

News - NAV evaluation

1 November 2022

Dairy cattle

The latest NAV official evaluation for yield, fertility, conformation, udder health, general health, calving traits, milkability, temperament, growth, longevity, young stock survival, claw health, saved feed and NTM took place as scheduled. NAV carried out three evaluations per trait group:

Holstein evaluation, including data from: Danish Holstein, Swedish Holstein, Norwegian Holstein, Finnish Holstein, Finnish Ayrshire and Finncattle.

Red Dairy Cattle evaluation, including data from: Danish Red, Swedish Red, Finnish Ayrshire, Finnish Holstein and Finncattle.

Jersey evaluation, including data from: Danish Jersey, Swedish Jersey, Finnish Jersey, Norwegian Jersey and French Jersey.

Extraction dates

Dates for extraction of data from national databases for the latest official evaluations are given in Table 1.

Table 1. Dates for extraction of data from the national databases

Trait	Denmark	Finland	Sweden
Yield	19.09.2022	06.09.2022	08.09.2022
Type, milkability and temperament	19.09.2022	06.09.2022	09.09.2022
Fertility	19.09.2022	06.09.2022	10.09.2022
Udder health and other disease	19.09.2022	06.09.2022	10.09.2022
Calving ¹⁾	19.09.2022	06.09.2022	10.09.2022
Longevity	19.09.2022	06.09.2022	10.09.2022
Growth ¹⁾	19.09.2022	06.09.2022	10.09.2022
Claw health	19.09.2022	06.09.2022	09.09.2022
Youngstock survival	19.09.2022	06.09.2022	10.09.2022
Saved feed	19.09.2022	06.09.2022	09.09.2022
Pure beef cattle	04.10.2022	11.10.2022	10.10.2022

¹⁾Including data for the evaluation of beef bulls used on dairy

Data used in genomic prediction

Genotypes were extracted from the joint Nordic SNP data base 3 October 2022. INTERBULL information from August 2022 was included in the genomic prediction.

News in relation to NAV dairy genetic evaluation

Dairy

Traditional evaluation

- Calving evaluation has been upgraded to follow the defined Eurogenomic Golden standards for Jersey, RDC and Holstein
- Jersey udder conformation - changed weights

Genomic prediction

- Single step for type traits for Jersey, RDC and Holstein

BeefxDairy

- Joint Nordic genetic evaluation for youngstock survival

Beef pure

- Danish Welsh Black data removed from Hereford evaluation

Upgrading of calving evaluation

In November 2022 calving evaluation has been upgraded to follow the defined European Golden standards for Jersey, RDC and Holstein by:

- Improved handling of heterogenous variance by applying the Snell score method
- Updating the genetic parameters
- Correction for inbreeding
- Including permanent cow effect in the model
- Excluding heterosis in the RDC model

The purpose of reviewing and optimizing the genetic evaluation for calving traits is to be able to calculate more accurate breeding values and fulfill common European guidelines also called Golden standard. Below is described the most important changes and the effect on breeding values for AI bulls and females.

Handling of heterogenous variance and editing of data

Registrations for still birth, calving ease and size of calf is not normally distributed like for instance milk yield, but the registration take place in a few classes e.g., alive, or dead etc. This is handled by transforming data by a method called Snell score. Furthermore, calving records from Danish Jersey bull calves born in 2022 and onwards are deleted. This is because killing of newborn calves has stopped from 1. January 2022 and there has been an unexpected increase in registered still born Jersey bull calves in 2022.

Genetic parameters

Based on data from improved editing and handling of heterogeneous variance new genetic parameters have been calculated on recent data. Results showed that heritability's for most traits and genetic correlations between traits in general were quite like the previously used, but a few parameters related to maternal traits for cows for RDC were somewhat different from earlier used estimates.

Improvements of genetic model

The genetic model was improved by removing heterosis for RDC, making it like the model for Holstein and Jersey. This is done because analysis showed that it is not possible to separate maternal and direct heterosis in breeds where there has been intensive import from foreign breeds over time. Further a correction for inbreeding is included in the model for all three breeds to consider that inbreeding is expected to affect the robustness in the fetus. Another addition to the model is an effect that makes it possible to take care of the permanent environment of the individual cow affecting all her calving's.

Changes for AI bulls

We have compared indices from an evaluation with previous parameters and model with an evaluation using updated parameters and model for both AI bulls and females. For all three breeds the estimated genetic trends are almost the same from the new and the old model. For Holstein and

Jersey bulls the correlations are high for both proven and young bulls (Table 2 and Table 3). This means that 80-95% of the bulls change less than 3 index units for calving or birth. So, in practice you will only see minor changes. For RDC the correlation is high for birth where 80-95% of the AI bulls change less than 3 index units (Table 2). For calving the correlations are a lower – especially for proven bulls. This means that 45% of the proven bulls change more than 2 index units (Table 3).

Table 2. Effect on EBV comparing new birth index to the previous birth index shown as frequency (%) of changes in EBV Based on 2982 RDC bulls, 4272 Holstein bulls, and 831 Jersey AI bulls

Change in EBV index units	Distribution of changes, %		
	Holstein	RDC	Jersey
≤ -6		2	
≥ -5 and < -3	4	7	3
≥ -3 and < -1	23	21	16
≥ -1 and ≤ 1	65	50	45
> 1 and ≤ 3	6	14	23
> 3 and ≤ 5	2	4	9
≥ 6		1	4

Table 3. Effect on EBV comparing new calving index to the previous birth index shown as frequency (%) of changes in EBV Based on 2857 RDC bull, 4121 Holstein bulls, and 774 Jersey AI bulls

Change in EBV index units	Distribution of changes, %		
	Holstein	RDC	Jersey
≤ -6		7	1
≥ -5 and < -3	2	11	7
≥ -3 and < -1	18	16	23
≥ -1 and ≤ 1	68	32	53
> 1 and ≤ 3	11	16	13
> 3 and ≤ 5	1	9	2
≥ 6		9	1

Changes for females

For Holstein and Jersey females the correlations are high for heifers and cows with or without a genomic test. More than 95% of the females change less than 3 index units for both calving and birth. For RDC females more than 95% change less than 3 index units for birth index, while it is 80-90% for calving index. Change for RDC females are therefore smaller than for proven RDC AI bulls.

Jersey udder conformation

The weighting of the linear traits for udder in the combined udder index have been changed (see Table 4)

Table 4. Optimum and weight for udder traits for Jersey

	Old		New	
	Optimum	Weight	Optimum	Weight
Fore udder attachment	9	20	9	20
Rear udder height	9	-	9	10
Rear udder width	9	-	9	-
Udder cleft/support	9	10	9	10
Udder depth	9	25	9	25
Teat length	5.5	-	5.5	-
Teat thickness	6	-	6	10
Teat placement (front)	7.5	-	7.5	-
Teat placement (back)	5	-10	5	-10
Udder balance	5	-10	5	-

The changed weights create changes in EBVs for udder. Correlation between old and new EBV for combined udder is about 0.90 indicating some reranking of animals caused by the changed weights. In Table 5 the changes in EBV for AI bulls born 2013-2017 having at least 15 daughters are shown.

Table 5. Effect on EBV when using new weights for the linear type traits in the Jersey udder conformation index compared to the previous udder index shown as frequency (%) of changes in EBV Based on 553 Jersey AI bulls born 2013-2017 with at least 15 daughters with classifier records.

Change in EBV index units	Distribution of changes, %
≤ -6	1.4
≥ -5 and < -3	5.4
≥ -3 and < -1	12.8
≥ -1 and ≤ 1	30.9
> 1 and ≤ 3	21.9
> 3 and ≤ 5	19.3
≥ 6	8.1

Improved genetic evaluation for type traits

A single step method for type traits is introduced in the November evaluation and replace the so called two step method where in the first step traditional breeding values without genomic information are calculated and in the second step breeding values weighted together across lactations are combined with genomic information. Single step uses all information from genotyped and non-genotyped animals simultaneously in the single step method. It means that all animals both genotyped and non-genotyped animals get breeding values from the same evaluation. In the single step approach only genotypes from animals born since 2009 are used, since results have shown that use of old genotypes create a bias in the genetic trend.

The benefit by the single step method is that:

- Reliabilities on breeding values will increase slightly. This is because pedigree, phenotypes, and genotypes will be weighted together in a more optimal way, and all three information sources contribute to breeding values for all animals.
- Genomic preselection bias is avoided. The traditional genetic models used so far builds on the assumption that AI bulls and dams of next generation of heifer calves have a genetic

level that is equal to parent average. This is not the case when genomic selection is used intense. The result is that a bias is introduced in the traditional breeding values.

- Genomic breeding values are calculated for each lactation. In the two-step method genomic breeding values are only calculated for an overall trait across lactation 1-3.

All information is used during the AI bull's life

In the publication of breeding values for AI bulls from the two-step system, we use all available information. However, when a bull gets a high reliability based on own daughters, the genomic information is excluded. When using the single step method all information is always used.

Changes in breeding values

Changes in breeding values for linear type traits and for the combined indices for frame, feet&legs and udder are minor, but there are some reranking of AI bulls and females. Below are only mentioned changes for udder, but changes of similar magnitude are seen for frame and feet&legs.

Almost no changes for proven AI bulls

Changes for proven bulls will be minor for all breeds. Ranking within year is almost unchanged, but the trend across years will be a bit steeper. Results shows that the trend will be 1-3 index units larger in the last 7 years depending on breed. This means that around 80% of bulls born since 2010 will change less than 3 index units for udder and only 1-2% of the bulls will change more than 5 index units.

Minor changes for unproven AI bulls

For young unproven AI bulls, there are minor changes. Ranking within year is affected more than for proven bulls and in general, index for udder increases with 1-3 index units compared to two-step evaluation. This means that for RDC and Holstein, 50% of the bulls change less than 3 index units and nearly all other bulls will have indices that are higher (3 or more index units). For all breeds almost no bulls drop more than 2 index units for udder. For Jersey the changes are smaller. Around 60% of the bulls change less than 3 index units for udder and the rest of the bulls will have higher indices (3 or more index units).

Almost no changes for non-genotyped females

For cows and heifers that are not genotyped there are almost no changes for all breeds. Ranking within year is almost unchanged and trend is not affected. This means that around 90% of the animals change less than 3 index units for udder.

Minor changes for genotyped females

For cows and heifers that are genotyped, changes are larger than for non-genotyped females. Ranking within year is affected and in general index for udder increases with 1-2 index units compared to two-step evaluation. This means that 60-80% of the cows and 50-70% of the heifers change less than 3 index units. Most cows and heifers with changes larger than 2 index units have increasing indices for udder, but there are also females that have decreasing indices.

Metabolic efficiency – data included

Metabolic efficiency is based on feed intake data. The core trait for metabolic efficiency is residual feed intake, which is the observed feed intake minus the expected feed intake. The expected feed intake is calculated by use of information about yield and metabolic body weight change.

In Table 6 the amount of feed intake data available for the November 2022 run is shown for all three breeds. The amount of feed intake data has increased significantly during the last year. CFIT data is in November 2022 included from in total 18 herds and more than 6,500 cows

Table 6 Feed intake data for genetic evaluation of metabolic efficiency in November 2022

	Holstein			RDC		Jersey
	CFIT data	Danish research farm data	Abroad research farm data ^{a)}	CFIT data	Finnish research farm data	CFIT data
Cows with feed intake phenotypes	2896	1227	1581	2116	769	1657
Cows with feed intake phenotypes and genotypes	2059	819	1450	1839	416	1333
Lactations included	1-6	1-3	1-6	1-6	1	1-6
Number of herds	7	1	a)	6	4	5

a) Research farm data from Canada, US and Australia

GEBVs for dairyxdairy crossbreds

Joint Nordic GEBVs for dairyxdairy crossbred females were published for the first time 7th December 2021. The procedures for calculating GEBVs have not been changed since the introduction, but for a few animals it has been observed that the changes in GEBVs between two subsequent evaluations are significantly larger than expected. NAV is investigating what is causing these unexpected large changes.

Genetic base

EBVs for bulls and females are expressed on the same cow base. This genetic evaluation included cows born from 01.11.2017 to 01.11.2019 in the genetic base (average 100).

The GEBVs for crossbred are expressed on a genetic base of 1-7 year old crossbreds.

Publication of NTM for Nordic and foreign bulls

NTM is published if the bull has official EBVs (NAV (G)EBV or international EBV) for Yield, Mastitis and Type. By official means for NAV EBVs that the NAV thresholds are met, and for international EBVs (IB EBVs) that Interbull EBVs for the single bull exist. For traits without a NAV (G)EBV or an IB (G)EBV a NAV pedigree index is calculated.

For bulls with a Nordic herd book number the pedigree index follows the principles described in the October 2008 routine information. For foreign bulls without a Nordic herd book number the pedigree index is calculated in as $\frac{1}{2}(\text{EBVsire}-100) + \frac{1}{4}(\text{EBVmgs}-100) + 100$. If EBVsire or EBVmgs is not official NAV EBVs then 100 is used.

Publication of EBVs/GEBVs

Official EBVs/GEBVs for bulls used for AI in Denmark, Finland or Sweden are published at the [NAV Bull Search](#).

Official NAV GEBVs for foreign AI bulls not used for AI in Denmark, Finland and Sweden are published at [NAV homepage](#). The excel sheets also include GEBVs for bulls used for AI in Denmark,

Finland and Sweden. The excel sheets include AI bulls that are 10 months to 5 years old at the date of publication and is mainly useful for foreign AI-companies.

Interbull EBVs/GEBVs are published at the [NAV Interbull Search](#).

Genetic evaluation of beef bulls used in dairy herds

The latest NAV official evaluation for AI beef bulls based on their crossbred offspring from dairy cows for birth, youngstock survival and carcass traits took place as scheduled. Extraction date for the data can be found in table 1. Breeding values for AI beef bulls are estimated four times per year, in connection to the NAV routine genetic evaluation for dairy breeds (table 9), and EBVs are published at [NAV Beef Search](#).

Youngstock survival

Youngstock survival is a new trait group added to the joint Nordic Genetic evaluation of beef bulls used in dairy herds. Youngstock survival is evaluated as two traits: survival from day 1-30 (YSS1) and from day 31-200 (YSS2). It is assumed the trait within each period genetically is the same in both sexes. Average survival rate varies across country, sex and breed. Across all the data the survival rate is about 96-97% in the first period and 95-96% in the second period. The heritabilities for youngstock survival are 1.0-1.5%, and the genetic correlation between the two traits is 0.3 indicating that survival expressed in the two periods are genetically different traits (table 7).

Table 7. Heritabilities for youngstock survival

Trait	Heritabilities	Genetic correlation
Period I – survival 1-30 days	1.0 %	0.30
Period II – survival 31-200 days	1.5 %	

Three breeding values for youngstock survival are published: EBVs for youngstock survival in the two periods and a combined index for youngstock survival given equal weight to the two single EBVs. The weight used to calculate the combined index is a preliminary weight which will be updated early next year.

Youngstock survival is an economical important trait and will be included in NBDI primo 2023. Currently work is ongoing to estimate economic values for youngstock survival, and also update the preliminary weight used to construct the combined EBV for youngstock survival.

EBVs for youngstock survival is published if a bull has:

- EBV reliability $\geq 50\%$ on YSS2 or ≥ 500 offspring having YSS2 phenotypes
- or
- Official EBVs for Calving and Growth traits.

Table 8 show breed means for bull born since 2014 getting official EBV for youngstock survival. The results are based on a limited number of bulls and cover a significant within breed variation. The EBVs are expressed to the same genetic base as the other evaluated traits (see below).

Table 8 EBV breed mean for young stock survival for beef bulls born since 2014

Sire breed	Number of bulls	Mean YSS1	Mean YSS2
SIM	18	102.1	105.3
AAN	41	108.3	112.7
HER	12	105.3	111.1
BAQ	9	97.7	102.0
CHA	17	101.2	100.0
LIM	12	96.8	94.0
BBL	67	112.5	121.1

For survival 1-30 days the effect of 10 index units difference in breeding value between two bull is equivalent to a difference of 0.5% among offspring. For survival 31-200 days the effect of 10 index units difference in breeding value between two bull is equivalent to a difference of 0.75% among offspring

Genetic base

The genetic base for beef bulls evaluated based on dairy crosses is defined as relative breeding values with a mean of 100 and standard deviation of 10. The genetic base animals for beef bulls evaluated based on dairy crosses constitutes of 2-5 year old crossbreds born after beef breeds which can be used in all 3 countries.

Fee for EBV of beef bulls based on beef x dairy crossbred offspring

Nordic Cattle Genetic Evaluation (NAV) conducts a genetic evaluation of AI beef bulls based on beef x dairy crossbred offspring for calving and carcass traits. A fee system was introduced 1.1.2020 for the service. It means a fee must be paid for all bulls getting publishable EBVs for the first time after 1.1.2020. No fee needs to be paid for bulls already having official EBVs before 1.1.2020. To get published EBVs the following criteria should be fulfilled for each bull:

- The EBV should meet the criteria for publication
- A one-time fee of currently 1,000 euro per bull should be paid

More information about the genetic evaluation and the publication criteria can be found at [NAV homepage](#).

Genetic evaluation for Purebred Beef animals

The latest genetic evaluation of purebred beef animals took place 1 November 2022. NAV publish EBVs for calving, growth and carcass traits based on phenotypes from purebred beef Angus, Charolais, Simmental, Hereford, and Limousine cattle. Extraction date for the data used in the November evaluation can be found in Table 1. Breeding values for pure beef cattle are estimated four times per year (table 9), and EBVs are published at [NAV Beef Search](#).

Danish Welsh Black data has been removed from the Herford evaluation for all traits

NAV – frequency and timing of official runs

NAV has 4 large dairy evaluations per year, which include updated phenotypic and genomic data, and additional eight small runs including updated genotypes. In Table 9 the NAV and INTERBULL release dates for 2022/23 are shown. The beef evaluation based on beef x dairy crossbreds take

place along with the large NAV dairy runs 4 times a year. The NAV pure beef evaluation has its own time schedule

Table 9. NAV and INTERBULL release dates in 2022/23. EBVs released at NAV dates in bold will be delivered to international genetic evaluation.

Month	Dairy Cattle			Beef Cattle	
	NAV Small run ¹⁾	NAV Large runs ²⁾³⁾	INTERBULL	NAV Pure Beef	INTERBEEF
October 2022	4				21
November 2022		1		1	
December 2022	6		6		
January 2023	3				
February 2023		7			
March 2023	7			7	3
April 2023	4		4	18	
May 2023		2			
June 2023	6			6	
July 2023	4				
August 2023		8	8		
September 2023	5				
October 2023	3				20
November 2023		7		7	
December 2023	5		5		

¹⁾ Genotypes updated; ²⁾ Genotypes and phenotypes updated; ³⁾ Beef x dairy evaluation

You can get more information about the joint Nordic evaluation:

General about Nordic Cattle Genetic Evaluation: www.nordicebv.info

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