News - NAV evaluation
2 November, 2021

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 are given in Table 1.

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

Trait	Denmark	Finland	Sweden
Yield	20.09.2021	13.09.2021	09.09.2021
Type, milkability and temperament	20.09.2021	13.09.2021	10.09.2021
Fertility	20.09.2021	13.09.2021	11.09.2021
Udder health and other disease	20.09.2021	13.09.2021	11.09.2021
Calving[1]	20.09.2021	13.09.2021	11.09.2021
Longevity	20.09.2021	13.09.2021	11.09.2021
Growth[1]	20.09.2021	13.09.2021	12.09.2021
Claw health	20.09.2021	13.09.2021	10.09.2021
Youngstock survival	20.09.2021	13.09.2021	11.09.2021
Saved feed	20.09.2021	13.09.2021	10.09.2021
Pure beef cattle	12.10.2021	11.10.2021	12.10.2021

[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 10th October 2021. INTERBULL information from August 2021 was included in the genomic prediction.

News in relation to NAV dairy genetic evaluation

Traditional evaluation

- Metabolic efficiency evaluation has been improved by including an eating rate filter to remove outlier data from the CFIT system
- Fertility evaluation has been upgraded to follow the defined Eurogenomic Golden standards by:
  - Correcting for inbreeding for all fertility traits
  - Considering insemination sire breed in the evaluation of conception rate
- Udder trait evaluation – include Danish AMS data

- Growth – updated standardisation factors

Genomic prediction
- No changes

Metabolic efficiency – improved editing of CFIT data
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 the November run a new method for filtering the feed intake data from the CFIT system is introduced. The filter removes unrealistic amounts of feed registered by the system as eaten in a short time. Analyses of the data after introducing the filter showed that data quality is significantly improved. Furthermore, in the November run information about concentrate given next to total mixed rations in some of the herds are added to the feed intake for the single cows.

In table 2 the amount of feed intake data available for the November run is shown for all three breeds, the amount of feed intake data has increased significantly. Relative largest amount of new CFIT data has been added to RDC followed by Holstein and Jersey.

Table 2 Feed intake data for genetic evaluation of metabolic efficiency in November 2021

	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	1502	967	1581	1003	725	1130
Cows with feed intake phenotypes and genotypes	1043	532	1450	881	372	971
Lactations included	1-6	1-3	1-6	1-6	1	1-6
Number of herds	4	1	a)	4	4	4

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.

Changes in GEBVs
Improved editing of feed intake, and access to more feed intake data have caused significant reranking in the published GEBVs for metabolic efficiency for all 3 breeds, as illustrated in table 3. Correlations are relatively low 0.47-0.60.

Table 3. Correlation between August and November GEBV for AI bulls born after 2017

	Holstein	RDC	Jersey
Correlation	0.55	0.60	0.47
Number of bulls	689	572	150

Fertility upgraded to Golden standard

The fertility evaluation has been improved to fulfil the defined Eurogenomic Golden standard by including a correction for inbreeding depression and reduced variance caused by inbreeding for all the evaluated fertility traits. Furthermore, an effect of insemination sire breed is added to the conception rate evaluation to take a potential effect of the increased use of beef semen into account.

Changes in EBVs

The effect of the changes in the fertility model is very limited. Correlations between EBV with or without the new effects are over 0.99 for all 3 breeds, and less than 1% of the animals change more than 1 index units.

Udder evaluation – AMS data

In the November evaluation significant more Danish AMS data from primarily 2018 and onwards had been made available for the genetic evaluation of udder traits. It means the amount of AMS data used in the evaluation has increased significantly. In table 4 the amount of new AMS data used in the November evaluation is shown.

Table 4. AMS data added in the November 2021 run for udder.

	1. lactation	2. lactation	3. lactation
Holstein	54,625	44,764	31,742
RDC	3,744	3,174	2,172
Jersey	3,845	3,045	2,110

Changes in EBVs

The AMS data is used as correlated traits to evaluate the linear udder traits. The significant amount of extra data added to the November 2021 evaluation cause somewhat larger EBV changes between two subsequent evaluation than usually observed. Table 5 shows the changes in EBV for progeny tested bulls by including the extra AMS data. Only a few bulls change more than 3 index units. The effect is largest for Jersey and Holstein having the largest cow populations in Denmark.

Table 5. Effect on EBV by including more AMS data to the November 2021 evaluation shown as frequency (%) of changes in EBV for progeny tested Nordic AI bulls born 2013-2017.

Change in EBV index units	Holstein, % N = 2,269	RDC, % N = 1,626	Jersey, % N = 446
≤ -4	3.8	1.4	2.5
≥ -3 and ≤ -2	15.0	4.2	19.1
≥ -1 and ≤ 1	71.1	89.7	72.6
≥ 2 and ≤ 3	7.1	3.3	4.0
≥ 4	3.0	1.4	1.8

Growth – updated standardisation factors

The procedure for calculating standardisation factors for growth traits has been aligned with the procedures applied for all other traits. The change had no effect on the ranking of animals and very limited effect on size EBVs, except for Jersey females where and error in the standardisation procedures for carcass conformation had a significant effect on size of published EBV, some old figures were unrealistic high.

Genetic base

EBVs for bulls and females are expressed on the same cow base. This genetic evaluation included cows born from 02.11.2016 to 02.11.2018 in the genetic base (average 100).

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 3), 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 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 1,000 euro per bull should be paid

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

NAV official genetic evaluation for Purebred Beef animals

In November 2021, NAV publish, for the first time, breeding values for calving, growth and carcass traits for purebred beef animals from a joint Nordic evaluation. 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 10), and EBVs are published at [NAV Beef Search](#).

Breeding values for calving traits

The NAV calving evaluation for purebred Beef includes calf survival, calving ease and birth weight and all three traits are subdivided into two categories: 1st parity calvings versus 2nd+ parity calvings.

This division considers the differences in the degree of difficulties between first calving compared to later calvings. Of the twelve estimated breeding values, only eight are published since birth weight is only used as indicator trait in this evaluation. The resulting breeding values from the NAV Purebred Beef evaluation for calving traits are in Table 6.

Table 6. Calving traits in the model and resulting breeding values

Traits in the model	Resulting EBVs
Calf survival – 1st parity	2 official EBVs: DIR* + MAT**
Calf survival – 2nd+ parity	2 official EBVs: DIR + MAT
Calving ease - 1st parity	2 official EBVs: DIR + MAT
Calving ease - 2nd+ parity	2 official EBVs: DIR + MAT
Birth weight – 1st parity	DIR + MAT but only to be used as indicator trait
Birth weight - 2nd+ parity	DIR + MAT but only to be used as indicator trait

*Direct, **Maternal

Genetic parameters for both calving and weight/growth and carcass traits have been estimated from Swedish data using Charolais and Hereford breeds and these were applied within breed group (Continental and British).

The magnitude of heritabilities in table 7 agree with commonly low heritabilities also found in the literature. The pattern of genetic correlations among traits was remarkably similar for Charolais and Hereford.

Genetic correlations between 1st parity and 2nd+ parity within the same trait are high (~0.80) but not one, meaning that calving ease and calf survival traits expressed at the first parity are not genetically the same as in later parities. In general, direct-maternal genetic correlations are unfavorable.

Genetic correlations between maternal calf survival and calving ease are relatively high within and across parities and very similar to the direct genetic correlations. Direct birth weight in first parity is unfavorable correlated with direct calving ease in first and later parties (0.70 and 0.54, respectively), but moderate to low with direct calf survival in first and later parities (0.20 and 0.16, respectively).

Table 7. Heritabilities (h_d^2 **direct and** h_m^2 **maternal**) for calving traits used in the NAV Purebred Beef evaluation

	British (HER)		Continental (CHA)	
	h_d^2	h_m^2	h_d^2	h_m^2
Calf survival - 1st parity	0.06	0.03	0.02	0.02
Calf survival - 2nd+ parity	0.00	0.01	0.01	0.00
Calving ease - 1st parity	0.09	0.04	0.11	0.10
Calving ease - 2nd+ parity	0.02	0.02	0.02	0.01
Birth weight – 1st parity	0.47	0.11	0.42	0.12
Birth weight - 2nd+ parity	0.46	0.11	0.37	0.10

Breeding values for weight/growth and carcass traits
The NAV Purebred Beef evaluation for growth and carcass traits includes seven traits: birth weight, weaning weight gain, yearling weight (only Denmark), post-weaning weight gain (only Finland and Sweden), carcass daily gain, carcass conformation score and carcass fat score.

The calculation of post-weaning weight gain requires information on weights at weaning and at one-year age, and in occasions this data can be limited, such is the case of weaning weights records especially from Denmark. For this reason, it was agreed that Danish records on yearling weight will be used instead of post-weaning weight in the evaluation so that there is no information lost on weight records. The resulting breeding values from the NAV Purebred Beef evaluation for weight/growth and carcass traits are in Table 8.

Table 8. Weight/growth and carcass traits in the model and resulting breeding values

Traits in the model	Resulting EBVs
Birth weight	2 official EBVs: DIR + MAT
Weaning weight gain	2 official EBVs: DIR + MAT
Yearling weight	2 official EBVs: DIR + MAT
Post-weaning weight gain	1 official EBV: DIR
Slaughter daily gain	1 official EBV: DIR
Carcass score	1 official EBV: DIR
Fat score	1 official EBV: DIR

In general, direct heritabilities estimated for weight/growth and carcass traits are moderate. Heritabilities for maternal and direct weaning weight gain are at the same level 13-16%. Maternal heritabilities are lower than the direct heritabilities for birth weight and yearling weight with estimates of around 10%.

Genetic correlations between birth weight and slaughter daily gain are relatively low ranging from 0.17 to 0.24. For weaning weight gain and yearling weight with slaughter daily gain, genetic correlations are moderate (0.50 to 0.61). Slaughter daily gain is positive and moderately (~0.4) correlated with carcass score and between carcass score and fat class the genetic correlations are generally close to zero.

The pattern of heritabilities and genetic correlations among traits were remarkably similar for Charolais and Hereford.

Table 9. Heritabilities for weight/growth and carcass traits used in the NAV Purebred Beef evaluation

	British (HER)		Continental (CHA)	
	h_d^2	h_m^2	h_d^2	h_m^2
Birth weight	0.47	0.11	0.38	0.10
Weaning weight gain	0.15	0.16	0.17	0.13
Yearling weight	0.29	0.10	0.31	0.10
Post-weaning weight gain	0.20		0.20	
Slaughter daily gain	0.46		0.36	
Conformation score	0.28		0.31	
Fat class	0.30		0.34	

Presentation of EBVs

The genetic base for pure beef animals is defined as relative breeding values with a mean of 100 and standard deviation of 10. The selection of animals to form the genetic base includes males and females with birth years 5 to 9 years prior to the publication date and having observations or having at least 5 offspring with observations for one trait in each trait group. For calving traits an additional requirement is known sire identity.

The NAV purebred Beef evaluation provides breed-specific estimated breeding values and therefore individual estimated breeding values cannot be compared across breeds.

Changes moving from national to joint Nordic genetic evaluation

Compared to the national evaluation done up to now in Denmark, Sweden and Finland the joint Nordic model have
- A better handling of heterogenous variance correction
- A better handling of genetic level of imported animals
- New genetic parameters - heritabilities and genetic correlations.

Nordic beef evaluation outlook

NAV genetic evaluation is expected to be further developed within 2022 by:
- Including more beef breeds
- Estimate joint Nordic combined indices
- Include more traits like fertility

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 2022 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 10. NAV and INTERBULL release dates in 2021/22. 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
December 2021	7		7		
January 2022	5				
February 2022		1			
March 2022	1			1	4
April 2022	5		5	12	
May 2022		3			
June 2022	7			7	
July 2022	5				
August 2022		9	9		
September 2022	6				
October 2022	4				21
November 2022		1		1	
December 2022	6		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
Contact person: Gert Pedersen Aamand, Ph.: +45 87405288 gap@seges.dk,

Denmark: www.landbrugsinfo.dk
Contact person: Ulrik Sander Nielsen, Seges Cattle, Ph. +45 87405289, usn@seges.dk

Sweden: www.vxa.se
Contact person: Freddy Fikse, Växa, Ph +46 10 4710615. Genetic.Evaluation@vxa.se

Finland: www.faba.fi
Contact person: Jukka Pösö, Faba co-op, Ph +358-400614035 jukka.poso@faba.fi