News - NAV evaluation
4 February 2025

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	10.12.2024	11.12.2024	6.12.2024
Type, milkability and temperament	10.12.2024	11.12.2024	6.12.2024
Fertility	10.12.2024	11.12.2024	7.12.2024
Udder health and other disease	10.12.2024	11.12.2024	7.12.2024
Calving[1]	10.12.2024	11.12.2024	7.12.2024
Longevity	10.12.2024	11.12.2024	7.12.2024
Growth[1]	10.12.2024	11.12.2024	7.12.2024
Claw health	10.12.2024	11.12.2024	7.12.2024
Youngstock survival[1]	10.12.2024	11.12.2024	9.12.2024
Saved feed	10.12.2024	11.12.2024	6.12.2024
Pure beef cattle	23.09.2024	23.09.2024	14.10.2024

[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 10 January 2025. INTERBULL information from December 2024 was included in the genomic prediction.

News in relation to NAV dairy genetic evaluation

Dairy pure

- New Saved feed evaluation for Holstein, RDC and Jersey
- New weight for Saved feed in NTM for Holstein
- Data for Rib Structure until 1st January 2020 has been deleted.

DairyxDairy

- Swedish crossbred animals which contain Holstein, RDC, Jersey or Montbéliard are included in the Swedish pedigree file. Swedish non genotyped crossbred animals will get pedigree index corrected for genetic difference between the breed proportion in the animal. The

crossbred animals will get index for yield including milk, fat and protein index, fertility and mastitis index. NTM for the animals will be calculated according to yield, fertility and mastitis.

BeefxDairy
- No changes

Beef pure
- Latest evaluation took place 5.11.2024

Genetic evaluation of dairy breeds
Saved feed version 3.0
In February 2025, the new saved feed version 3.0 will be implemented. This version is quite different from the old one and should be seen as a new index. It offers higher reliability and economic value, making it one of the most important indexes for future dairy farmers.

Amount of data

The saved feed index is still built on the same data from CFIT that gives information about the feed intake. In table 2 the amount of feed intake data available for the February 2025 run is shown for all three breeds. The amount of feed intake data has increased significantly during the last years. In February 2025 CFIT data include 26 herds and around 12,000 cows and around 900 cows from research center Foulum in Danmark and Luke in Finland.

Table 2. Feed intake data for genotyped cows in the genetic evaluation of saved feed in February 2025

Breed	HOL	RDC	JER
Herds CFIT	12	7	7
Genotyped cows CFIT	5,104	3,828	3,040
Genotyped cows Foulum	528	-	-
Genotyped cows Luke	-	356	-

Outline of the saved feed index

Saved feed is not calculated directly but instead based on indexes for:
- Dry matter intake (DMI) 14-280 days in the lactation
- Energy corrected milk production (ECM) 14-280 days in the lactation
- Weight change 30-280 days in the lactation

The indexes are calculated using random regression models. For each farm trait specific curves throughout the lactation are estimated. Based on the single cow's deviations from these trait specific curves, daily GEBVs for each cow are calculated. GEBVs are estimated. Afterwards an accumulated GEBV is calculated for the whole lactation.

First and later lactations (2. to 5. lactation) are handled as two different traits. However, there is a high genetic correlation between the lactations.

Calculation of saved feed

For saved feed the animals with lowest dry matter intake (DMI), when energy requirements for production in ECM (ECM) and weight change (BWC) are considered get the highest index value. Saved feed is calculated according to this formula:

Saved feed = -1 * (DMI – 0.4 * ECM – 4 * BWC)

Energy requirements for ECM production and weight change are the same value as used in Germany with 0.4 kg DMI/kg ECM and 4 kg DMI/kg BWC.

Saved feed is afterwards standardized to the official relative index for saved feed. The mean is 100 for cows which are 3-5 years old and with CFIT registrations. The standard deviation is 10 for the same group of cows. Bull candidates have a standard deviation on 6-7 while it is approximated 10 for the proven sires. Weight between first and later lactations is 1:2 which means that the later lactation has double weight according to the first lactation.

Correlation between saved feed and the traits in saved feed
For all breeds there is a negative correlation between saved feed and DMI, weight and BWC while there is a positive correlation to production.

Table 3. Correlations between saved feed and the traits included in saved feed.

Breed	HOL	RDC	JER
DMI (dry matter intake)	-0,55	-0,75	-0,55
ECM (production)	0,45	0,30	0,55
Weight	-0,55	-0,60	-0,55
Weight change	-0,25	-0,20	-0,05

Correlations with other traits
All breeds have low correlations between fertility, health traits, survival traits and saved feed. A negative correlation to health traits is not caused directly by saved feed since there is small negative correlations between health traits and DMI and ECM.

Table 4. Correlation between saved feed 3.0 and other traits in NTM for Holstein.

Holstein	Saved Feed	DMI	ECM	Weight
Fertility	-0,05	-0,10	-0,20	0,00
Udder health	-0,10	-0,05	-0,15	0,05
General health	-0,10	-0,15	-0,30	0,00
Youngstock survival	0,10	-0,20	0,10	-0,20
Longevity	0,05	0,00	0,00	-0,20

Table 5. Correlation between saved feed 3.0 and other traits in NTM for RDC.

RDC	Saved Feed	DMI	ECM	Weight
Fertility	0,15	-0,30	-0,25	-0,25
Udder health	0,10	-0,15	-0,15	0,00
General health	-0,10	0,00	-0,20	0,00
Youngstock survival	0,15	-0,15	0,05	-0,20
Longevity	0,20	-0,20	0,05	-0,20

Table 6. Correlation between saved feed 3.0 and other traits in NTM for Jersey.

Jersey	Saved Feed	DMI	ECM	Weight
Fertility	-0,15	-0,05	-0,30	0,00
Udder health	-0,10	-0,05	-0,20	0,00
General health	-0,05	-0,10	-0,20	0,00
Youngstock survival				
Longevity	-0,05	0,00	-0,10	-0,05

Low correlation with the old index for saved feed

The new and old saved feed index are two different indexes and the correlation between the two indexes is low. The correlation is 0.30 for Holstein, 0.50 for RDC and 0.25 for Jersey. The low correlations indicate that very large changes in saved feed index will occur and there will be a large reranking between the animals. The two main reasons for the low correlation are: 1. The energy sink in the old saved feed index was estimated too low and animals with a high production were punished. 2. The residual feed efficiency was estimated per week for the old saved feed, and the weekly measurement uncertainties were accumulated over time.

High economic value for saved feed

When the saved feed index increases by one unit for a cow, it reduces the dry matter intake by 60 gram per day, which accumulates to 15-20 kg of dry matter per lactation. If the feed price is set to 0.2 Euro per kg of dry matter, the reduction in feed cost is 3-4 Euro per lactation for a saved feed index unit. To compare the value of an NTM unit is around 9 Euro per lactation.

Change in NTM weight for saved feed for Holstein

In connection with the introduction for the new saved feed index it has been a wish for Holstien to increase the weight in NTM for saved feed. The weight in NTM for saved feed has increased from 0.08 to 0.18. The weight 0.18 was the calculated economic value for the old saved feed index. A new calculation for the economic value is necessary to find the new optimal weight for the new saved feed index in NTM. The preliminary calculations show that the weight for saved feed should increase further in the future.

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 04.02.2020 to 04.02.2022 in the genetic base (average 100). For growth EBVs are expressed on a genetic base of 3-5 year old bull calves. For Finncattle 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 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 ½(EBVsire-100) +1/4(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, 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 5 November 2024. 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. Genomic breeding values are published for weight, growth, and carcass traits for the five largest breeds (AAN, CHA, HER, LIM, and SIM) for genotyped animals. 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 7), and all breeding values are published at [NAV Beef Search](#).

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 7 the NAV and INTERBULL release dates for 2025/2026 are shown. The beef evaluation based on beef × dairy crossbreeds take place along with the large NAV dairy runs 4 times a year. The NAV pure beef evaluation has its own time schedule.

Table 7. NAV and INTERBULL release dates in 2025/2026. 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 2025	7				
February 2025		4			25
March 2025	4			4	
April 2025	1		1	15	
May 2025		6			
June 2025	3			3	
July 2025	1				
August 2025		12	12		
September 2025	2				
October 2025	7				14
November 2025		4		4	
December 2025	2		2		
January 2026	6				

[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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