News - NAV evaluation
November 3, 2020

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, 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 are given in Table 1.

Table 1. Dates for extraction of data from the national databases

Trait	Denmark	Finland	Sweden
Yield	22.09.2020	09.09.2020	12.09.2020
Type, milkability and temperament	22.09.2020	09.09.2020	11.09.2020
Fertility	22.09.2020	09.09.2020	12.09.2020
Udder health and other disease	22.09.2020	09.09.2020	12.09.2020
Calving[1]	22.09.2020	09.09.2020	12.09.2020
Longevity	22.09.2020	09.09.2020	12.09.2020
Growth[1]	22.09.2020	09.09.2020	12.09.2020
Claw health	22.09.2020	09.09.2020	11.09.2020
Youngstock survival	22.09.2020	09.09.2020	12.09.2020
Saved feed	22.09.2020	09.09.2020	11.09.2020

[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 15th October 2020. INTERBULL information from August 2020 was included in the genomic prediction.

News in relation to NAV dairy genetic evaluation
Traditional evaluation

- Updated pedigree file for RDC and Holstein
- Improved editing of mastitis data in the NAV evaluation for udder health
- Jersey data from France are included in the NAV Jersey evaluation for conformation and longevity
- Jersey data from Norway are included in the NAV Jersey evaluation for longevity
- Holstein Jersey data from Norway are included in the NAV Holstein evaluation for yield, fertility, udder health, calving traits, and longevity
- Metabolic efficiency calculated based on feed intake data are included in the EBV for saved feed for RDC, Holstein and Jersey

Genomic prediction
- Metabolic efficiency predicted based on feed intake data from research farms and the CFIT camera system for RDC, Holstein and Jersey

Updated pedigree file

An upgraded pedigree file has been implemented for the RDC and Holstein evaluation, the upgraded pedigree file was implemented for Jersey in August. The upgrades include:
- A better handling of international id
- Inclusion of French Jersey and Norwegian Jersey animals
- Updates of some old pedigree information from Sweden and Finland

The upgrade of the pedigree file had hardly any effect on the EBVs for bulls but make it possible to include French and Norwegian data and will ensure the use of international IDs can follow international standards in the future.

Improved editing of mastitis data

The editing of the mastitis data has been improved by removing a mix up of herd ids among primary old Finnish and Swedish mastitis data. The mix up had previously caused some instability in the mastitis evaluation for a few Holstein and RDC cows. The correction of the mix up had a very limited impact on EBVs for bulls, and ensure the instability observed earlier for older cows is fixed. Furthermore, Finnish RDC data is no longer included in the Holstein evaluation.

Jersey evaluation including data from France and Norway

In the November evaluation French and Finnish phenotypes for longevity and conformation, and Norwegian phenotypes for longevity are included in the NAV Jersey evaluation.

The impact of including French, Norwegian and Finnish Jersey phenotypes on the EBV for progeny tested Jersey bulls is limited, but a few bulls mainly foreign bulls having limited daughter information in Denmark and Sweden and many daughters in France change in EBVs. But the changes are in line with expectations when information from more daughters is included.

Holstein evaluation including data from Norway

In the November evaluation phenotypes for yield, fertility, calving, longevity and udder health from Holstein in Norway are included in the NAV Holstein evaluation. For udder health it is SCC data only which are included since the amount of mastitis registration data is very limited. The Holstein population in Norway is small, the number of cows with yield data is between 1,700-2,000 cows per birth year in the most recent birth year classes.

The impact of including Norwegian Holstein phenotypes on the EBV for progeny tested Holstein bulls is limited, but a few bulls mainly, foreign bulls having limited daughter information in Denmark, Finland and Sweden and several daughters in Norway, change somewhat in EBVs. But the changes are in line with expectations when information from more daughters is included.

NTM is calculated for all Norwegian Holstein females. For traits where phenotypes are not included from Norway the published EBVs are pedigree indices. NTM is calculated for all females from Norway like for Holstein females from Finland, Sweden and Denmark.

Metabolic efficiency based on feed intake data is a new component in saved feed

Metabolic efficiency based on feed intake data is a new important component in the genetic evaluation for saved feed. 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. The bottleneck to get more reliable breeding values for metabolic efficiency is the amount of feed intake data.

In table 2 the amount of feed intake data available for the November run is shown. The data is research farm data only for RDC and Holstein. For Jersey all feed intake data comes from the camera system for feed intake registration, called CFIT, developed by VikingGenetics. For all breeds the amount of data is limited. For Holstein quite a bit of data from abroad is used, but it must be noted that the value of that information is limited due to recording under quite different conditions. Furthermore, it is important to remember that all research farm data comes from a set up where the cows are included in different research trials as well. The data for Holstein and Jersey includes data from more lactations, while the RDC data is from first lactation cows only. Due to limited amount of data so far, it has been assumed that residual feed intake is the same trait in all lactations; this might be a strong assumption that will be revisited once more data is available. Residual feed intake is assumed to have a heritability of 15% for all breeds.

Table 2 Feed intake data for genetic evaluation of metabolic efficiency in November 2020

	Holstein		RDC	Jersey
	Danish research farm data	Abroad research farm data[a]	Finnish research farm data	CFIT data
Cows with feed intake phenotypes	799	1581	725	505
Cows with feed intake phenotypes and genotypes	436	1450	372	475
Lactations included	1-3	1-6	1	1-6

a) Research farm data from Canada, US and Australia

A single step model – a model using phenotypes and genotypes simultaneously - is used for the genomic prediction for metabolic efficiency. The number of cows with a genotype and a phenotype – the so called reference population – is limited and much lower that for all other traits that are evaluated for dairy cattle. It means that the reliabilities of the GEBVs for metabolic efficiency are low (<5%). The reliability will increase for all breeds when more feed intake data will be recorded by the CFIT system in the future. In spring 2021 it is expected that the first CFIT data will be included in the RDC and Holstein evaluation.

The breeding values for metabolic efficiency and for maintenance efficiency are standardized so that one index unit of both EBVs express the same amount of kg dry matter. It means that the two breeding values can be summed together in the Saved Feed index as:

EBV(Saved feed) = (EBV(Maintenance eff)-100) + (EBV(Metabolic eff)-100) + 100

The standard deviation of GEBV for metabolic efficiency for heifers and candidate bull born 2017-2019 is about 1.8 index unit compared with about 8 index units for maintenance efficiency. A standard deviation of 1.8 shows the low reliability of GEBV for metabolic efficiency. In table 3 the distribution of GEBVs for metabolic efficiency for AI bulls born 2017-2018 is shown.

Table 3. Distribution of GEBV for metabolic efficiency for AI bulls born 2017-2018, number of bulls

GEBV metabolic Efficiency	Holstein	RDC	Jersey
<97	4	6	1
97	16	12	1
98	30	24	9
99	33	30	12
100	**39**	**54**	**15**
101	40	28	18
102	16	28	4
103	4	7	4
>103	5	5	2

The relative weights of information from the two component EBVs in Saved Feed are shown in table 4. The majority of the information in the Saved feed index comes from maintenance efficiency because the GEBV for maintenance is much more reliable than the GEBV for metabolic efficiency.

Table 4. Approx. relative information coming from maintenance efficiency and metabolic efficiency in Saved feed for genomic evaluated bull calves and heifer calves

Relative weight	Holstein	RDC	Jersey
Maintenance efficiency	80	80	80
Metabolic efficiency	20	20	20

In table 5 the correlations between maintenance efficiency, metabolic efficiency, and Saved feed are shown for candidate bulls born 2018 and later. The correlation between maintenance efficiency and metabolic efficiency is expected to be close to zero, since the metabolic efficiency is adjusted for metabolic body weight. The correlation between saved feed and maintenance efficiency is much higher than the correlation between saved feed and metabolic efficiency due to large differences in the reliabilities of the GEBV for maintenance efficiency and metabolic efficiency.

Table 5. Correlations between maintenance efficiency, metabolic efficiency, and Saved feed for genomic evaluated bull calves born

	Holstein		RDC		Jersey	
	Saved feed	Maintain. efficiency.	Saved feed	Maintain efficiency	Saved feed	Maintain efficiency
Maintenance eff.	0.97	-	0.98	-	0.97	-
Metabolic eff.	0.21	-0.01	0.17	-0.01	0.21	-0.02

Saved feed was introduced in NTM in the evaluation in August 2020. The correlations between GEBV for metabolic efficiency and the single NTM traits are all low - close to zero – due to the low reliability on the GEBV for metabolic efficiency, which make it impossible to make any conclusion based on such correlations.

Genetic base
EBVs for bulls and females are expressed on the same cow base. This genetic evaluation included cows born from 3.11.2015 to 3.11.2017 in the genetic base (average 100). The genetic base for Jersey includes now also Jersey cows from France and Norway which are 3-5 year old at publication.

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 routine evaluation for AI beef bulls based on their crossbred offspring from dairy cows for birth 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 6), and EBVs are published at NAV Beef Search.

No news has been introduced in the NAV genetic evaluation of beef bulls used in dairy herds

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 calving and carcass traits. A fee system is 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 1,000 euro per bull should be paid

More information about the genetic evaluation and the publication criteria can be found at NAV homepage.

NAV – frequency and timing of routine runs

NAV has 4 large evaluations per year, which include updated phenotypic and genomic data, and additional eight small runs including updated genotypes. In Table 6 the NAV and INTERBULL release dates for 2020 are shown. The beef evaluation based on beef × dairy crossbreeds takes place along with the large NAV runs 4 times a year.

Table 6. NAV and INTERBULL release dates in 2020. EBVs released at NAV dates in bold will be delivered to international genetic evaluation.

Month	NAV Small run[1]	NAV Large runs[2][3]	INTERBULL
January 2020	7		
February 2020		4	
March 2020	3		
April 2020	7		7
May 2020		5	
June 2020	2		
July 2020	7		
August 2020		11	11
September 2020	1		
October 2020	6		
November 2020		3	
December 2020	1		1

[1] Genotypes updated; [2] Genotypes and phenotypes updated; [3] Beef × dairy evaluation

You can get more information about the joint Nordic evaluation:
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