News - NAV evaluation
6 February 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	14.12.2023	03.12.2023	09.12.2023
Type, milkability and temperament	14.12.2023	03.12.2023	08.12.2023
Fertility	14.12.2023	03.12.2023	11.12.2023
Udder health and other disease	14.12.2023	03.12.2023	11.12.2023
Calving[1]	14.12.2023	03.12.2023	11.12.2023
Longevity	14.12.2023	03.12.2023	11.12.2023
Growth[1]	14.12.2023	03.12.2023	11.12.2023
Claw health	14.12.2023	03.12.2023	11.12.2023
Youngstock survival[1]	14.12.2023	03.12.2023	11.12.2023
Saved feed	14.12.2023	03.12.2023	08.12.2023
Pure beef cattle	25.09.2023	10.09.2023	16.10.2023

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

News in relation to NAV dairy genetic evaluation

Data extraction

- Finland has updated its system of extracting data from the national data base. Parts of the new system have already been used for some traits, e.g. for fertility. When constructing data for February 2024 evaluation, the new system has been applied for all traits. The new extraction system gives slightly more phenotypic data (more animals and more calvings) than the old system did. This means that the estimated breeding values for some animals have changed a bit.

Dairy pure
Traditional evaluation
- RDC yield model has been upgraded.
- RDC growth errors in calculation of heterosis and genetic base have been corrected.

Genomic prediction
- Single step for growth for Jersey, RDC and Holstein

DairyxDairy
- No changes

BeefxDairy
- No changes.

Beef pure
- No changes

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 2 the amount of feed intake data available for the February 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 February 2024 included from in total 20 herds and close to 10,000 cows.

Table 2. Feed intake data for genetic evaluation of metabolic efficiency in February 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	4012	1226	1581	3279	769	2395
Cows with feed intake phenotypes and genotypes	3184	725	1450	2927	416	2163
Lactations included	1-6	1-3	1-6	1-6	1	1-6
Number of herds	7	1	a)	7	4	6

a) Research farm data from Canada, US and Australia

Improved genetic evaluation for yield for RDC
The yield model for RDC has been upgraded by:
- Improved handling of Finnish AMS milk data
- Leave FIN HOL data out from RDC model
- Updated genetic parameters

Improved handling of Finnish AMS data
In the NAV genetic evaluation for yield data from both automatic milking systems (AMS) and conventional milking systems (CMS) are included, and the model handle standard errors differences between AMS and CMS data. So far it has been assumed that standard error was the same over years. But Finland had changed the milk recording in AMS herds over years (table 3), and a method

having a significant higher standard error was used from 2015-2017. The methods for genetic evaluation for yield for RDC have been modified to take the changes in standard error into account. The changes in the Finnish yield recording might also affect Holstein and Jersey. NAV will investigate that at a later stage.

Table 3. Overview changes over years in Finish milk recording in AMS herds

Time period	Number of days used to calculate kg of milk	Comment
2003-2015	30/31 days	Data used when methods for heterogenous variance was implemented
2015-2017	2 milkings within 24 hours	Method has very large standard error
2017-	2 milkings within 24 hours or 96 hours	More than one method used

Finnish Holstein yield data

Finland has relatively small herds and many herds with both Holstein and RDC cows. Finnish Holstein cows have been included in the RDC genetic evaluation to improve estimation of herd management effect. New analyses have shown that leaving Finnish Holstein data out from the RDC genetic evaluation improved the results.

Updated genetic parameters.

A new set of genetic parameters estimated on Finnish RDC - heritabilities and genetic correlations have been tested. The new parameters show better predictability than the earlier used genetic parameters, which were estimated in 2011 based on a Swedish RDC data set. The main difference between the two set of parameters is that the new heritabilities are lower than the old (table 4), and the genetic correlations between lactations are higher (table 5 results for protein). The same magnitude holds for milk, fat and protein.

Table 4. Heritabilities for RDC yield traits

	Heritability		
	Old	**New**	**Difference**
Milk 1. lact	0.44	0.39	-0.05
Protein 1. lact	0.43	0.33	-0.10
Fat 1. lact	0.43	0.34	-0.09
Milk 2. lact	0.32	0.29	-0.03
Protein 2. lact	0.34	0.27	-0.07
Fat 2. lact.	0.34	0.26	-0.08
Milk 3 lact	0.34	0.26	-0.08
Protein 3 lact	0.35	0.25	-0.10
Fat 3 lact	0.35	0.21	-0.14

Table 5. Genetic correlation for RDC protein

	Old		New	
	Protein 2. lact	**Protein 3. lact**	**Protein 2. lact**	**Protein 3. lact**
Protein 1. lact	0.79	0.69	0.83	0.81
Protein 2. lact		0.98		0.97

Effect of upgrading the RDC Yield model

Implementation of the three elements improve the validation results for RDC for yield. The estimated genetic trend for yield is the same from the old and new model, but the new model ranks animals differently, and especially EBVs for 2nd and 3rd lactation for bulls having no or few daughters in later lactations are improved (figure 1 and 2). EBVs from the traditional model are used as inputs for the genomic prediction. Changes in in the traditional model leads also to some changes in genomic breeding values (GEBVs).
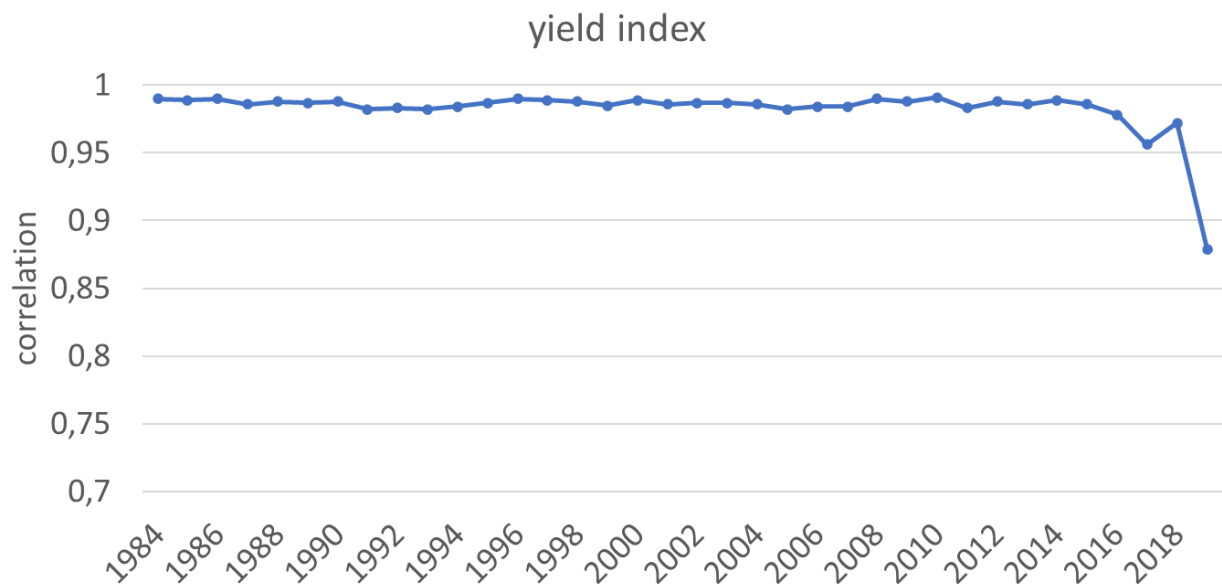

Figure 1. Correlations between Y-index, from old and new model for RDC bulls having at least 50 lactating daughters.
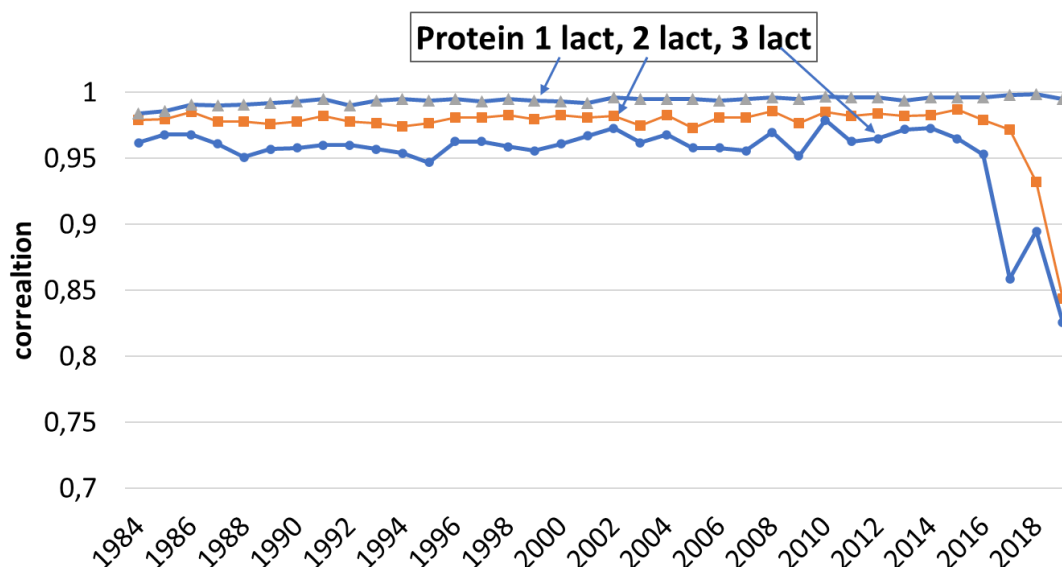
Figure 2. Correlations between EBV for protein for 1st, 2nd and 3rd lactation for RDC bulls having at least 50 lactating daughters.

Table 6 show the changes in EBVs between the old and the new model. The changes are largest for the youngest bulls having 1st lactating daughters only and are caused by the more accurate prediction of EBV in 2nd and 3rd lactation with the upgraded model. For birthyear classes before 2017 only minor changes are observed.

Table 6. Changes in Y-index for AI bulls born after 2016 having at least 50 lactating daughters, number of bulls.

Change in Y- index units	Birth year			
	2016	**2017**	**2018**	**2019**
≤ -4	1	2	4	1
≥ -3 and ≤ -2	2	6	5	1
≥ -1 and ≤ 1	46	30	20	4
≥ 2 and ≤ 3	23	12	11	4
≥ 4	1	16	11	8
Number of bulls	70	66	51	18

Cow EBV
The correlation between Y-index for cows from the old and the new model is high about 0.96. Also, for cows the 3rd lactation EBVs change most. 90% of the cow EBVs change less than 4 index units.

GEBVs for males and females
EBV from the traditional model is used as input for the genomic prediction. The changes in the traditional model also cause slightly larger changes in GEBVs than normally observed between two subsequent evaluations. The correlation between GEBV from the old and new model is in the range og 0.90 for birth year class 2021, while it without model changes but only update of phenotypes is about 0.95 between two subsequent runs.

Improved genetic evaluation for growth.
A single step method for growth is introduced in the February 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.
- Genomic breeding values are calculated for each trait. In the two-step method genomic breeding values are only calculated for daily carcass gain and carcass conformation score.

Changes in breeding values for growth
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 growth between breeding values from the new and the old model is high (table 7). For bulls having progeny the correlation is over 0.97 for all breeds. For genotyped young bulls and genotyped heifers, the correlations are about 0.90 for Holstien and about 0.80 for RDC and Jersey indicating some reranking of animals.

Table 7. Correlation between growth breeding values from the new and old model

	HOL	RDC	JER
AI bulls and with genotype and progeny	0.98	0.97	0.97
Heifers and AI bulls with genotype no progeny	0.90	0.80	0.80

High stability in general
In general, the changes for the Growth index have been small for Holstein and RDC. There is a small increase in the index level for RDC, while Holstein is 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.
For Jersey the changes are larger than for the two other breeds. Since growth is calculated from slaughter data for purebred animals the information level for Jersey is very limited and the reliability is therefore significantly lower for Jersey. This gives a larger variation for Jersey and thereby larger reranking according to growth. Since the value of beef production from Jersey is very limited the change in growth index has a minimal effect for the Jersey breed.

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 the general level for growth increases a bit while it is stable for Holstein. For RDC around 95 percent of the bulls change less than 3 index units while 98 percent of the Holstein bulls change less than 3 index units.

Largest changes for the genomic bulls
For both Holstein and RDC 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 both breeds. For Holstein and RDC around 60 percent of the bulls change maximum 3 index units, while 20 percent of the bulls change more than 5 index units in growth.

Genotyped females show good stability
The index level for RDC increases a bit, while it is stable for Holstein. For the animals born in the same year, there will be a smaller reranking, but the stability is in general high. The change in index-es follow the same pattern as for the genomic tested bulls. For the genotyped females 65 percent of them change maximum 3 index units, while only 15 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 both Holstein and RDC. Close to 50 percent of the animals will not have a changed index in growth due to implementation of the new single step model, while only 5 percent of the animals change more 3 index units.

Reliabilities for growth
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 substi-tutes the method used so far for growth, 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 8 it is shown that the new estimates of reliabilities for growth for all three breeds are 9-17% units lower than with the old method, but at a more realistic level. The reliabilities are very low for Jersey because of limited amount of slaughter data for bull calves. Please note that this has no impact on the estimated breeding values but only change the figures telling how accu-rately the breeding value is estimated to a more realistic level.

Table 8. Average reliabilities for growth for RDC, Holstein and Jersey AI bull born 2021 or later.

	Holstein		RDC		Jersey	
	New	Old	New	Old	New	Old
Growth	0.56	0.73	0.47	0.56	0.19	0.30

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 06.02.2019 to 06.02.2021 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 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 (table 9), 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 7 November 2023, 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 9), and EBVs are published at NAV Beef Search.

The NAV breeding values from the November 2023 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 10 the NAV and INTERBULL release dates for 2023 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 9. 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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