News - NAV routine evaluation
3 February 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	16.12.2014	14.12.2014	19.12.2014
Type, milkability and temperament	18.12.2014	14.12.2014	22.12.2014
Fertility	18.12.2014	14.12.2014	22.12.2014
Udder health and other disease	18.12.2014	14.12.2014	22.12.2014
Calving	18.12.2014	14.12.2014	22.12.2014
Longevity	18.12.2014	14.12.2014	22.12.2014
Growth	16.12.2014	14.12.2014	14.12.2014
Claw health	18.12.2014	14.12.2014	23.12.2014
Young stock survival	18.12.2014	14.12.2014	22.12.2014

Data used in genomic prediction
Genotypes were extracted from the joint Nordic SNP data base 21 January 2015. INTERBULL information from December 2014 and national information from present run were included in genomic prediction.

News in relation to NAV genetic evaluation
Genomic prediction
- Improved Deregressed proofs (DRP) for Holstein
- Changes in genomic prediction for Holstein

Traditional evaluation
- Genetic evaluation for youngstock survival

Genomic prediction
Deregressed proofs
NAV has in routine run in the autumn 2014 observed some instability in the DRPs. The problem has been carefully investigated, and the following modifications have been introduced for Holstein:
- Minimum reliability for foreign animals to be included set to 50%
- Limitation for outliers with extreme deviations from pedigree index - Bulls deviation from PA > 20 index units set to 20 index units, and cows deviation from PA >15 index units set to 15 index units

- Stopping criteria for the MIX99 DRP program modified

The modifications will also be introduced for Jersey and RDC in the near future to improve the stability.

Holstein

Improvements are introduced in the genomic prediction for Holstein traits - the method is identical to the method applied for Holstein yield (starting 2 November 2014) and RDC and Jersey (starting 12 August 2014). It means the following changes are introduced:

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

About 8500 cows are now included in the Holstein reference population for yield, type traits, milkability, mastitis and temperament.

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

	Reference population	
	Bulls	Cows
Holstein	27500[a)]	8400
RDC	8150[b)]	12700
Jersey	2450[c)]	8550

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

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

The genomic prediction for Holstein has been improved a bit by adding genotyped females. The increase in reliabilities for Holstein is on average about 0-2% (table 4).

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

	Reference population	
	Bulls	**Bulls + cows**
Yield	0,33	**0,35**
Growth	0,24	0,24
Fertility	0,32	0,32
Birth index	0,31	0,31
Calving index	0,22	0,22
Mastitis	0,39	**0,41**
Other diseases	0,06	0,06
Frame	0,36	**0,36**
Feet & Legs	Calculated from linear traits	
Mammary	0,52	**0,52**
Milkability	0,46	**0.46**
Temperament	0,14	0.14
Longevity	0,21	0.21

The changes in the genomic prediction for Holstein traits have some impact on the ranking of bulls. Results show, that the correlations between GEBVs in November 2014 and February 2015 are about

0.96-0.98 for most traits. For yield the correlations is 0.99 since the changes in the use of Animal Model pedigree, blending procedure, and females in the reference population took place in November 2014 for yield traits.

Traditional evaluation
<u>Genetic evaluation for young stock survival</u>
NAV published the first official genetic evaluation for young stock survival for progeny tested bulls November 28th 2014.

Survival in calves and young stock is described by means of four traits.
- Heifer period 1(HP1): Heifer calf survival in period: 1 to 30 days
- Heifer period 2(HP2): Heifer calf survival day in the period: 31 – 458 days
- Bull period 1(BP1): Bull calf survival day in the period 1 to 30 days
- Bull period 2 (BP2): Bull calf survival day in the period 31- 183 days

From the 3rd February run the young stock survival evaluation follow the normal evaluation schedule. Genomic prediction for young stock survival is expected to be introduced during 2015. More details about EBV for young stock survival can be found at www.nordicebv.info

Genetic base
EBVs for bulls and females are expressed on the same cow base. This genetic evaluation included cows born from 3.2.2010 to 3.2.2012 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 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 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

Contact person: Gert Pedersen Aamand, Ph.: +45 87405288 gap@vfl.dk,

Denmark: https://www.landbrugsinfo.dk

Contact person: Ulrik Sander Nielsen, VFL Cattle, Ph. +45 87405289, usn@vfl.dk

Sweden: www.sweebv.info, www.vxa.se

Contact person: Jan-Åke Eriksson, Swedish Dairy Association, Ph. +46 08-790 58 67
Jan-Ake.Eriksson@vxa.se

Finland: www.faba.fi

Contact person: Jukka Pösö, Faba co-op, Ph +358-(0)207472071 jukka.poso@faba.fi