45 minutes about improvements of NAV genetic evaluation

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Nordic Cattle Genetic Evaluation

Implemented 2016 (I)

Implemented December 14th 2015

- Weekly genomic prediction

Implemented February 2nd 2016

- Genomic breeding values youngstock survival
- GEBV for fat and protein percentage

Implemented April 2016

- New NAV Interbull search page
- GEBV for foreign bulls without herd book number on NAV scale

Implemented 2016 (II)

Implemented May 2016

- Young stock survival in NTM

Implemented June 2016

- Monthly publication of GEBVs for bulls
- Fee system Holstein Interbull traits

Implemented September 2016

- Fee system Holstein Nordic traits (Claw health, Other diseases, Young stock survival, growth)

Implemented 2016 (III)

Implemented November 2016

- Udder coordinates included in udder conformation
- Fertility model handling sexed semen, conception rate (Eurogenomics harmonization) – CR published instead of NRR56
- Yield handling – AMS/CMS and outlier
- Animal model for calving traits
- Improved genomic prediction - polygenic effect included and revised standardization to handle inflation of GEBV

Reference population

January 2017

	Reference population	
	Bulls	Cows
Holstein	33,600[a)]	22,900
RDC	7,900[b)]	26,500
Jersey	2,570[c)]	17,500

a) Includes proven bulls from NLD, FRA, DEU, ESP, POL
b) Includes proven bulls from NOR
c) Includes proven bulls from USA

Tested females per country and birth year

Year	Holstein			RDC			Jersey		
	DNK	FIN	SWE	DNK	FIN	SWE	DNK	FIN	SWE
2010	1,123	353	151	506	1,850	1,309	2,226	1	43
2011	1,719	1,137	364	899	3,608	1,875	4,084	6	90
2012	2,550	1,814	585	1,306	3,758	2,084	4,513	1	112
2013	3,930	2,613	1,631	1,633	3,483	2,362	3,282	17	84
2014	4,196	2,800	2,257	1,796	3,623	2,756	3,969	28	92
2015	5,398	3,445	2,589	2,080	4,640	3,831	4,276	35	126
2016	4,663	2,825	2,489	1,464	4,416	3,522	2667	26	94
Total	**26,039**	**15,258**	**10,381**	**9,915**	**25,991**	**17,967**	**25,513**	**126**	**659**
	HOL total : 51,678 **Last year: 16,063**			**RDC total : 53,873** **14,540**			**Jersey total : 26,298** **5,230**		

Level of genomic tested Holstein

November 2016

	Bulls with HB		Bulls with out HB		Females	
Born	Number	NTM	Number	NTM	Number	NTM
2010	248	5.2	903	-1.5	1,627	-0.6
2011	192	9.6	1,541	2.1	3,220	0.5
2012	211	14.3	1,971	5.2	4,949	2.5
2013	173	17.6	2,224	8.0	8,174	4.8
2014	130	22.0	3,046	10.1	9,253	7.1
2015	97	28.0	2,608	15.1	11,372	10.5
2016	20	31.0	2,276	18.5	9,977	13.3

Level of genomic tested RDC

November 2016

	Bulls with HB		Bulls without HB		Females	
Born	**Number**	**NTM**	**Number**	**NTM**	**Number**	**NTM**
2010	256	3.6	738	0.1	3,665	-2.3
2011	257	5.4	1,555	3.2	6,382	-0.7
2012	205	11.6	2,134	4.4	7,148	1.2
2013	188	12.4	2,163	5.4	7,478	3.6
2014	138	16.6	2,194	7.8	8,175	5.8
2015	100	22.0	2,177	11.9	10,550	9.0
2016	32	23.8	1,751	14.4	9,396	10.8

Level of genomic tested Jersey

November 2016

	Bulls with HB		Bulls without HB		Females	
Born	Number	NTM	Number	NTM	Number	NTM
2011	73	5.9	325	0.9	5.103	0.4
2012	58	7.7	370	3.0	5.100	1,2
2013	67	8.8	390	4.2	3,479	2.9
2014	64	11.8	430	5.6	4,090	4.1
2015	53	17.6	492	9.4	4,437	6.5
2016	5	20.2	362	11.9	2,787	8.8

Genetic level of HB bulls born in 2015

- Genetic level of tested bulls for all traits
- Effect of selection for all traits
- Correlation between NTM and all traits based on:
  - Selected bulls (HB)
  - All tested bulls (All)
  - All cows born in 2013 with production data

Genetic level of selected HOL bulls born in 2015

	Genetic level			
	Selected bulls (HB)	All tested bulls	Difference	All cows born 2012-2013
Yield	114.3	109.7	4.6	100
Fertility	110.3	104.1	6.2	100
Udder health	108.9	104.5	4.4	100
Udder	116.0	107.5	8,5	100
NTM	28.0	15.5	12.5	0

Genetic level of selected RDC bulls born in 2015

	Genetic level			
	Selected bulls (HB)	All tested bulls	Difference	All cows born 2012-2013
Yield	111.9	108.0	3.9	100
Fertility	103.9	101.0	2.9	100
Udder health	106.7	102.4	4.3	100
Udder	110.4	104.7	5.7	100
NTM	22.0	12.3	9.7	0

Correlations with NTM (HOL)

	Correlation with NTM		
Trait	Selected bulls (HB)	All tested bulls	All cows born 2012-2013
Yield	0.03	0.39	0.68
Fertility	0.42	0.47	0.33
Udder health	0.52	0.48	0.48
Udder	0.34	0.44	0.21

Correlations with NTM (RDC)

	Correlation with NTM		
Trait	Selected bulls (HB)	All tested bulls	All cows born 2012-2013
Yield	0.55	0.64	0.85
Fertility	0.15	0.21	0.14
Udder health	0.04	0.32	0.26
Udder	0.18	0.37	0.15

Correlation estimates to NTM based on different animal groups

- Selected bulls (HB) are intensively selected and a small group
- Genomic tested bulls are a bigger group but still intensively selected based on pedigree information
- Cows are unselected

Correlations and genetic progress

- Cow correlations express the relative genetic progress for different traits which can be obtained with the accuracy on the breeding values for none genotyped cows
- Genetic progress for genomic tested animals will be relatively larger for low heritability traits because of higher relative increase in accuracy

Correlations and genetic progress

- **Selection differences for HB bulls will also be effected by:**
    - **Control of inbreeding**
    - **Selecting the best out of half and full sib groups**
    - **Coincidences**

- ***Note - in the genomic selection era we should be careful with conclusions about genetic progress based on correlation between NTM and single traits***

Self-study Holstein

	Selection bull candidates			Correlation with NTM		
	HB	All	Dif.	HB	All bulls	Cows
Yield	114.3	109.7	4.6	0.03	0.39	0.68
Growth	99.0	98.6	0.4	0.02	0.01	0.10
Fertility	110.3	104.1	6.2	0.42	0.47	0.33
Birth	105.3	102.7	2,6	0.23	0.29	0.29
Calving	109.1	104.1	5,0	0.32	0.37	0.28
Udder health	108.9	104.5	4.4	0.52	0.48	0.48
Other diseases	106.6	104.1	2.5	0.44	0.34	0.49
Frame	105.1	103.9	1.2	-0.08	0.04	-0.17
Feet & Legs	108.5	104.5	4.0	0.34	0.28	0.12
Udder	116.0	107.5	8.5	0.34	0.44	0.21
Milking speed	106.4	101.2	5.2	-0.12	0.04	0.19
Temperament	105.1	102.9	2.2	0.10	0.11	0.17
Longevity	113.2	106.2	7.0	0.57	0.62	0.52
Claw health	106.8	104.8	2.0	0.27	0.27	0.38
Young st. survival	100.8	101.5	-0.7	0.24	0.18	0.33
NTM	28.0	15.5	12.5			

Self-study RDC

	Selection bull candidates			Correlation to NTM		
	HB	All	Dif	HB	All bull	Cows
Yield	111.9	108.0	3.9	0.55	0.64	0.85
Growth	99.5	100.2	-0.7	-0.18	-0.06	0.26
Fertility	103.9	101.0	2.9	0.15	0.21	0.14
Birth	103.1	101.4	1.7	0.36	0.21	0.19
Calving	102.9	101.7	1.2	0.12	0.18	0.24
Udder health	106.7	102.4	4.3	0.04	0.32	0.26
Other diseases	104.2	102.3	1.9	-0,06	0.17	0.27
Frame	103.7	101.7	2.0	-0.18	0.09	0.06
Feet & Legs	106.9	102.7	4.2	0.25	0.30	0.17
Udder	110.4	104.7	5.7	0.18	0.37	0.15
Milking speed	106.8	103.9	2.9	-0.13	0.13	0.25
Temperament	102.5	101.9	0.6	-0.16	0.09	0.23
Longevity	111.2	105.2	6.0	0.19	0.51	0.51
Claw health	102.5	101.8	0.7	0.20	0.11	-0.06
Young st. survival	100.1	99.2	0.9	0.21	0.24	0.17
NTM	22.0	12.3	9.7			

Self-study JER

	Selection bull candidates			Correlation with NTM		
	HB	All	Dif	HB	All bull	Cows
Yield	111.5	107.4	4.1	0.40	0.58	0.76
Growth	98.8	99.0	-0.2	-0.09	-0.07	0.10
Fertility	102.8	101.4	1.4	-0.04	0.18	0.16
Birth	100.3	100.6	-0.3	-0.06	0.07	0.15
Calving	102.2	101.0	1.2	0.17	0.22	0.21
Udder health	106.5	103.1	3.4	0.60	0.57	0.46
Other diseases	100.6	100.5	0.1	0,20	0.25	0.22
Frame	107.8	104.1	3.7	0,21	0.14	0.11
Feet & Legs	104.4	102.5	1.9	-0.03	0.11	0.09
Udder	109.0	104.5	4.5	0.49	0.44	0.39
Milking speed	101.3	100.5	0.8	0.03	0.02	0.20
Temperament	100.2	99.0	1.1	0.23	0.04	0.11
Longevity	108.7	105.2	3.5	0.19	0.46	0.49
Claw health	99.6	100.2	-0.6	-0.13	-0.02	0.08
Young st. survival	105.0	100.8	4.2	0.17	0.30	0.15
NTM	17.6	10.1	7.5			

Genomic prediction Implementation plan 2017

- Cows in reference more traits
  - Fertility, calving, claw health
- Single traits within other diseases
- Use of more SNPs on LD chip
- “Quick step blending”
  - Include more dam information

Traditional evaluation Implementation 2017

- Include Norwegian Jersey and Holstein in NAV evaluations

- Upgrade other disease evaluation

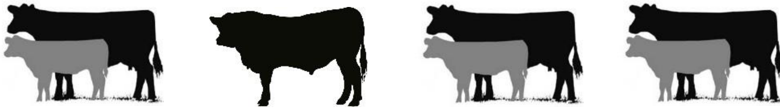
Upgrade other disease evaluation

Aim

- Apply an animal model
- Use NAV model for JER
- Include BHB, acetone data

Implications

- EBV for dams
- Slightly higher EBV reliability for sires
- Increased reliability of GEBV by having cows in the reference population



Sub-index for Other diseases

- **Describes:** Genetic potential to resist reproductive, metabolic and feet and leg diseases.

- **Includes:** Breeding values for
  - Early reproductive disorders
  - Late reproductive disorders
  - Metabolic diseases
  - Feet and leg problems

- **Data**: Based on health records made by veterinarian and farmers from first three lactations

- More than 80 different disease codes are used to describe the diagnoses and codes vary by country

Disease traits and sub-traits used in the current genetic evaluation

Early reproductive disorders (DIM 0-40)	Late reproductive disorders (DIM 41-305)	Metabolic diseases	Feet and leg problems
• Retained placenta • Hormonal reproductive disorders • Infective reproductive disorders • Other reproductive disorders	• Hormonal reproductive disorders • Infective reproductive disorders • Other reproductive disorders	• Ketosis • Milk fever • Other metabolic diseases • Other feed related disorders • Other diseases	• Feet and legs disorders

New trait in the genetic evaluation of OD to increase reliability of EBV on metabolic disorders

- ***β-hydroxybutyrate(BHB) / Acetone***

Early reproductive disorders	Late reproductive disorders	Metabolic diseases	Feet and leg problems
• **Retained placenta** • **Hormonal reproductive disorders** • **Infective reproductive disorders** • **Other reproductive disorders**	• **Hormonal reproductive disorders** • **Infective reproductive disorders** • **Other reproductive disorders**	• **Ketosis + *β-hydroxybutyrate(BHB) Acetone*** • **Milk fever** • **Other metabolic diseases** • **Other feed related disorders** • **Other diseases**	• **Feet and legs disorders**

Physiological relationship between ketosis and BHB

- Large demand for energi for milk production

- Feed absorption cannot compensate

- Mobilization of body fat reserves

- Large turnover in liver

- Liver fails to be able to handle mobilization of fat

- More ketone bodies in milk (among these BHB)

Ketosis

Search for better indicator of disease

Depending on farmer threshold

Other more objective measures

BHB and acetone in milk samples

History of measuring BHB and Acetone in Denmark

- Started measuring both BHB and Acetone in few herds in 2012
- Started measuring BHB and Acetone in all herds in 2013

Purpose was to use as a management tool for detecting ketosis

Results from study on Danish Holstein BHB data done in 2015

- Calving's between August 2012 and June 2014
- Only data from DIM 3-60
- 460,000 TD records
- 5,000 vet. diagnoses of ketosis

Genetic parameters from study on Danish Holstein BHB data done in 2015

	BHB	Acetone	Ketosis
BHB	**0,09**	0,85	0,69
Acetone	0,53	**0,05**	0,79
Ketosis diagnoses	0,07	0,09	**0,01**

Note

h^2 higher for BHB and acetone than for diagnoses

BHB and acetone tells about both clinical and subclinical ketosis

Ketose diagnoses tells about clinical ketosis

BHB and acetone data available

	Holstein	RDC	Jersey
Denmark	2013-	2013-	2013-
Sweden	Not yet collected on a regular basis		
Finland	Not yet collected on a regular basis		
% of population	75%	10%	95%

Including BHB and acetone will improve the reliability of EBV and GEBV for ketosis considerably for Holstein and Jersey

Very important for RDC to get registrations from Sweden and Finland

Upgrade NTM

1. During 2017 - NAV project – collect input from owner organizations and re estimate economic values
2. January 2018 - NAV workshop presentation and discussion of results
3. January 2018-Mid 2018 Fine-tuning based on workshop feed back - follow up work by NAV NTM project group
4. Mid/Autumn 2018 NAV workshop final recommendation
5. NAV Board decision based recommendations from the NAV workshop
6. November 2018 implementation

Joint Nordic genetic evaluation for beef bulls based on beef and beefXdairy data

- State of art
  - Use of beef semen on dairy increases significantly
  - Current national beef evaluations are difficult to keep up to date
  - Interbeef might be a door to get access to international genomic prediction for beef
  - Unofficial Nordic evaluations developed for LIM, CHA and SIM for a few traits to take part jointly in Interbeef

In 2017 a NAV project will be initiated to establish joint Nordic genetic evaluation for beef bulls based on beef and beefXdairy data

- Will include all beef breeds and traits currently evaluated nationally
- Aim to develop joint Nordic official breeding values for single traits and sub-indices