Nordic breeding values for beef breed sires used for crossbreeding with dairy dams

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Abstract

The use of beef semen in dairy herds has increased considerably during the past years in Denmark, Finland and Sweden. This has created a need for the dairy farmers to be able to, select the beef breed sires best suited for crossbreeding with dairy cattle. Nordic Cattle Genetic Evaluation has developed joint Nordic breeding values that will aid farmers in their choice of the right beef sires to use on their dairy cows. An important feature of the breeding values is that they are comparable across sire breed and country of origin. Breeding values are currently estimated for seven traits belonging to one of two trait groups: calving and carcass traits. This paper describes the new beef × dairy evaluation that gives the Nordic dairy farmers a better opportunity for a profitable production of beef × dairy crossbred animals.

Key words: crossbreeding, genetic evaluation, calving traits, carcass traits

Introduction

In the last decade there has been a large increase in the use of beef semen in dairy cattle herds in both Denmark, Finland and Sweden. The strategy of inseminating dairy cows not needed to produce replacement heifers with beef semen has several advantages for the profitability of the dairy farms. Combining this strategy with other modern breeding tools at herd level such as the use of sexed semen and genomic breeding values has been proven efficient (Ettema *et al.*, 2017) and is expected to increase even further in the future.

Nordic Cattle Genetic Evaluation (NAV) has for more than 10 years run a joint genetic evaluation and breeding goal for the dairy breeds Red dairy cattle (RDC), Holstein and Jersey in Denmark, Finland and Sweden (http://www.nordicebv.info/about-nav). More recently the cooperation has been extended to also develop joint evaluations for beef breeds; both for beef breed sires used on dairy cattle and for pure breeding. Due to the rapidly increased use of beef semen in dairy herds, it was of high priority to develop breeding values for beef breed AI-bulls based on their beef × dairy crossbred offspring (in this paper referred to as beef × dairy evaluation). The new breeding values make it possible for the Nordic dairy farmers to select the beef breed sires that produce the economically best crossbred calves, that is calves that are easily born and with a high growth capacity and carcass quality. An important feature of the evaluation is that all beef bulls are comparable across sire breed, dam breed and country.

The aim of this paper is to describe the newly developed joint Nordic beef × dairy evaluation, including available data and its structure, trait definitions, evaluation model and results. Further, a brief status of future developments for the beef × dairy evaluation is given.

Material and methods

Data

The national cattle data bases in Denmark, Finland and Sweden contain most important information on both purebred and crossbred animals such as pedigree, production results and inseminations. 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. Beef sire breeds considered were Belgian Blue (BBL), Blonde d'Aquitaine (BAQ), Aberdeen Angus (AAN), Limousin (LIM), Charolais (CHA), beef Simmental (BSM) and Hereford (HER).

There has been an increase in the use of beef semen in dairy herds in both Denmark, Finland and Sweden (Figure 1). 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. In the August 2019 evaluation, calving records from 714 380 beef × dairy crossbred calves were included. The corresponding number for the carcass traits was 273 417.

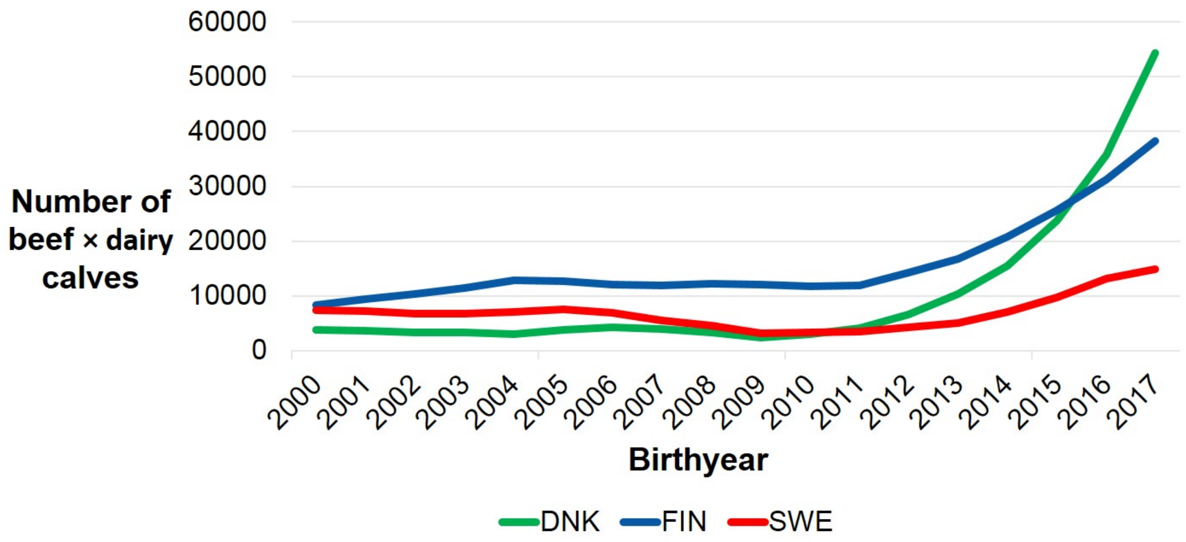

Figure 1. Number of beef × dairy crossbred calves born in Denmark (DNK), Finland (FIN) and Sweden (SWE) from year 2000 and onwards.

Data structure

The distribution of sire breeds has varied greatly over time. Figure 2 displays the proportion of crossbred calves, across all countries, after the major beef sire breeds. Considering crossbred calves born in 2018, the majority have either a BBL (41%) or BAQ (28%) sire. The remaining calves are more evenly distributed on the other sire breeds, and none of them exceeding 10%.

The use of sire breeds however differs across countries. Again, considering crossbred calves in 2018, BBL was the dominating breed used in Danish dairy herds (accounts for over 80% of Danish crossbred calves). BAQ sires are especially used in Finnish dairy herds and have increased in popularity over recent years (currently they account for around 50% of

Finnish crossbred calves). In Sweden, on the other hand, there is a more equal use of the remaining sire breeds (BSM, HER, CHA, LIM and AAN each accounting for about 30 to 15% of the Swedish crossbred calves). Another difference between countries in the use of beef semen in dairy herds is that Sweden to a larger extent uses beef semen on heifers. However, the vast majority of inseminations of beef on dairy cows are on cows in all three countries.

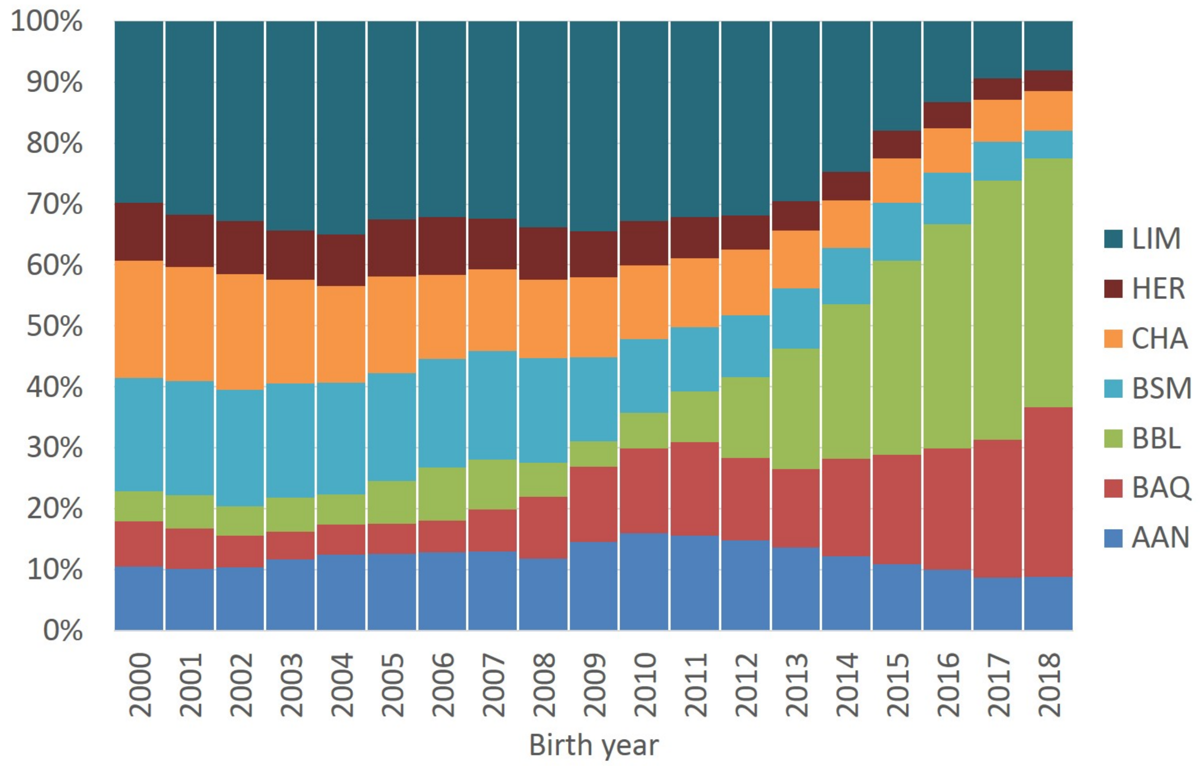

Figure 2. The distribution of sire breeds for beef × dairy crossbreeds born between 2000 and 2018. AAN: Aberdeen Angus; BAQ: Blonde d'Aquitaine; BBL: Belgian Blue; BSM: beef Simmental; CHA: Charolais; HER: Hereford; LIM: Limousin

The connection between sire breeds is good since many of the dairy herds use several beef sires per year and also beef sires from different breeds. Furthermore, all beef breeds are used on all dam breeds. This enables a fair comparison of beef bulls across breed. Table 1 illustrates that connectedness between beef sire breeds by listing the number of common herd-years by sire breed for multiparous cows. An exception from the use of several beef breeds per year occurs in some Danish herds where only BBL sires have been used.

Another difference between the countries is related to the rearing system of animals for slaughter, which affects the average age at slaughter for both males and females (Figure 3). In Denmark, crossbred calves are reared more intensively with an average age at slaughter below 550 days (18 months) for both males and females. In Finland and Sweden, on the other hand, the rearing period is longer and more extensive with an average age at slaughter above 550 days. In Finland, females are slaughtered at an earlier age, whereas in Sweden the opposite is true. In Denmark there is no clear sex difference for age at slaughter. The differences in rearing systems, explained by differences in pricing systems between countries, are important to consider and they have affected the trait definitions in the beef × dairy evaluation.

Table 1. Cross table of common herd-years by sire breed for multiparous cows.

Sire breed	BAQ*	BBL	BSM	CHA	HER	LIM
AAN	4673	162	3393	2967	2583	8446
BAQ		387	3589	3602	1423	8996
BBL			623	444	55	1302
BSM				5028	2679	7936
CHA					2643	7414
HER						3852

* AAN: Aberdeen Angus; BAQ: Blonde d'Aquitaine; BBL: Belgian Blue; BSM: beef Simmental; CHA: Charolais; HER: Hereford; LIM: Limousin.

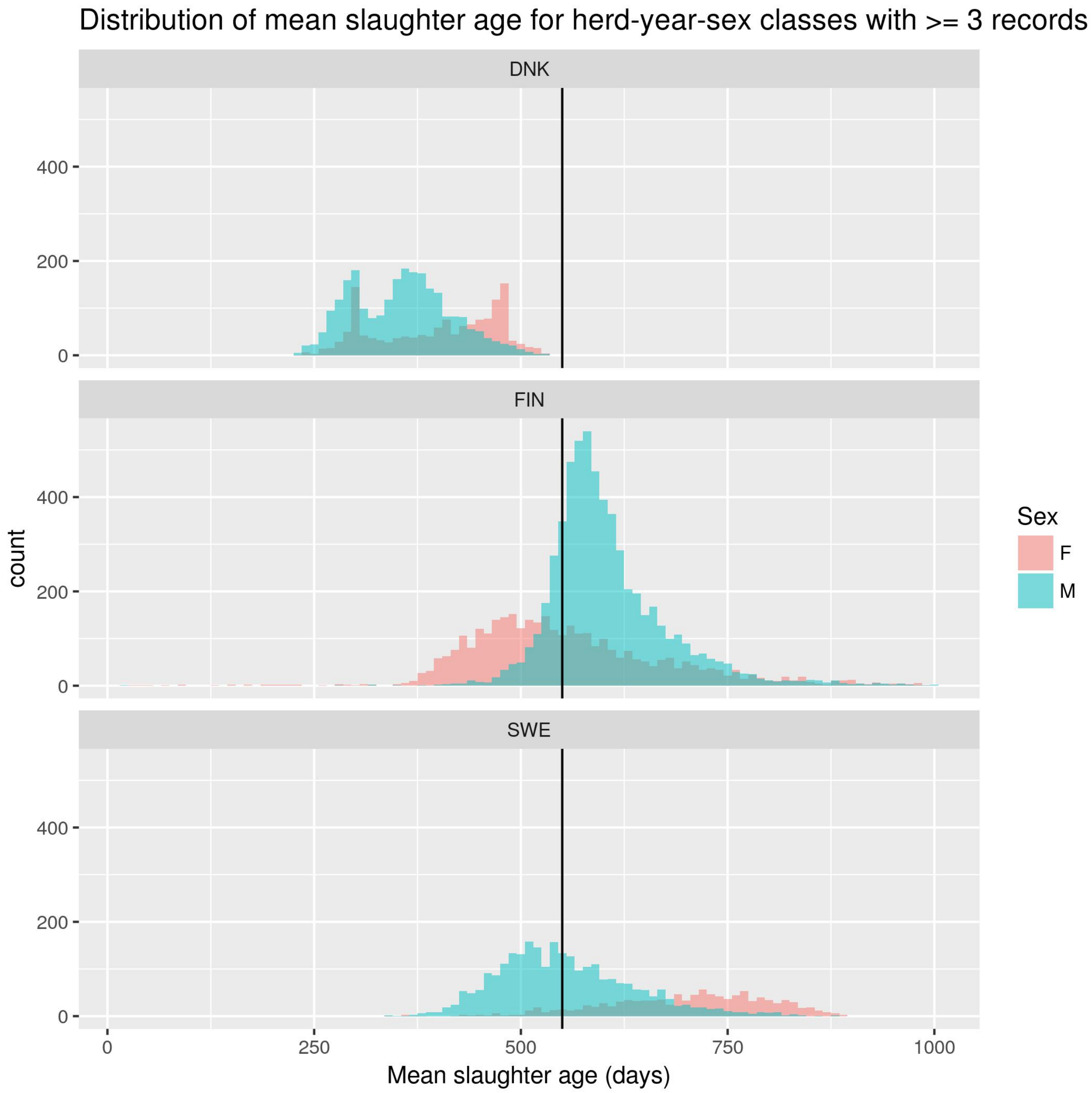

Figure 3. Distribution of mean slaughter age (days), by country) and sex.
DNK: Denmark; Finland: FIN; Sweden: SWE; Female: F; Male: M

Trait definitions

In the Nordic beef × dairy evaluation, there are in total seven breeding values published from two trait groups.

The calving evaluation has a core of four traits recorded in all three countries: calf survival and calving ease based on cows in 1st and later lactations, respectively**.** Calf survival is defined as calves born alive and still alive 24 hours after birth. Calving ease is scored according to international standards on a scale 1(easiest) to 4 (most difficult). The reason for treating records from first and later lactation as genetically different traits is that the genetic correlation is generally different from one (e.g. Eriksson *et al.*, 2004). Information on calf size is used as an indicator trait in the evaluation (data only available from Denmark). Calf size is a subjective assessment made by the farmer and is scored in four categories from small to large.

The carcass evaluation is based on slaughterhouse records, comprised of cold carcass weight and EUROP scores for carcass conformation and carcass fat (both scored in 15 categories) for slaughtered animals. Age at slaughter is calculated as the difference between date of slaughter and date of birth. The trait carcass daily gain (kg/day) is calculated as the difference between cold carcass weight and half the birth weight, divided by age at slaughter (in days). Individual birth weight records are not available, and tabulated breed averages are therefore used.

About 60% of the slaughter records are for male beef × dairy crossbreds, and the other 40% pertain to females. Growth and carcass traits in males and females are treated as genetically different but correlated traits. This is done to account for differences between males and females in phenotypic variances of growth and carcass traits, and because the genetic background of these traits is slightly different between sexes.

Rearing practices and targets for slaughter weight differ substantially between the three countries, resulting in rather different average slaughter ages. As the growth typically follows a sigmoid curve, the trait carcass daily gain was split into two traits, carcass daily gain for short and long rearing period, to ease modeling of the trait.

Genetic evaluation model

Two multiple-trait linear sire models, one for calving traits and one for carcass traits, are used in the Nordic beef × dairy evaluation.

Fixed effects

- Sire beef breed
- Herd-year of calving/slaughter
- Country-year-month of calving
- Age of dam at calving/age of crossbred animal at slaughter
- dam breed-year

Random effects

- Genetic effect of sire

Comments to the models

The effect of sire beef breed is included to adjust for systematic sire breed differences. The breed effect is added back to the individual sire solutions to get the final breeding value of a bull. The dam breed-year effect is included to account for the fact that we have three different dam breeds with different genetic levels (and trends) over the years.

Beef sires are only evaluated for the direct genetic effect. The maternal genetic effects that are usually included in the analyses of calving traits are not included here as it is assumed that crossbred animals are only produced for slaughter and not to be used as suckler cows. Maternal effects expressed by dairy dams are modelled through the dam breed effect.

Variance components were estimated from the complete dataset. Variance components and breeding values were estimated using the DMU software package (Madsen & Jensen, 2008).

Publication of breeding values

Four breeding values are published for calving traits: calf survival in first and later lactations and calving ease in first and later lactations. These breeding values are published if the bull has a minimum reliability of 50 for breeding value for calf survival or stillbirth in later lactations.

For carcass traits, three combined breeding values are published: daily carcass gain, carcass conformation score and carcass fat score. Carcass gain is based on combining breeding values for bulls and heifers with short (<550 days) and long fattening periods, respectively, with equal weights. Conformation and fat score are based on combing breeding values for bulls and heifers with equal weights. All three breeding values are published if the bull has a minimum reliability of 50 for breeding value for carcass conformation score.

Breeding values are expressed such that:

1) a recent cohort of beef × dairy crossbreds (born 2-5 years prior to the publication date) have an average sire breeding value equal to 100, and 2) the genetic variance on the published scale is equal to 10. This expression of breeding values follows that for breeding values of dairy bulls; we chose this practice as the target users of the Beef × Dairy breeding values, the dairy producers, are familiar with it.

Results & Discussion

Genetic parameters

Estimated heritabilities for calving traits were generally low, ranging from 0.01 for calf survival, multiparous cows to 0.11 for calving ease, primiparous cows (Table 2). Calf size had moderately high heritabilities. Estimated genetic correlations among the same trait recorded in primi- versus multiparous cows were around 0.9. The genetic correlations between calf survival and calving ease were moderately high, around 0.6-0.7. By and large, these parameters are similar to the genetic parameters used by NAV in the calving traits evaluation of dairy breeds (NAV, 2019).

Carcass traits were moderately highly heritable, with values ranging from 0.2 to 0.4 (Table 3). Genetically, growth in the short and long rearing period appears to be the same, as indicated by a genetic correlation larger than 0.95. The genetic correlation between traits recorded in male and female was high, around 0.8-0.9.

Table 2. Genetic parameters for calving traits; estimated heritabilities on the diagonal and estimated genetic correlations on the off-diagonals.

	CSu1*	**CSu2+**	**CE1**	**CE2+**	**CSi1**	**CSi2+**
CS1	**0.049**	0.88	0.70	0.67	0.80	0.58
CS2+		**0.013**	0.61	0.62	0.53	0.43
CE1			**0.114**	0.97	0.89	0.93
CE2+				**0.049**	0.80	0.84
CS1					**0.171**	0.83
CS2+						**0.091**

* CSu1, CSu2+ : calf survival in first respectively later parities; CE1, CE2+ : calving easy in first respectively later parities; CSi1, CSi2+: calf size in first respectively later parities

Table 3. Genetic parameters for carcass traits; estimated heritabilities on the diagonal and estimated genetic correlations on the off-diagonals.

	dgs,♂ *	dgl,♂	bcs,♂	fats,♂	dgs,♀	dgl,♀	bcs,♀	fats,♀
dgs,♂	**0.19**	0.97	0.30	-0.21	0.83	0.86	0.22	-0.27
dgl,♂		**0.21**	0.34	-0.10	0.85	0.86	0.25	-0.21
bcs,♂			**0.32**	-0.17	0.31	0.24	0.92	-0.12
fats,♂				**0.23**	-0.20	-0.13	-0.19	0.88
dgs,♀					**0.33**	0.97	0.35	-0.30
dgl,♀						**0.33**	0.25	-0.22
bcs,♀							**0.36**	-0.18
fats,♀								**0.25**

* Dgs: carcass daily gain, short fattening period; dgl carcass daily gain, long rearing period; bcs: carcass conformation score; fats: carcass fat score; ♂ and ♀ specifies whether it is a trait male respectively female trait

Distribution of breeding values

There is a negative genetic correlation between the calving and carcass traits. Comparing breeds, a similar pattern is observable where breeds good for carcass traits generally are not as good for calving traits. It is apparent that lighter breeds, such as AAN, have higher average breeding values for calving traits, compared to the heavier breeds, such as BBL (Figure 4). There is also a large variation within breed for the calving traits. In Figure 5, the distribution of breeding values for carcass daily gain is shown. Here 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. However, there is large variation within all sire breeds. It is therefore very important that the dairy farmers should look at the breeding values of individual beef sires regardless of breed since there is large variation not only across but also within breed.

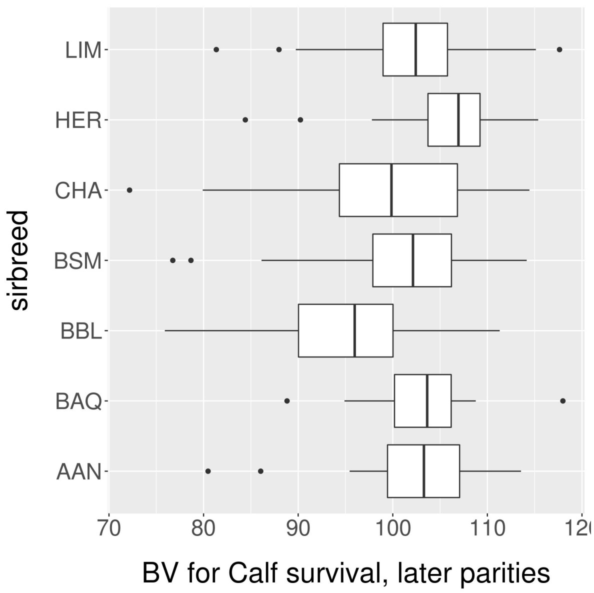

Figure 4. The distribution of breeding values for calf survival in later parities by sire breed: AAN: Aberdeen Angus; BAQ: Blonde d'Aquitaine; BBL: Belgian Blue; BSM: beef Simmental; CHA: Charolais; HER: Hereford; LIM: Limousin

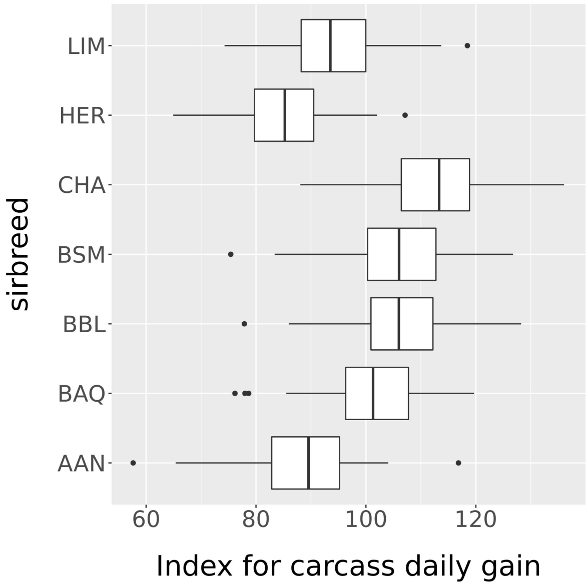

Figure 5. The distribution of the index for carcass daily gain by sire breed: AAN: Aberdeen Angus; BAQ: Blonde d'Aquitaine; BBL: Belgian Blue; BSM: beef Simmental; CHA: Charolais; HER: Hereford; LIM: Limousin

The performance of the beef × dairy crossbreds is affected by heterosis. However, a heterosis effect is not included in the model as the data structure (only F1) does not enable separating additive effects from heterosis effects. Thus, the breeding values include (part of) the heterosis effects. The primary purpose of the beef × dairy evaluation is to chose 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 no effect when selection beef bull for producing cross breed offspring.

Future perspectives

Communication and improved advisory service related to the new beef × dairy breeding values are ongoing activities. To make a more efficient selection tool available for the dairy farmers, development on combining the calving and carcass traits in a total merit index for beef × dairy has been nearly completed. The Nordic beef × dairy index (NBDI) will be implemented in the end of 2019. NBDI will be available for both short and long rearing period since the length of the rearing period has a large impact on the economic weight for growth and carcass traits. In the future, the NBDI can be further improved by including other traits of relevance to the production of crossbred beef × dairy animals.

Furthermore, new traits are currently planned to be developed. The first trait that will be investigated is young stock survival. Breeding values for young stock survival on beef × dairy crossbred calves are already published in Denmark (Davis *et al.*, 2019).

Conclusions

The new breeding values for beef breed sires based on their crossbred beef × dairy offspring was first published by NAV in December 2018. Breeding values are routinely published four times a year. They offer the opportunity for Nordic dairy farmers to select the best beef breed sires across breed to be used for insemination on the dairy cows in their herd. For a profitable production of crossbred animals, it is important to consider both calving and carcass traits. An important message is that the dairy farmer should look at the breeding values of individual beef sires regardless of breed since there is large variation not only across but also within breed.

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