News - NAV evaluation
5 November 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	23.09.2024	23.09.2024	06.09.2024
Type, milkability and temperament	23.09.2024	23.09.2024	06.09.2024
Fertility	23.09.2024	23.09.2024	07.09.2024
Udder health and other disease	23.09.2024	23.09.2024	07.09.2024
Calving[1]	23.09.2024	23.09.2024	07.09.2024
Longevity	23.09.2024	23.09.2024	07.09.2024
Growth[1]	23.09.2024	23.09.2024	07.09.2024
Claw health	23.09.2024	23.09.2024	07.09.2024
Youngstock survival[1]	23.09.2024	23.09.2024	07.09.2024
Saved feed	23.09.2024	23.09.2024	06.09.2024
Pure beef cattle	23.09.2024	23.09.2024	14.10.2024

[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 4 October 2024. INTERBULL information from August 2024 was included in the genomic prediction.

News in relation to NAV dairy genetic evaluation

Dairy pure
- Single step for fertility for Jersey, RDC and Holstein
- Changed weight and optimum for single traits in combined EBV for udder for Holstein
- Correction of weight on stature in combined EBV for Frame for RDC
- Changed procedures for calculation of combined indices for type traits

DairyxDairy
- No changes

BeefxDairy
- Youngstock survival included, and economic values updated in NBDI

Beef pure
- Including genomic information in the breeding evaluation for growth and carcass traits for Angus, Charolais, Simmental, Hereford, and Limousin

Genetic evaluation of dairy breeds
Metabolic efficiency
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 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 November 2024 included from in total 23 herds and more than 12,000 cows.

Table 2. Feed intake data for genetic evaluation of metabolic efficiency in November 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	5445	1226	1581	3883	769	2924
Cows with feed intake phenotypes and genotypes	4579	730	1450	3519	416	2599
Lactations included	1-6	1-3	1-6	1-6	1	1-6
Number of herds	9	1	a)	8	4	7

a) Research farm data from Canada, US and Australia

NAV has observed some weakness in the genetic evaluation of metabolic efficiency evaluation, and work is ongoing to improve the statistical model. The current metabolic feed efficiency evaluation takes place in two steps. In the first step the residual feed intake is estimated by correcting the feed intake for the energy sinks used for producing milk, maintenance, and changes in body weight during lactation. The estimated energy in one kg ECM by this method is somewhat lower than one should expect from feeding norms indicating a weakness in the current model. Furthermore, we observe an unexpected negative genetic trend in Holstein and to some extent also RDC, which is linked to the problems estimating correct effects of the energy sinks. Currently intense development work is ongoing to improve the statistical model for metabolic efficiency. The expectation is that it will be possible to introduce an improvement of the metabolic efficiency evaluation in the February 2025 run, which makes better use of the CFIT data than what we are doing today.

Improved genetic evaluation for fertility
A single step method for fertility 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. It means that all animals, both genotyped and non-genotyped get breeding values from the same evaluation. In the single step approach only geno-

types 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 build 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.

Changes in breeding values for fertility
The estimated genetic trend is slightly steeper with the new model compared to the old model for all three breeds. However, introduction of single step causes some reranking of animals because single step simultaneously combines all information, which is more optimal.

The correlation for fertility between breeding values from the new and the old model is high (table 3). For bulls having progeny the correlation is 0.97 or higher for all breeds for the most recent birth year classes. For genotyped young bulls and genotyped heifers, the correlations are lower for all breeds 0.85-0.91 indicating slightly more reranking of animals.

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

	HOL	RDC	JER
AI bulls with genotype and progeny	0.97	0.97	0.98
Heifers and AI bulls with genotype and no progeny	0.85	0.88	0.91

Good stability for proven sires
All breeds show high stability for the proven sires, and the reranking between the bulls born in the same year is minor. For the proven sires born after 2009, 75 percent of the bulls across all breeds will change by no more than 3 index units. For Holstein around 10 percent of the bulls will drop by more than 5 index units, for Jersey and RDC, the figure is around 5 percent.

Some changes for the genomic bulls and genomic tested heifers
For all three breeds, the average index level for genomic bulls will increase, with Holstein showing the largest increase of 2-3 index units. The reranking for the genomic bulls born in the same year will be larger compared to the proven sires, as the reliability for genomic bulls is lower. The genomic level is the same in the new and old model for Holstein and RDC, while Jersey shows a small positive increase, indicating that younger animals with the new model are estimated to be slightly better compared to the older ones.
For Holstein and Jersey, around half of the bulls change by a maximum of 3 index units, while for RDC, this figure is 75 percent. In Holstein, 70 percent of the bulls change by no more than 5 index units and around 25 percent increase more than 5 index units. For Jersey, 75 percent of the animals change by a maximum of 5 index units, while for RDC, this is close to 85 percent. For both RDC and Jersey, 15 percent of the animals increase by more than 5 index units.

Females having both a genotype and a phenotype show good stability
Among females having both a phenotype and a genotype RDC is the most stable breed, with 65 percent of the animals changing by a maximum of 3 index units, compared to 55 percent for Jersey and 50 percent for Holstein. Only 15 percent of RDC animals change by more than 5 index units, while the figure is 25 percent for Jersey and 30 percent for Holstein. The small increase in index

level means that most of the animals that change more than 5 index units will show an increase in the fertility index.

High stability for none genotyped females
The breeding values for none genotyped females show the greatest stability. Across all three breeds, there is minimal reranking between the animals born in the same year. In all breeds, close to 85 percent of the animals will change by a maximum of 2 index units, with only 1-2 percent changing by more than 5 index units.

Reliabilities for fertility
A method for calculating reliabilities from a single step model is implemented. The new method sub-stitutes the method used so far for fertility, which belongs 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 4 it is shown that the new estimates of reliabilities for fertility for all three breeds are significantly lower than with the old method.

Table 4. Average reliabilities for fertility for RDC, Holstein and Jersey AI bulls born 2021.

	Holstein		RDC		Jersey	
	New	Old	New	Old	New	Old
Fertility	0.54	0.78	0.43	0.64	0.42	0.62

NAV will in the coming months conduct some additional checks of the estimated reliabilities for single step GEBVs for fertility. Please note that this has no impact on the estimated breeding values but only changes the figures telling how accurately the breeding value is estimated.

Changes in the calculation of combined indices for type traits
In the November 2024 run, there are changes in the calculation of combined indices for: frame, feet and legs and udder, which affect all three dairy breeds. Furthermore, Holstein has decided to change the weight of the sub-indices in udder. Both changes create some reranking of animals especially for Frame for Jersey and RDC, and Udder for Holstein, as indicated by the correlation in table 5.

Table 5. Correlations for AI bulls between current official (G)EBVs from AUG24 with (G)EBVs calculated with new method including updated breed means for all breeds, and new weights and optimum for Holstein.

Birth year	HOL			RDC			JER		
	Frame	F&L	Udder#	Frame	F&L	Udder	Frame	F&L	Udder
2010	1.00	0.97	0.92	0.84	0.99	1.00	0.37	1.00	1.00
2011	1.00	0.98	0.87	0.84	0.99	1.00	0.71	1.00	0.99
2012	1.00	0.98	0.93	0.87	0.99	1.00	0.68	1.00	1.00
2013	1.00	0.97	0.91	0.83	0.99	0.99	0.70	1.00	0.99
2014	1.00	0.98	0.93	0.84	1.00	1.00	0.57	1.00	1.00
2015	1.00	0.98	0.96	0.83	0.99	1.00	0.50	1.00	1.00
2016	1.00	0.98	0.94	0.90	0.99	0.99	0.53	1.00	0.98
2017	1.00	0.97	0.93	0.88	0.99	1.00	0.46	1.00	1.00
2018	1.00	0.97	0.94	0.90	0.99	1.00	0.72	1.00	0.99
2019	1.00	0.97	0.91	0.86	0.99	1.00	0.41	1.00	1.00
2020	1.00	0.97	0.94	0.86	0.99	1.00	0.36	1.00	1.00
2021	1.00	0.97	0.94	0.86	0.99	1.00	0.44	1.00	1.00
2022	1.00	0.97	0.95	0.80	0.99	1.00	0.42	1.00	1.00
2023	1.00	0.96	0.92	0.82	1.00	0.99	0.40	1.00	1.00

Update of breed mean

The breed averages for the single traits are updated for all breeds. When the breed average changes, it can affect the ranking of the individual animals within the breed. This is because the breed average can move to the other side of the breed optimum for traits having a breed mean close to the assumed optimum. For a trait where that happen, the contribution into the index for frame, feet and legs or udder can change significantly.

Large reranking for frame for Jersey

For Jersey there are big changes for frame. Over the past years, Jersey cows have become larger in size, which has significantly shifted the breed average. For Jersey 1st lactation cows, the breed optimum for stature is 129 cm, while the breed average assumed in the breeding evaluation has increased from 125.9 cm to 129.8 cm. This means that previously Jersey aimed to breed taller cows, but now the goal is to breed smaller cows. The changed breed average means that the optimum on the index scale changes from >130 to 89 for stature. There are also other sub traits in frame that will change the optimum. For example, the optimum for body depth will change from index 105 to index 122. These changes have caused major re-rankings for frame at the November evaluation for Jersey.

Table 6. Old and new breed average and breed optimum for frame for Jersey

Sub traits in Frame	Jersey average old	Jersey average new	Optimum old	Optimum new
Stature	125,9	129,8	>130	89
Body depth	5,9	5,7	105	122
Chest width	4,8	4,9	113	109
Rib structure	5,5	4,9	>130	>130
Top line	5,6	6,0	>130	>130
Rump width	5,2	5,0	126	>130
Rump angle	5,2	5,2	91	92

Minor changes for RDC and Holstein according to updated breed average

For RDC and HOL, a technical optimum for frame is used, where the frame index explains the size of the cow, so higher index indicates taller, wider and deeper cows. Therefore, the change in breed average does not affect the calculation of frame for these two breeds. Only the position of the optimum dot on the graph will change, as it indicates the real optimum for frame for these breeds. For example, the optimum point for stature for Holstein was index 115, but from November it will be index 83, because Holstein on average is taller than the 148 cm breed optimum. For RDC, the optimum point for body depth will change from index 118 to the farthest right on the scale (index >130). This is because the new breed average is lower than the breed average earlier used in the index calculation for frame.

For udder and feet and legs, the breed average update will only have a limited effect for all three breeds. Either because the change in the breed averages is very small, the optimum is still far away from the breed average, so it is really a matter of breeding in one direction, or the breeds do not have any weight on the sub traits in the combined index for udder and feet and legs.

Correction in Frame for RDC

For RDC, an incorrect weight has unfortunately been used in the past to calculate frame. The error caused that relatively too little weight was put on stature compared to the other sub traits in the weighting for frame. This means that RDC bulls that breed taller cows have generally got higher index for frame in the November 2024 evaluation.

Changed weights and optimum in udder for Holstein

Holstein has decided to change weights and optimum for the sub traits in the udder index
In addition to the changed optimum for teat placement back and udder balance, Holstein also has decided to adjust the weight of the sub-traits in udder giving a small weight on both teat length and thickness. In the table below the old and new weights and optimum that are included in udder index for Holstein are shown.

Table 7. Old and new optimum on the linear scale and the weights of the sub-traits in udder index for Holstein. The negative weight for teat placement back and udder balance simply indicates that the optimum on the index scale is below 100.

Sub traits in udder	Optimum, old	Optimum, new	Weight, old	weight, new
Fore udder attachment	9	9	20	18
Rear udder height	9	9	10	5
Rear udder wide	9	9		5
Udder support	8	8	20	17
Udder depth	9	9	25	18
Teat length	5.5	5.5		3
Teat thickness	5	5		4
Teat placement front	8	8		
Teat placement back	5.0	6.2	-15	-15
Udder balance	5.0	5.4	-10	-15

In general, changes in weights and optimum in udder index for Holstein have a moderate effect on the ranking of the bulls, but there are some animals that have changed significantly in the udder index. This particularly affects animals with very low breeding values for teat placement back, udder balance and teat size. These animals have previously had a large positive contribution to udder index from the teat placement back and udder balance, while not being penalized for breeding shorter and thinner teats.

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 05.11.2019 to 05.11.2021 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, and EBVs are published at NAV Beef Search.

Youngstock survival included, and economic values updated in NBDI
NBDI has been updated in the November run by:
- Updating the economic values behind NBDI to reflect current production circumstances.
- Including Youngstock survival

The upgraded NBDI consider the following updates compared to the old NBDI:
- Average growth rates, age at slaughter, live and carcass weight at slaughter (daily gain and daily net gain) for crossbreed calves
- Assumptions on EUROP form and fat scores. That includes separate assumptions for male and female calves.

- Assumptions on calf mortality and calving ease for crossbred calves. That includes separate assumptions for male and female calves.
- Assumptions related to youngstock survival (average survival rates and age at death).
- Economic assumption with respect to beef prices for crossbreed calves including deduction or additions due to EUROP form and fat score.
- Besides the model has been modified in order to take into account the use of Y-sorted beef semen.
- The calculation of feed consumption for the long growth period has been changed such that the crossbred calves are slaughtered at a fixed weight when growth rate is increased. In the previous version of model all calves were slaughtered at a fixed age when growth rate increased.
- Besides, feed consumption has been adjusted for crossbred heifer calves – such that it corresponds to observations from practice. Continue publishing one youngstock survival index, as ranking of beef sires on youngstock survival was found to be similar for short and long fattening periods. Emphasis on survival in the late period is increased by 25% compared to the economic calculations, to reflect that the late period covers until day 200 and that some losses occur after that. Labour costs have been added to the model to consider all costs associated with premature death.

In table 8 and 9 weight factors for NBDI and correlations between NBDI and single traits are presented.

Table 8. New and old weights factors for NBDI short and NBDI long.

	Old		New	
	NBDI short	**NBDI long**	**NBDI short**	**NBDI long**
Birth	1.08	1.01	0.50	0.45
Growth short	0.79	-	0.55	-
Growth long	-	1.07	-	0.79
Young stock survival	0	0	0.73	0.66

Table 9. Correlations between single and combined traits and NBDI based all bulls with publishable breeding values.

	Old		New	
	NBDI short	**NBDI long**	**NBDI short**	**NBDI long**
Birth	**0.60**	**0.37**	**0.37**	**0.18**
Still birth	*0.60*	*0.39*	*0.38*	*0.20*
Calving ease	*0.55*	*0.33*	*0.33*	*0.15*
Growth short	**0.50**	**0.58**	**0.50**	**0.66**
Growth long	**0.39**	**0.70**	**0.43**	**0.72**
Daily carcass gain	*0.46*	*0.48*	*0.46*	*0.56*
EUROP Form score	*0.23*	*0.62*	*0.21*	*0.58*
EUROP fat score	*0.14*	*-0.27*	*0.12*	*-0.16*
Young stock survival	**0.15**	**0.06**	**0.69**	**0.51**
YSS early	*0.13*	*0.06*	*0.46*	*0.33*
YSS late	*0.12*	*0.04*	*0.68*	*0.51*

The correlation between the old and new NBDI short is 0.76 and between the old and new NBDI long it is 0.83. This indicates significant reranking caused by inclusion of youngstock survival and updating economical weights.

More details about the upgraded NBDI can be found at NAV homepage.

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

NAV publish EBVs for calving, growth and carcass traits based on phenotypes from purebred beef Angus, Charolais, Simmental, Hereford, Limousin, Highland Cattle, Blonde d 'Aquitaine, Belgian Blue, Dexter, Galloway, Grauvieh, Piemontese, Salers, Shorthorn cattle. Extraction date for the data used in the June evaluation can be found in Table 1. Breeding values for pure beef cattle are estimated four times per year, and EBVs are published at NAV Beef Search.

The NAV breeding values from the November 2024 evaluation can be found at the NAV Beef search page for all animals and all 18 traits included in the evaluation.

Including of genomic information for weight, growth, and carcass traits

In November 2024, NAV published, for the first time, genomic breeding values for weight, growth, and carcass traits for the five largest breeds (AAN, CHA, HER, LIM, and SIM). The genomic breeding values are calculated by a so-called single step model using all information from genotyped and non-genotyped animals simultaneously in one evaluation.

Table 10, show the list of breeds and number of genotypes available for the November 2024 evaluation.

Table 10. List of breeds with number of genotypes by country included in the November 2024 ssGBLUP evaluation.

Breed name	DNK	FIN	SWE	Other	Total
Aberdeen Angus	1608	4504	2241	154	8507
Charolais	408	3912	5289	188	9797
Hereford	1518	4807	5723	86	12134
Limousin	2538	2474	1584	162	6758
Simmental	1546	3029	2386	102	7063

Breeding value changes when adding genotype information

By adding genomic information, the reliability of breeding values increases especially for genotyped animals. The extra information leads to changes in breeding values compared to results from the old

model not using genomic information. For animals with only pedigree and phenotype records the changes in breeding values are expected to be limited.

In table 11 the results from the old NAV purebred beef evaluation (pedigree-based model) are compared with the new NAV purebred beef genomic evaluation (genotype and pedigree-based model) showing high agreement in breeding values across breeds and traits and for all three countries. As expected, the biggest differences were found in animals where their genotype was used in the new evaluation, compared to just using pedigree information in the old evaluation.

Table 11. Correlation of combined breeding values for growth, production, and slaughter quality from the old NAV purebred beef evaluation (pedigree-based model) with the new NAV purebred beef genomic evaluation (genotype and pedigree-based model), split between non-genotyped and genotyped animals within country and breed. (Males and females born after 2012 with at least one phenotypic record)

	DNK		FIN		SWE	
	Non-genotyped	Genotyped	Non-genotyped	Genotyped	Non-genotyped	Genotyped
Aberdeen Angus						
Growth index	0.97	0.87	1	0.94	0.98	0.94
Production index	0.97	0.86	1	0.94	0.97	0.93
Slaughter quality index	0.97	0.88	1	0.93	0.93	0.79
Charolais						
Growth index	0.97	0.9	1	0.96	0.98	0.93
Production index	0.98	0.91	1	0.96	0.98	0.93
Slaughter quality index	0.99	0.95	1	0.97	0.98	0.94
Hereford						
Growth index	0.97	0.85	0.99	0.92	0.98	0.89
Production index	0.97	0.86	1	0.92	0.98	0.88
Slaughter quality index	0.98	0.88	1	0.93	0.97	0.87
Limousin						
Growth index	0.99	0.92	1	0.95	0.98	0.94
Production index	0.99	0.92	0.99	0.95	0.98	0.93
Slaughter quality index	0.99	0.93	0.99	0.95	0.99	0.93
Simmental						
Growth index	0.93	0.99	0.99	0.96	0.98	0.94
Production index	0.93	0.99	0.99	0.96	0.98	0.93
Slaughter quality index	0.96	0.99	0.99	0.96	0.99	0.94

A summary of the publication of breeding values for all breeds and traits for the November 2024 evaluation are shown in table 12 having genomic breeding values in place for weight/growth and carcass traits.

Table 12. Type of breeding value, genomic (GEBV) or pedigree-base (EBV) calculated in the No-vember 2024, for all breeds, traits, and indexes.

Breed name	Growth & carcass traits	Calving traits	Growth, car-cass quality and produc-tion index	Dam index	Calving index	Birth index
Aberdeen Angus	**GEBV**	EBV	**GEBV**	**GEBV**+EBV	EBV	EBV
Charolais	**GEBV**	EBV	**GEBV**	**GEBV**+EBV	EBV	EBV
Hereford	**GEBV**	EBV	**GEBV**	**GEBV**+EBV	EBV	EBV
Limousin	**GEBV**	EBV	**GEBV**	**GEBV**+EBV	EBV	EBV
Simmental	**GEBV**	EBV	**GEBV**	**GEBV**+EBV	EBV	EBV
Blonde D'Aquitaine	EBV	EBV	EBV	EBV	EBV	EBV
Highland Cattle	EBV	EBV	EBV	EBV	EBV	EBV
Other	EBV	EBV	EBV	EBV	EBV	EBV

Next step

Genomic information increases the reliability of the breeding values for genotyped animals with about 10% units. The published reliabilities in the November run are estimated without considering genomic information. Next steps for NAV are to:

- Improve the calculation of reliabilities so it considers genomic information
- Look at possibilities for establishing genomic prediction for beef breeds having relative few geno-typed animals
- Analyze the possibilities to conduct genomic prediction for calving traits

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 13 the NAV and INTERBULL release dates for 2024/2025 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 13. NAV and Interbull release dates in 2024/2025. 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 2024		5		5	
December 2024	3		3		
January 2025	7				
February 2025		4			Not decided yet
March 2025	4			4	
April 2025	1		1	15	
May 2025		6			
June 2025	3			3	
July 2025	1				
August 2025		12	12		
September 2025	2				
October 2025	7				Not decided yet
November 2025		4		4	
December 2025	2		2		

[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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