

Multi-breed genetic evaluation of beef bulls used in dairy herds – Emphasis on newest development

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Abstract

Since 2018, Nordic Cattle Genetic Evaluation (NAV) routinely estimates across breed breeding values for beef sires based on data from their offspring when used on dairy cows and since 2019, the Nordic farmers have access to the Nordic Beef × Dairy overall economic Index (NBDI). To fulfill requests expressed by the industry, the NAV Beef × Dairy evaluation traits portfolio has recently been expanded to include two new trait groups, youngstock survival and gestation length. The aim of this paper is to describe the current Nordic routine evaluation for beef bulls used on dairy cows with focus on the recent developments.

Key words: beef x dairy, genetic evaluation, multi-breed, youngstock survival, gestation length

Introduction

The interest in utilizing beef bulls with dairy cows has grown significantly over time. The integration of beef semen into dairy herds, particularly when paired with sexed dairy semen, has proven to be highly beneficial for farmers in terms of economic advantages. By ensuring replacements from the genetically superior animals in the herd and generating value-added beef × dairy calves from the remaining females, this practice helps improving the profitability of the dairy farm.

The selection of the appropriate beef bulls to be used on the farm is an important factor to ensure the success of this practice. Considerable across but also within beef breed genetic differences have been reported for many traits (Davis et al., 2019) which emphasizes the need for a multi-breed genetic evaluation of the beef bulls used in dairy herds.

To help farmers in their choice of the right beef sires to use, Nordic Cattle Genetic Evaluation (NAV) has developed a joint Nordic multibreed genetic evaluation of beef bulls used in dairy farms (Carlén et al., 2019).

The aim of this paper is to briefly describe the current Nordic routine evaluation for beef bulls used on dairy cows with focus on the recent developments.

The Joint Nordic Beef × Dairy Genetic Evaluation

The joint Nordic Beef × Dairy evaluation includes data from Finland, Denmark, and Sweden and crossbred calves from purebred Holstein, Jersey and Red Dairy Cattle (RDC) cows. Up to eight individual breeding values may be made publicly available for each bull, subject to compliance with publication rules. Since its launch in 2018, the evaluation is publishing 4 breeding values for calving traits: calf survival and calving ease based on cows in 1st and later lactations, respectively and 3 combined breeding values for carcass traits: daily carcass gain, carcass conformation score and carcass fat score.

In 2019, the Nordic Beef x Dairy economic Index (NBDI) was implemented. This index assesses the economic value of beef bulls based on their genetic potential for producing crossbred beef × dairy offspring that benefit farmers economically. The NBDI currently consists of two sub-indices: one for birth traits, which includes calf survival and calving ease in later lactations and another for growth traits, including daily carcass gain, carcass conformation score, and carcass fat score. As

the rearing period's length and intensity affect the economic values of the growth traits, both the growth index and NBDI are available for short (below 550 days) and long (above 550 days) rearing periods.

Since the launch of the current evaluation, industry stakeholders have voiced their desire to introduce two additional traits into the evaluation framework: Youngstock survival (YSS) and gestation length (GL). The addition of YSS is particularly pertinent due to its far-reaching implications for both economic viability and animal welfare, thus warranting its integration into the NBDI. GL also holds significant economic importance as it plays a crucial role in effective calving pattern management on dairy farms. This importance is amplified for dairy farmers participating in beef on dairy programs, as gestation length varies across different beef breeds (Norman et al. 2009). This insight underscores the potential for managing this trait through careful selection of the beef bull used for breeding with the cow. However, many studies such as Hansen et al., 2004 and Eaglen et al., 2013 did not support selection for shorter neither longer duration but rather opt for intermediate values which were found by many studies to be optimal for other traits like productive life and calving ease (Norman et al., 2011). Consequently, at this point, there is no plan to incorporate GL into the NBDI. To address the industry's requests, YSS was implemented in November 2022, followed by GL in May 2023.

Materials and Methods

Data

For both YSS and GL, as with the other beef × dairy traits (Davis et al., 2019), the data used in the evaluation includes crossbred calves born in the three countries from the year 2000 onward, provided they meet the following criteria:

- (i) Born to a purebred dairy dam of the RDC, Holstein, or Jersey breed.
- (ii) Sired by a purebred beef breed AI sire with a minimum of 50 beef-on-dairy crossbred offspring.
- (iii) Born in a milk-producing herd.

Survival data from Swedish males born prior to 2008 and all Finnish data from before 2004 were omitted from the evaluation due to concerns about the completeness of information gathered for animals born before respective years. For all countries, survival data were excluded for all calves born with malformation or from multiple births/embryo transfer, those that do not survive the first 24h after calving, those that are slaughtered or exported within the considered period for survival.

Regarding GL, a similar data editing process was applied as that used for the calving traits (Fikse et al., 2019). After this editing process, data were subject to outlier removal. The Interquartile Range (IQR) statistical method (Smiti, 2020) was used to identify and discard outliers within each sire breed.

For both YSS and GL, a very limited number of records were obtained from Jersey cows in Sweden and Finland, which may pose a limitation when attempting to account for variance heterogeneity within this breed (see the "Heterogenous variance adjustment" section later in this document). Furthermore, these calves born from Jersey cows did not hold significant interest in both countries. Therefore, records collected from Jersey cows in both countries were subsequently excluded from the evaluation.

The final data set included data from 871,524 records for YSS and 1,157,256 records for GL. The data distribution per dam breed and country for both trait groups, is shown in Table 1.

Table 1. Number of survival and gestation length records per dam breed and country.

YSS			
	Denmark	Finland	Sweden
Holstein	262335	152056	59905
RDC	28356	248622	64485
Jersey	55765		
GL			
Holstein	361974	183625	93955
RDC	34184	305230	96969
Jersey	81319		

Trait definitions*Youngstock survival*

YSS is divided on rearing period to create two separate single traits:

- Survival day 1-30 (YSS1): equal to 1 if the calf is alive at day 30, otherwise, it is set to 0
- Survival day 31-200 (YSS2): equal to 1 if the calf is alive at day 200, otherwise, it is set to zero.

In the context of beef production from dairy cattle, both male and female animals are typically raised under similar conditions and for the shared purpose of meat production. Consequently, it is reasonable to assess the YSS as one trait for both heifers and bull calves. This initial assumption was subsequently validated during the validation process, the detailed results of which are not presented here.

Gestation length

Gestation length is defined as the time interval, measured in days, from the moment of conception to the subsequent occurrence of parturition. Distinct traits are defined for heifers (GL1) and cows (GL2).

Heterogeneous variance adjustment

To account for the heterogeneity of variance of YSS across different countries, sexes, birth years and dam breeds, Snell scores were used (Snell, 1964). Groups used for the transformation are subclasses of country – sex – year – dam breed. Years with less than 1000 records were regrouped. Regarding gestation

length, a simple correction for phenotypic variance was applied with respect to sex, addressing a noticeable systematic difference observed in the phenotypic standard deviation for both traits.

Genetic evaluation model

A multiple-trait linear sire model was used to evaluate YSS and GL in the Nordic beef × dairy evaluation.

Fixed effects

The fixed effects included in the model are described in Table 2. The sire beef breed effect is integrated into the model to account for systematic differences among sire breeds. However, it's important to note that this effect is subsequently added to the individual sire solutions to derive the final breeding value of a bull. Furthermore, it has to be noted that the estimated breeding values express the total genetic value meaning that they include both additive and non-additive genetic effects. The transfer effect in the model is defined as a binary variable equal to 1 if the calf was transferred during the first 100 days of its life and zero otherwise. The herd used to create the herd-year contemporary group effect for YSS2 in this case is the herd to which the calf is first transferred otherwise it is the birth herd.

Table 2. Fixed effects included in the model per trait.

	YSS	GL
Sire breed	x	x
Country – herd – year	x	x
Country – year – month	x	x
Country – year – sex	x	x
Dam breed – year	x	x
Country – parity	x	
Country – transfer*	x	
Country – age of the dam		x

* Only for YSS2

Genetic parameter estimation

The genetic parameters were estimated using the DMU software package (Madsen and Jensen 2013) with a multiple-trait model including data from all countries and breeds.

Genetic base

The genetic base is defined as 2-5 years old crossbreds born after beef breeds which can be used in all 3 countries.

Expression of breeding values

Like for the other beef × dairy traits except the NBDI (Fikse et al., 2019), YSS breeding values are presented as relative values, with a standardized mean of 100 and a genetic standard deviation of 10.

GL breeding values differ from the other traits within the NAV portfolio. They are expressed in days and as a deviation from a standard dairy gestation length average fixed at 280 days. This makes it easier to interpret by the farmers since the primary use of the GL breeding values is to help management of the calving patterns.

Results & Discussion

Survival rates

In line with what was observed in the Nordic purebred dairy YSS data (Carlén et al. 2016) and the Danish YSS beef on dairy data (Davis et al., 2020), females had a slightly higher average survival rate for both evaluation periods and survival rates for early period were slightly higher than those for later period (Table 3). Calves born from Jersey cows had a lower survival rate than Holstein and RDC for both traits (Table 4). This finding aligns with the results reported for the Danish YSS beef × dairy data by Davis et al. (2020).

Table 3. Average phenotypic survival rates per sex and trait.

	Number of calves	YSS1	YSS2
Males	429974	0.96	0.95
Females	441550	0.97	0.96

Table 4. Average phenotypic survival rates per dam breed and trait.

	Number of calves	YSS1	YSS2
Holstein	474296	0.97	0.96
RDC	55765	0.97	0.96
Jersey	341463	0.95	0.94

Gestation length data

All data combined, GL was about two days shorter on average for heifers (282 days) compared to cows (284 days) and about one day on average shorter for females (283 days) compared to males (284 days).

Phenotypic means of GL varied per sire breed with Angus and Belgian Blue having the shortest GL and Limousine and Blonde d'Aquitaine the longest (Table 5).

Table 5. Number of records (N), Mean, SD and Median of gestation length per country and sire breed.

Sire breed*	N	Mean	SD	Median
AAN	123012	280.5	5.2	280
BAQ	236749	287.4	5.6	288
BBL	289264	280.8	5.1	281
CHA	98781	283.5	5.6	284
HER	51168	281.6	5.3	282
LIM	168572	287.1	5.8	287
SIM	96720	284.5	5.6	285

*AAN: Aberdeen Angus; BAQ: Blonde d'Aquitaine; BBL: Belgian Blue; CHA: Charolais; HER: Hereford; LIM: Limousine; SIM: Simmental

Genetic parameters

The estimated heritabilities for YSS traits were low (0.01 for YSS1 and 0.015 for YSS2),

and there was a moderate genetic correlation of 0.3 between the two traits. These findings are consistent with what has been reported in other studies for YSS traits (Davis et al., 2020; Buch, 2012). The low heritabilities are expected due to the nature of survival data, where only a small proportion of animals experience mortality and the environmental variation is quite high.

In contrast, high heritabilities were estimated for GL (0.56 and 0.57 for GL1 and GL2 respectively) and a very high genetic correlation of 0.99 was estimated between both traits. These results are consistent with the literature on GL (Eaglen et al., 2013; Hansen et al., 2004; Haile-Mariam & Pryce, 2019; Amer et al 2016; Norman et al., 2009).

Relative breeding values

Figures 1 to 3 present a boxplot summarizing the breeding values per sire breed for YSS1, YSS2 and GL2 respectively. In each graph, the central box represents the interquartile range (IQR) of the data, with the horizontal line inside indicating the median breeding value. The lower and upper whiskers extend to the minimum and maximum values within 1.5 times the IQR, respectively. Data points outside this range are identified as outliers, representing sires with extreme breeding values compared to the rest of the population.

The graphs provide an insightful overview of the distribution of breeding values across different sire breeds, highlighting both the genetic variation among breeds and the variability within each breed. The results underscore the importance of a multi-breed evaluation, highlighting that breed selection alone may not suffice. Instead, farmers should pay close attention to individual bulls to make their breeding decisions.

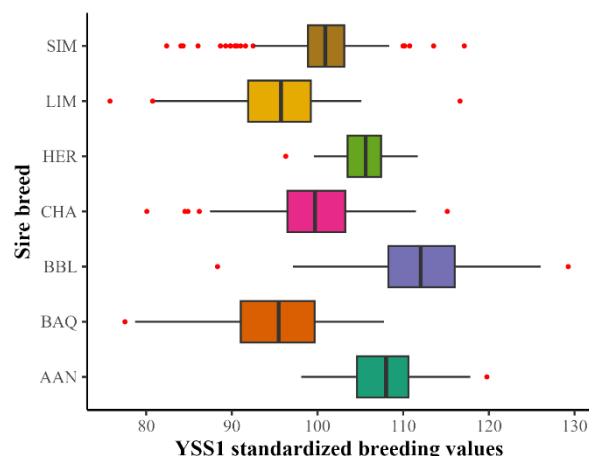


Figure 1. Box and Whisker Plot of YSS1 Relative Breeding Values by Sire Breed: AAN: Aberdeen Angus; BAQ: Blonde d'Aquitaine; BBL: Belgian Blue; CHA: Charolais; HER: Hereford; LIM: Limousine; SIM: Simmental

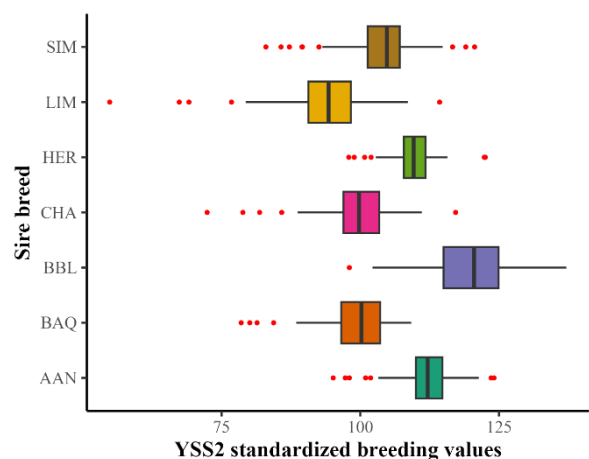


Figure 2. Box and Whisker Plot of YSS2 Relative Breeding Values by Sire Breed: AAN: Aberdeen Angus; BAQ: Blonde d'Aquitaine; BBL: Belgian Blue; CHA: Charolais; HER: Hereford; LIM: Limousine; SIM: Simmental

Due to the high genetic correlation between GL1 and GL2, suggesting that they represent the same trait, a decision has been made to exclusively publish GL2.

Both YSS1 and YSS2 breeding values, as well as a combined breeding value derived from both sources, are now made available for publication. Proper economic weights to be used for both the combined YSS index and inclusion in the NBDI are being calculated and are planned to be implemented by the end of 2023.

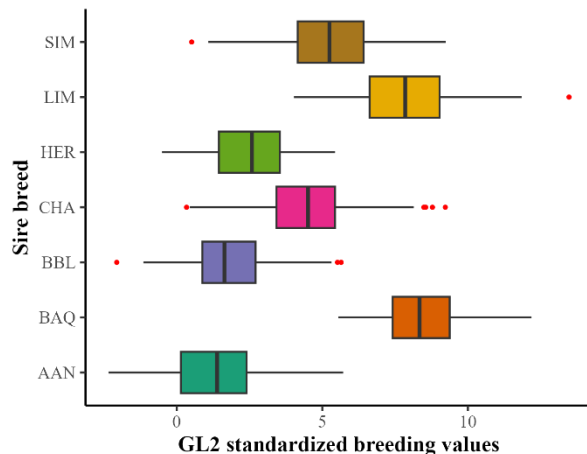


Figure 3. Box and Whisker Plot of GL2 Relative Breeding Values (expressed in days) by Sire Breed: Aberdeen Angus; BAQ: Blonde d'Aquitaine; BBL: Belgian Blue; CHA: Charolais; HER: Hereford; LIM: Limousine; SIM: Simmental

Conclusions

The study's findings reinforce the necessity of conducting multibreed evaluations when estimating breeding values for beef bulls used in dairy herds. Significant within-breed variation was observed for both YSS and GL traits, highlighting the importance of considering individual sire results rather than relying solely on specific breeds.

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