News - NAV routine evaluation
2 November 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	29.09.2014	21.09.2014	26.09.2014
Type, milkability and temperament	30.09.2014	21.09.2014	22.09.2014
Fertility	29.09.2014	21.09.2014	27.09.2014
Udder health and other disease	29.09.2014	21.09.2014	27.09.2014
Calving	29.09.2014	21.09.2014	27.09.2014
Longevity	29.09.2014	21.09.2014	27.09.2014
Growth	30.09.2014	21.09.2014	23.09.2014
Claw health	30.09.2014	21.09.2014	26.09.2014

Data used in genomic prediction

Genotypes were extracted from the joint Nordic SNP data base 16 October 2014. INTERBULL information from August 2014 and national information from present run were included in genomic prediction.

News in relation to NAV genetic evaluation

- Changes in genomic prediction for Holstein for yield traits
- Cows omitted from the Jersey reference population for feet and legs
- Improved traditional genetic evaluation for type traits and temperament.

Genomic prediction

Holstein

Improvements are introduced in the genomic prediction for Holstein yield traits 2 November – the method is identical to the method applied for RDC and Jersey (12 August 2014)

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

Inclusion of females gives a slightly higher reliability on genomic breeding values (1- 2 %).

Table 2. Overview of changes in the genomic prediction for yield traits in Holstein 2 November 2014 for genotyped females and genotyped young bulls

	Old model	**New model 2 November**	**Comments**
Pedigree in genomic prediction	Sire-Maternal grandsire	Animal Model	
Reference population	Bulls	Bulls + cows	8500 Holstein
Blending method	Method developed by MTT in 2010	Revised blending method developed by MTT in 2013/14	Revised method is better to avoid double counting, which make it possible to include females in ref population

About 8500 cows are included in the Holstein reference population 2 November for yield. Preliminary studies indicate that adding bull dams to the reference population has no significant effect on the GEBVs of the offspring.

The changes in the genomic prediction for Holstein yield traits have some impact on the ranking of bulls. Results show, that the correlations between GEBVs in August and October for genotyped heifers and young bulls are 0.97 for milk, fat and protein. For genotyped cows the corresponding correlations is 0.96. The estimated genetic trend is a bit steeper using the new model and the standard deviation of GEBVs slightly smaller.

For yield this means that for about 10% of the heifers, young bulls and cows the breeding value changes more 4 index units.

Improvements in the genomic prediction for udder health type traits, milkability and temperament in Holstein are planned to take place in February 2015. Use of females in reference population for more NTM traits will be investigated in 2015 for all breeds.

Jersey

Cows are omitted from the reference population for Jersey for feet and legs. Shortly before deadline for publication of breeding values NAV has identified unexpected results, which could not be investigated in details before deadline. NAV will in November try to solve the problem. The unfortunate situation creates larger changes in GEBV for feet and legs for Jersey than one should expect between two subsequent evaluations.

Traditional evaluation

The genetic evaluation for type traits and temperament has been improved by:

- An update of genetic parameters
- Introducing a multi lactation model (only type traits)
- Harmonisation of fixed effects.

All NAV EBVs for conformation traits are based on classification records on cows made by official classifiers in Denmark, Finland and Sweden. Previously only records from first lactation cows were included from Sweden, whereas later lactation records were included from Finland and Denmark to estimate EBVs for cows and/or bulls. The model is now extended to include second and third lactation records from all three countries for both bulls and cows, see table 1.

Table 3. From which lactations classifications records are used to estimate bull and cow breeding values for conformation in genetic evaluation before (old model) and after (new model) November 2014.

	Bulls		**Cows**	
	Old	**New**	**Old**	**New**
Denmark	1	1-3	1-3	1-3
Finland*	1-10	1-3	1-10	1-3
Sweden	1	1-3	1	1-3

How much of the information included in the genetic evaluation that is from classifications in later lactation varies a lot both between countries and breeds. The proportion of records from later lactations is highest (38 %) in RDC (Red Dairy Cattle) from Finland and lowest in RDC (5 %) from Sweden.

New genetic parameters are estimated for all traits. In table 4 the heritabilities are show and in table 5 the genetic correlation between 1 and 3 lactation.

The genetic correlations between the same traits in different lactations were assumed to be 1.00 in the old model, but the new model is a multi-lactation model and the estimated genetic correlations are used in the evaluation.

Table 4. Heritabilities in 1. lactation for type traits and temperament

	Holstein	RDC	Jersey
Stature	0.60	0.77	0.41
Body depth	0.25	0.29	0.24
Chest width	0.17	0.12	0.16
Dairy form	0.27	0.15	0.22
Top line	0.17	0.19	0.18
Rump width	0.28	0.40	0.27
Rump angle	0.32	0.27	0.29
Rear legs, side view	0.20	0.19	0.14
Rear legs, back rear view	0.11	0.11	0.06
Hock quality	0.17	0.30	0.12
Bone quality	0.21	0.47	0.14
Foot angle	0.12	0.10	0.13
Fore udder attachment	0.21	0.22	0.22
Rear udder height	0.19	0.23	0.23
Rear udder width	0.21	0.25	0.25
Udder cleft/support	0.20	0.17	0.17
Udder depth	0.39	0.34	0.34
Teat length	0.35	0.44	0.44
Teat thickness	0.29	0.27	0.27
Teat placement (front)	0.32	0.27	0.27
Teat placement (back)	0.28	0.26	0.26
Udder balance	0.16	0.16	0.16
Temperament	0.11	0.14	0.11

Table 5. Estimated genetic correlations between 1 and 3 lactation

	Holstein	RDC	Jersey
Stature	0.98	0.99	0.99
Body depth	0.96	0.98	0.98
Chest width	0.94	1.00	1.00
Dairy form	0.97	0.97	0.97
Top line	0.91	0.92	0.92
Rump width	0.99	0.98	0.98
Rump angle	0.98	0.97	0.97
Rear legs, side view	0.95	0.99	0.95
Rear legs, back rear view	0.98	0.99	0.94
Hock quality	0.96	0.98	0.99
Bone quality	0.97	0.99	0.98
Foot angle	0.94	0.98	0.97
Fore udder attachment	0.91	0.91	0.90
Rear udder height	0.93	0.96	0.84
Rear udder width	0.88	0.97	0.88
Udder cleft/support	0.96	0.91	0.95
Udder depth	0.93	0.95	0.95
Teat length	0.99	0.99	0.99
Teat thickness	0.96	0.95	0.99
Teat placement (front)	0.96	0.98	0.96
Teat placement (back)	0.93	0.98	0.97
Udder balance	0.94	0.94	0.87

The genetic correlations between lactations are very high. It means that it is nearly the same genes which control the traits expressed in the different lactations, and that selection on first lactation results improves conformation in later lactations efficiently.

For an overview of all the EBVs for conformation traits and how these are combined into indices, see figure 1. The new thing from November 2014 is the single EBVs for second and third lactation and how lactation 1-3 are weighted together into one index per trait (50, 30 and 20 % weight on 1st, 2nd and 3rd lactation, respectively).

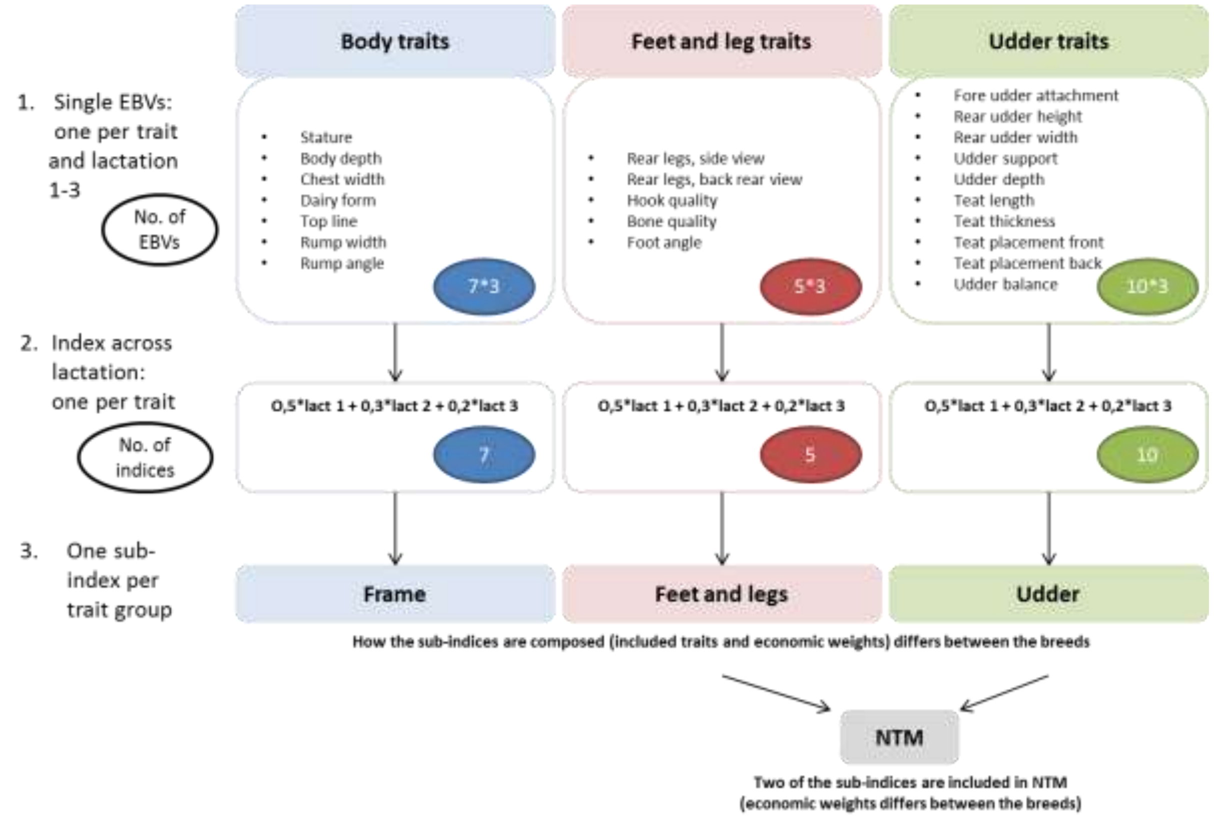

Figure 1. Illustration of which single estimated breeding values (EBVs) are published for conformation traits in lactation 1-3 and how these are combined into indices across lactations as well as across traits within trait group.

In table 6 the correlations between EBVs from the new and old model are shown. For bulls the correlation are 0.97-0.98 for conformation traits, and we do only see minor changes in EBVs. For cows the correlations for conformation traits are somewhat lower 0.94-0.98 indicating that we do see larger changes in EBVs for cows comparing EBVs from the old and the new model. The main reasons for the changes are the updated heritabilities, and the harmonization of the systematic effects across countries. For Swedish cows the changes are also due to adding information from later lactation . The changes mean that EBVs change less than 5 index point for 95% of the animals for conformation traits.

For temperament the correlation is 0.95-0.97% for both cows and bulls for RDC and Holstein, but for Jersey we do see significant lower correlation 0.90-0.92 and relatively large changes in EBV due to a quite large difference between the estimated heritability used in the new and old model.

Table 6. Correlations between EBV from old and new model

		Frame	Feet and Legs	Mammary	Temperament
Holstein	Bulls	0.97	0.97	0.97	0.95
RDC	Bulls	0.98	0.97	0.98	0.97
Jersey	Bulls	0.97	0.97	0.98	0.90
Holstein	Cows	0.97	0.96	0.95	0.96
RDC	Cows	0.95	0.94	0.97	0.97
Jersey	Cows	0.98	0.97	0.98	0.92

Genetic base

EBVs for bulls and females are expressed on the same cow base. This genetic evaluation included cows born from 2.11.2009 to 2.11.2011 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 7 describes how different categories of genotyped animals are handled in the evaluation. All non genotyped animals get traditional EBVs.

Table 7. Publication of Genomic breeding values (GEBVs) for different categories of animals

Category of animals		Status	Published Breeding value
Genotyped males	Bulls without a progeny test	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	AI bulls with a Nordic progeny test	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 12 August 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 ½(EBVsire-100) +1/4(EBVmgs-100) +100. If EBVsire or EBVmgs is not official NAV EBVs then 100 is used.

NAV search page

NAV publish (G)EBVs for herd book registered AI bulls from all three countries at a joint Nordic search page http://www3.mloy.fi/NAV/

NAV – frequency and timing of routine runs

NAV has 4 evaluations per year including all phenotypic data. In table 8 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 2015 takes place 6.1, 3.3, 7.4, 2.6, 7.7, 1.9, 6.10, and 1.12. After the extra runs GEBVs for females are published on national data bases

NAV will in 2015 publish breeding values the first Tuesday in a month instead the 2nd in month, which has been the procedure so far (see table 8).

Table 8. NAV and INTERBULL release dates in 2015. EBVs released at NAV dates in bold will be delivered to international genetic evaluation.

Month	NAV	INTERBULL
January 2015		
February 2015	**3**	
March 2015		
April 2015		7
May 2015	5	
June 2015		
July 2015		
August 2015	**11**	11
September 2015		
October 2015		
November 2015	**3**	
December 2015		1

You can get more information about the joint Nordic evaluation:

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