News - NAV routine evaluation
2 May 2011

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	22.03.2011	20.03.2011	17.03.2011
Type, milk ability and temperament	23.03.2011	20.03.2011	21.03.2011
Fertility	23.03.2011	20.03.2011	19.03.2011
Udder health and other disease	23.03.2011	20.03.2011	19.03.2011
Calving	23.03.2011	20.03.2011	19.03.2011
Longevity	23.03.2011	20.03.2011	19.03.2011
Growth	23.03.2011	20.03.2011	15.03.2011
Claw health	23.03.2011	20.03.2011	29.03.2011

News in relation to NAV genetic evaluation

Claw health
NAV published for the first time an EBV for claw health. It is planned that the claw health index will be included in the NTM in the August 2011 evaluation.

Genomic EBVs (GEBVs)
NAV published for the first time GEBVs. GEBVs combine genomic and phenotypic information. GEBVs are estimated for all combined traits in NTM and for NTM. GEBVs will replace traditional EBVs for genotyped young animals (more information in table 8) and farmers will still just get one EBV per trait, which for some categories of animals include an additional information source – genomic information.

Other traits
No changes

Genetic base

EBVs for bulls and females are expressed on the same cow base. This genetic evaluation included cows born from 02.05.2006 to 02.05.2008 in the genetic base (average 100).

Table 2. Definition of genetic base for cows and bulls

Trait	**Genetic base**
Yield, type, milk ability, temperament, longevity, mastitis resistance, growth*, fertility, calving, claw health and resistance against other diseases	Cows born 02.05.2006 - 02.05.2008

*Bull calves born in the same period

Claw health

NAV published for the first time an EBV for claw health. The joint model is a multi trait linear Animal Model.

Seven traits within the 3 first lactations are used in the evaluation. Table 3 gives the diseases used in each trait.

Table 3. Diseases used in each country for each trait

Trait	Denmark	Finland	Sweden
Dermatitis (DE)	Digital de + spaltebetaendelse	Sorkkavälin ihon tulehdus + Sorkka-alueen ihotulehdus	Digital de + klövspalteksem
Heel Horn Erosion (HH)	Balleråd	Kantasyöpymä	Klövröta
Sole Haemorrhage (SH)	Såleblödning	Vertymiä anturassa	Sulblödning
Sole Ulcer (SU)	Sålesår	Anturahaavauma + Valkoviivan paise	klövsulesår
Cork screw claws (CSC)	Proptraekker klov	Sorkkakiertymä	Korkskruvsklöv
Skin Proliferation (SP)	Nydannelse+Digital vorte	Sorkkavälin liikakasvu+Sorkkasyylä	Limax+vårta
White line separation+ double sole (WLS)	Hul vaeg+ dobbelt sål	Valkoviivan repeämä	Hålvägg+ dubbelsula

Recording period is from calving to calving or from calving to 430 days after calving, depending on which comes first. Only 3 trimmings are allowed per lactation. Trimmings should be at least 12 weeks apart.

Table 4 Number of claw trimmings recorded from 01.04.2010-31.03.2011 per breed and country

	RDC	Holstein	Jersey
Sweden	68,206	77,102	1,303
Finland	12,012	6,598	-
Denmark	13,271	148,751	23,319

Table 5 Genetic parameters simple overview

Trait	Heritability – range 1-3 lact	Genetic correlation across lactation
Dermatitis (DE)	0.04-0.05	0.94-0.99
Heel Horn Erosion (HH)	0.05-0.06	0.84-0.98
Sole Haemorrhage (SH)	0.03-0.04	0.82-0.90
Sole Ulcer (SU)	0.02-0.02	0.79-0.91
Cork screw claws (CSC)	0.02-0.06	0.66-0.98
Skin Proliferation (SP)	0.04-0.05	0.88-0.97
White line separation+ double sole (WLS)	0.01-0.02	0.71-0.88

Genetically claw traits can be separated in two groups of traits: group 1(Dermatitis, Skin Proliferation, Heel Horn Erosion) group 2 (Sole Haemorrhage, Sole Ulcer, Cork screw claws, White line separation+ double sole). The genetic correlation between traits within each group is 0.5-0.9 whereas the genetic between traits in group 1 and traits in group 2 is close to 0.00.

Relative breeding values were calculated for all individual traits, for each trait over lactations, and for an index trait containing all 7 traits. In table 6 the relative weights given to each trait is shown. The economically most important trait is sole ulcer.

Table 6 Relative weights for unstandardized EBVs

	Holstein	RDC	Jersey
Sole Ulcer	1.000	1.000	1.000
Sole Hemorhage	0.134	0.134	0.136
Horn Heel Erosion	0.215	0.215	0.219
Digital Dermatitis	0.215	0.215	0.219
Skin Proliferation	0.394	0.394	0.363
White Line disease	0.134	0.134	0.136
Cork Screw claws	0.149	0.149	0.193

EBVs are published for all bull having a minimum reliability of 40%. Since regular registration of claw trimmer data has only taken placed during the most recent years all bulls having reliability over 40% are included in the standardization procedure for Holstein and RDC and all bulls having reliability over 30% for Jersey to get a sufficient number of bulls.

Table 7. Correlations between EBVs for claw traits and claw index

	Holstein	RDC	Jersey
Sole Ulcer	0.90	0.79	0.84
Sole Hemorhage	0.66	0.83	0.74
Horn Heel Erosion	0.62	0.76	0.77
Digital Dermatitis	0.50	0.63	0.62
Skin Proliferation	0.41	0.41	0.56
White Line disease	0.78	0.53	0.66
Cork Screw claws	0.57	0.34	0.68

The correlation between the old Swedish claw health index and the NAV claw health index is about 80%. The main difference is that data from later lactations is used in the NAV evaluation whereas the old Swedish model was based on first lactation records only. Furthermore three more claw diseases are included in the index.

The plan is to include the claw health index in the NTM starting in the August 2011 evaluation.

Genomic EBVs (GEBVs)

NAV published for the first time GEBVs. GEBVs combine genomic and phenotypic information. GEBVs are estimated for all combined traits in NTM and for NTM. Table 8 describes how different categories of genotyped animals are handled at the 2nd May evaluation. All non genotyped animals get traditional EBVs.

Table 8 Publication of Genomic breeding values (GEBVs) for different categories of animals 2nd May

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 20 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		**GEBV**
	Cows		**GEBV** for traits with pedigree information only (e.g. Other disease, fertility, calving) and EBVs for all other traits

- 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

Genotyped DRH animals will be included in GEBV calculation in the near future. NAV will in the coming months work with:

- GEBVs for DRH
- GEBVs for single traits
- GEBVs for genotyped bulls with daughters
- Genotyped cows with own records

Reliabilities

The reliability of genomic information varies between traits and breeds. Table 9 give a general picture of the reliability of the genomic information used when weighting genomic information and phenotypic information together in GEBV.

Table 9 Reliability of genomic information

	Reliability genomic information
RDC	0.30-0.40
Holstein	0.40-0.50
Jersey	0.20-0.30

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. In Table 10 the future NAV and INTERBULL release dates are shown.

Table 10. NAV and INTERBULL release dates in 2011. EBVs released at NAV dates in bold will be delivered to international genetic evaluation.

	2011	
Month	NAV	INTERBULL
January 2011		
February 2011	**2**	
March 2011		
April 2011		5
May 2011	2	
August 2011	**9**	9
September 2011		
October 2011		
November 2011	**2**	
December 2011		6

You can get more information about the joint Nordic evaluation:

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