News - NAV routine evaluation
November 6, 2018

The latest NAV routine evaluation for yield, fertility, conformation, udder health, general health, calving traits, milkability, temperament, growth, longevity, young stock survival, claw health 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 Finn Cattle.

Red Dairy Cattle evaluation, including data from: Danish Red, Swedish Red, Finnish Ayrshire, Finnish Holstein and Finn Cattle.

Jersey evaluation, including data from: Danish Jersey, Swedish Jersey and Finnish 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	27.09.2018	16.09.2018	21.09.2018
Type, milkability and temperament	27.09.2018	16.09.2018	21.09.2018
Fertility	27.09.2018	16.09.2018	21.09.2018
Udder health and other disease	27.09.2018	16.09.2018	21.09.2018
Calving	27.09.2018	16.09.2018	21.09.2018
Longevity	27.09.2018	16.09.2018	21.09.2018
Growth	27.09.2018	16.09.2018	21.09.2018
Claw health	27.09.2018	16.09.2018	21.09.2018
Youngstock survival	27.09.2018	16.09.2018	21.09.2018

Data used in genomic prediction
Genotypes were extracted from the joint Nordic SNP data base 18th October 2018. INTERBULL information from August 2018 was included in the genomic prediction.

News in relation to NAV genetic evaluation
Genomic prediction
No changes

Traditional evaluation
- Swedish bull calf data are included in evaluation of young stock survival
- Lactation weights changed for all traits
- Yield index weights changed all breeds
- Udder conformation changed in Holstein
- Frame changed in RDC
- NTM has been updated

Swedish bull calf data are included in evaluation of young stock survival
Previously survival data from Swedish bull calves has not been available for genetic evaluation. A data pipeline has now been developed and information about calf survival for a proportion of Swedish bull calves can now be included in the evaluation of young stock survival. The data is available

from 2009 and onwards comprising a total of 884.000 records (August 2018 test run) from Holstein (44.9 %), RDC (54.5 %) and Jersey (0.6 %) for calf survival up to day 30 (early period). In comparison 1.016 mill. records from Swedish heifer calves were used in the evaluation from the same time period (Swedish heifer data has been collected from 1999). From day 31 to 184 (late period) a large proportion of the Swedish bull calves are moved to other herds for fattening from these herds records are not available, thus, the number of observations on Swedish bull calves in the late period is much lower compared to the early period. Comparison between EBV were made using Nordic AI bulls born after 2009 and with reliability of the young stock survival index >0.40. The correlations between EBV with and without Swedish bull calf data were 0.99, 0.97, and 1.00 for Holstein, RDC and Jersey, respectively, indicating no or minimal re-ranking of bulls in Holstein and Jersey and slightly more re-ranking in RDC. In line with expectations, a greater proportion of the progeny in RDC is from Sweden compared to Holstein and the proportional increase in the number of Swedish progeny when Swedish bull calf data is added is also seem in RDC. This explains why the investigated bulls change slightly more for RDC compared to Holstein. For Jersey, the changes are minimal given the low number of records from Swedish Jersey bull calves.

Table 2. Effect on EBV from adding Swedish bull calf data to routine data (August 2018 evaluation test) shown as frequency (%) of changes in EBV Based on Nordic AI bulls born 2008-2010 with reliability of young stock survival index > 0.40.

Change in EBV index units	Holstein, %; N = 1,010	RDC, % N = 567	Jersey, % N = 157
≤ -6	1.3	1.8	-
≥ -5 and < -1	4.6	7.6	-
≥ -1 and ≤ 1	87.8	77.4	100
> 1 and ≤ 5	5.3	10.6	-
≥ 6	1.0	2.6	-

Table 2 shows the distribution of changes in the young stock survival index when Swedish bull calf data is included in the evaluation. For HOL 87.8 % of the included bulls change less than 2 index units for RDC this is the case for 77.4 % of the bulls. A limited effect was seen for the Jersey bulls.

Lactation weights for NTM sub-traits have been updated

EBVs for several NTM sub-traits are based on phenotypic records from multiple lactations. These traits are yield, fertility, udder health, general health, claw health, and conformation traits (frame, feet & legs, udder). The previous lactation weights were 0.50, 0.30 and 0.20 for 1st, 2nd, and 3rd lactation, respectively. The relative high weight on 1st lactation considered that 1st lactation is expressed early in a progeny testing scheme resulting in higher reliabilities of the combined EBV for e.g. yield at an early stage. However, genomic selection schemes have now completely replaced progeny testing; thus, a large weight on 1st lactation is no longer necessary because EBV have more equal reliabilities across lactations.

New lactation weights were calculated in conjunction with the 2018 NTM review (see below). They must reflect the distribution of lactations in a future production system with a lower replacement rate than is currently observed. For calculation of economic values for the NTM traits, it was decided to use a replacement rate of 32 % for all Nordic breeds across countries. Using the NTM model this resulted in a new distribution of 1st, 2nd, and 3rd+ lactation: **0.30:0.25:0.45**. This set of weights reflects the future distribution of lactations and signals that older cows (3rd lactation and older) also are important in a breeding goal. For comparison, the distribution of lactations in 2016 for Danish Holstein was 0.38:0.28:0.34 indicating a slightly higher replacement rate than 32 %.

Table 3 illustrates the effect of changing lactation weights from the previous of 0.50:0.30:0.20 to the new of 0.30:0.25:0:45. The yield traits and selected claw health traits are used as examples, but the results also apply to the remaining NTM sub-traits. The correlations for all the investigated traits were

~0.99, indicating minimal effect of a relative large change and a very limited effect on re-ranking of animals. This is because the genetic correlations between lactations are high, for example the genetic correlation between protein yield in different lactation is ~0.90 across the NAV breeds.

Table 3. Correlations between breeding values based on current lactation weights and new weights based on the 2018 NTM model for selected traits in Holstein, RDC and Jersey. Based on Nordic AI sires born 2008-2010 with reliability above 0.50.

Breed	Holstein	RDC	Jersey
Number of sires	914	678	164
M-index	0.992	0.991	0.997
F-index	0.992	0.989	0.994
P-index	0.997	0.988	0.995
Number of sires	905	669	162
Digital dermatitis	0.997	0.998	0.998
Sole ulcer	0.995	0.995	0.996

Weights on M-, F-, and P-yield in the yield index have been updated

During the NTM 2018 review new proposals were given regarding the relative weighting of fat, protein, and milk yield within the yield index. The relative weighting of the three yield traits depends on expected relative payment of milk, fat and protein when the breeding goal is realized 5-7 years ahead. Currently we are seeing an increased payment for fat relative to protein and more focus on milk solids instead of milk yield – this trend is expected to continue well into the future. The previous yield index weights do not reflect this and should, therefore, be updated.

Background information and details for this study can be found on NAVs homepage. The final weights as proposed by the Nordic breed organizations are shown in Table 4. Common for all breeds is a changed protein-fat ratio towards more weight on fat yield. For Jersey, equal weights are put on fat and protein yield. For Holstein and RDC a greater negative weight is put on milk yield indicating more emphasis on increased amounts of milk solids rather than milk yield.

Table 4. Final relative weights for M, F, and P yield in the yield index for Holstein, RDC and Jersey (new) and alternative weighing (alt.) using fat and protein yield and fat and protein percentage. Previous weights are shown for comparison.

	M-index	F-index	P-index	F%-index	P%-index
Holstein, new	-0.25	0.55	0.70	-	-
Holstein, alt.	-	0.40	0.55	0.20	0.10
Holstein, previous	-0.20	0.40	0.80	-	-
RDC, new	-0.25	0.55	0.70	-	-
RDC, alt.	-	0.40	0.55	0.20	0.10
RDC, previous	-0.20	0.40	0.80	-	-
Jersey, new	-0.30	0.65	0.65	-	-
Jersey, alt.	-	0.50	0.50	0.25	0.15
Jersey, previous	-0.30	0.50	0.80	-	-

Alternatively, the yield index can be constructed by weighing fat and protein yield and fat and protein percentage. The alternative weights are also shown in Table 4 but it should be noted that yield index values based on the two methods of weighting the yield traits are not 100 % identical because the alternative weights are approximate because of rounding off values in several places during the calculations. This results in a correlation between the yield and alternative yield index values for all three breeds ≥ 0.99.

Correlations between new and previous GEBV for the yield index were 0.98 for Holstein and RDC and 0.99 for Jersey when based on genotyped Nordic bulls born in 2015-2016. This indicates minimal re-ranking of the bulls. In Table 5, expected genetic response for milk, fat and protein using the old and new weights are shown as correlation between milk, fat and protein yield and the yield index. Also, expected genetic progress is shown for fat and protein percentages.

The changes in expected genetic response reflect the changed weights. For all breeds, genetic progress is expected to be a bit lower for milk yield and protein yield and increase a bit for fat yield. Because of the decreased weight on milk yield, genetic response for fat and protein percentage is expected to increase compared to the old yield index.

Table 5. Expected genetic response for milk, fat and protein yield and fat and protein percentages shown as correlations between EBV for the sub-traits and the yield index. The values are based on genotyped Nordic bulls born in 2015-2016.

		Milk	Fat	Protein	Fat %	Protein %
Holstein	New yield index	0.28	0.92	0.75	0.39	0.33
5,218 bulls	Old yield index	0.44	0.83	0.87	0.20	0.22
RDC	New yield index	0.47	0.91	0.86	0.24	0.19
4,368 bulls	Old yield index	0.57	0.85	0.93	0.09	0.11
Jersey	New yield index	0.41	0.95	0.80	0.06	0.12
867 bulls	Old yield index	0.50	0.92	0.87	-0.05	0.04

New relative weights within udder conformation index for Holstein

The relative weighting of the linear type traits within the udder conformation index for Holstein have been changed. In Table 6 the new weights are presented together with the previous weights. The new udder conformation index puts more emphasis on a stronger udder that is able handle increasing future yield; mainly genetic response for udder cleft is expected to increase considerably. The correlation between the new and previous udder conformation index is 0.92 indicating that some re-ranking of the bulls can be expected.

Table 6. New and previous weights for linear type traits within the udder conformation index and expected genetic response for sub-traits in new and previous udder conformation index for Holstein shown as correlations between EBV for the sub-traits and the udder conformation index. The values are based on 1,128 Nordic Holstein bulls born in 2007-2011 with at least 15 daughters with classifier records.

Sub-trait within udder conformation			Expected genetic response	
	Previous weights	New weights	Previous index	New index
Fore udder attachment	0.17	0.20	0.71	0.72
Rear udder height	0.10	0.10	0.52	0.57
Rear udder width	-	-	0.22	0.28
Udder cleft	0.10	0.20	0.01	0.23
Udder depth	0.24	0.25	0.89	0.80
Teat length	0.05	-	0.14	0.00
Teat thickness	0.05	-	0.06	-0.04
Teat placement, front	0.07	-	0.16	0.07
Teat placement, rear	-0.12	-0.15	-0.02	0.06
Udder balance	-0.10	-0.10	0.14	0.00

Table 7 shows the distribution of differences between the previous udder conformation index and the new index with changed weighting of the linear type traits. Considerable changes in EBV were observed – 66 % of investigated bulls changed more than 2 index units.

Table 7. Effect on EBV when using new weights for the linear type traits in the Holstein udder conformation index compared to the previous udder index (based on data from September 2018 evaluation) shown as frequency (%) of changes in EBV Based on 1,109 Nordic AI Holstein bulls born 2007-2011 with at least 15 daughters with classifier records.

Change in EBV index units	Distribution of changes, %
≤ -6	4.1
≥ -5 and < -1	28.3
≥ -1 and ≤ 1	33.5
> 1 and ≤ 5	25.7
≥ 6	8.4

New relative weights within frame index for RDC

The relative weighting of the linear type traits within the frame index have been changed for RDC. In Table 8 the new weights are presented together with the previous weights. Expected genetic response for the traits with the frame index was calculated using 743 Nordic RDC bulls born from 2009 with at least 15 daughters with classifier records (Table 8). The correlation between the new and old frame index was 0.78 indicating that re-ranking of bulls can be expected. The result is less emphasis on stature and more emphasis towards cows with greater capacity compared to the old frame index.

Table 8. New and old weights for linear type traits within the frame index and expected genetic response for sub-traits in new and old frame index for RDC shown as correlations between EBV for the sub-traits and the frame index. The values are based on 743 Nordic RDC bulls born 2009 with at least 15 daughters with classifier records.

Sub-trait within frame	Previous weights	New weights	Expected genetic response	
			Previous index	New index
Stature	10	15	0.79	0.56
Body depth	15	25	0.56	0.80
Chest width	20	30	0.40	0.74
Dairy form	10	10	0.27	0.08
Top line	10	0	0.07	-0.17
Rump width	15	20	0.57	0.62
Rump angle	20	0	-0.39	-0.11

Table 9 shows the distribution of differences between the previous frame conformation index and the new index with changed weighting of the linear type traits. Considerable changes in EBV were observed – only 22.1% of investigated bulls changed less than 2 index units.

Table 9. Effect on EBV when using new weights for the linear type traits in the RDC frame conformation index compared to the previous frame index (based on data from September 2018 evaluation) shown as frequency (%) of changes in EBV Based on 525 Nordic AI RDC bulls born from 2009 with at least 15 daughters with classifier records.

Change in EBV index units	Distribution of changes, %
≤ -6	17.3
≥ -5 and < -1	22.5
≥ -1 and ≤ 1	22.1
> 1 and ≤ 5	24.0
≥ 6	14.1

NTM has been updated

For the last 2 years NAV has been upgrading the Nordic Total Merit Index (NTM) in co-operation with the Nordic breed and AI organizations. This work is now complete, and we can present new relative NTM weights are implemented in the November 2018 run. Focus has been on preparing NTM for production circumstances for the Nordic dairy farms when the new NTM is realized 8-10 years ahead. Since NTM was introduced in 2008, genomic selection has been introduced. The use of sexed semen has been introduced and is often combined with the use of beef semen. This affects the number and type of animals for slaughter and needs to be accounted for when calculating economic values for the NTM traits. Also, the number of organic dairy farms has increased during the last decade. Participation in health agreement schemes enabling the herd personnel to treat certain diseases with antibiotics has also been considered. The economic value of feed efficiency has been investigated during the NTM review but is not yet included in NTM. Finally, both biological and economic assumption have been reviewed in detail and updated. The results of the NTM reviews have been discussed at two NAV workshops in January and May 2018 before the final sets of weights for Holstein, RDC and Jersey were agreed upon. In Table 10, the updated relative NTM weights are presented. The previous relative NTM weights are shown for comparison.

Table 10. New relative weights for each sub-index in NTM after standardization for Holstein, RDC and Jersey. Previous (prev) relative NTM weights are shown for comparison.

	Holstein		RDC		Jersey	
	Prev NTM	**New NTM**	**Prev NTM**	**New NTM**	**Prev NTM**	**New NTM**
Yield	0.75/0.68[1]	0.90/0.81[1]	1.00/0.91[1]	1.02/0.93[1]	0.87/0.78[1]	0.83/0.75[1]
Growth	0.06	0.08	0.00	0.10	0.00	0.00
Fertility	0.31	0.36	0.24	0.36	0.20	0.26
Birth	0.15	0.14	0.13	0.11	0.06	0.04
Calving	0.17	0.14	0.11	0.10	0.06	0.07
Udder health	0.35	0.30	0.30	0.26	0.44	0.44
General health	0.11	0.14	0.11	0.11	0.04	0.14
Frame	0.00	0.00	0.00	0.00	0.00	0.00
Feet & legs	0.12	0.05	0.08	0.06	0.04	0.07
Udder	0.25	0.18	0.35	0.26	0.26	0.15
Milkability	0.08	0.09	0.09	0.11	0.10	0.09
Temperament	0.03	0.04	0.03	0.03	0.03	0.03
Longevity	0.11	0.06	0.07	0.06	0.08	0.09
Claw health	0.08	0.10	0.05	0.07	0.05	0.04
Young stock surv.	0.14	0.13	0.22	0.19	0.12	0.10

[1]Weight factor for cows with own yield record but without genomic information.

Compared to the previous NTM, the weights on production traits, fertility and general health have increased, and the weights on conformation traits, longevity and to some degree udder health have decreased. The relative weights on the remaining traits are unchanged.

Expected genetic response can be assessed by calculating the correlation between each sub-trait index and the NTM index. For example, a value of 0.40 for a trait means that 40 % genetic progress can be expected compared to selection for that trait only. Table 11 shows the expected genetic response for each NTM sub-trait using the new relative NTM weights. Expected responses based on the previous relative NTM weights are shown for comparison. The values in Table 11 are based on the November 2017 evaluation run which has also been used for values in all presentations in relation to the NTM revision from January 2018 to August 2018. It should be noted that the values only include changes to the yield index. Effect of changes in udder conformation index in Holstein and the young stock survival index is not included. Therefore, expected genetic response based on the November 2018 can be expected to be slightly different compared to the values in Table 11. Further-

more, more data are included in the November 2018 evaluation compared to November 2017 evaluation. The results show that the new NTM will result in a slightly increased response on production (yield and growth). Overall, the expected genetic response for the functional and conformation traits is slightly lower compared to the previous NTM. However, for fertility and general health in RDC and Jersey genetic response is expected to increase slightly.

Table 11. Expected genetic response for the new NTM based on genotyped 5,218, 4,368, and 867 Nordic Holstein, RDC, and Jersey bulls born 2015-2016. Values are based on the November 2017 evaluation. Expected genetic response for the previous (Prev) NTM is shown for comparison.

	Holstein		RDC		Jersey	
	Prev NTM	**New NTM**	**Prev NTM**	**New NTM**	**Prev NTM**	**New NTM**
Yield	0.41	0.58	0.65	0.69	0.59	0.63
Growth	0.03	0.08	-0.10	0.02	-0.02	0.02
Fertility	0.48	0.45	0.16	0.25	0.23	0.31
Birth	0.27	0.25	0.18	0.16	0.09	0.09
Calving	0.37	0.33	0.19	0.18	0.19	0.16
Udder health	0.51	0.39	0.35	0.29	0.58	0.57
General health	0.36	0.35	0.17	0.19	0.28	0.33
Frame	0.01	0.02	0.04	0.04	0.17	0.11
Feet & legs	0.30	0.19	0.28	0.23	0.15	0.20
Udder	0.42	0.28	0.37	0.27	0.42	0.30
Milkability	0.05	0.08	0.14	0.20	0.00	0.08
Temperament	0.09	0.09	0.05	0.07	0.00	-0.01
Longevity	0.63	0.52	0.45	0.45	0.49	0.52
Claw health	0.26	0.24	0.16	0.15	0.16[1]	0.16[1]
Young stock survival	0.26	0.23	0.32	0.28	0.32[1]	0.33[1]

[1]Based on progeny tested Nordic Jersey bulls born 2009-2010 – GEBV not estimated for JER.

With all the new changes (explained above) combined for the November evaluation, the new NTM was compared with the previous NTM. Changes were assessed using both progeny tested Nordic bulls born 2009-2010 and genotyped Nordic bulls born 2015-2016. The reason for adding results from the progeny tested bulls is that when EBV from two evaluations (October 2018 and November 2018) are compared changes are also caused by adding new phenotype information. For the progeny tested bulls with many milking daughters, changes caused by new information are minor; thus, the correlation between new and previous NTM is expected not to reflect changes caused by new daughter information. In contrast, changes are expected to be larger when assessed by the genotyped bulls because new phenotypic information is added to the reference population for the November evaluation.

In Table 12 correlations between new and previous NTM are shown for both progeny tested and genotyped Nordic bulls. The changes caused by the upgrade of NTM can best be seen by comparing NTM for progeny tested bulls from August (August daughter also used in October evaluation) to November, since the NTM for genotyped young bulls are also affected by the extra information added to the reference population from August to November. The lowest correlation based on the progeny tested bulls was seen for Holstein (0.95), mainly caused by the new weighting of M, F, and P within the yield index, the weighting within the udder conformation index and some by adding Swedish bull calves to the young stock survival index which also affect the correlation for RDC (0.96) besides changes to the yield index. Based on the genotyped bulls, the lowest correlation was seen for RDC because the effect of updating reference information (adding new phenotypic information to the reference population) is substantial. Therefore, the correlations based on the genotyped bulls are expected to be relatively lower for RDC and Jersey than for Holstein compared to the progeny tested bulls.

Table 12. Correlations between new and previous NTM based on either progeny tested Nordic bulls born in 2009-2010 and genotyped Nordic bulls born 2015-2016. Number of bulls in ( ).

Breed	Progeny tested bulls (N)	Genotyped bulls (N)
Holstein	0.95 (792)	0.94 (5,224)
RDC	0.96 (303)	0.92 (4,369)
Jersey	0.98 (100)	0.95 (859)

In Table 13 and 14 the distribution of differences between previous and new NTM for Holstein, RDC and Jersey are shown. Like the correlations, changes are shown for both progeny tested (Table 13) and genotyped (Table 14) bulls.

For Holstein, the distribution of changes based on progeny tested bulls shows that 60 % of the bulls change more than 2 NTM index units with the majority decreasing in NTM value. The proportion of genotyped Holstein bulls changing more than 2 NTM index units is also around 60 % but the proportions of bulls with decreased and increased NTM values, respectively, are equally distributed.

For RDC, the proportion of bulls changing more than 2 NTM index unit is around 60 % for both progeny tested and genotyped bulls. However, the proportion of genotyped bulls with decreased NTM values is much larger than the proportion of bulls with increased NTM values. For the progeny tested bulls, the proportion of bulls with increased or decreased NTM values is almost the same.

For Jersey, the distribution of bulls changing more than 2 NTM index units is around 50 % for both progeny tested and genotyped bulls. In both cases most of the bulls decrease in NTM values the highest proportion for the genotyped bulls.

Table 13. Distribution of differences between new NTM (based on data from November 2018 evaluation) and previous NTM (based on data from October 2018 evaluation). Based on 792, 303, and 100 progeny tested Nordic Holstein, RDC and Jersey bulls, respectively, born 2009-2010

	Distribution of changes, %		
Change in EBV index units	Holstein	RDC	Jersey
≤ -6	4.3	1.7	1.0
≥ -5 and < -1	37.2	29.7	30.0
≥ -1 and ≤ 1	40.2	42.2	55.0
> 1 and ≤ 5	17.0	24.1	14.0
≥ 6	1.3	2.3	-

Table 14. Distribution of differences between new NTM (based on data from November 2018 evaluation) and previous NTM (based on data from October 2018 evaluation). Based on 5,224, 4,369, and 859 genotyped Nordic Holstein, RDC, and Jersey bulls, respectively, born 2015-2016.

	Distribution of changes, %		
Change in EBV index units	Holstein	RDC	Jersey
≤ -6	2.2	4.8	0.9
≥ -5 and < -1	29.7	41.3	41.1
≥ -1 and ≤ 1	43.9	41.1	48.2
> 1 and ≤ 5	22.7	12.5	9.8
≥ 6	1.6	0.3	-

Economic value of NTM

Following the update of NTM, the economic value of 1 NTM index unit changes slightly for all breeds (Table 14). For Holstein, the economic value per NTM index unit decreases slightly whilst it increases slightly for RDC and JER.

Table 14. Economic value in Euros per NTM index unit per annual cow for HOL, RDC and JER

	Holstein	RDC	Jersey
New NTM	9.89	9.20	7.96
Previous NTM	10.15	9.05	7.80

For a sire, the economic value per NTM unit is half the values in Table 14 because only half his genes are transferred to the offspring. The economic potential for a heifer at 1st calving can also be calculated. Based on the assumptions used for the updated NTM, the average number of lactations per cow has increased to 2.8 for an average cow. Male growth is assumed not to be expressed in females, i.e. the economic value of the growth index is zero in females. Also, young stock survival has already been expressed in a heifer at 1st calving, thus, the value of the young stock survival index is also zero for a heifer at 1st calving. Thus, the average economic value of 1 NTM index unit for a heifer at 1st calving is:

- HOL: €25.54
- RDC: €23.12
- JER: €21.35

Genetic base
EBVs for bulls and females are expressed on the same cow base. This genetic evaluation included cows born from 06.11.2013 to 06.11.2015 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.

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 15 the NAV and INTERBULL release dates for 2018 are shown.

Table 15. NAV and INTERBULL release dates in 2018/2019. EBVs released at NAV dates in bold will be delivered to international genetic evaluation.

Month	NAV Small run[1]	NAV Large runs[2]	INTERBULL
November 2018		6	
December 2018	4		4
January 2019	3		
February 2019		5	
March 2019	5		
April 2019	2		2
May 2019		7	
June 2019	4		
July 2019	2		
August 2019		13	13
September 2019	3		
October 2019	1		
November 2019		5	
December 2019	3		3

[1] Genotypes updated; [2] Genotypes and phenotypes updated

You can get more information about the joint Nordic evaluation:
General about Nordic Cattle Genetic Evaluation: www.nordicebv.info
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Denmark: https://www.landbrugsinfo.dk
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