

News - NAV routine evaluation

5 May 2015

The latest NAV routine evaluation for yield, fertility, type, udder health, other diseases, calving traits, milk ability, 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, 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	23.03.2015	16.03.2015	12.03.2015
Type, milkability and temperament	23.03.2015	16.03.2015	23.03.2015
Fertility	23.03.2015	16.03.2015	14.03.2015
Udder health and other disease	23.03.2015	16.03.2015	14.03.2015
Calving	23.03.2015	16.03.2015	14.03.2015
Longevity	23.03.2015	16.03.2015	14.03.2015
Growth	23.03.2015	16.03.2015	11.03.2015
Claw health	23.03.2015	16.03.2015	13.03.2015
Young stock survival	23.03.2015	16.03.2015	15.03.2015

Data used in genomic prediction

Genotypes were extracted from the joint Nordic SNP data base 21 April 2015. INTERBULL information from April 2015 and national information from present run were included in genomic prediction.

News in relation to NAV genetic evaluation

Genomic prediction

- No changes

Traditional evaluation

- Improved model for genetic evaluation for fertility
- Yield index for Holstein bull VH Bynke

Traditional evaluation

Yield Index VH Bynke, DNK HB 254176

The Holstein bull VH Bynke has changed more than expected in his daughter based EBV from February 2015 evaluation to May 2015 evaluation. In table 2 is the EBV for Y-index and persistency shown

Table 2 Information about the Holstein bull VH Bynke

	Reliability	No daughters with TD yield	No daughters >100 Days in milk	EBV yield	EBV persistency
Nov 2014	87	83	18	106	94
Feb 2015	95	363	107	102	89
May 2015	98	1777	355	113	102

VH Bynke had a GEBV for yield index of 110 in August 2014. The EBVs for VH Bynke in November 2014 were based on quite a lot of daughters in early lactation which give VH Bynke reliabilities at 87%. The phenotypic means (table 3) behind the EBVs reflect very well the observed change in VH Bynke's breeding value.

Table 3 Phenotypic means for VH Bynke, kg milk per day (kg), number of daughters included (N)

	Days in Milk									
	0-29		30-59		60-89		90-119		120-149	
	N	Kg	N	Kg	N	Kg	N	Kg	N	Kg
Nov 2014	83	27,5	80	32,1	49	31,3	18	28,1	9	27,7
Feb 2015	270	26,8	212	31,5	153	31,5	107	29,9	74	29,3
May 2015	1333	28,5	1180	33,1	758	33,6	394	32,2	221	31,2

The observed fluctuations in Y-index EBV for VH Bynke are only caused by daughter phenotypes. Use of a blended index GEBV including also the genomic information will only to a very little degree have an influence on the observed fluctuations in VH Bynke's Y-index, since VH Bynke in all three traditional evaluations since November 2014 have had lots of information from milking daughters.

Improved fertility evaluation

Fertility was among the first traits, which got a joint Nordic evaluation in 2005. In the May 2015 evaluation significant improvements are introduced in the evaluation model. The major changes are listed in table 4.

Table 4 Major differences between May 2015 and old fertility model

Old model	May 2015 model	Comments
Sire model	Animal model	Cows get breeding values from the model, which in the future can be used in reference population for genomic prediction.
Repeatability model	Multi lactation model	Fertility in 1, 2 and 3 rd parity treated as different but correlated traits
Correction for month effect	Month x year effect	Improved correction for development in month effects over years
Old genetic parameters	Updated genetic parameters	Up to date genetic parameters
Genetic base included cows with pedigree information	Genetic base include cows with fertility records	Cows with pedigree information only are not included in the current genetic base

Implementing the changes in the fertility evaluation create some changes in the EBV for fertility. The correlations between old fertility index and May 2015 fertility index are around 0.95 to 0.98 for proven bulls. This means that we see somewhat larger changes than at an ordinary update of breeding values in fertility index, and in separate fertility traits of individual bulls. About 75% of the RDC and Holstein have changes within plus minus 3 index point, and about 7 % of the RDC and Holstein bulls

have changes over 5 index points. For Jersey about 65% of the bulls have changes within plus minus 3 index point, and about 15% of the Jersey bulls have changes over 5 index points.

The changes in definition of the genetic base for fertility by introducing an AM for fertility causes an average drop of about 2 index point in fertility EBV for bulls.

With the change to an animal model cows get fertility indices based also on their own records and not only on information from their relatives. This explain why the correlation between the old fertility index and new fertility index for cows is, around 0,9 and thus, some more re-ranking occurs for cows than for bulls.

The use of an animal model for fertility traits makes it possible to include females in the reference population for genomic prediction also for fertility traits. NAV expects to test this possibility later in 2015.

Genetic base

EBVs for bulls and females are expressed on the same cow base. This genetic evaluation included cows born from 5.5.2010 to 5.5.2012 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 5 describes how different categories of genotyped animals are handled in the evaluation. All non genotyped animals get traditional EBVs.

Table 5. 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 GEBVs are available for genotyped Holstein bulls from the countries participating in the GMACE routine evaluation.

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

<https://fabaweb.mloy.fi/SKJOWeb/WWW/jasu/NAV/BullSearch.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 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 6 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 6. 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:

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

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