

News - NAV routine evaluation August 12th 2014

The latest NAV routine evaluation for yield, fertility, type, udder health, other diseases, calving traits, milk ability, temperament, growth, longevity, claw health and NTM took place as scheduled. NAV carried out three evaluations per trait group:

Holstein evaluation, including data from: Danish Holstein, Danish Red 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 and Swedish Jersey (only yield and type).

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	25.06.2014	15.06.2014	13.06.2014
Type, milk ability and temperament	01.07.2014	15.06.2014	23.06.2014
Fertility	01.07.2014	15.06.2014	14.06.2014
Udder health and other disease	01.07.2014	15.06.2014	14.06.2014
Calving	01.07.2014	15.06.2014	14.06.2014
Longevity	01.07.2014	15.06.2014	14.06.2014
Growth	25.06.2014	15.06.2014	14.06.2014
Claw health	01.07.2014	15.06.2014	16.06.2014

Data used in genomic prediction

Genotypes were extracted from the joint Nordic SNP data base July 9th 2014. Interbull information from April 2014 and national information according to extraction dates in table 1 were included in genomic prediction.

News in relation to NAV genetic evaluation

- Changes in genomic prediction for RDC and Jersey
 - Females are included in the reference population
 - Animal Model pedigree used in genomic prediction
 - Revised blending procedure introduced

- More electronic recorded milking speed data added to the genetic evaluation for all breeds
- Body is renamed and is called Frame for all breeds
- Weight and optimum for Frame changed for Holstein and Red Holstein

Genomic prediction

Significant improvement is introduced in the genomic prediction for RDC and Jersey July 2nd – the changes have an impact of female GEBVs published July 2nd and male GEBV published August 12th:

- Females are included in the reference population
- Animal Model pedigree used in genomic prediction
- Revised blending procedure introduced

Inclusion of females gives a considerably higher reliability on genomic breeding values. This means that we more accurately can find the best males for AI, and the best females for ET or to inseminate with sexed semen.

The limited size of the reference group has been the major problem for RDC and especially Jersey since the beginning of calculation of breeding values with genomic information. Holstein has a much larger reference group, because the breed is considerably larger than RDC and Jersey, and because proven bulls from the EuroGenomics cooperation are also included. The possibilities to cooperate with other populations are limited for RDC and Jersey and the only other possibility to increase the reference population is to include females. At the moment Jersey is exchanging genotypes with US Jersey and RDC is exchanging with NRF.

VikingGenetics started in 2012 a cooperation with RDC and Jersey farmers in Denmark, Sweden and Finland genotyping all females of a certain age in the herds. This has increased the number of tested females considerably. Simultaneously with the testing of more females NAV has in close cooperation with MTT and AU developed and tested the genetic models and methods necessary to be able to include genotypes from females in the reference group. Table 2 gives an overview over the changes in the prediction, and table 3 an overview over the used reference populations for the three breeds in the August 12th evaluation.

Table 2. Overview over changes in the genomic prediction for RDC and Jersey introduced July 2nd for genotyped females and August 12th for genotyped young bulls 2014

	Old model	New model 2 nd July	Comments
Pedigree in genomic prediction	Sire-Maternal grandsire	Animal Model	
Reference population	Bulls	Bulls + cows	6800 Jersey cows and 10000 RDC Cows included
Blending method	Method developed by MTT in 2010	Revised blending method developed by MTT in 2013/14	Revised method better avoid double counting, which make it possible to include females in ref population

Table 3. Reference population for the different breeds used in routine evaluation August 12th 2014

	Reference population	
	Bulls	Cows
Holstein	25700 ^{a)}	-
RDC	7800 ^{b)}	10000
Jersey	2400 ^{c)}	6800

a) Including NLD, FRA, DEU, ESP ref bulls; b) including NO ref bulls; c) including US ref bulls

About 10,000 RDC cows are included in the RDC reference population July 2nd and about 6,800 cows in the Jersey reference population. Preliminary studies indicate that adding a bull dam to the reference population has not a significant effect on the offspring's GEBVs. In the coming months we will study in more details the effect of using different groups of females in reference population.

Genotyped females are used in the reference population for the following traits: yield, udder health, conformation, temperament (only RDC) and milking speed. These are the traits where the breeding values of cows today are affected by own performance.

The genomic prediction for RDC and Jersey has been significantly improved, by adding genotyped females and modifying the blending method. The increase in reliabilities for RDC is on average about 5% and for Jersey about 8 % (table 4 and 5).

Table 4. Extra reliabilities next to pedigree information for RDC using bulls or bulls+cows in the reference population – female information is included for traits market with **bold**

	Reference population	
	Bulls	Bulls + cows
Milk	0.17	0.23
Fat	0.16	0.23
Protein	0.12	0.18
Yield	0.13	0.18
Fertility	0.14	0.14
Birth index	0.18	0.18
Calving index	0.02	0.02
Mastitis	0.17	0.23
Other diseases	0.14	0.14
Frame	0.24	0.29
Feet & Legs	0.24	0.33
Mammary	0.23	0.30
Milkability	0.17	0.22
Temperament	0.18	0.21
Longevity	0.07	0.07

Table 5. Extra reliabilities next to pedigree information for Jersey using bulls or bulls+cows in the reference population - female information is included for traits market with **bold**

	Reference population	
	Bulls	Bulls + cows
Milk	0.23	0.37
Fat	0.13	0.21
Protein	0.18	0.32
Yield	0.16	0.22
Fertility	0.17	0.17
Birth index	0.00	0.00
Calving index	-0.02	-0.02
Mastitis	0.09	0.16
Other diseases	-0.11	-0.11
Frame	0.19	0.30
Feet & Legs	0.05	0.13
Mammary	0.26	0.29
Milkability	0.15	0.34
Temperament	0.00	0.00
Longevity	0.11	0.11

Compared with Holstein the GEBV reliabilities for RDC and Jersey are still about 12-15% units lower, but significantly higher than before. In the near future more genotyped RDC and Jersey females will be lactating and be included in the reference population, and the GEBV reliabilities are expected to increase further.

The improvements in the genomic prediction also have the effect that the underestimation of genetic level that has previously been observed in RDC and Jersey is removed. For RDC the genotyped young bulls and heifers increase on average 4 index point for yield index and NTM, and between 0-2 index point for the other traits where cow information contribute to the reference population. For Jersey the corresponding results show an increase of 2 index point for Y-index and NTM, and 0-1 index point for the other traits where cow information contribute to the reference population.

The increase in reliabilities (table 4 and 5) - due to use of significant more information - makes it possible to more accurately identify the genetically best animals. However it also means that some re-ranking occurs among the already tested bulls and females. Results show, that the correlations between GEBVs in May and August are in the range 0.80-0.90 for traits where cows have been added to the reference population (yield, udder health, conformation, temperament and milking speed). Jersey gain relatively more in reliabilities by adding female to the reference population, since the Jersey bull reference population is quite small, creating the largest re-ranking of animals.

Table 6. Correlations between GEBVs calculated May and August 2014

	RDC		Jersey	
	Genotyped young bulls and heifers	Genotyped cows	Genotyped young bulls and heifers	Genotyped cows
Traits without genotyped cows in reference population	0.97-0.99	0.97-0.99	0.94-0.96	0.94-0.96
Traits with genotyped cows in reference population	0.88-0.93	0.89-0.92	0.77-0.85	0.87-0.90

For yield this means that for about 20% of the heifers, young bulls and cows the breeding value changes 5 or more index units.

Additional to this effect of reliability we should add the effect of improved mean when looking at changes in GEBV from May to August for genotyped heifers and young bulls. The mean effect is as mentioned earlier largest for yield and NTM about 4 units for RDC and 2 units for Jersey.

We do see considerable changes in GEBV for RDC and Jersey, but in fact it is a positive story because adding cows to the reference population has increased the reliability of the GEBV for RDC and Jersey significantly, and justified the investment in genotyping females in large scale.

Use of females in reference population for more traits in RDC and Jersey, and inclusion of females in the reference group for Holstein will be investigated in the future.

Traditional evaluation

Milkability

Routine genetic evaluation for milkability has until August 12th been based on scoring data from the questionnaire system and milk flow data from Danish trutest meters. An increasing number of farms have permanent installed milking meters and flow data from the equipment is transferred to the national databases.

Data from permanent installed milking meters is included in the routine milkability evaluation August 12th. The milk flow data from the permanent installed milking meters replace - like data from TruTest meters - the scoring record when both observations are available for the cow. Table 7 show the number of extra flow data from permanent installed milking meters added to the milkability evaluation from each country

Table 7. Extra flow data from permanent installed milking meters added to milkability evaluation

	Holstein	RDC	Jersey
Denmark	40,000	2,700	2,900
Sweden	17,000	13,000	200
Finland	600	1,100	-

The correlation between the May and August routine evaluations for milkability for bulls is very high over 99% for all breeds, reflecting that the EBVs for only 15% of all bulls change more than 1 index units. For cows the correlation are also very high for cows having the same phenotypic information

included in both runs, whereas as expected significant changes in EBVs can be observed for cows getting milk flow records included from permanent installed milking meters. The correlation for this group of cows is about 75%.

Frame

The name Body index will not be used anymore. The name Frame will be used as the English name for the combined EBV for body traits interpreting the size of the cow for all breeds. In the national languages Frame will be called *Kokoindexi* in Finland, *Kroppstorlek* in Sweden, and *Kropskapacitet* in Denmark

For RDC and Jersey the weight in frame is the same as in the old body index, but for Holstein and Red Holstein new weights and a technical optimum is used in the calculations of frame (table 8 and 9).

Table 8. Optimum and weight used for calculation of Frame in Holstein

	Old		Current frame		
	Breeding goal Optimum	Weight	Breeding goal Optimum	Technical Optimum	Weight
Stature	148	3	148	155	5
Body depth	6	15	6	9	25
Chest width	5	15	5	9	30
Dairy form	6	20	6	9	20
Topline	7	12	7	7	0
Rump width	5,5	15	5,5	9	20
Rump angle	5	20	5	5	0

Table 9. Optimum and weight used for calculation of Frame in Red Holstein

	Old		Current frame		
	Breeding goal Optimum	Weight	Breeding goal Optimum	Technical Optimum	Weight
Stature	146	10	146	155	5
Body depth	6,5	20	6,5	9	25
Chest width	6	16	6	9	30
Dairy form	5,5	15	5,5	9	20
Topline	7	10	7	7	0
Rump width	6	11	6	9	20
Rump angle	5,2	8	5,2	5	0

The new definition of frame for Holstein and Red Holstein gives a significant reranking of animals comparing with the old body index. The correlations between EBVs for the old body and the new frame EBVs is about 75%.

Genetic base

EBVs for bulls and females are expressed on the same cow base. This genetic evaluation included cows born from 12.08.2009 to 12.08.2011 in the genetic base (average 100)

Genomic EBVs (GEBVs)

GEBVs combine genomic and phenotypic information. GEBVs are estimated for all combined traits in NTM, single type traits, and NTM. Table 10 describes how different categories of genotyped animals are handled in the evaluation. All non genotyped animals get traditional EBVs.

Table 10. Publication of Genomic breeding values (GEBVs) for different categories of animals

Category of animals	Status	Published Breeding value
Genotyped males	Culled	None
	AI bulls with a Nordic herd book number and genotype	GEBV when at least 10 month old at publication date
	Foreign AI bulls with a Nordic herd book number and a genotype abroad only	IB-GEBV when at least 10 month old at publication date
	Bulls with a Nordic progeny test or a progeny test abroad	EBV
	Foreign AI bulls with a Nordic herd book number and a progeny test abroad	IB EBV for all international traits available. GEBV for traits with pedigree information only
Genotyped females	Heifers & cows	GEBV

- EBV=Estimated breeding value based on phenotypic data only
- IB EBV = Interbull breeding value based on phenotypic data only
- GEBV=Genomic Enhanced breeding value – based on phenotypic data and genomic information

For genotyped females and young bulls the GEBV is published as the official index instead of the EBV

GMACE

Interbull run the first official GMACE evaluation in August 12th 2014 and results are released. It means that Interbull GEBVs are available for genotyped bulls from 10 countries participating in the GMACE routine evaluation.

The figures can be found on the NAV search page for Interbull EBVs

<http://www2.mloy.fi/SKJOWeb/WWWjasu/NAVbullSearch.asp?strLang=DNK&strBreed=&strBirthCountry=&strBirthCountryID=&strName>

Publication of NTM for Nordic and foreign bulls

A NTM is published if the bull has official EBVs (NAV (G)EBV or international (G) 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. EBVs are used in the following priority NAV EBVs, IB EBVs, NAV GEBV, IB GEBV and Pedigree index. 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 $\frac{1}{2}(\text{EBVsire}-100) + \frac{1}{4}(\text{EBVmgs}-100) + 100$. If EBVsire or EBVmgs is not official NAV EBVs then 100 is used.

NAV – frequency and timing of routine runs

NAV has 4 evaluations per year including all phenotypic data. In Table 11 the future NAV and INTERBULL release dates are shown. NAV does eight extra genomic predictions to get GEBVs based on the newest information for all genotyped bull calves and females. The extra runs in 2014 takes place 2.1, 3.3, 2.4, 2.6, 2.7, 2.9, 2.10, and 2.12. After the extra runs GEBVs for females are published on national data bases

NAV search page

NAV has early July introduced a new search page showing (G)EBVs for herd book registered AI bulls from all three countries – see <http://www3.mloy.fi/NAV/>

Table 11. NAV and INTERBULL release dates in 2014. EBVs released at NAV dates in bold will be delivered to international genetic evaluation.

Month	2014	
	NAV	INTERBULL
January 2014		
February 2014	2	
March 2014		
April 2014		1
May 2014	2	
June 2014		
July 2014		
August 2014	12	12
September 2014		
October 2014		
November 2014	3	
December 2014		2

You can get more information about the joint Nordic evaluation:

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