
- If P1 is 'did not survive' or P1 is missing
- If the heifer is slaughtered, exported or otherwise lost during day 31-200
- If the crossbred calf is less than 200 days old at the date of data extraction.

If the crossbred calf dies in this period, the P2 variable is set to 0, otherwise it is 1.

Basic editing rules

For all traits a general editing is done. Calves are included if they are:
1. Born in Denmark, Sweden, or Finland 2000 and onwards
2. Born by a purebred dairy dam of the breed RDC, Holstein or Jersey
3. Sired by a purebred beef AI sire of one of the major beef breeds
4. Born in a milk producing herd.

The purpose of these edits is to ensure that data 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.

The general editing rules are followed by a specific editing for young stock survival traits:
- Stillborn calf or calves euthanized right after birth (euthanized up to day 7 after birth) are deleted
- Records for aborted and defect calves were deleted
- Records for calves from multiple birth (twins, triplets) were deleted
- Records for ET-calves, calves with unknown sex, or castrates were deleted
- Records with missing vitality, herd, birth date or invalid parity were deleted
- Finnish young stock survival data from before 2003 was deleted
- Swedish young stock survival data for males from before 2009 was deleted.

Pre-adjustment

All traits were transformed using the Snell score method (Snell, 1964). The transformation was done within subclasses of country – year – sex – dam breed.

Genetic evaluation

Model

A multitrait and multibreed sire model is used. Below are the effects in the model:

- Country – herd – year of birth of crossbred   fixed
- Country – year – month of birth of crossbred   fixed
- Country – year – sex of crossbred   fixed
- Country – parity of dam of crossbred   fixed
- Country – transfer (0/1) – 5 birth years (only for period 2)   fixed
- Breed – year of birth of dam of crossbred   fixed
- Breed of (beef) sire   fixed
- Sire   random
- Residual   random

No heterosis effect is included in the model, and the EBV expresses the sum of additive effect and effect of heterosis that can be observed in beef × dairy crossbred offspring.

Genetic parameters

The parameters used in the genetic evaluation for youngstock survival traits are shown in Table 5.2.

Table 5.2. Estimated genetic parameters for youngstock survival traits[1]: heritability on the diagonal and genetic correlations above the diagonal.

	P1	P2
P1	**0.01**	0.30
P2		**0.015**

[1] P1 = young stock survival, early period; P2 = young stock survival, late period

Index

Effect of "Breed of sire" from the genetic model is added to the EBV's for young stock survival before standardization. The standardization of the relative breeding values is described in the chapter "Expression and standardization".

The young stock survival index includes standardized indices for young stock survival early and late period, combined with weight factors (Table 5.3).

Table 5.3. Weights in calculation of the young stock survival index.

	Young stock survival
Young stock survival, early period	0.36
Young stock survival, late period	0.83

All three breeding values are published when bull's reliability for late period is 50 %, or when the bull has at least 500 offspring with youngstock survival records, or when the bull has published breeding values for calving and growth traits.

Correlation between the Youngstock survival index and the underlying traits

The expected progress of each trait, when Youngstock survival index is selected for, expressed as a proportion of maximum progress for that trait, is shown in Table 5.4. The maximum progress is obtained if selection is solely based on the trait in question.

Table 5.4. Correlations between index for youngstock survival and breeding values for young stock survival early and late period.

	Correlation
Young stock survival, early period	0.63
Young stock survival, early period	0.96

Expected effect of the breeding values

The effect of subindices for youngstock survival expressed on the original scale is shown in Table 5.5. It is expressed as the difference in performance of two progeny groups, where there is a difference of 1 index units in the sires.

Table 5.5. Effect of 1 index unit larger EBV for a beef bull on phenotypic performance of BxD crossbred progeny. Average in parentheses.

Period and sex	Scale	Denmark	Finland	Sweden	High values mean
Period 1, males	0-1	0.0009 (0.953)	0.0009 (0.954)	0.0008 (0.979)	Higher survival
Period 1, females	0-1	0.0009 (0.936)	0.0009 (0.970)	0.0008 (0.984)	Higher survival
Period 2, males	0-1	0.0013 (0.922)	0.0012 (0.961)	0.0011 (0.980)	Higher survival
Period 2, females	0-1	0.0013 (0.959)	0.0012 (0.970)	0.0011 (0.977)	Higher survival

References
Joint Nordic Beef x Dairy Genetic Evaluation of Youngstock Survival

6. Gestation length

The index for Gestation length is calculated separately for primiparous and multiparous cows, and only the index values for multiparous pregnancies are published. The index for gestation length describes a bull's crossbred offspring's gestation length. The breeding values are based on gestation lengths records, derived nationally from routinely registered insemination and calving records.

Trait definitions

In the evaluation of gestation length, two traits are considered (Table 6.1).

Table 6.1. Abbreviations and definitions of traits included in evaluation of growth.

Abbreviation	Definition
GL_1	Gestation length in first parity
$GL_{\geq 2}$	Gestation length in later parities

Basic editing rules

For all traits a general editing is done. Calves are included if they are:
1. Born in Denmark, Sweden, or Finland 2000 and onwards
2. Born by a purebred dairy dam of the breed RDC, Holstein or Jersey
3. Sired by a purebred beef AI sire of one of the major beef breeds
4. Born in a milk producing herd.

The purpose of these edits is to ensure that data 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.

The general editing rules are followed by a specific editing for gestation length traits:
- In Denmark, gestation lengths are limited to 260 - 300 days. Sweden includes gestation lengths ranging from 260 to 310 days. Gestation lengths from Finland are limited to 260 to 310 days.
- Outliers detected with the IQR method for outlier detection, applied within sire breed, are deleted.

Outlier detection
The IQR method for outlier detection defines data points as outliers if they fall below the first quartile minus 1.5 times the IQR or above the third quartile plus 1.5 times the IQR. The interquartile range (IQR) is the range between the first quartile (25th percentile) and the third quartile (75th percentile) of the data. This method assumes that most of the data should lie within the central range. The IQR method is applied within sire breeds.

Pre-adjustment
All traits were pre-adjusted for heterogeneous variance within subclasses of sex.

Genetic evaluation

Model

A multitrait and multibreed sire model is used. Below are the effects in the model:

- Country – herd – year of birth of crossbred   fixed
- Country – year – month of birth of crossbred   fixed
- Country – year – sex of crossbred   fixed
- Country – age of dam of crossbred   fixed

- Breed – year of birth of dam of crossbred   fixed
- Breed of (beef) sire   fixed
- Sire   random
- Residual   random

No heterosis effect is included in the model, and the EBV expresses the sum of additive effect and effect of heterosis that can be observed in beef × dairy crossbred offspring.

Genetic parameters

The parameters used in the genetic evaluation for gestation length traits are shown in Table 6.2.

Table 6.2. Estimated genetic parameters for gestation length[1]: heritability on the diagonal and genetic correlations above the diagonal.

	GL_1	$GL_{\geq 2}$
GL_1	0.56	0.99
$GL_{\geq 2}$		0.57

[1] GL_1 = gestation length in first parity; $GL_{\geq 2}$ = in later parities

Index

Effect of "Breed of sire" from the genetic model is added to the EBV's for young stock survival before standardization. The genetic base is defined as 2-5 years old crossbreds born after beef breeds which can be used in all 3 countries. Gestation length breeding values are expressed in days and as a deviation from a standard dairy gestation length average fixed at 280 days.

Due to the very high genetic correlation between heifers and cows breeding values only the index for gestation length for cows is published. The index for gestation length is published if the beef bull has got official breeding values for calving traits and the reliability for gestation length is higher than 50%.

Expected effect of the breeding values

The effect of subindices in gestation length expressed on the original scale is shown in Table 6.3. It is expressed as the difference in performance of two progeny groups, where there is a difference of 1 index units in the sires.

Table 6.3. Effect of 1 index unit larger EBV for a beef bull on phenotypic performance of BxD crossbred progeny. Average in parentheses.

Trait and sex	Scale	Denmark	Finland	Sweden	High values mean
GL_1, males	days	1 (281)	1 (284)	1 (281)	Longer gestations
GL_1, females	days	1 (280)	1 (282)	1 (280)	Longer gestations
$GL_{\geq 2}$, males	days	1 (284)	1 (288)	1 (283)	Longer gestations
$GL_{\geq 2}$, females	days	1 (283)	1 (287)	1 (282)	Longer gestations

References
Joint Nordic Beef x Dairy Genetic Evaluation of Gestation length

7. Expression and standardization

Standardization
EBVs for all traits (except gestation length) are standardized in the same way. The formula for adjusting the mean and standard deviation of EBV is:

EBV = (EBV$_{animal}$ – Mean) × Standardization factor

Breeding values for sub-indices are standardized to an average breeding value of 100 and a standard deviation of 10. NBDI is standardized to have a standard deviation of 10, and the mean is (by definition) close to zero.

Mean of the relative breeding values
The genetic base is a relative breeding value, where 100 reflects the present genetic level. Hence, the genetic base is a rolling base, that is updated at each evaluation.

The genetic base is defined as the mean EBV of the sire of all calf's born 2-5 years before publication date. The genetic base includes BxD calves of all beef sire breeds, except BBL. This is because BBL is not used in all three Nordic countries.

Standard deviation of the relative breeding values
The standard deviation of the relative EBVs is constant over time to ease interpretation.

Genetic standard deviation taken from the estimated genetic parameters are used to standardize EBV variation. The standard deviation would be 10 within breed if reliability of published bulls were 100 %. However, because reliability of proven bulls is below 100% this reduces standard deviation – most for traits with low heritability. On the other hand, addition of effect of breed of sire means that the observed standard deviation among bulls for most traits are considerably above 10, because there are considerable breed differences for most traits.