

News - NAV evaluation

7 May 2024

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, and Finncattle.

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

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	19.03.2024	18.03.2024	07.03.2024
Type, milkability and temperament	19.03.2024	18.03.2024	08.03.2024
Fertility	19.03.2024	18.03.2024	09.03.2024
Udder health and other disease	19.03.2024	18.03.2024	09.03.2024
Calving ¹⁾	19.03.2024	18.03.2024	09.03.2024
Longevity	19.03.2024	18.03.2024	09.03.2024
Growth ¹⁾	19.03.2024	18.03.2024	09.03.2024
Claw health	19.03.2024	18.03.2024	09.03.2024
Youngstock survival ¹⁾	19.03.2024	18.03.2024	09.03.2024
Saved feed	19.03.2024	18.03.2024	08.03.2024
Pure beef cattle	02.04.2024	26.03.2024	29.03.2024

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 5 April 2024. INTERBULL information from April 2024 was included in the genomic prediction.

News in relation to NAV dairy genetic evaluation

Dairy pure

Genomic prediction

- Single step for milkability for Jersey, RDC and Holstein

DairyxDairy

- No changes

BeefxDairy

- No changes.

Beef pure

- Latest evaluation took place 16.4.2024.

Metabolic efficiency

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 2 the amount of feed intake data available for the May 2024 run is shown for all three breeds. The amount of feed intake data has increased significantly during the last year. CFIT data is in May 2024 included from in total 21 herds and close to 10,500 cows.

Table 2 Feed intake data for genetic evaluation of metabolic efficiency in May 2024

	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	4685	1226	1581	3444	769	2476
Cows with feed intake phenotypes and genotypes	3848	730	1450	3087	416	2395
Lactations included	1-6	1-3	1-6	1-6	1	1-6
Number of herds	9	1	a)	7	4	6

a) Research farm data from Canada, US and Australia

NAV has observed some weakness in the genetic evaluation of metabolic efficiency evaluation, and work is ongoing to improve the statistical model. The current metabolic feed efficiency evaluation take place in two steps. In the first step the residual feed intake is estimated by correcting the feed intake for the energy sinks used for producing milk, maintenance, and changes in body weight during lactation. The estimated energy in one kg ECM by this method is somewhat lower than one should expect from feeding norms indicating a weakness in the current model. Furthermore, we observe an unexpected negative genetic trend in Holstein and to some extent also RDC, which is linked to the problems estimating correct effects of the energy sinks. Currently intense development work is ongoing to improve the statistical model for metabolic efficiency. The expectation is that it will be possible to introduce an improvement of the metabolic efficiency evaluation in the November 2024 run, which make better use of the CFIT data than what we are doing today.

Improved genetic evaluation for milkability

A single step method for milkability is introduced in the May evaluation. Single step method replaces 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 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 benefits of the single step method are:

- Prediction of breeding values will be more precise. This is because pedigree, phenotypes, and genotypes are 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 intensively. The result is that a bias is introduced in the traditional breeding values.

Changes in breeding values for milkability

The estimated genetic trend is nearly the same in the new and the old model for all three breeds. However, introduction of single step causes some reranking of animals because single step simultaneous combine all information, which is more optimal.

The correlation for milkability between breeding values from the new and the old model is high (table 3). For bulls having progeny the correlation is 0.99 for all breeds for the most recent birth year classes having progeny r. For genotyped young bulls and genotyped heifers, the correlations are slightly lower for all breeds 0.93-0.96 indicating slightly more reranking of animals.

Table 3. Correlations between milkability breeding values from the new and old model.

	HOL	RDC	JER
AI bulls and with genotype and progeny	0.99	0.99	0.99
Heifers and AI bulls with genotype no progeny	0.95	0.93	0.96

High stability in general

In general, the changes for the Milkability index have been small for all three breeds. There is a small increase in the index level for Holstein, while RDC and Jersey are unchanged. There is a high stability for the proven sires and non-genotyped females. For the genomic tested animals, the changes are a bit larger, but the stability of the indexes are still high.

Minimal changes for the proven sires

The proven sires show a very high stability, and there are few cases of reranking between the bulls. For RDC around 93 percent of the bulls change less than 4 index units. Corresponding figure for Jersey and Holstien is 94% and 96% respectively.

Slightly larger changes for the genomic bulls and genomic tested heifers

For all three breeds the index level is stable between the two models. However, the variation is higher than for the proven sires, so there will be a small reranking between bulls born in the same year for all breeds, and between 20-30 of the bulls change more than 3 index units.

Cows having both a genotypes and a phenotype show good stability

The change in indexes follow the same pattern as for the genomic tested bulls, and limited reranking has taken place. For the genotyped females about 70 percent of them change maximum 3 index units, while only 10 percent changes more than 5 index units.

High stability for none genotyped females

The index level for none genotyped females is unchanged, and only a few cases of reranking can be seen for the three breeds.

Reliabilities for milkability

Calculation of reliabilities takes place in runs separated from the estimation of breeding values. A method for calculating reliabilities from a single step model is implemented. The new method substitutes the method used so far for milkability, which belong to the two step setup.

Reliabilities are an estimate of the precision of the breeding values and is estimated in a separate run next to the estimation of breeding values. It means that by changing the method for calculation of reliabilities the true precision of the breeding values is unchanged, but the estimate of the reliability will be more correct. In table 4 it is shown that the new estimates of reliabilities for milkability for all three breeds are 5-11% units lower than with the old method, but at a more realistic level. Please note that this has no impact on the estimated breeding values but only change the figures telling how accurately the breeding value is estimated to a more realistic level.

Table 4 Average reliabilities for milkability for RDC, Holstein and Jersey AI bull born 2021 or later.

	Holstein		RDC		Jersey	
	New	Old	New	Old	New	Old
Milkability	0.68	0.77	0.65	0.76	0.61	0.66

Genetic base

EBVs for RDC, Holstein and Jersey bulls and females are expressed on a cow base except for growth where the EBV are expressed on bull calf base. This genetic evaluation included cows born from 07.05.2019 to 07.05.2021 in the genetic base (average 100). For growth EBVs are expressed on a genetic base of 3-5 year old bull calves. For Finn Cattle the EBVs are expressed on base of 3-7 year old cows. The GEBVs for crossbred are expressed on a genetic base of 1-7 year old cross-breds.

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 gestation length, 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 5), and EBVs are published at [NAV Beef Search](#).

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 × dairy crossbred offspring

Nordic Cattle Genetic Evaluation (NAV) conducts a genetic evaluation of AI beef bulls based on beef × dairy crossbred offspring for young stock survival, gestation length, 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 1,300 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 16 April 2024, and include 9 new breeds. NAV publish EBVs for calving, growth and carcass traits based on phenotypes from purebred beef Angus, Charolais, Simmental, Hereford, Limousine, Highland Cattle, Blonde d'Aquitaine, Belgian Blue, Dexter, Galloway, Grauvieh, Piemontese, Salers, Shorthorn 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 5), and EBVs are published at [NAV Beef Search](#).

The NAV breeding values from the April 2024 evaluation can be found at the NAV Beef search page for all animals and all 18 traits included in the evaluation.

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 5 the NAV and INTERBULL release dates for 2024 are shown. The beef evaluation based on beef × 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 5. NAV and INTERBULL release dates in 2024. 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
January 2024	9				
February 2024		6			28
March 2024	5			5	
April 2024	2		2	16	
May 2024		7			
June 2024	4			4	
July 2024	2				
August 2024		13	13		
September 2024	3				
October 2024	1				16
November 2024		5		5	
December 2024	3		3		

¹⁾ Genotypes updated; ²⁾ Genotypes and phenotypes updated; ³⁾ Beef × 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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