

News - NAV routine evaluation November 1st 2016

Description of improvements

NAV introduce several improvements in the November 1st genetic evaluation. In this note a detailed description is given of the different changes, and the effect on breeding values.

News in relation to NAV genetic evaluation

Traditional evaluation

- Improved evaluation for fertility evaluation
- Improved evaluation for calving trait evaluation
- Improved evaluation for yield trait evaluation
- Udder coordinates included in the genetic evaluation for udder traits

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Genomic prediction

- Improved standardization of GEBVs taking care of over evaluated GEBVs, and introduction of a polygenic effect in the genomic prediction model smoothing transition from GEBV to EBV

Fertility model handling sexed semen and including conception rate (CR)

The main change for fertility is correction for sexed semen in the model. This will have an insignificant effect on EBV's for bulls because sexed semen is rarely used more in daughter groups after one bull compared to another bull. The change will have a larger effect on EBV's for the individual cows. It is important to account for this because cows need to have most accurate EBVs and it is even more important in the future when cows will be a part of the reference group used to calculate genomic EBV's. Other changes are minor. A complete list of changes in the November 2016 evaluation is shown in table 2.

Table 2. Major differences between November 2016 evaluation and old fertility evaluation

Old evaluation	November 2016 evaluation	Comments	Effect
NRR	Conception rate (CR)	EBV for conception rate is published instead of EBVs for NRR. Conception rate is defined as non-return rates for all inseminations and not only NRR for 1. ins	Some change in EBV – but no effect in fertility index
No correction for sexed semen	Correction for sexed semen	The model now corrects for the use of sexed semen for the following fertility traits: Interval from first to last insemination, Number of insemination, and Conception rate.	Has small effect on bulls, but a bigger effect for cows inseminated with sexed semen
Danish Jersey data only	Swedish and Finnish Jersey data included	Fertility data from all three countries are included in the Jersey evaluation	Effect on Swedish and Finnish Jersey cows
	Improved data quality	The data quality has been improved by including Finnish pregnancy test, and updated editing on Swedish heifer data	Some effect on genetic trend for Swedish heifer traits and Finnish females
Heterosis correction in RDC and Jersey evaluation	Heterosis correction also included in Holstein evaluation	Heterosis correction takes place for all three breeds	Minor effect

Implementing the changes listed in table 2 in the fertility evaluation; create some minor changes in the EBVs for fertility. The correlations between old fertility index and November 2016 fertility index are over 0.98 for proven bulls, and over 0.97 for cows. 97% of the Holstein bulls change less than 4 index units (table 3). For RDC and Jersey 90 % and 89 % of the bulls change less than 4 index units. The observed changes are slightly larger in RDC and Jersey compared to Holstein because of a more intensive use of sexed semen in Jersey, and relative more RDC bulls having offspring in Finland (effect of improved data quality). The same pattern are observed on cow EBVs (table 4)

Table 3 Frequency (%) of changes in EBVs for fertility index between November 2016 evaluation and the old evaluation for bulls born 2008-2011

Change in fertility index (units)	Holstein	RDC	Jersey
Less than 2	74	58	52
2-3	23	32	37
More than 3	3	10	11

Table 4. Frequency (%) of changes in EBVs for fertility index between November 2016 evaluation and the old evaluation for cows born after year 2012

Change in fertility index (units)	Holstein			RDC			Jersey
	Denmark	Sweden	Finland	Denmark	Sweden	Finland	Denmark
Less than 2	96.6	87.3	74.1	95.0	91.5	80.2	76.2
2-3	3.3	12.0	11.0	4.8	8.2	8.8	23.1
More than 3	0.1	0.7	4.9	0.2	0.3	1.6	0.7

As a consequence of harmonization across countries involved in Eurogenomics, conception rate is introduced as a new trait and is published instead of NRR. Conception rate handles non return rates from all inseminations whereas previous NRR only included data from 1st insemination. The correlation between EBVs for NRR and CR is around 0.85. The breeding goal for fertility expressed in the fertility index is however unchanged – CR is not included in the breeding goal, as neither was the case for NRR.

Udder coordinates increase reliability for udder conformation

Data from AMS are easy to collect as the recording is done automatically. They describe important udder conformation traits on a daily basis. Adding AMS data have only a limited effect on bull EBVs because their reliabilities for conformation traits are already high. However they will give considerably more information to cows. This is important in mating plans, and because cows are an important part of the reference group used to calculate genomic EBVs.

Genetic evaluations for udder conformation traits in NAV countries have been based on a subjective linear classification system. Now, with a large number of dairy cows being milked using AMS udder coordinates are registered automatically repeatedly. By using udder coordinates, it is possible to calculate measures that resemble the present linear udder conformation traits registered by classifiers. Only data from Danish AMS are available. Measures from AMS are included as correlated traits to four linear traits; front and rear teat distance, udder depth and udder balance. Within lactation 1 to 3 AMS measures are calculated as average distance using data from day 30 to 60 after calving.

Udder coordinates has been stored in the Danish data base since 2008. The dataset includes about 53.000 Holstein cows, 3.400 RDC cows and 3.700 Jersey cows.

Teat and udder traits calculated from AMS data showed significantly higher heritability's than the linear scored udder traits (table 5). The genetic correlations between udder coordinate measures,

and linear scored traits are close to unity (above 0.90) indicating that they genetically are the same traits. Genetic parameters for udder coordinate traits based on Holstein data are used for all three breeds.

Table 5. Genetic parameters for udder conformation traits based on either linear classification done by classifiers or AMS

Trait	Heritability			Heritability AMS coordinates, 1. lact	Genetic correlation, 1. Lact,
	Linear score, 1. lact				
	HOL	RDC	Jersey	HOL,RDC, JER	HOL,RDC, JER
Front Teat Placement	0.32	0.27	0.27	0.61	0.91
Rear Teat Placement	0.28	0.26	0.26	0.48	0.93
Udder Balance	0.16	0.16	0.16	0.48	0.90
Udder Depth	0.39	0.34	0.34	0.67	0.97

The effect of including AMS data is limited for bulls. The correlation between EBVs from new and old model is over 0.99. Only a few proven bulls, which all have many daughters with AMS data, change more than 2 index units.

Changes in udder index for cows due to inclusion of AMS data are considerably larger. This is because AMS information often adds a significant amount of new information from up to 3 lactations for the individual cows. The effect depends on how much information the cow had in advance. When cows get AMS information from 3 lactations, and they previously only had pedigree information it might change EBV for udder a lot. However, also cows that already have a linear classification will get more information, and EBV's might change considerably.

In addition to the changes mentioned above, we have also corrected an error in the Holstein evaluation. For Holstein the previously used heritability for udder balance was, by mistake, set to a too low value (0.04). The correct heritability for udder balance is 0.16. This correction creates somewhat larger changes in EBVs for udder balance for Holstein animals than between normal routine runs

Animal model for calving and birth traits – fundament for females in reference

The main improvement for calving and birth traits is the change from a sire model to an animal model (table 6). This has some impact on EBV's for bulls. However it has a larger effect on EBV's for individual cows. Change of model means that cows can be an important part of the reference group used to calculate genomic EBV's for calving traits. NAV expects to test this possibility during the winter 2016/17. A change in coding of Swedish calving ease data has an effect on EBVs for bulls having the majority of the progeny in Sweden. Inclusion of data from Swedish and Finnish Jersey are minor changes.

The old Swedish calving ease data is coded 1-2. In 2012 Sweden started stepwise implementation of a 1-4 coding of calving ease as used in Denmark and Finland. Previously the Swedish data recorded on the 1-4 scale have been pooled in 2 classes before being used to estimate breeding values to fit the old Swedish 1-2 scale. Starting from November 1st the use of Swedish data are changed so records from the new 1-4 coding scheme is used in estimation of breeding values.

Table 6. Major differences between November 2016 evaluation and old calving and birth traits evaluation

Old evaluation	November 2016 evaluation	Comments	Effect
Sire model	Animal model	Cows get breeding values including own information. Cows can be used in reference population for genomic prediction.	Some effect on EBVs for bulls, and larger effect on cow EBVs
Swedish calving ease from 1-4 scale recoded to 1-2 scale	Swedish calving ease recorded on 1-4 scale not recoded		Effect on bulls with offspring in Sweden
Danish Jersey data	Danish, Swedish and Finnish Jersey	Calving data from all three countries are included in the Jersey evaluation	Swedish and Finnish cows get more precise EBVs

In total the introduced changes create some changes in EBVs for calving and birth traits for both bulls and cows. Overall correlations for progeny tested bulls born after 2009 are between 0.94 and 0.97. By looking at correlations per birth country of the bull it becomes clear that the changes in EBV are larger for Swedish bulls – bulls having majority of their offspring in Sweden (table 7). Correlations for Swedish born bulls vary from 0.89-0.92 indicating significant larger changes in EBVs for Swedish born bull compared to Danish and Finnish bulls. This is caused by the change of recording scheme in Sweden from 2 to 4 classes for calving ease introduced in 2012.

Table 7. Correlations between EBVs from the new evaluation and the old evaluation for calving and birth index, progeny tested bulls born after 2009

Birth country of the bull	Across countries		DNK		FIN		SWE	
	Birth	Calving	Birth	Calving	Birth	Calving	Birth	Calving
Holstein	0.95	0.96	0.97	0.97	0.96	0.96	0.89	0.92
RDC	0.96	0.94	0.98	0.94	0.98	0.96	0.92	0.87
Jersey	0.97	0.97						

99% of the Holstein bulls change less than 4 index units for birth index. For RDC and Jersey 98 % and 89 % of the bulls change less than 4 index units for birth index. For calving traits 97% of the Holstein bulls change less than 5 index units, and 91% and 92% for RDC and Jersey respectively.

Table 8. Frequency (%) of changes in EBVs Between the new evaluation and the old evaluation for bulls born after year 2000

Change in EBV index units	Holstein		RDC		Jersey	
	Birth	Calving	Birth	Calving	Birth	Calving
Less than 3	79	70	81	59	64	60
3-5	20	27	17	32	29	32
More than 5	1	3	2	9	7	8

With the change to an Animal Model cows also get calving indices based also on their own records and not only on information from their parents (pedigree index). This explains why the correlation between the old calving indices (pedigree index) and new calving indices for cows is in the range 0.80-0.85. This means that a lot more re-ranking occurs for cows than for bulls, which is indicating that the cows are getting much more reliable EBVs. Table 9 show changes from old to new evaluation for cows e.g. that 11% of the RDC cows changes 6-10 index units in calving traits ,and 3% change more than 10 index units.

Table 9. Frequency (%) of changes in EBVs Between the new evaluation and the old evaluation for cows born after year 2000

Change in EBV index units	Holstein		RDC		Jersey	
	Birth	Calving	Birth	Calving	Birth	Calving
Less than 6	77	90	79	86	91	91
6-10	19	9	18	11	7	7
More than 10	4	1	3	3	2	2

Yield – improved handling of data

Fat and protein yield based on milk samples from AMS has larger standard deviation than fat and protein yield based on samples from conventional milking system (CMS). This is mainly due to the fact that distance between milking varies more in AMS than in CMS. It is difficult to correct for milking distance in AMS.

Starting November 1st NAV corrects for differences in standard deviation between AMS and CMS. However the effect on EBVs is very limited for bulls. Besides this change NAV has also improved the method to detect outlier (extreme) data – data which are so extremely high or low that they hardly can be true, and can be seen as registration errors. The effect is very limited for bulls, but it is somewhat higher for single cows. Some cows can have a registration which earlier was included, but with the new improved method is defined as an outlier (=error) and deleted from the evaluation.

Correlations between old and new EBVs, both for bulls and cows, are above 0.995, indicating very little reranking of animals. No RDC or Jersey bulls change more than 3 Y-index units, and only 7 Holstein bulls change more than 3 index units. 98% of the cows change less than 2 Y-index units, and very few cows change more than 5 index units. Cows with large changes in Y-index have earlier had a very deviating single observation included in the estimation of breeding values.

Upgrade genomic prediction - polygenic effect included and revised standardization to handle over evaluation of GEBVs

NAV introduces improvements in the genomic prediction November 1st. An overview of the improvements having an effect on the genomic prediction is shown in table 10.

Table 10. Major differences between November 2016 evaluation and old genomic prediction model

Old model	November 2016 model	Comments	Effect
Old traditional models for fertility, yield, calving and udder conformation	Improved traditional models for fertility, yield, calving and udder conformation		Model changes in the traditional evaluation create changes of the same size in GEBVs as observed in EBVs
	GEBV standardisation improved to handle that overrating is “accumulated” in youngest candidates because genetic trend was over evaluated	Genomic tested young bull and genomic tested heifers get lower GEBVs according to the observed over evaluation	Minor effect on ranking of genomic tested young bulls or genomic tested heifers within birth year, but genetic level is lower for young genotyped animals
Genotype (SNPs) expected to explain all the genetic variation	Polygenetic effect of 10% - genotype (SNPs) expected to explain 90% of the genetic variation	A bit less weight is given to genomic information – more weight on pedigree + own information/daughter information	Have a minor effect on GEBVs for genotyped cows and bulls with no or small progeny groups

Polygenic effect

It was observed that the difference between EBVs based on daughter information only and GEBVs based on daughter information and genomic information for bulls having large daughter groups (over 90% reliability) were larger than theoretically expected. This is illustrated by the blue bars in figure 1. The figure shows that a few Holstein bulls have a difference between GEBV and EBV larger than 8 index units. This is because the weight on genomic information in the genomic prediction model was too high. The effect was that bulls with positive genomic information for a particular trait in some cases had GEBV's that were too high even, when they had a considerable number of daughters included, and that conversely some bulls with a negative genomic information for a particular trait in some cases had GEBV's that were too low when daughters were included. To handle this, a polygenic effect is included. In practice, this reduces the weight on genomic information a bit and put more weight on daughter information. As a consequence the transition from having only genomic information over genomic + daughter information to almost entirely daughter information is smoother – the magnitude of change is nearly the same.

Previously the genomic prediction model allowed genomic information to explain up to 100% of the genetic variation. A polygenic effect of 10% is now included in the prediction model, which ensure that the genomic information only can explain up to 90% of the total genetic variation. But daughter information can explain the entire genetic variation, when a bull has an infinite number of daughters. A polygenic effect is used in the majority of countries around the world.

The effect of including a polygenetic effect for protein for Holstein is shown by the red bars in figure 1 showing a narrower distribution than the blue bars, which is in agreement with theoretical expectations. The same pattern as illustrated for Holstein protein yield is observed for all traits, and

also for RDC and Jersey. A polygenic effect of 10% had been included for all traits and all three breeds.

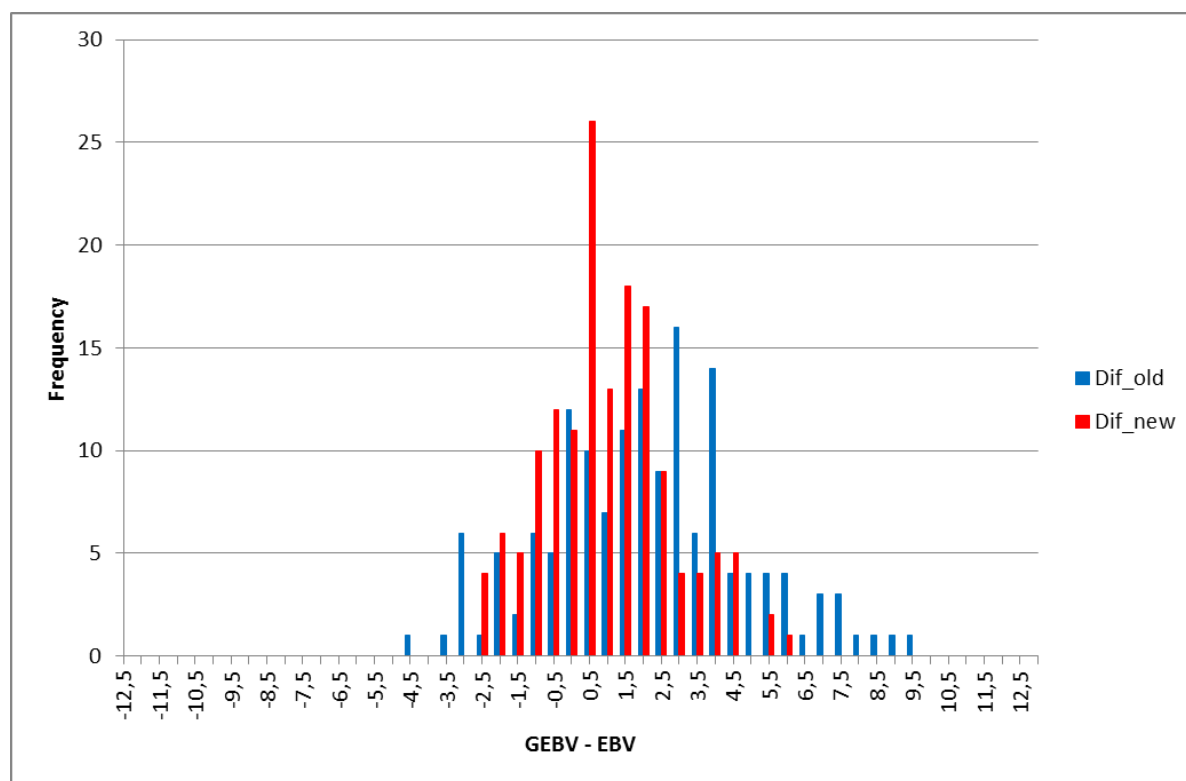


Figure 1. Effect of a model including (Dif_new) or excluding (Dif_old) a polygenic effect of 10% on the difference between EBV and GEBV for protein for Holstein bulls having a reliability of EBV >90% (the study is done before correction of standardisation is considered), 152 bulls born after 2010.

Improved standardisation of GEBV

It has been found that the genetic trend has been over evaluated for genomic tested young animals for several traits in all three breeds. The over evaluation can be removed by improving the method used for correcting variance of GEBV. We have previously only standardized variation within year. Now we also standardize genetic trend across years using the two last birth year classes of bulls with lactating daughters as base value for genetic trend from year to year. In practice it means that the genetic trend is reduced with the same reduction factor as the within year standard deviation, and that the genetic level of young genotyped bulls and females are reduced. The effect is largest for the youngest animals.

NTM for animals with genomic information is affected by sum of changes

All the changes in both traditional and genomic evaluations have an effect on NTM for all genomic tested animals. Improvements of traditional evaluation create some reranking of all genomic tested animals; polygenic effect gives a more smooth change in GEBVs during the lifetime and is especially interesting for live genotyped cows, and newly proven bulls. Changed standardization will especially affect genomic tested young AI bulls and genomic tested heifers.

The results of all three changes (listed in table 10) affect the breeding values for animals with genomic information. In table 11-13 the effect on NTM and the single traits included in NTM is shown for AI bulls born in 2015 for Holstein, RDC and Jersey.

The effects on yield traits are between 2.6-3.0 index units for the 3 breeds. For longevity the overrating has been 6.6 index units in Holstein, and 3 index units in RDC. In general the overrating is 0-2 index units for sub-indices in NTM. But since animals having high NTM have positive breeding values for most traits the effect of the overestimation of NTM is relative larger than for single traits: 4.7 for Holstein, 4.3 for RDC, and 2.5 for Jersey – bulls born in 2015.

Table 11. New GEBV, Old GEBV and Difference ($GEBV_{new} - GEBV_{old}$) for 99 Holstein AI bulls born in 2015

Trait	New GEBV	Old GEBV	Difference
Yield	115.1	118.1	-3.0
Milk	108.3	109.9	-1.7
Fat	114.8	116.8	-2.0
Protein	113.8	116.8	-3.1
Growth	99.6	99.6	-0.1
Fertility	108.9	110.6	-1.7
Birth	105.5	106.8	-1.3
Calving	109.2	110.2	-1.1
Udder health	109.4	111.2	-1.8
Other Disease	106.9	107.5	-0.7
Frame	105.7	105.4	0.3
Feet& Legs	108.5	109.1	-0.6
Udder	117.3	117.2	0.1
Milkability	106.7	107.1	-0.5
Temperament	105.2	105.2	0.1
Longevity	114.2	120.8	-6.6
Claw health	107.4	108.3	-0.9
Youngstock survival	101.4	102.8	-1.3
NTM	28.7	33.4	-4.7

Table 12. New GEBV, Old GEBV and Difference ($GEBV_{new} - GEBV_{old}$) for 98 RDC AI bulls born in 2015

Trait	New GEBV	Old GEBV	Difference
Yield	112.4	115.3	-2.9
Milk	106.9	109.0	-2.0
Fat	110.8	112.9	-2.1
Protein	111.9	115.0	-3.1
Growth	99.5	99.6	-0.1
Fertility	104.1	104.7	-0.6
Birth	102.6	103.3	-0.7
Calving	103.5	104.8	-1.3
Udder health	107.8	109.1	-1.3
Other Disease	105.4	106.0	-0.6
Frame	103.9	103.9	0.0
Feet& Legs	106.9	108.8	-1.9
Udder	110.3	11.3	-1.0
Milkability	106.9	106.9	0.0
Temperament	102.5	103.3	-0.8
Longevity	111.9	114.4	-3.0
Claw health	102.6	103.0	-0.3
Youngstock survival	99.7	99.6	0.1
NTM	22.1	26.4	-4.3

Table 13. New GEBV, Old GEBV and Difference ($GEBV_{new} - GEBV_{old}$) for 49 Jersey AI bulls born in 2015

Trait	New GEBV	Old GEBV	Difference
Yield	111.5	114.1	-2.6
Milk	104.6	105.7	-1.1
Fat	109.5	111.9	-2.4
Protein	110.6	112.3	-1.7
Growth	99.1	99.5	-0.3
Fertility	102.6	102.6	0.1
Birth	100.4	100.0	0.4
Calving	103.3	104.3	-1.0
Udder health	107.2	107.6	-0.4
Other Disease	100.3	100.1	0.2
Frame	106.7	107.6	-0.9
Feet& Legs	104.3	104.3	-0.1
Udder	109.2	108.6	0.5
Milkability	101.7	103.0	-1.3
Temperament	100.1	100.6	-0.5
Longevity	108.1	108.9	-0.8
Claw health	-	-	-
Youngstock survival	-	-	-
NTM	17.3	19.8	-2.5

For genomic tested young bulls born in year 2012-2014 the decrease will be smaller than for bulls born in 2015 since the effect of the changed standardization is less. This is illustrated in figure 2 (NTM for RDC). Note that the genetic level is unchanged for proven bulls (up to birth year 2012). Decrease in NTM will be similar for genomic tested heifers.

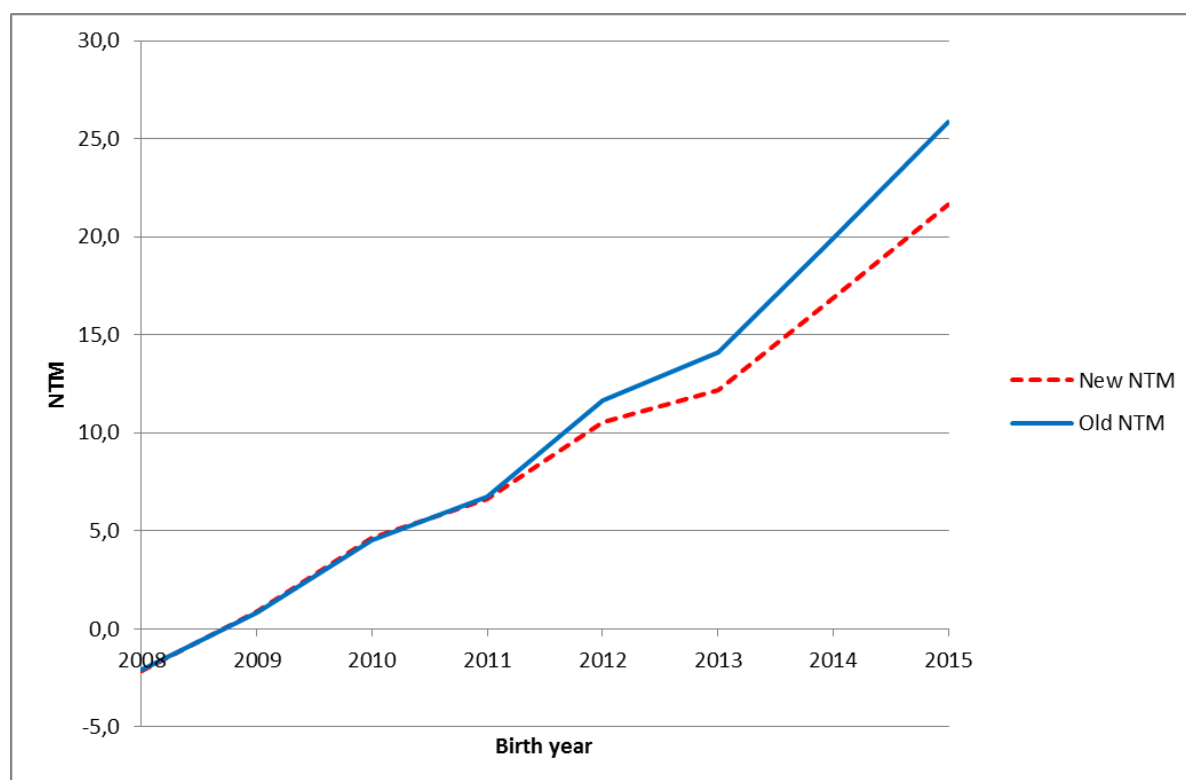


Figure 2 Illustration of the effect of improved standardisation on the genetic trend. RDC NTM. Note the effect is largest in the youngest birth year classes.

NTM for an animal will change due to standardization, but besides that bulls and females can rerank mainly due to changes in the traditional evaluation for calving, fertility, udder conformation, and yield. In table 14 correlations between new and old NTM for genomic tested AI bulls and females are

shown. The correlations for bulls are a bit lower than for heifers for all 3 breeds which also are expected since the AI bulls are stronger selected.

Table 14 Correlations between NTM from new and old evaluation for AI bulls born in 2013-2015 and cows and heifers born after 2010

	Bulls	Heifers	Cows
Holstein	0.95	0.98	0.98
RDC	0.95	0.98	0.98
Jersey	0.96	0.98	0.99

Table 15-17 show the distribution of changes in NTM for genomic tested young bulls (table 15), genomic tested heifers (table 16), and genomic tested cows (table 17).

Table 15. Frequency (%) of changes in NTM between the new evaluation and the old evaluation for genomic tested I bulls born in year 2015

Change in NTM	Holstein	RDC	Jersey
-10	0.0	0.0	0.0
-9	0.0	0.0	0.0
-8	2.2	0.0	0.0
-7	3.2	4.1	0.0
-6	18.3	10.2	2.0
-5	33.3	33.7	0.0
-4	26.9	22.4	12.2
-3	8.6	20.4	34.7
-2	7.5	8.2	30.6
-1	0.0	1.0	20.4
0	0.0	0.0	0.0
Average change	-4.7	-4.3	-2.5

Table 16. Frequency (%) of changes in NTM between the new evaluation and the old evaluation for genomic tested heifers born in year 2015

Change in NTM	Holstein	RDC	Jersey
-10	0.0	0.0	0.0
-9	0.1	0.0	0.0
-8	0.9	0.1	0.0
-7	5.5	0.8	0.0
-6	15.3	3.9	0.2
-5	26.8	13.8	1.4
-4	27.6	27.5	10.0
-3	16.5	29.9	29.5
-2	5.9	17.8	34.9
-1	1.3	5.1	19.6
0	0.2	1.0	4.2
1	0.0	0.1	0.3
Numbers	10,956	10,218	4,077

Table 17. Frequency (%) of changes in NTM between the new evaluation and the old evaluation for genomic tested cows born after 2010

Change in NTM	Holstein	RDC	Jersey
-10	0.0	0.0	0.0
-9	0.0	0.0	0.0
-8	0.0	0.0	0.0
-7	0.2	0.0	0.0
-6	1.2	0.1	0.0
-5	4.7	0.6	0.0
-4	12.8	2.9	0.1
-3	22.7	9.8	1.6
-2	26.1	21.2	8.2
-1	20.0	26.9	23.1
0	9.4	22.2	33.2
1	3.3	11.5	24.2
2	0.7	3.8	8.2
3	0.1	0.8	1.3
4	0.0	0.1	0.1
5	0.0	0.0	0.0
Numbers	16.364	20.220	12.704

You can get more information about the joint Nordic evaluation:

General about Nordic Cattle Genetic Evaluation: www.nordicebv.info

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