Genomic prediction, status

NAV workshop

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Tested females per country and birth year

Year	Holstein			RDC			Jersey		
	DNK	FIN	SWE	DNK	FIN	SWE	DNK	FIN	SWE
2007	350	35	54	32	79	25	74	0	1
2008	629	56	74	59	160	33	118	0	0
2009	820	136	132	83	288	100	146	1	5
2010	1010	341	119	338	1206	806	1196	1	36
2011	1232	752	227	465	1883	632	1797	3	72
2012	1679	920	191	504	1371	421	1172	10	31
2013	1272	700	65	184	414	26	106	1	0
Total	7514	2970	958	1907	6765	3264	5527	18	167
	Holstein total : 11442			RDC total : 11936			Jersey total : 5712		

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Level of genomic tested Holstein

January 2014

	Bulls with HB		Bulls with out HB		Females	
Born	Number	NTM	Number	NTM	Number	NTM
2008	304	8,9	528	1,6	759	6,8
2009	292	11,9	827	4,6	1088	7,6
2010	248	17,1	888	8,2	1471	11,1
2011	200	21,6	1499	11,9	2211	12,5
2012	213	26,6	1935	16,1	2760	15,4
2013	35	29,1	1912	22,3	2007	20,4

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Level of genomic tested RDC

January 2014

	Bulls with HB		Bulls without HB		Females	
Born	Number	NTM	Number	NTM	Number	NTM
2008	258	5,0	60	2,2	254	11,0
2009	247	5,8	343	1,1	474	10,0
2010	258	8,6	736	4,0	2957	6,7
2011	294	12,5	1515	8,1	3998	6,9
2012	248	17,7	2088	11,0	3061	8,3
2013	95	19,5	1792	14,8	910	13,8

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Level of genomic tested Jersey

January 2014

	Bulls with HB		Bulls without HB		Females	
Born	Number	NTM	Number	NTM	Number	NTM
2008	47	6,6	33	0,0	118	8,4
2009	59	8,6	124	2,7	152	8,9
2010	73	8,9	178	3,7	1377	5,5
2011	75	13,1	323	6,9	2209	6,6
2012	58	15,1	368	9,2	1543	6,1
2013	8	19,0	370	13,2	133	12,4

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Stability of NTM

- Comparison of breeding values for bulls where breeding values were based on:
  - Only genomic information in May 2011
  - Only progeny information in November 2013

Bulls are nearly all selected as young bulls before start of genomic prediction

Bulls are grouped according to GEBV's in May 2011

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Stability of NTM

EBV's based on progeny information are indicator of the efficiency of genomic prediction, but remember:

- **Reliability is not 100 %**
- **Genomic test and a progeny test are two independent tests of the same animal, and the changes will be bigger compared to a progeny test based on few daughters and a later test based on more daughters**

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Stability of NTM – level

HOL November 2013 EBV's versus May 2011 GEBV's

Level Nov. 2013	Level of GEBV, May 2011									
	-8	-4	0	4	8	12	16	20	24	28+
10	14	34	57	64	117	95	65	29	12	3
11-12				2	6	12	16	13	3	3
13-14				1	5	7	12	5	7	1
15-16				2	2	4	9	14	7	2
17-18					1	2	10	10	8	3
19-20					1		6	3	6	4
21-22						2	2	3	4	3
23-24						1	1	1	3	1
25-26								1	1	1
27-28										2
>=29							1		1	

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Stability of NTM - level

RDC November 2013 EBV's versus May 2011 GEBV's

Level Nov. 2013	Level of GEBV, May 2011							
	-8	-4	0	4	8	12	16	>20
10	13	43	62	88	73	57	20	2
11-12			3	8	4	7	6	1
13-14			2	3	3	8	1	1
15-16			1	2	2	6	3	1
17-18			1	1	4	8	4	1
19-20					2	4	1	2
21-22						2	2	2
23-24					2	1	2	
25-26								
27-28							2	

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Stability of NTM - level

Jersey November 2013 EBV's versus May 2011 GEBV's

Level Nov. 2013	Level of GEBV, May 2011					
	-4	0	4	8	12	16
10	4	6	28	31	17	6
11-12		1	3	3	3	
13-14				1	6	2
15-16				3	2	1
17-18		1		1	2	
19-20					1	1
21-22				1		
23-24				1		
25-26				1	1	
27-28						
29-30						

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GenVik-Plus bulls - level

November 2013 EBV's

Level Nov. 2013	HOL	RDC	JER
<=10	5	1	2
11-12	2		
13-14	3		1
15-16	4	2	1
17-18	9		
19-20	5		
21-22	2		
23-24		1	
25-26	2		
27-28	2	1	
>=29	1		

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Stability of GenVik-Plus bulls

NTM

	Bulls	NTM May 2011	NTM Nov 2013	Diff NTM	Genetic progress
HOL	35	23.7	16.8	-6.9	5
RDC	5	18.6	16.4	-2.2	4
JER	4	15.5	10.0	-5.5	4

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Female in reference group

Opportunity:

- Increase reference group and reliabilities of GEBV

Challenge:

- Avoid bias because of preferential treatment

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LD-project

Females with and without production
January 2014

	DNK	FIN	SWE	Total
RDC				
With prod.	328	1505	1218	3051
Without prod.	313	1416	1039	2768
JER				
With prod.	2300		37	2337
Without prod.	2120	1	48	2169

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Max increase in reference group by inclusion of females

	HOL	RDC	JER
Bulls	25600	7800	1240
Total	30700	13200	4300
Increase	20%	69%	247%

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Females in reference population

Remember:

- Cows have lower reliability and they are less informative
- EBV's for elite cows may be biased
- Cows are only informative if EBV's are calculated by an Animal model, not a Sire model

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Preliminary results of inclusion of females in reference group

	RDC	JER
Production	X	XXX
Udder health	XX(X)	XXX
Body	XX	XXX
Feet and legs	-	X
Mammary	XXX	XXX
Milking speed	XXX	XXX
Temperament	-	-

XXX ≈ 5 pct. units

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Current challenges

Especially RDC and Jersey

- Bulls - increased in NTM, when getting progeny (NTM > gNTM)
- Heifers from LD project - lower GEBV than pedigree index
- The difference is biggest for yield (largest genetic trend)

Improvements are in test

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Optimal use of all information

- More reference animals
  - Exchanged bull genotypes and genotyped cows
  - More ref animals – hopefully higher reliability – has to do restandardization
  - Changes expected
- Improved combination of genomic and phenotypic information

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Blending – routine (GEBV)

Phenotypic information

Genomic information

Challenge to avoid double counting of information

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Blending – future (GEBV)?

Phenotypic information

Genomic information

Can we better avoid double counting of information?

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One step (research focus)

Phenotypic information

Genomic information

All information utilised in the same step:

- No risk of double counting
- Optimal use of information
- Handling selection

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Focus coming months

- Include more genotypes in ref population
  - Jersey include ref bulls from USA/CDN
  - Cows in ref population (which cows and traits)
- Optimal blending
  - Avoid double counting
- Reliabilities
- One step
- Follow up GMACE

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NAV expects to make stepwise improvements in the routine genomic prediction in the coming months

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