News - NAV evaluation
6 May 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	18.3.2025	18.3.2025	7.3.2025
Type, milkability and temperament	18.3.2025	18.3.2025	7.3.2025
Fertility	18.3.2025	18.3.2025	8.3.2025
Udder health and other disease	18.3.2025	18.3.2025	8.3.2025
Calving[1)]	18.3.2025	18.3.2025	8.3.2025
Longevity	18.3.2025	18.3.2025	8.3.2025
Growth[1)]	18.3.2025	18.3.2025	8.3.2025
Claw health	18.3.2025	18.3.2025	8.3.2025
Youngstock survival[1)]	18.3.2025	18.3.2025	8.3.2025
Saved feed	18.3.2025	18.3.2025	7.3.2025
Pure beef cattle	1.4.2025	1.4.2025	27.3.2025

[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 4 April 2025. INTERBULL information from April 2025 was included in the genomic prediction.

News in relation to NAV dairy genetic evaluation

Dairy pure

- Improved genetic evaluation for yield
- Methane index for Holstein AI bulls
- More yield information included in saved feed calculation

DairyxDairy

- No changes

BeefxDairy

- No changes

Beef pure

- Latest evaluation took place 15.4.2025

Genetic evaluation of dairy breeds

Improved genetic evaluation for yield

A single step method for yield is introduced in the May evaluation. Single step method replaces the so called two step method where the traditional breeding values without genomic information are calculated in the first step and in the second step breeding values are weighted together across lactations and are combined with genomic information. Single step uses all information from genotyped and non-genotyped animals simultaneously. It means that both genotyped and nongenotyped animals get breeding values from the same evaluation. In the single step approach only genotypes from animals born since 2009 are used, since 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 build 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 yield

For all breeds and for all traits (milk kg, protein kg, fat kg and yield index), the genetic trends get more steep with the new model compared to the old one. This means that breeding values for older animals decrease compared to younger animals.

Applying single step method for genetic evaluation of yield traits causes genetic trends to become stronger as expected. Overall changes in GEBVs are moderate but there are individual animals with large changes in index values.

Proven sires are very stable

Correlations between the old two step evaluation and the new single step evaluation are very high across breeds for proven bulls. This means few indices change and implying that reranking between bulls within the same birth years are minimal.

Table 2. Correlations for yield index pr year between single step and the old two step model.

Trait	HOL	RDC	JER
Daughter proven AI bulls	0.97–1.00	0.98–1.00	0.95–1.00
Young genomic bulls without daughters	0.92-0.94	0.81-0.99	0.91-0.98

More changes for young genomic bulls

For young genomic bulls the correlations between the old and the new yield model are a bit lower, but still high. This means that young genomic bulls have more changes in yield indices compared to proven bulls. For young genomic Holstein bulls indices for milk and protein production increase, while fat production and overall yield index slightly decrease. The average change in yield index is about 1-2 index units. For young genomic RDC and Jersey bulls changes are positive for all traits. The average change in yield index is about two index units.

Minor changes for genomic females
For genomic tested females changes are very small for all breeds in yield index. For all breeds changes are positive and the change in yield index is about 1-2 index units. For the youngest females (born 2023-2024) changes are slightly larger and more re-ranking might be seen. However, in average the changes are still small.

Methane index for Holstein AI bulls

In the May evaluation, the first Nordic methane index is released. It is necessary to collect many methane registrations to make a methane index. In total, across different projects, there are today methane registrations from 16,000 cows, including 8,000 Holstein cows, 5,000 Jersey cows, 2,300 RDC cows, and 700 crossbreeding cows. The data are collected in 40 herds, and at the moment, methane registrations are collected in 15 herds.

The overall goal is to breed for lower methane production in the rumen of the cow, thereby reducing methane emissions. The phenotypic registration used in the methane index is the methane concentration. The assumption is that a lower methane concentration from a cow indicates lower methane production. Breeding for lower methane concentration should therefore lead to lower methane production in the rumen of the cow for future generations.

Methane is a new trait, and the amount of collected methane data is limited. The low amount of data gives a low reliability for the index. The index was first developed for Holstein since they had the biggest amount of data. In the May evaluation, the released methane index will only be for Holstein AI bulls.

On the NAV homepage, there is a page about methane production under dairy cattle. At the methane page there is a link to the methane index list. Since data has mostly been collected in the last five years, it is only bulls born after 2008 that will get a methane index. To get on the list, the bull needs to be genomic tested in the Nordic system and has paid the Nordic fee or has official NTM and a minimum of 10 daughters with methane observations.

More yield information included in saved feed calculation

Yield information from the period where cows do not have methane registrations are included in the saved feed calculation. The extra yield information increases the reliability for the saved feed index.

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 15 April 2025. 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. Breeding values for growth, slaughter quality, and milk for the five breeds AAN, CHA, HER, LIM, and SIM are estimated in a genomic SS model. Breeding values for pure beef cattle are estimated four times per year (table X), 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 3 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 3. NAV and INTERBULL release dates in 2025/2026. EBVs released at NAV dates in bold will be delivered to international genetic evaluation.

	Dairy Cattle			Beef Cattle	
Month	**NAV Small run1)**	**NAV Large runs2)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

Denmark: www.landbrugsinfo.dk
Contact person: Kevin Byskov, Seges Innovation, Ph. +45 2662 1307, mailto:kvb@seges.dk

Sweden: www.vxa.se
Contact person: Andrei Kudinov, Växa, Genetic.Evaluation@vxa.se

Finland: www.faba.fi
Contact person: Jukka Pösö, Faba co-op, Ph +358 400 614 035 jukka.poso@faba.fi