

News - NAV evaluation

7 February 2023

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	15.12.2022	04.12.2022	08.12.2022
Type, milkability and temperament	15.12.2022	04.12.2022	10.12.2022
Fertility	15.12.2022	04.12.2022	10.12.2022
Udder health and other disease	15.12.2022	04.12.2022	10.12.2022
Calving ¹⁾	15.12.2022	04.12.2022	10.12.2022
Longevity	15.12.2022	04.12.2022	10.12.2022
Growth ¹⁾	15.12.2022	04.12.2022	10.12.2022
Claw health	15.12.2022	04.12.2022	10.12.2022
Youngstock survival	15.12.2022	04.12.2022	11.12.2022
Saved feed	15.12.2022	04.12.2022	10.12.2022
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 10 January 2023. INTERBULL information from December 2022 was included in the genomic prediction.

News in relation to NAV dairy genetic evaluation

Dairy

Traditional evaluation

- No changes

Genomic prediction

- New methods for calculating reliability for type traits for Jersey, RDC and Holstein

BeefxDairy

- No changes

Beef pure

- Latest run November 2022

Reliability for type traits

A single step method for type traits was introduced in November 2022. 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. Calculation of reliabilities takes place in runs separated from the estimation of breeding values. In the February run a method for calculating reliabilities from a single step model is implemented. The new method substitutes the method used so far for type traits, 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 reliabilities the true precision of the breeding values is unchanged, but the estimate of the reliability will be more correct. In table 2 it is shown that the new estimates of reliabilities for frame, feet&legs and udder for all three breeds are 10-15% units lower than with the old method, but still at a high level. Please note that this has no impact on the estimated breeding values but only change the figures telling how accurate the breeding value is estimated to a more realistic level.

Table 2 Average reliabilities for Frame, Feet&Legs, and udder for RDC, Holstein and Jersey AI bull born 2019 or later

	Holstein		RDC		Jersey	
	New	Old	New	Old	New	Old
Frame	0.59	0.76	0.49	0.67	0.49	0.67
Feet&Legs	0.59	0.72	0.49	0.65	0.48	0.65
Udder	0.62	0.76	0.58	0.69	0.47	0.68

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 3 the amount of feed intake data available for the February 2023 run is shown for all three breeds. The amount of feed intake data has increased significantly during the last year. CFIT data is in February 2023 included from in total 19 herds and more than 7,000 cows

Table 3 Feed intake data for genetic evaluation of metabolic efficiency in February 2023

	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	3011	1227	1581	2139	769	1981
Cows with feed intake phenotypes and genotypes	2223	819	1450	1886	416	1663
Lactations included	1-6	1-3	1-6	1-6	1	1-6
Number of herds	7	1	a)	6	4	6

a) Research farm data from Canada, US and Australia

In the February 2023 run larger changes than expected have been observed for metabolic efficiency GEBVs for Holstein. Ongoing work investigates the reasons for the instability.

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 07.02.2018 to 07.02.2020 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 4), 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 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 1,300 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 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 3), and EBVs 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 4 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 4. NAV and INTERBULL release dates in 2023. 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 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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