News - NAV routine evaluation
August 13th 2013

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	26.06.2013	16.06.2013	14.06.2013
Type, milk ability and temperament	01.07.2013	16.06.2013	10.06.2013
Fertility	01.07.2013	16.06.2013	15.06.2013
Udder health and other disease	01.07.2013	16.06.2013	15.06.2013
Calving	01.07.2013	16.06.2013	15.06.2013
Longevity	01.07.2013	16.06.2013	15.06.2013
Growth	26.06.2013	16.06.2013	16.06.2013
Claw health	01.07.2013	16.06.2013	16.06.2013

Data used in genomic prediction
Genotypes were extracted from the joint Nordic SNP data base July 5th 2013. Interbull information from April 2013 and national information according to extraction dates in table 1 were included in genomic prediction.

News in relation to NAV genetic evaluation
Genomic prediction
RDC reference bulls
Last 2-3 birth years of NRF bulls with a progeny test have been added to the reference population for RDC in June

Low Density (LD) chip
LD (10K) genotypes is included in the routine evaluation from July 2nd an onwards. The X-chromosome has until July 2nd been included in the genomic prediction for RDC and Jersey. But imputation from 10K to 54K is complicated for the X-chromosome and requires more research, and the X-chromosome has been removed from the genomic prediction starting July 2nd. It has earlier been shown that the effect of including SNPs on the X-chromosome was very minor.

The imputation is done by either the Beagle or FImpute software. Beagle has been shown to do best in all imputation studies, but Beagle is very time consuming when the reference panel is large. FImpute is fast and has performed among the best imputations programme next to Beagle. Main difference is that FImpute use pedigree information more than Beagle when doing the imputation. NAV can currently

handle Beagle on a routine basis within Jersey and RDC (with some restrictions in the reference panel). For RDC only bull genotypes from Finland, Sweden and Denmark are used in the imputation. FImpute is used for Holstein. In table 2 results from imputations studies are shown for the three breeds.

Table 2. Genotype error rates (number of animals) – imputation from 10K to 54K.

Breed	Imputation software	Only sire genotyped	Sire and dam genotyped
Holstein	FImpute	3.2 (1213)	0.7 (432)
Holstein	Beagle	Cannot be handled on routine basis	
RDC – all genotypes	FImpute	4.3 (1147)	0.7 (234)
RDC – all genotypes	Beagle	1.3 (1147)	1.0 (234)
RDC- genotypes from Danish, Swedish and Finnish bulls	Beagle	1.4 (1147)	1.1 (234)**
Jersey	FImpute	1.5 (110)	0.5 (75)
Jersey	Beagle	Not investigated, but Beagle is expected to perform better than FImpute	

The imputation has been applied on:
- 54K genotypes – all missing SNPs are imputed – major effect across Illumina version 1 and version 2
- Imputation from 10K to 54K

The changes in editing of SNPs create a little bit bigger changes in GEBV than we normally have seen when comparing GEBVs from two subsequent evaluations. Furthermore we do see a slightly higher standard deviation and genetic trend for all breeds after introducing the new editing and imputation of 54K genotypes.

In the August run more than 7500 new female genotypes have entered the system mainly Jersey and RDC heifers and cows from VikingGenetics female testing program. We have observed that RDC females on average drop about 4-5 NTM units when the genomic information are added to the traditional EBV. This is mainly due to a discrepancy in yield index. The drop is biggest for the youngest birth year classes. We due to a smaller extent observe the same for Jersey where the effect seems to be 2-3 NTM index units. Since the major part of the females are tested in VikingGenetics female testing program and unselected – we do think this discrepancy is due to problems with scaling in relation to the prediction model. We expect we are able to solve the problem within the coming months. As along as the discrepancy exists it also means that we do not have a 100% fair ranking across genotyped and not genotyped animals, which has to be taken into account in the selection process in practice.

NTM
Starting August 13rd the reduced weights on yield in NTM calculation is only be applied for cows with own yield record without genomic information

Table 3. Current weight factors for NTM

	Holstein	RDC	Jersey	Red Holstein
Yield*	0.75/0.68	0.92/0.84	0.87/0.78	0.75/0.68
Growth	0.06	0.00	0.00	0.11
Fertility	0.31	0.26	0.20	0.23
Birth index	0.15	0.14	0.06	0.17
Calving index	0.17	0.12	0.06	0.17
Udder health	0.35	0.32	0.44	0.35
Other diseases	0.11	0.12	0.04	0.12
Body	0.00	0.00	0.00	0.00
Feet&Legs	0.12	0.09	0.04	0.15
Udder	0.25	0.32	0.26	0.24
Milk ability	0.08	0.10	0.10	0.08
Temperament	0.03	0.03	0.03	0.03
Longevity	0.11	0.07	0.08	0.11
Claw health	0.08	0.05	0.05	0.10

*Weight factor for bulls/weight factor for cows with own yield record, but without genomic information

Genetic base
EBVs for bulls and females are expressed on the same cow base. This genetic evaluation included cows born from 13.08.2008 to 13.08.2010 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 4 describes how different categories of genotyped animals are handled in the evaluation. All non genotyped animals get traditional EBVs.

Table 4 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	**GEBV** when at least 17 month old at publication date
	Bulls with a Nordic 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 animals having a GEBVs the GEBV is published as the official index instead of the EBV

Publication of NTM for Nordic and foreign bulls

A NTM is published if the bull has official EBVs (NAV EBV or international 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 estimates EBVs for the single bull. EBVs are used in the following priority NAV EBVs, IB EBVs and Pedigree index. For traits without a NAV EBV or an IB 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 – frequency and timing of routine runs

NAV has 4 evaluations per year including all phenotypic data. In Table 5 the future NAV and INTERBULL release dates are shown. NAV does seven extra genomic predictions to get GEBVs based on the newest information for all genotyped bull calves and females. The extra runs in 2013 take place 2.3, 2.4, 2.6, 2.7, 2.9, 2.10, 2.12. After the extra runs GEBVs for females are published on national data bases

Table 5. NAV and INTERBULL release dates in 2013. EBVs released at NAV dates in bold will be delivered to international genetic evaluation.

	2013	
Month	NAV	INTERBULL
January 2013		
February 2013	**4**	
March 2013		
April 2013		9
May 2013	2	
August 2013	**13**	13
September 2013		
October 2013		
November 2013	**2**	
December 2013		3

You can get more information about the joint Nordic evaluation:

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