News - NAV routine evaluation
3 May 2016

The latest NAV routine evaluation for yield, fertility, type, udder health, other diseases, calving traits, milkability, temperament, growth, longevity, youngstock 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	17.03.2016	09.03.2016	10.03.2016
Type, milkability and temperament	17.03.2016	09.03.2016	16.03.2016
Fertility	16.03.2016	09.03.2016	12.03.2016
Udder health and other disease	16.03.2016	09.03.2016	12.03.2016
Calving	17.03.2016	09.03.2016	12.03.2016
Longevity	17.03.2016	09.03.2016	12.03.2016
Growth	17.03.2016	09.03.2016	10.03.2016
Claw health	16.03.2016	09.03.2016	13.03.2016
Youngstock survival	30.03.2016	09.03.2016	28.02.2016

Data used in genomic prediction

Genotypes were extracted from the joint Nordic SNP data base 20 April 2016, but due to an unfortunate error genotypes from 712 DNA samples of females were not included in the genomic prediction, and these females have not get official GEBV in the May 3rd routine evaluation. The missing genotypes will be included in the June 7th run and the females will get official GEBVs.

News in relation to NAV genetic evaluation

Genomic prediction

- No changes

Traditional evaluation

- Youngstock survival included in NTM for all breeds
- Modified weights in NTM for RDC

Youngstock survival included in NTM for all breeds, and modified weights in NTM for RDC.

Starting May 3rd Youngstock survival is included in NTM for all 3 breeds. The old weightings of sub-indices (column marked old) and the new weightings when Youngstock survival is included in NTM are presented in table 2 (column marked new). For RDC the relative weight on yield and udder has been slightly increased, and as a consequence weight on all traits are reduce a bit to keep an unchanged standard deviation of NTM.

Table 2. Weights of sub-indices in NTM.

	RDC		Holstein		Jersey		Red Holstein	
	Old NTM	New NTM	Old NTM	New NTM	Old NTM	New NTM	Old NTM	New NTM
Yield*	0.96/0.88	**1.00/0.91**	0.75/0.68	0.75/0.68	0.87/0.78	0.87/0.78	0.75/0.68	0.75/0.68
Growth	-	**-**	0.06	0.06	0.00	0.00	0.11	0.11
Fertility	0.26	**0.24**	0.31	0.31	0.20	0.20	0.23	0.23
Birth	0.14	**0.13**	0.15	0.15	0.06	0.06	0.17	0.17
Calving	0.12	**0.11**	0.17	0.17	0.06	0.06	0.17	0.17
Udder health	0.32	**0.30**	0.35	0.35	0.44	0.44	0.35	0.35
Other diseases	0.12	**0.11**	0.11	0.11	0.04	0.04	0.12	0.12
Claw health	0.05	**0.05**	0.08	0.08	0.05	0.05	0.10	0.10
Longevity	0.07	**0.07**	0.11	0.11	0.08	0.08	0.11	0.11
Frame	0.00	**0.00**	0.00	0.00	0.00	0.00	0.00	0.00
Feet & legs	0.09	**0.08**	0.12	0.12	0.04	0.04	0.15	0.15
Udder	0.32	**0.35**	0.25	0.25	0.26	0.26	0.24	0.24
Milkability	0.10	**0.09**	0.08	0.08	0.10	0.10	0.08	0.08
Temperament	0.03	**0.03**	0.03	0.03	0.03	0.03	0.03	0.03
Youngstock survival	**-**	**0.22**		**0,14**		**0.12**		**0,14**

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

The correlations between NTM and the sub-indices of NTM are presented in table 3 for both the new and the old NTM. The correlation between the new NTM and Youngstock survival is positive for all breeds (0.26-0.36). It means that selection for NTM will results in a genetic increase in youngstock survival. Correlations between the new NTM including Youngstock survival and the old NTM excluding Youngstock survival are for all breeds over 0.97.It means that inclusion of Youngstock survival has a moderate effect on NTM rankings for bulls.

Table 3. Correlations between NTM and the sub-indices of NTM for NTM with (New) and without (Old) Youngstock survival based on 358, 472, and 179 bulls born 2008-2010, 2008-2009 and 2007-2010 for RDC, HOL and JER, respectively.

	RDC		HOL		JER	
	Old NTM	New NTM	Old NTM	New NTM	Old NTM	New NTM
Yield	0.65	0.63	0.50	0.48	0.57	0.55
Growth	0.10	0.02	0.10	0.10	0.18	0.20
Fertility	0.24	0.22	0.43	0.43	0.32	0.32
Birth	0.21	0.25	0.35	0.35	0.14	0.14
Calving	0.25	0.22	0.29	0.30	0.36	0.38
Udder health	0.30	0.27	0.42	0.42	0.56	0.56
Other diseases	0.21	0.15	0.44	0.45	0.16	0.18
Claw health	0.10	0.05	0.34	0.36	0.12	0.10
Longevity	0.49	0.49	0.60	0.61	0.62	0.62
Frame	0.05	-0.00	-0.06	-0.10	0.18	0.18
Feet & legs	0.26	0.33	0.19	0.19	0.13	0.12
Udder	0.19	0.26	0.16	0.14	0.29	0.30
Milkability	0.14	0.16	0.01	0.02	0.18	0.17
Temperament	0.04	0.04	-0.01	0.00	0.07	0.07
Youngstock survival	0.02	0.26	0.12	0.27	0.24	0.36
Old NTM	1.00	0,97	1.00	0.99	1.00	0.99

Genetic base

EBVs for bulls and females are expressed on the same cow base. This genetic evaluation included cows born from 03.05.2011 to 03.05.2013 in the genetic base (average 100).

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. 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 pages

NAV publish (G)EBVs for herd book registered AI bulls from all three countries at *NAV bull search* and Interbull (G)EBVs at *NAV Interbull search.* Links to the two search pages can be found at http://www.nordicebv.info/

NAV – frequency and timing of routine runs

NAV has 4 evaluations per year including all phenotypic data. In table 4 the future NAV and INTERBULL release dates are shown. NAV does eight extra genomic predictions to get GEBVs based on the newest information for females. The extra runs in 2016 takes place 5.1, 1.3, 5.4, 7.6, 5.7, 6.9, 4.10, and 6.12. After the extra runs GEBVs for females are published on national data bases

Table 4. NAV and INTERBULL release dates in 2016. EBVs released at NAV dates in bold will be delivered to international genetic evaluation.

Month	NAV	INTERBULL
January 2016		
February 2016	**2**	
March 2016		
April 2016		5
May 2016	3	
June 2016		
July 2016		
August 2016	**9**	9
September 2016		
October 2016		
November 2016	**1**	
December 2016		6

You can get more information about the joint Nordic evaluation:
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