News - NAV evaluation
7 November 2023

Dairy cattle

The latest NAV official evaluation for yield, fertility, conformation, udder health, general health, calving traits, milkability, temperament, growth, longevity, youngstock 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	25.09.2023	10.09.2023	08.09.2023
Type, milkability and temperament	25.09.2023	10.09.2023	08.09.2023
Fertility	25.09.2023	10.09.2023	09.09.2023
Udder health and other disease	25.09.2023	10.09.2023	09.09.2023
Calving[1]	25.09.2023	10.09.2023	09.09.2023
Longevity	25.09.2023	10.09.2023	09.09.2023
Growth[1]	25.09.2023	10.09.2023	10.09.2023
Claw health	25.09.2023	10.09.2023	10.09.2023
Youngstock survival[1]	25.09.2023	10.09.2023	10.09.2023
Saved feed	25.09.2023	10.09.2023	08.09.2023
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 6 October 2023. INTERBULL information from August 2023 was included in the genomic prediction.

News in relation to NAV dairy genetic evaluation
Dairy pure
Traditional evaluation
- Genetic groups in yield evaluation modified so it can be used for single step evaluation.

Genomic prediction
- Single step for claw health for Jersey, RDC and Holstein
- Single step for general health for Jersey, RDC and Holstein

DairyxDairy
- No changes, but a problem with the handling of the genotypes cause that the GEBVs will be a few days delayed.

BeefxDairy
- No changes.

Beef pure
- Joint Nordic genetic evaluation introduced for: Highland Cattle, Blonde d 'Aquitaine, Belgian Blue, Dexter, Galloway, Grauvieh, Piemontese, Salers, Shorthorn
- Pedigree index calculated for animals without phenotypes.

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 November 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 November 2023 included from in total 20 herds and close to 9,000 cows.

Table 2. Feed intake data for genetic evaluation of metabolic efficiency in November 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	3503	1227	1581	3050	769	2321
Cows with feed intake phenotypes and genotypes	2693	819	1450	2709	416	2094
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

Genetic groups for yield
The definition of genetic groups in yield evaluation is modified to prepare for introduction of single step models. The change in the genetic group definition have a very minor impact of breeding values for actual animals but change slightly the genetic trend over years and cause some changes in EBVs for very old animals with very limited amount of information.

Improved genetic evaluation for claw health and general health.
A single step method for claw health and general health is introduced in the November 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 will be 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 lactation. In the two-step method genomic breeding values are only calculated for an overall trait across lactation 1-3.

Changes in breeding values for claw health
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 between breeding values from the new and the old model is high (table 3). For bulls having progeny and females with phenotypes the correlation is over 0.97 for all breeds. For genotyped young bulls and genotyped heifers the correlations are slightly lower (0.91-0.95) indicating somewhat more reranking of animals.

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

	HOL	RDC	JER
AI bulls with genotype and progeny	0.98	0.97	0.97
AI bulls with genotype no progeny	0.94	0.92	0.91
Cows with genotype and phenotype	0.95	0.94	0.93
Cows with phenotype and no genotype	0.98	0.97	0.97
Heifers with genotype	0.93	0.92	0.90

Almost no changes for proven AI bulls
The proven AI sires show a high stability per year, so the yearly reranking is limited for all breeds. For Holstein 99 % of the bulls change maximum 4 index units while it is 92 % for RDC. Jersey is the breed with fewest claw health problems, and due to those low frequencies for the different claw diseases Jersey has the largest changes. For Jersey the standard deviation of the bulls breeding values increases by 2-3 index units by the introduction of single step. In Jersey 76 % of the proven bulls change less than 5 index units.

Changes for unproven AI bulls
For young unproven AI bulls, the ranking within year is affected more than for proven bulls. This means that for Holstein 87% of the bulls change less than 5 index units, for RDC 77% and for Jersey 58% respectively. Also, for the young genomic tested bulls the standard deviation for Jersey has increased by the new model which causes more changes in breeding values.

Almost no changes for non-genotyped females
For cows that are not genotyped there are almost no changes for all breeds. Ranking within year is almost unchanged. This means that around 90% of the animals change 3 index units or less for claw health.

Genotyped females
For cows and heifers that are genotyped, changes are larger than for non-genotyped females. This means that 48-81% of the cows and 46-76% of the heifers change less than 4 index units. The lowest correlation is observed for Jersey due to the increased standard deviation of the breeding values.

Changes in breeding values for general health
The estimated genetic trend is nearly the same in the new and the old model for RDC and Jersey and slightly higher for Holstein. However, introduction of single step for general health also causes some reranking of animals, because single step simultaneously combines all information, which is more optimal.

The correlation between breeding values from the new and the old model is high (table 4). For bulls having progeny and females with phenotypes the correlation is over 0.95 for all breeds. For genotyped young bulls and genotyped heifers the correlations are lower (0.84-0.88) indicating somewhat more reranking of animals.

Table 4. Correlation between breeding values from the new and old model

	HOL	RDC	JER
AI bulls with genotype and progeny	0.98	0.95	0.97
AI bulls with genotype no progeny	0.88	0.84	0.88
Cows with genotype and phenotype	0.91	0.88	0.91
Cows with phenotype and no genotype	0.95	0.95	0.95
Heifers with genotype	0.87	0.85	0.87

Almost no changes for proven AI bulls
The proven AI sires show a high stability per year, so the yearly reranking is limited for all breeds. For Holstein 95 % of the bulls change maximum 4 index units while it is 90 % for RDC, and 95% for Jersey.

Changes for unproven AI bulls
For young unproven AI bulls, the ranking within year is affected more than for proven bulls. This means that for Holstein 77% of the bulls change less than 5 index units, for RDC 83% and for Jersey 91% respectively.

Almost no changes for non-genotyped females

For cows that are not genotyped there are almost no changes for all breeds. Ranking within year is almost unchanged. This means that over 95% of the animals change 3 index units or less for general health.

Genotyped females
For cows and heifers that are genotyped, changes are larger than for non-genotyped females. This means that 68-79% of the cows and 63-77% of the heifers change less than 4 index units.

Reliabilities for Claw health and General health
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 general health and claw health, 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 5 it is shown that the new estimates of reliabilities for claw health and general health for all three breeds are 10-20% 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 5 Average reliabilities for claw health and general health for RDC, Holstein and Jersey AI bull born 2019 or later.

	Holstein		RDC		Jersey	
	New	Old	New	Old	New	Old
Claw health	0.60	0.70	0.47	0.60	0.41	0.60
General health	0.52	0.65	0.38	0.55	0.35	0.55

Genetic base
EBVs for bulls and females are expressed on the same cow base. This genetic evaluation included cows born from 07.11.2018 to 07.11.2020 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 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 7), 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 7), and EBVs are published at NAV Beef Search. Table 6 shows the list of additional breeds included in NAV Purebred Beef evaluation. As for the main five breeds, breeding values for breeds in Table 6 will be estimated 4 times per year (March, April, June, and November) and replace, fully or partly, the nationally calculated ones, depending on the country. The group Continental or British refer to the applied set of genetic parameters. The set up for the new breeds follow the set up for Angus, Charolais, Simmental, Hereford, Limousine for more details see NAV newsletter from November 2021.

Table 6. List of new breeds included in the Purebred beef evaluation from November 2023

Full name	Abbreviation	Group	Countries sending data to the evaluation
Blonde Aquitaine	BAQ	Continental	DNK, FIN and SWE
Danish Blue Cattle	BBL	Continental	DNK
Dexter	DXT	British	DNK
Galloway	GLW	British	DNK
Grauvieh	TGR	British	DNK
Highland Cattle	HLA	British	DNK, FIN and SWE
Piemontes	PIE	Continental	DNK
Salers	SAL	British	DNK
Shorthorn (beef)	BSH	British	DNK

Starting in the November run a pedigree index is calculated for all animals without phenotypes.

The NAV breeding values starting 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 7 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 7. NAV and INTERBULL release dates in 2023/24. 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
November 2023		7		7	
December 2023	5		5		
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
Contact person: Gert Pedersen Aamand, Ph.: +45 21717788 gap@lf.dk,

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