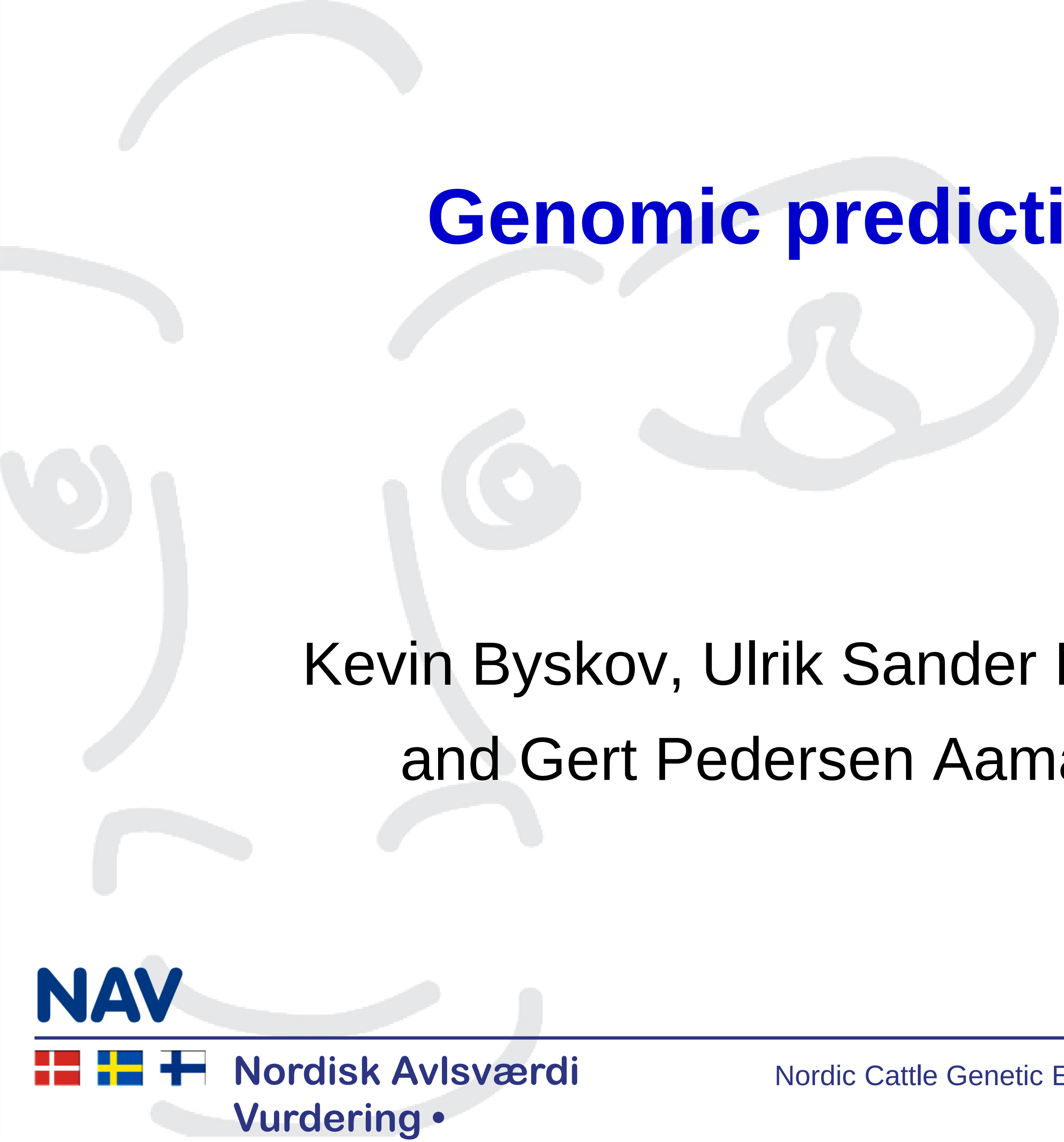


Genomic prediction

Kevin Byskov, Ulrik Sander Nielsen
and Gert Pedersen Aamand

Present 2-step method

(HOL), RDC ,JER

SNP and deregressed proof (DRP)

IMPROVEMENT

↓

Direct genomic values (DGV)

↓

Genomic enhanced breeding values (GEBV)

IMPROVEMENT

Basic data: Deregressed proof

Registered data (kg protein, mastitis diagnoses)

Systematic effects
(calving age, herd, ect.)

EBV

Depends on reliability

Adjusted phenotype

Deregressed proof (DRP)

Deregressed proof (DRP)

- genotyped animals

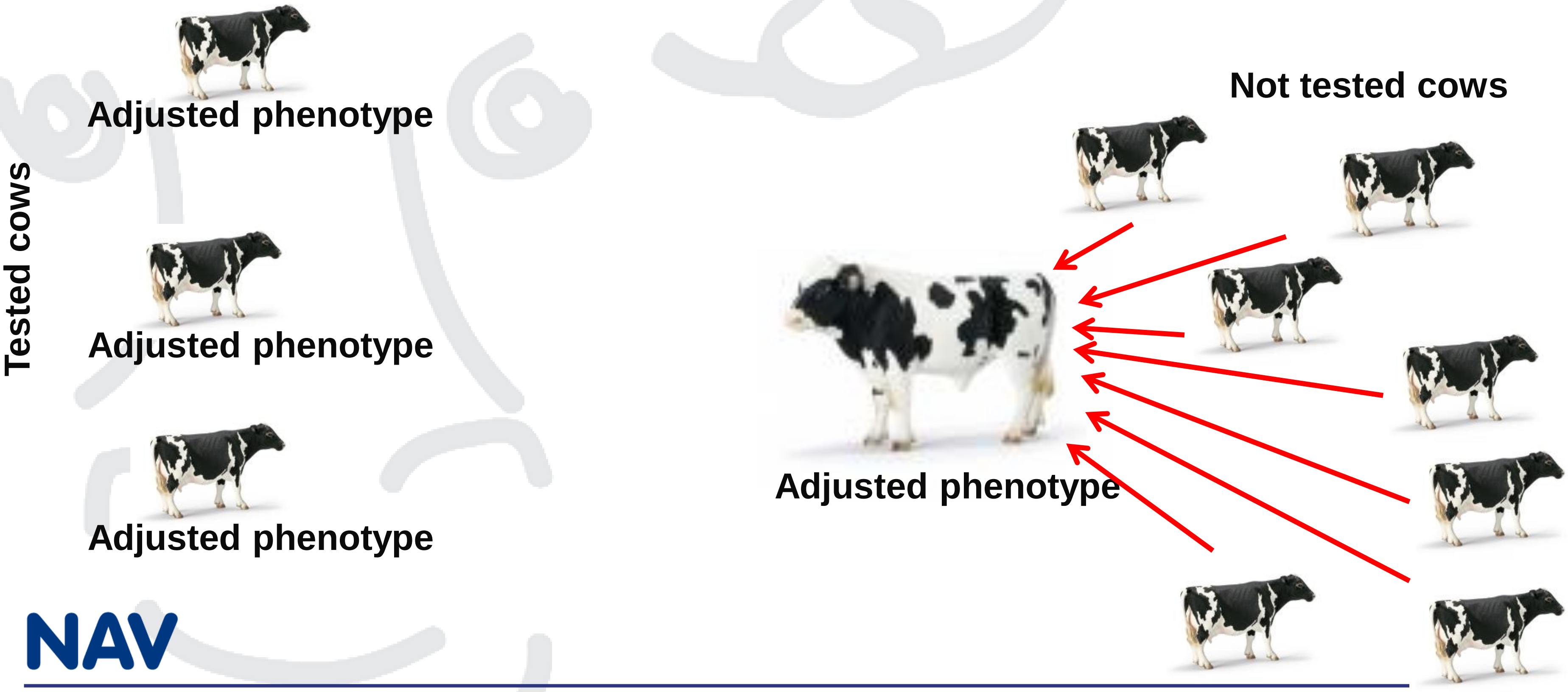
Females: Own phenotypic deviation from parent average – if animal should have the calculated EBV

Bulls: Phenotypic deviation of daughters is used as a phenotype of the bull. Deviation from parent average of the bull – if the bull should have the calculated EBV

Each phenotype is only included once!

Females in reference group

- information from 10 daughters of a bull with yield in 1. lactation



Tested cows

Adjusted phenotype

Adjusted phenotype

Adjusted phenotype

Not tested cows

Adjusted phenotype

DRP

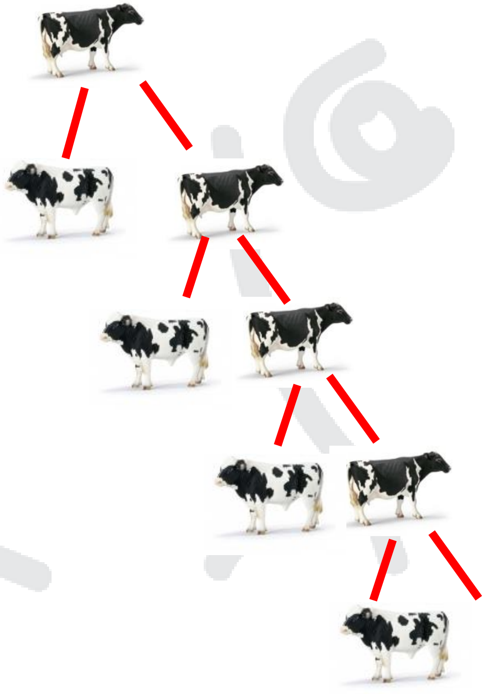
- use of pedigree information for tested animals

- Previous routine: Sire, MGS
- Now: Sire, Dam (Animal model)
- Advantage: DRP are closer to the true yield deviation of the animal

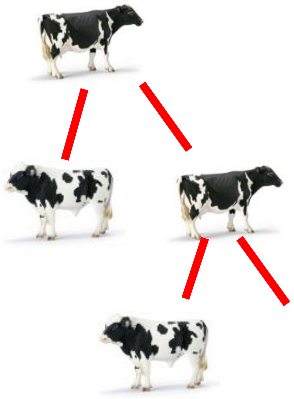
DRP

- use of pedigree information for tested animals

Now



Previously



Pedigree: 0,5 + 0,25 = 0,75 + genetic group

Pedigree: 0,5 + 0,25 + 0,125 + 0,0625 = 0,9375 + genetic group

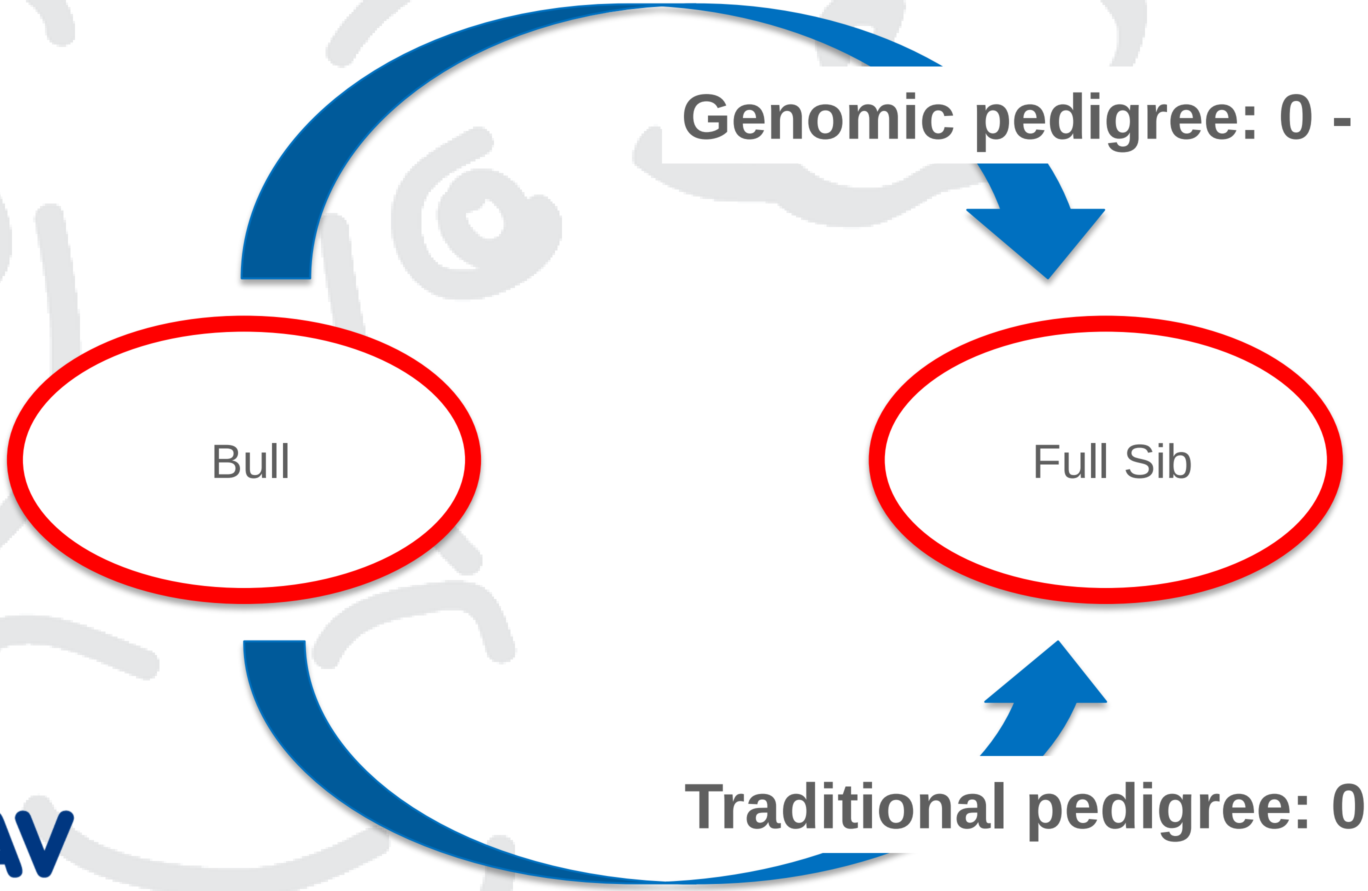
Calculation of BV

Tested cows and proven bulls with DRP

- DRP = μ + Animal + e

- Type of output BV depends on pedigree:
  - Genomic pedigree → DGV (genomic value)
  - Traditional pedigree → EBV (traditional value)

Pedigree on the basis of SNP



Genomic pedigree: 0 - 1

Bull

Full Sib

Traditional pedigree: 0,5

Calculation of BV

Tested heifers and young bulls without DRP

- ”Missing DRP” = μ + Animal + e
- Type of BV depends on used pedigree:
  - Genomic pedigree → DGV
  - Traditional pedigree → Pedigree index

Blending (GEBV)

- Combines DGV and EBV
- DGV: Pedigree (genomic), performance (DRP)
- EBV: Pedigree (traditional), performance (DRP)

Combination – BUT much overlap of information

New method better to avoid ”double counting” – makes it possible to include females in reference group

Reference population

January 2015

	Reference population	
	Bulls	Cows
Holstein	27500[a)]	(8400)
RDC	8150[b)]	12700
Jersey	2450[c)]	8550

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

Genomic information gives higher reliability for candidates!

Reliability for 4 latest birth years of proven bulls compared to reliability on pedigree information

Example:

Validation reliability on DGV	45%
Validation reliability on pedigree	20%
Extra reliability	25%

Extra reliability
– in addition to pedigree information for RDC

	Reference population	
	Bulls	**Bulls and cows**
Yield	0,13	**0,18**
Growth	0,13	**0,14**
Fertility	0,14	0,14
Birth	0,18	0,18
Calving	0,02	0,02
Udder health	0,17	**0,23**
Other diseases	0,14	0,14
Frame	0,24	**0,29**
Feet&Legs	0,24	**0,33**
Udder	0,23	**0,30**
Milking speed	0,17	**0,22**
Temperament	0,18	0,21
Longevity	0,07	0,07
Claw health	0,11	0,11

Extra reliability

– in addition to pedigree information for HOL

	Reference population	
	Bulls	**Bulls and cows**
Yield	0,33	**0,35**
Growth	0,24	0,24
Fertility	0,32	0,32
Birth	0,31	0,31
Calving	0,22	0,22
Udder health	0,39	**0,41**
Other diseases	0,06	0,06
Frame	0,36	**0,36**
Feet&Legs	-	**-**
Udder	0,52	**0,52**
Milking speed	0,46	**0.46**
Temperament	0,14	0.14
Longevity	0,21	0.21
Claw health	(0,00)	(0,00)

Extra reliability
– in addition to pedigree information for JER

	Reference population	
	Bulls	**Bulls and cows**
Yield	0,16	**0,22**
Fertility	0,17	0,17
Birth	0,00	0,00
Calving	0,00	0,00
Udder health	0,09	**0,16**
Other diseases	0,00	0,00
Frame	0,19	**0,30**
Feet&Legs	0,05	**0,13**
Udder	0,26	**0,29**
Milking speed	0,15	**0,34**
Temperament	0,00	0,00
Longevity	0,11	0,11

Difference in reliability between breeds

- Reliability for RDC and Jersey still 12-15% point lower than HOL – but higher than before!
- Expect increase in reliability when more genotyped RDC and Jersey cows are included in reference populationen

Correlations

- previously (May 2014) and now (since August 2014)

	RDC		Jersey	
Reference group:	Genotyped animals			
	Young bulls and heifers	Cows	Young bulls and heifers	Cows
Without cows	0.97-0.99	0.97-0.99	0.94-0.96	0.94-0.96
With cows	0.88-0.93	0.89-0.92	0.77-0.85	0.87-0.90

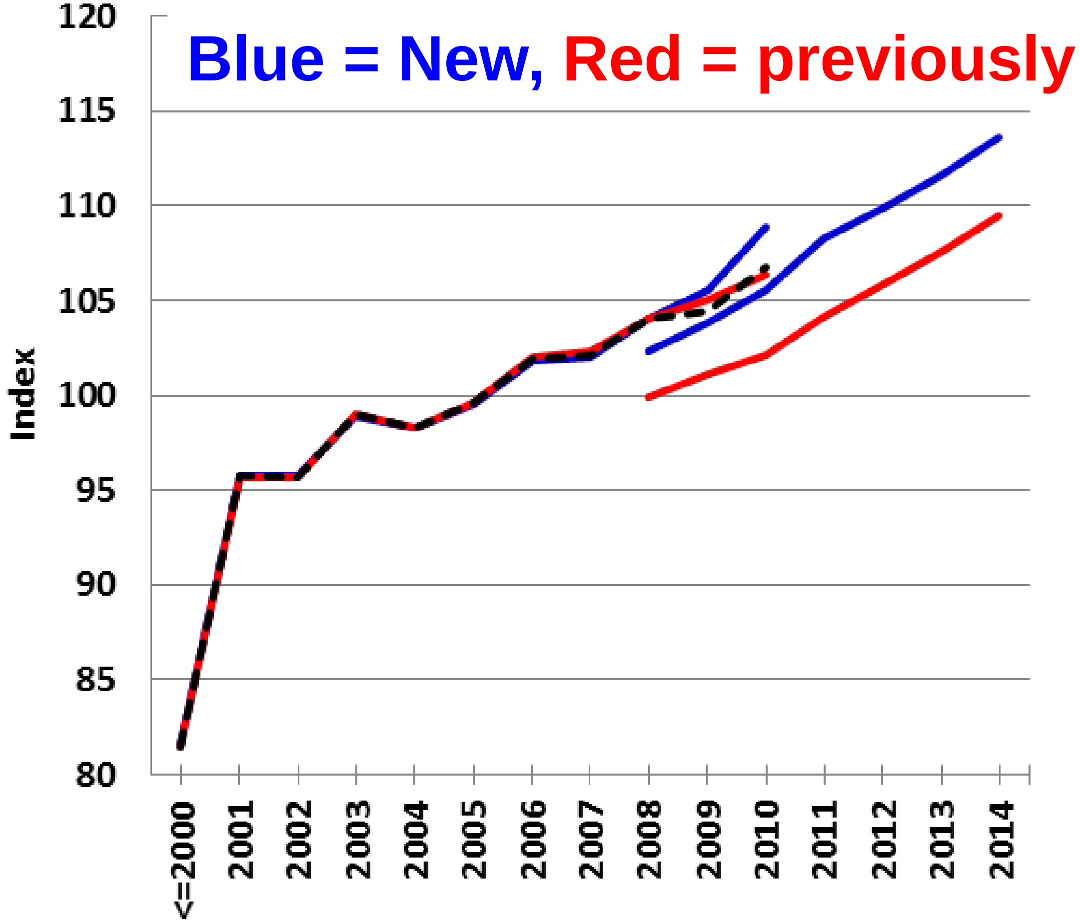
Genetic level

Genetic level for young bulls and heifers has increased

RDC:

- **4 index units for yield and NTM**
- **0-2 index units for other traits with cows in the reference population**

Yield: RDC Sire trends



Blue = New, Red = previously

Summary

– What is improved?

RDC/JER	Previous routine	New	
Pedigree	Sire-Maternal grandsire	Animal Model	Important for candidates and cows – only traits with strong trend
Reference population	Bulls	Bulls and cows	(8400 HOL), 12700 RDC, 8550 JER
Blending method	Developed by MTT (2010)	Improved by MTT (2013/14)	Better to avoid “Double counting”

Challenges

Calculation of DRP

- Method sensitive for traits with low heritability when females are included in reference group or reference group is not uniform
- Causes instability in DGV
- Improved method is expected to be introduced in February 2015
- Improvement of genomic prediction is a continuous process

Tested females per country and birth year

Year	Holstein			RDC			Jersey		
	DNK	FIN	SWE	DNK	FIN	SWE	DNK	FIN	SWE
2007	352	37	56	33	81	27	75	0	1
2008	641	58	75	66	166	33	118	0	0
2009	868	138	137	91	292	107	149	1	5
2010	1093	348	144	403	1842	1249	2175	1	42
2011	1547	1099	353	825	3556	1770	3925	6	87
2012	2153	1442	557	1098	3384	1908	4119	15	110
2013	3257	2045	1335	1360	2839	1920	2097	11	81
2014	1877	886	432	826	1001	561	990	7	37
Total	12371	6082	3184	4838	13230	7620	13742	41	375
	HOL total : 21.637 Last year: 10.195			RDC total : 25.688 13.752			Jersey total : 14.158 8.446		

Level of genomic tested Holstein

November 2014

	Bulls with HB		Bulls with out HB		Females	
Born	Number	NTM	Number	NTM	Number	NTM
2008	305	5,2	534	-0,9	774	3,5
2009	302	8,3	818	1,4	1141	4,3
2010	250	13,6	898	5,2	1583	8,9
2011	200	18,5	1529	9,6	2916	9,9
2012	223	23,2	1954	13,0	3972	12,1
2013	190	28,7	2183	18,2	6083	15,6
2014	8	30,5	2106	22,0	1996	19,2

Level of genomic tested RDC

November 2014

	Bulls with HB		Bulls without HB		Females	
Born	**Number**	**NTM**	**Number**	**NTM**	**Number**	**NTM**
2008	258	2,0	60	2,7	263	5,4
2009	247	4,8	343	2,5	488	5,2
2010	256	10,6	736	5,6	2957	3,9
2011	293	13,6	1517	9,6	5935	6,2
2012	267	18,6	2070	11,9	5863	8,6
2013	248	22,1	2098	14,5	5055	12,9
2014	78	25,6	1481	18,7	974	17,3

Level of genomic tested Jersey

November 2014

	Bulls with HB		Bulls without HB		Females	
Born	Number	NTM	Number	NTM	Number	NTM
2008	47	2,8	33	-1,6	204	5,4
2009	58	7,2	124	3,2	243	5,2
2010	72	9,2	179	3,0	2636	3,1
2011	73	10,5	325	5,2	4259	4,1
2012	58	12,9	370	7,8	4193	5,2
2013	66	15,9	381	10,2	2107	8,6
2014			345	12,8	565	10,8

Stated from practice

”First time a bull gets an EBV based on a progeny test it some times deviates/drops significantly from the GEBV but closes in on GEBV in subsequent runs”

and

“Top GEBV bulls tend to drop in level when daughters enter production”

Current thresholds going from GEBV to EBV

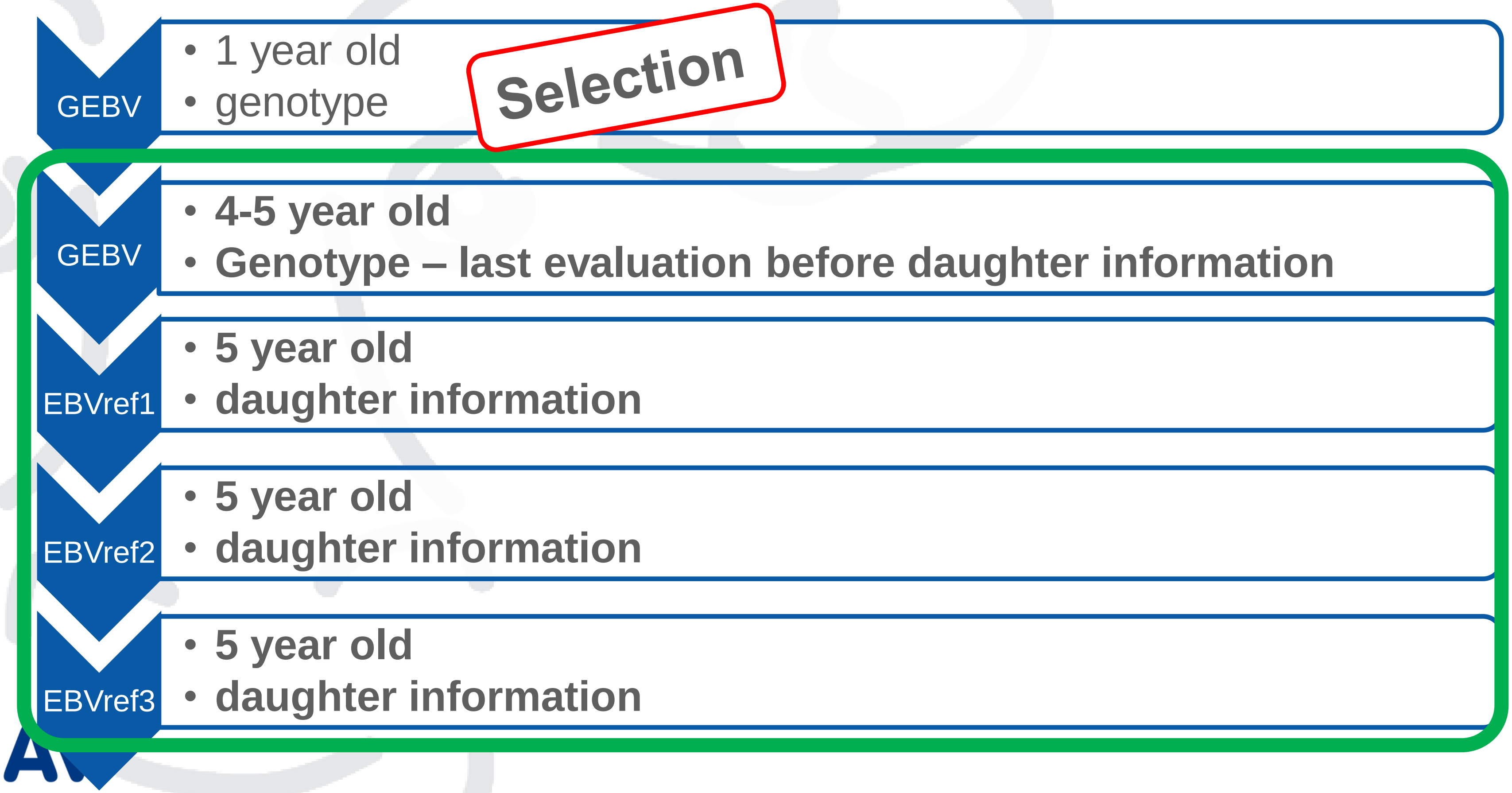
Trait	Reliability EBV
Yield, Beef	60%
Type traits, temperament, milkability	15 daughters
Longivity, calving traits direct	50%
Mastitis, claw health, calving traits maternal, young stock survival	40%
Fertility, other diseases	35%

- **GEBV reliability are > than EBV reliability threshold**

How well do the bulls meet expectations?

- HOL - Official GEBVs/EBVs for 2012-2014
  - Yield
  - Udder health
  - NTM
    - Depending on trait 554-586 bulls

- Standard deviations of (EBV – GEBV)
  - Do the 1st indices have larger STDVs



- 1 year old
- genotype

- **4-5 year old**
- **Genotype – last evaluation before daughter information**

- **5 year old**
- **daughter information**

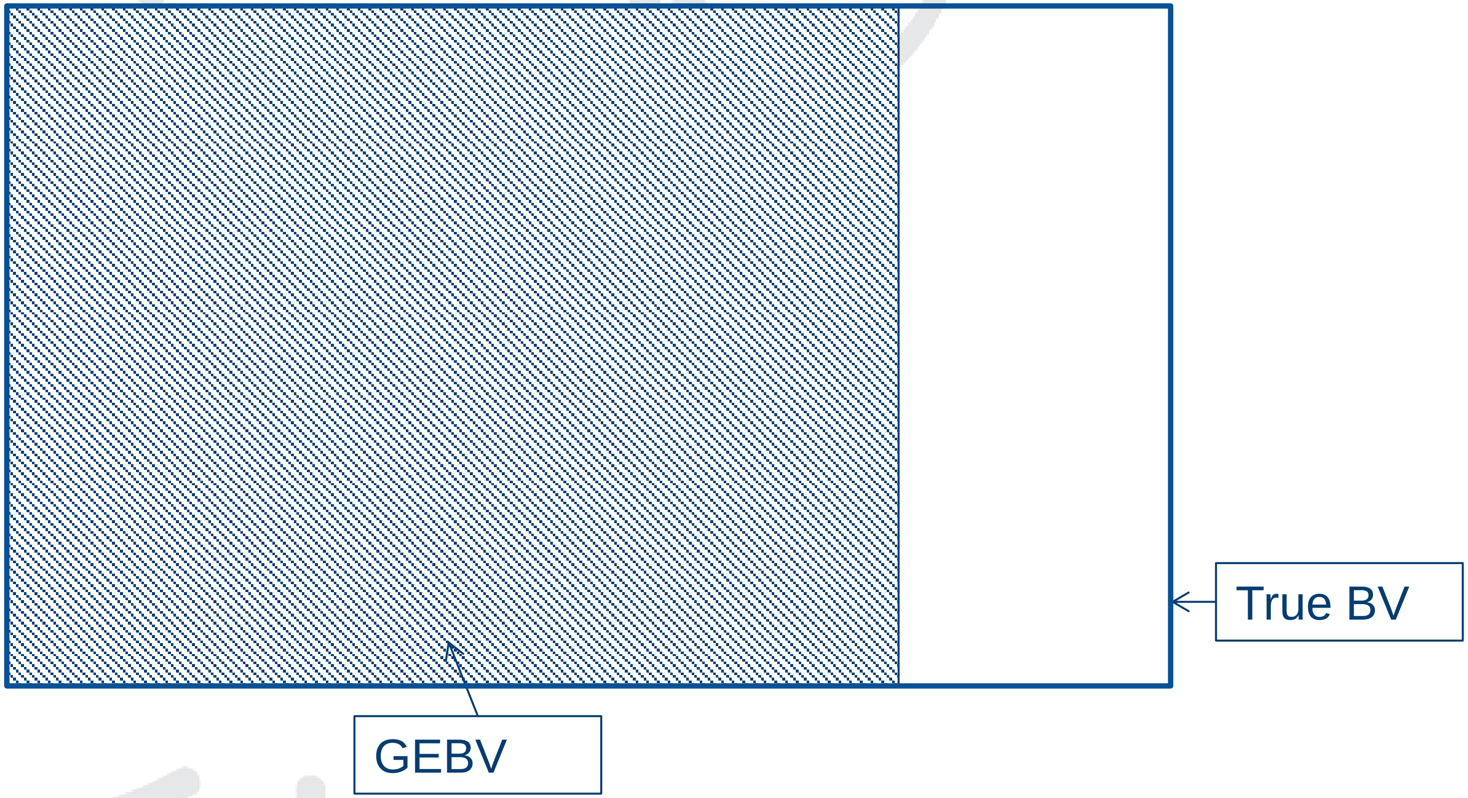
- **5 year old**
- **daughter information**

- **5 year old**
- **daughter information**

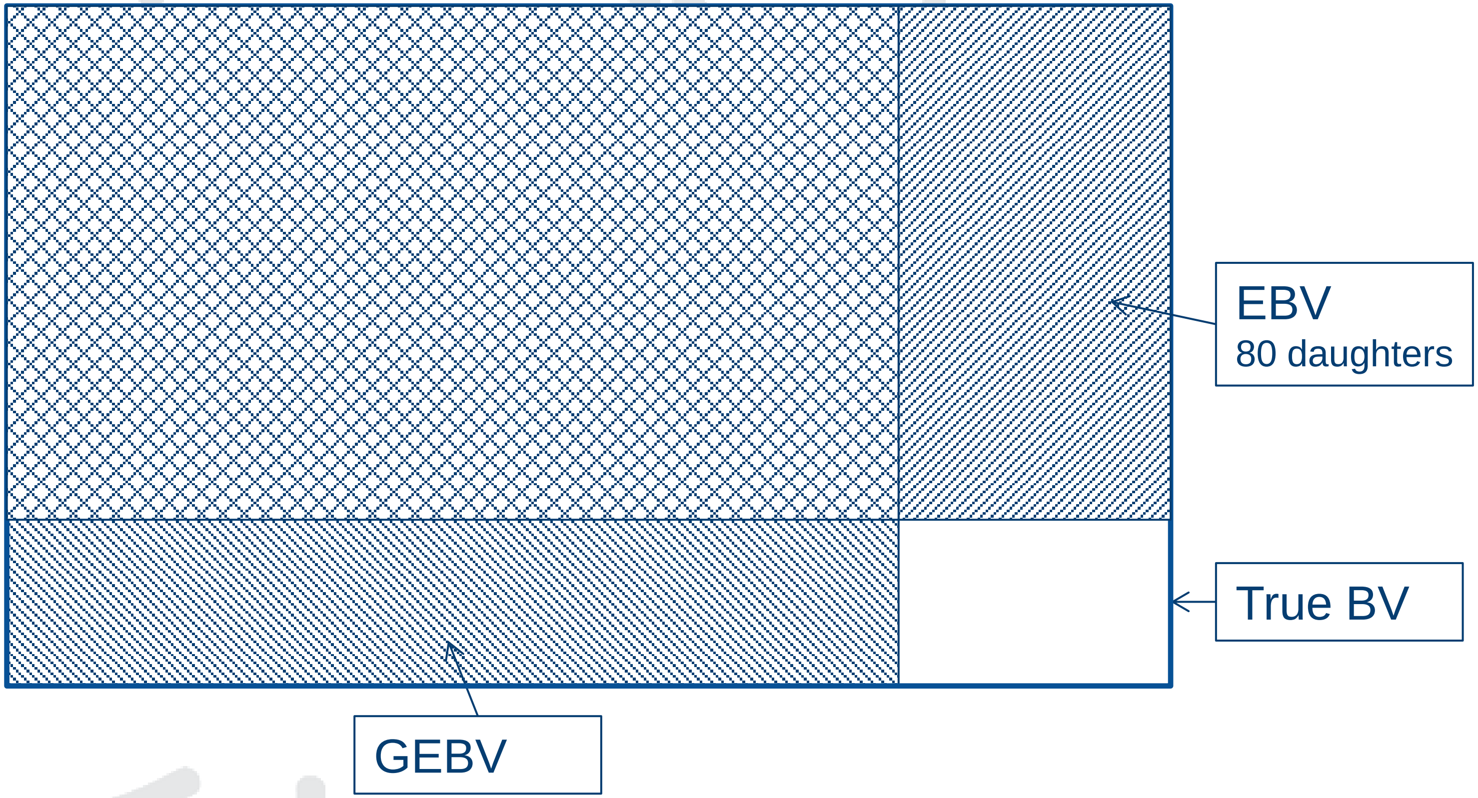
Expected results

- If a bull have GEBV NTM = 30 we do expect EBV NTM < 30!
  - The regression $\beta_{EBV,GEBV}$ expected < 1
  - …unless the bull has thousands of daughters.
- Why?
  - Not Part-Whole, but to some degree independent data in the two evaluations.
  - $E(\beta_{EBV,GEBV}) = r^2_{EBV}$ for independent tests

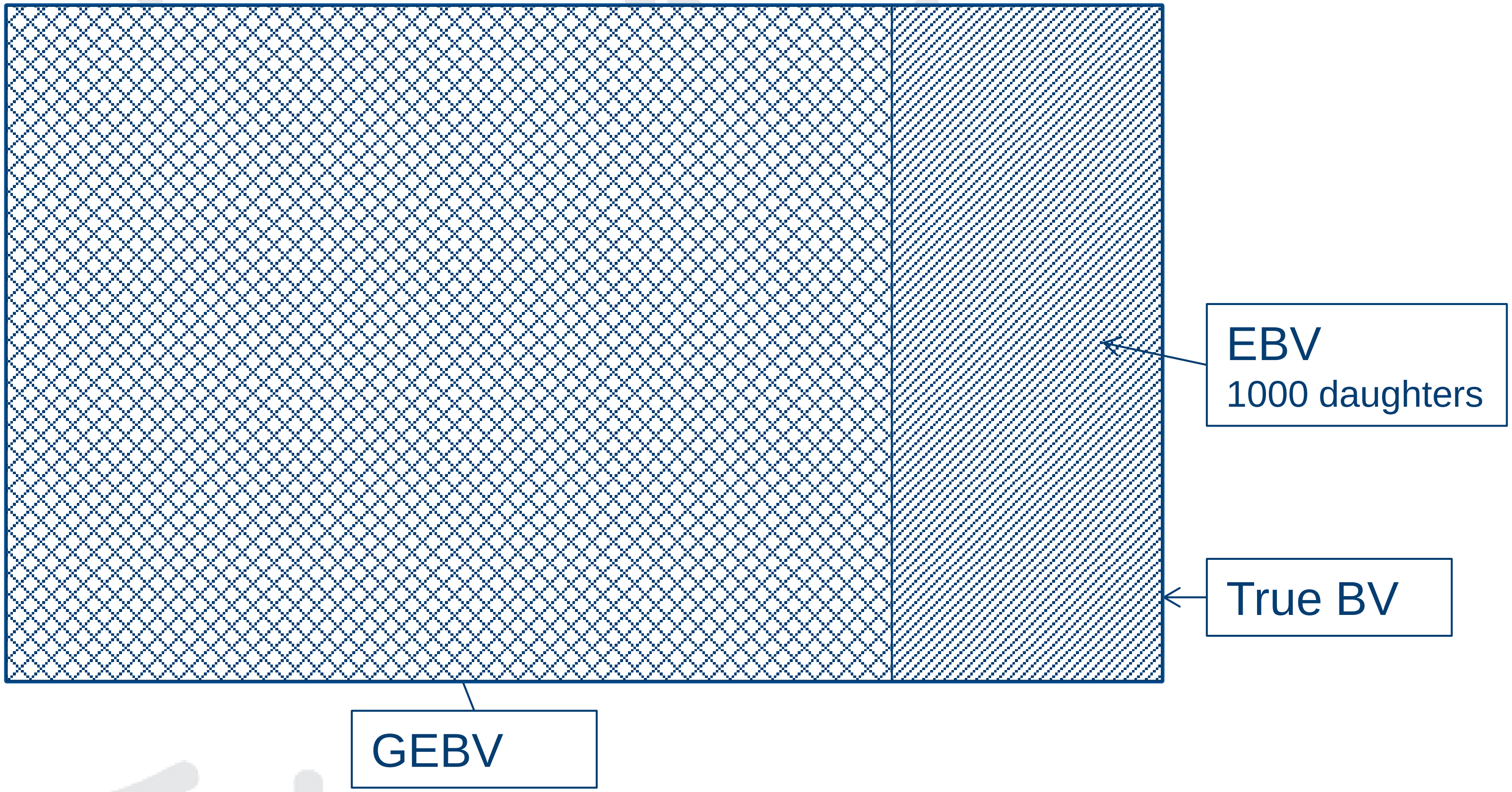
Expected results



Expected results
Not Part-Whole - $\beta_{EBV,GEBV} < 1$



Expected results
Part-Whole - $\beta_{EBV,GEBV} = 1$

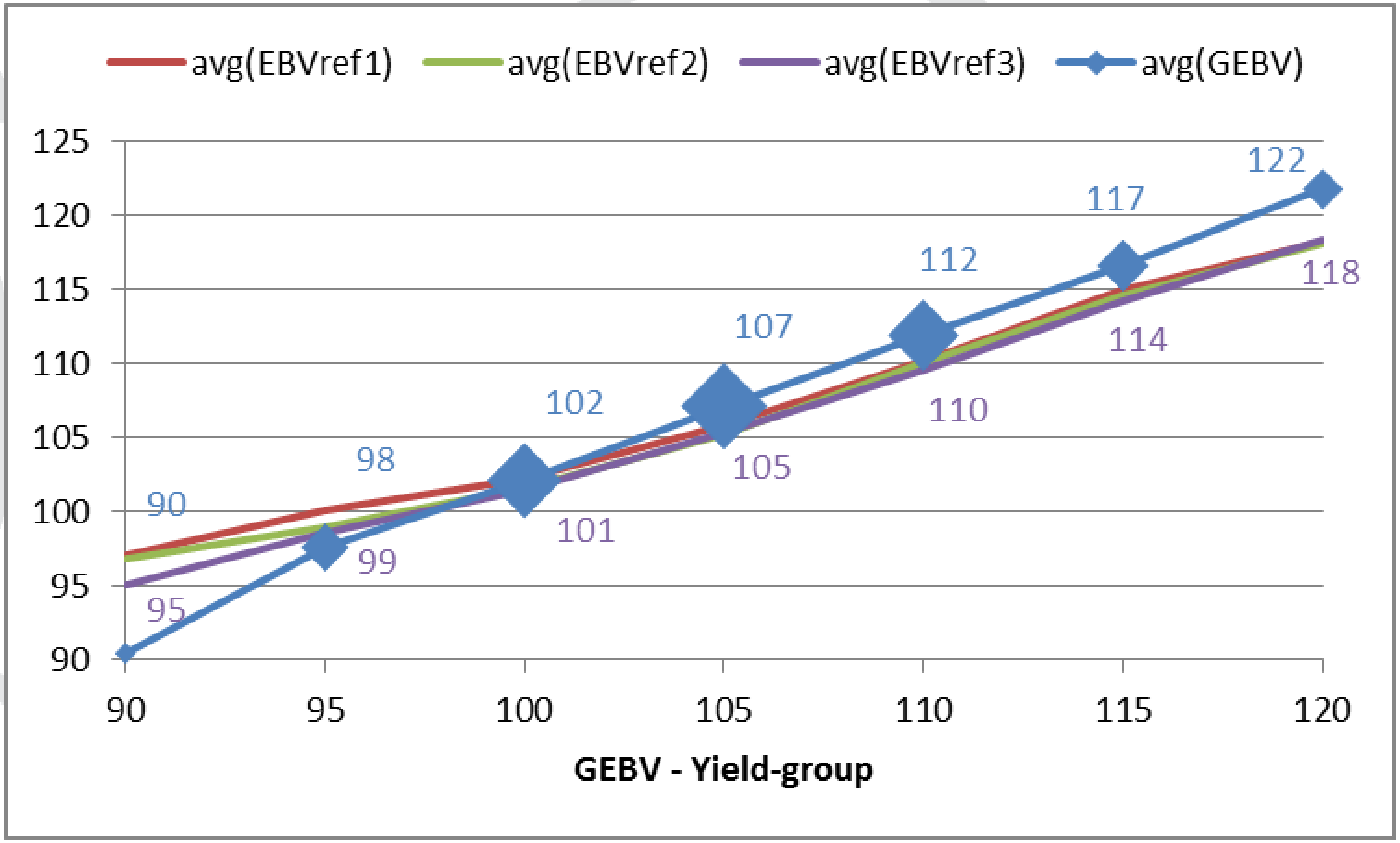


EBV
1000 daughters

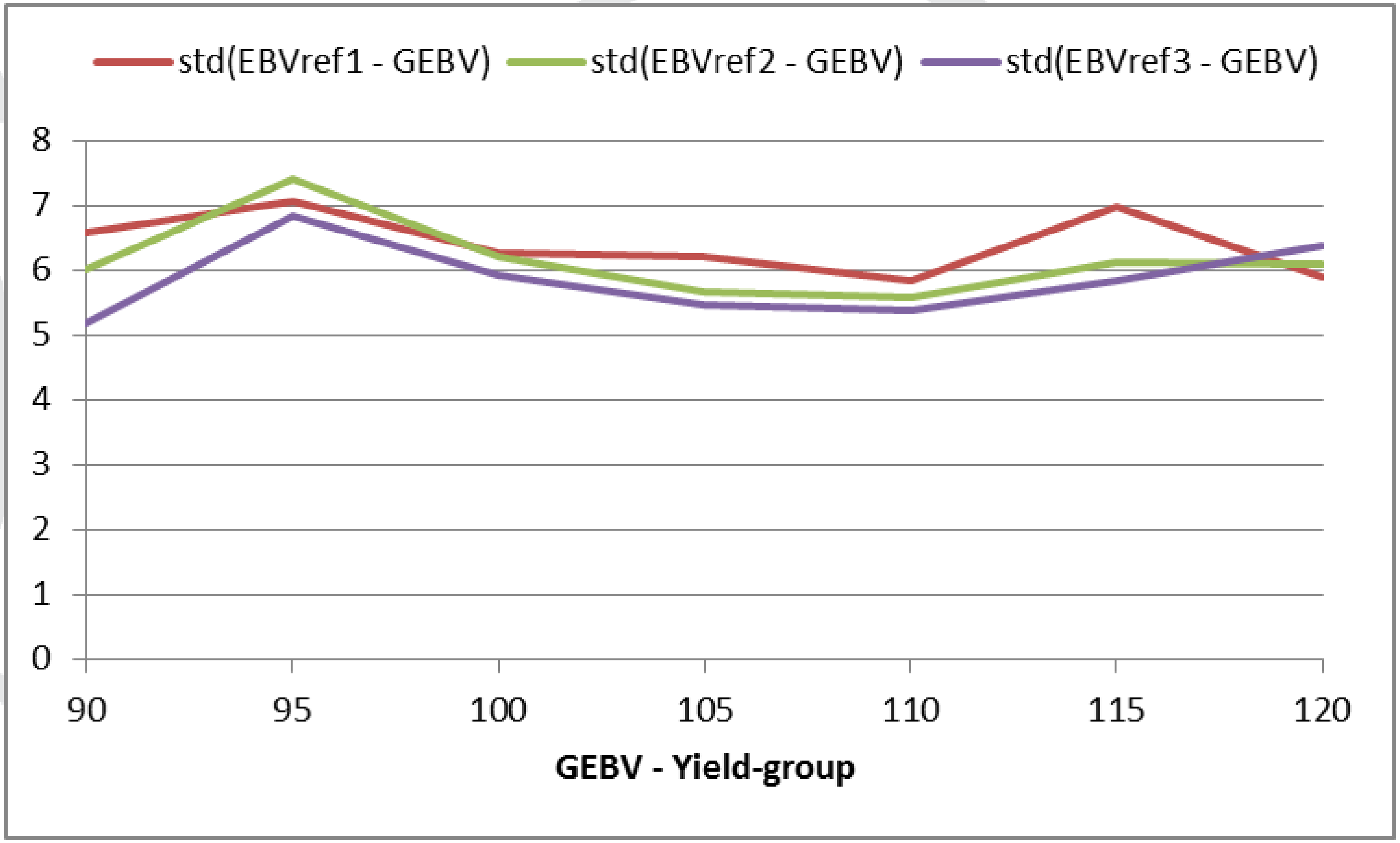
True BV

GEBV

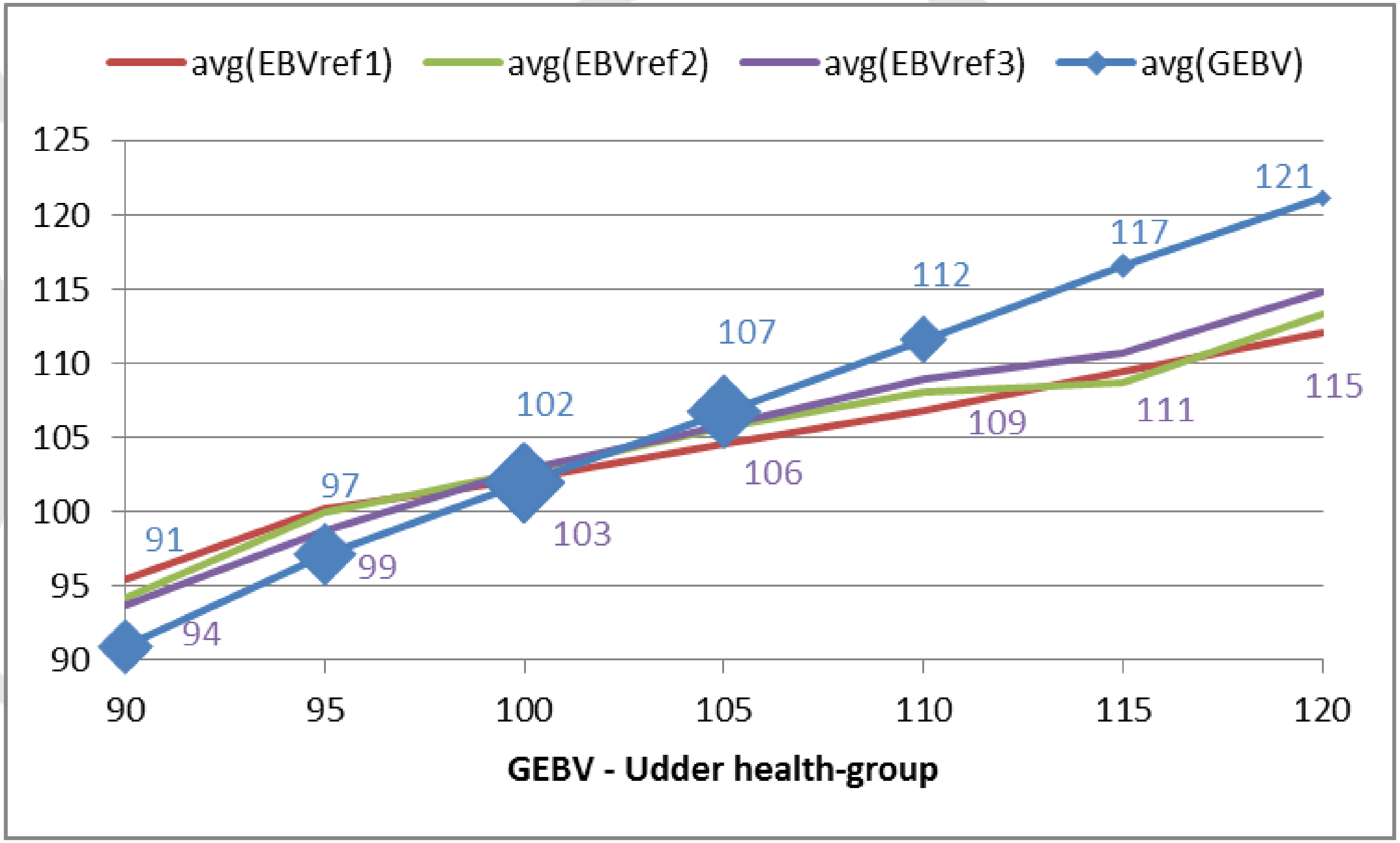
HOL Yield


avg(EBVref1)
avg(EBVref2)
avg(EBVref3)
avg(GEBV)
125
120
115
110
105
100
95
90
90
95
100
105
110
115
120
GEBV - Yield-group
90
98
102
107
112
117
122
95
99
101
105
110
114
118

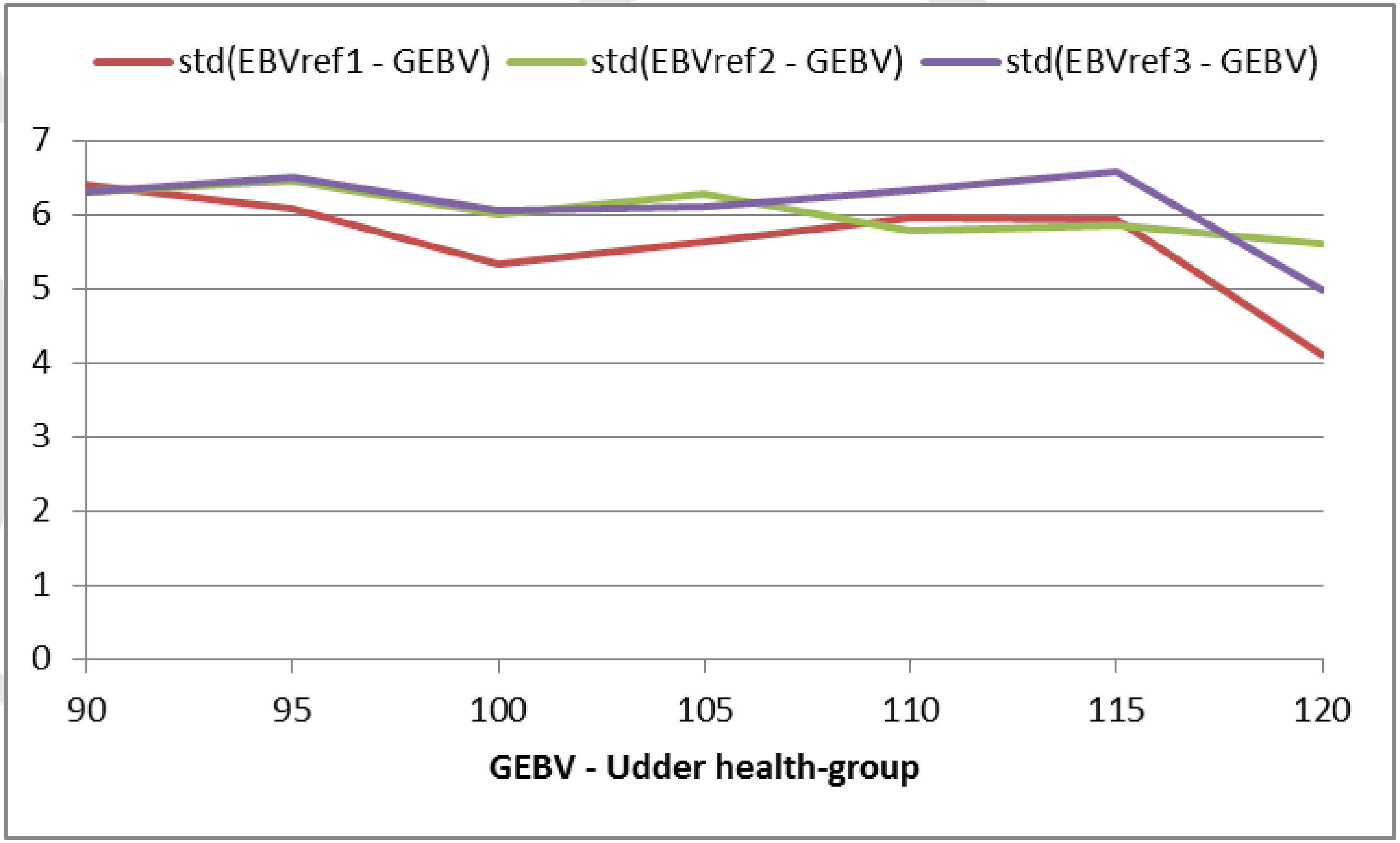
HOL Yield – (EBV-GEBV)



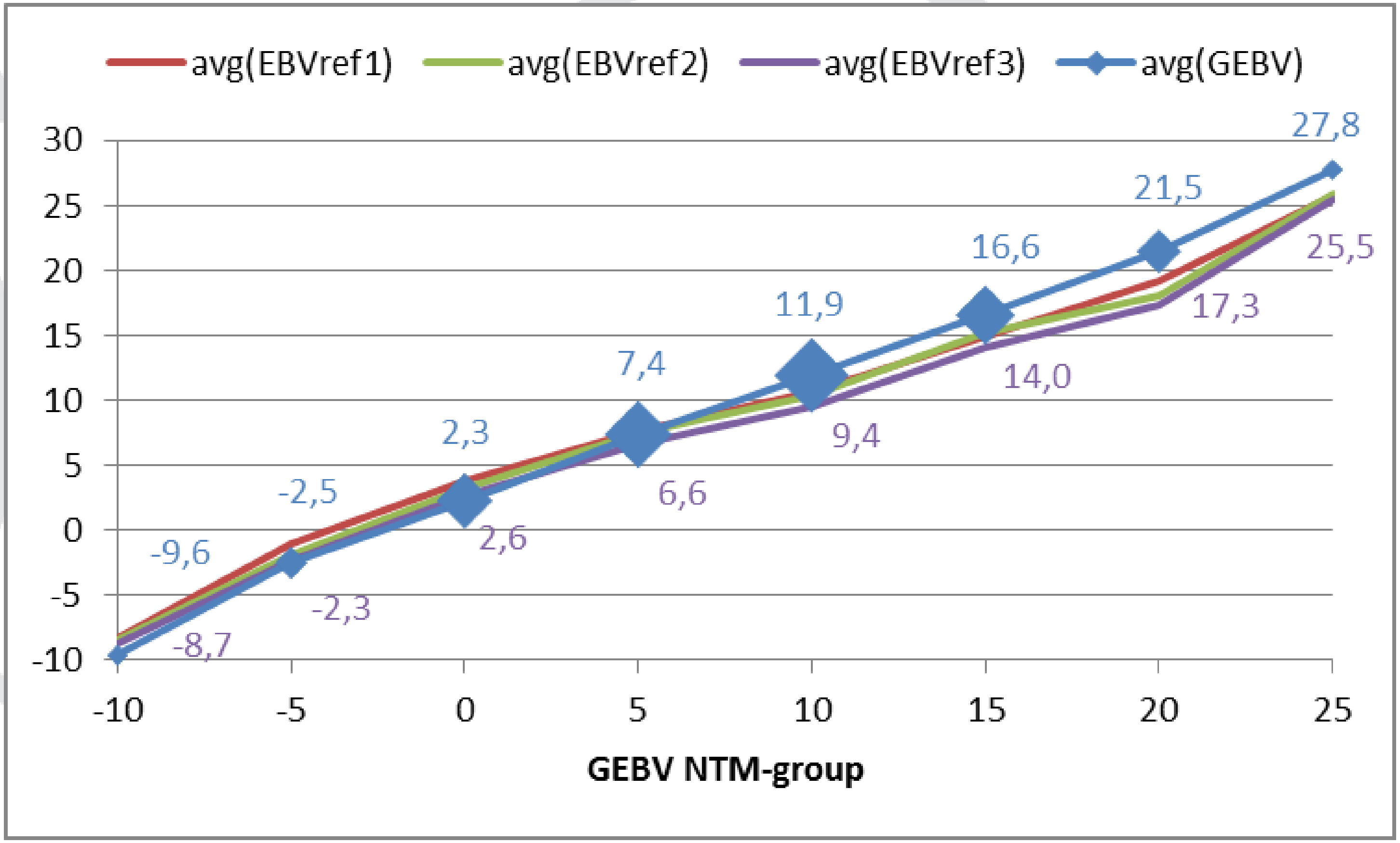
HOL Udder health



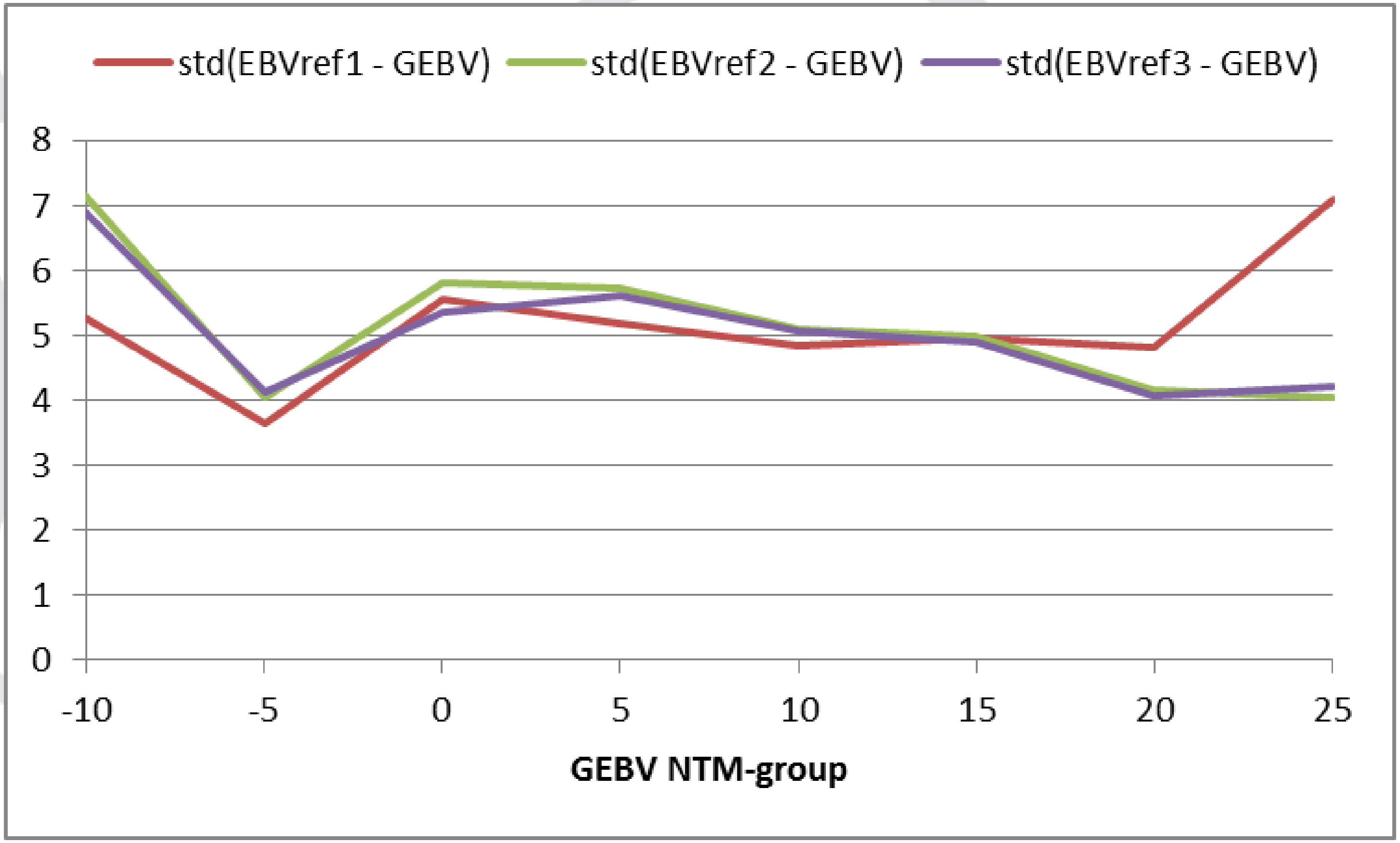
HOL Udder health – (EBV-GEBV)



HOL - NTM


avg(EBVref1)
avg(EBVref2)
avg(EBVref3)
avg(GEBV)
30
25
20
15
10
5
0
-5
-10
-10
-5
0
5
10
15
20
25
GEBV NTM-group
-9,6
-2,5
2,3
7,4
11,9
16,6
21,5
27,8
-8,7
-2,3
2,6
6,6
9,4
14,0
17,3
25,5

HOL NTM – (EBV-GEBV)

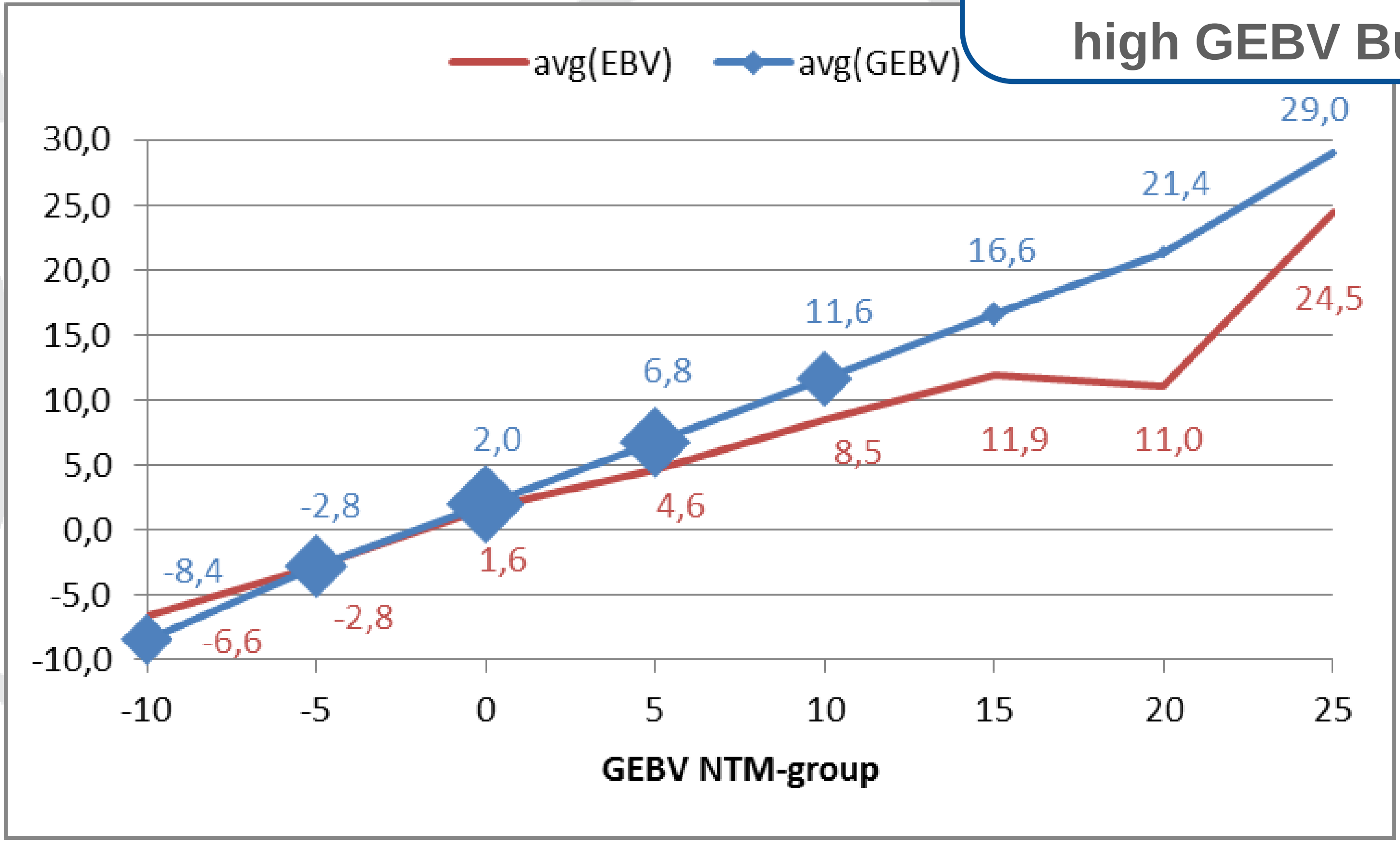


How well do the bulls meet expectations?

- RDC & JER changed genomic model in AUG14.
  - Changed to AM and cows in reference

- GEBVs calculated for 4 birth years of progeny tested bulls.
  - Bulls own EBVs and daughters EBVs not in reference population.

RDC - NTM

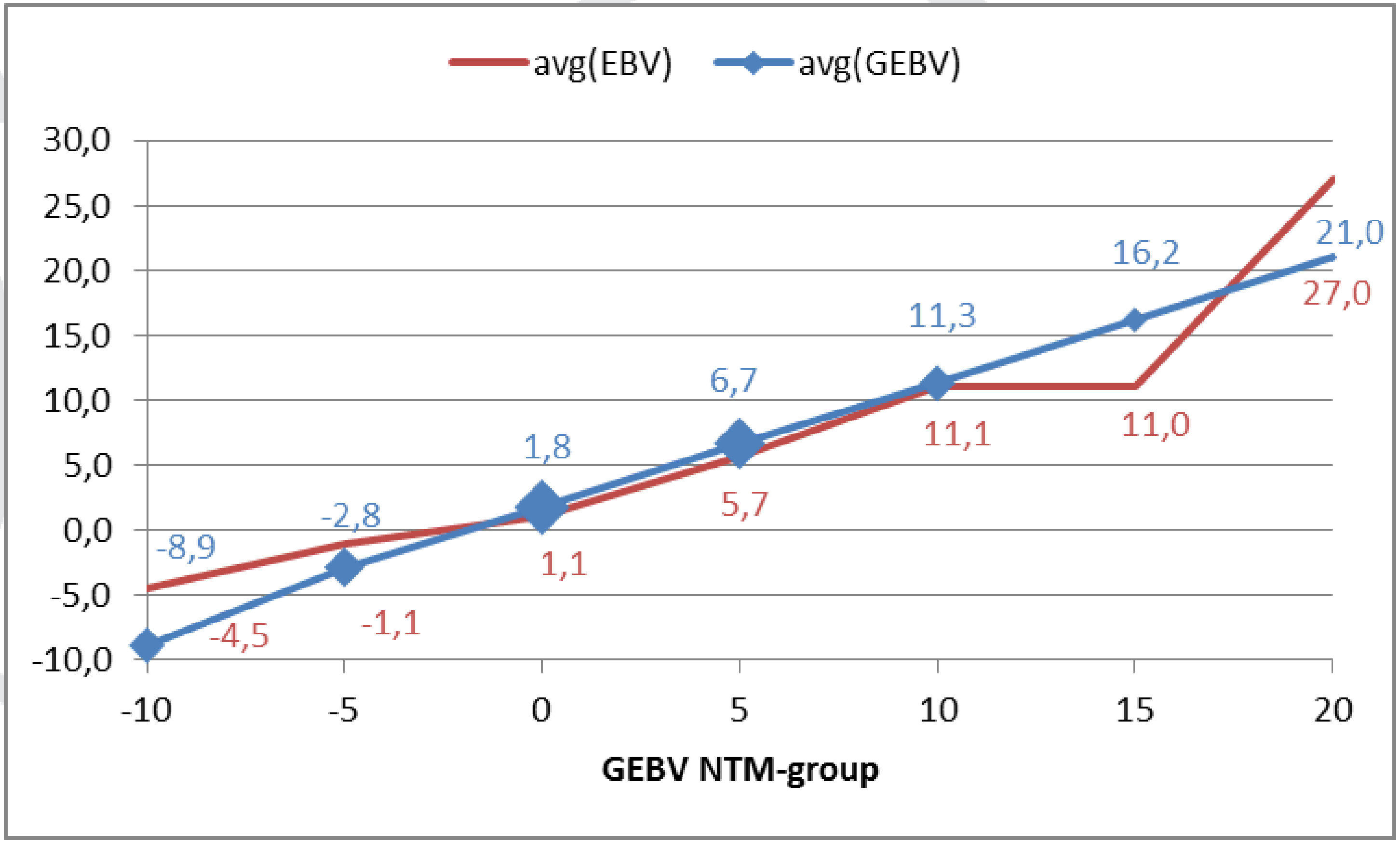


$\beta_{EBV,GEBV}$ **a little low**

↓

Tend to overestimate high GEBV Bulls

JER - NTM


avg(EBV)
avg(GEBV)
30,0
25,0
20,0
15,0
10,0
5,0
0,0
-5,0
-10,0
-10
-5
0
5
10
15
20
GEBV NTM-group
-8,9
-2,8
1,8
6,7
11,3
16,2
21,0
-4,5
-1,1
1,1
5,7
11,1
11,0
27,0

Conclusion

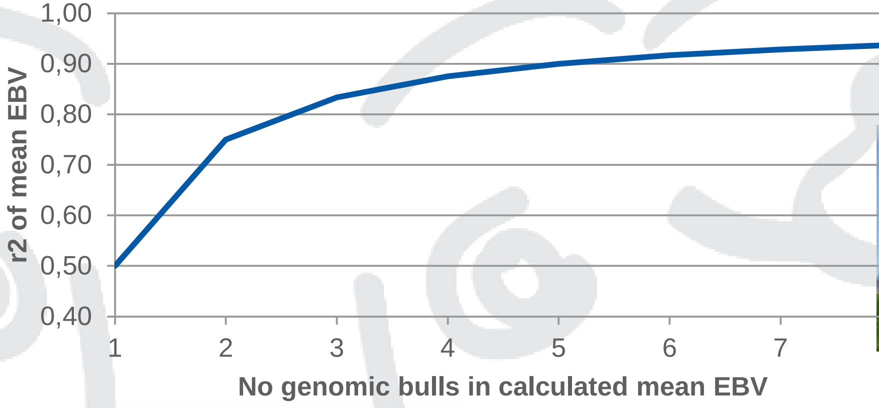
- Results generally looks as expected.
- Average EBV lower as not Part-Whole.
- $\beta_{EBV,GEBV}$ for RDC NTM looks a little low.
    - Quite different population structure.
    - Best GEBV group get best avg. EBV.
- Action
    - Keep focus that top bulls get expected results

Conclusion

- Lower threshold r^2_{EBV} than GEBV r^2
  - Larger STDV for (EBVref1-GEBV) HOL yield

- Actions
  - NAV will increase thresholds for r^2_{EBV} breedwise depending on GEBV r^2
  - Combine daughter information and genomic information (Part-Whole)

5-8 Genomic tested bulls has same expected change in EBV as one progeny tested bull



Focus less on single bulls and more on a group of bulls (5-8)

Implemented GEBV in 2014

Date	Comment
February 2014	Adjustment Holstein longevity
March 2014	US Jersey bulls included in ref population
May 2014	Publication age decreased from 17 month to 10 month
July/August 2014	Cows in reference populations and revised blending method applied for RDC and Jersey.
August 2014	Results from GMACE routine evaluation published
November 2014	Cows in reference populations and revised blending method applied for Holstein yield traits

Implementation plan GEBV 2015

Date	Comment
February 2015	Cows in reference populations and revised blending method applied for Holstein remaining traits
Spring 2015	All type traits at each evaluation – GEBV for females
Spring 2015	Official GEBV reliabilities
Spring/summer 2015	Young stock survival
2015	Weekly evaluations
2015	Cows in ref for more traits – fertility, claw health, longevity

More frequent genomic prediction

- Aim GEBV for bull calves available at a younger age than today
  1. Efficient registration of animal and collection of DNA (farmer and VG)
  2. More frequent and faster genotyping (GenoSkan)
  3. More frequent genomic prediction (NAV)

Room for improvement in all 3 steps!

Steps in routine genomic prediction

Step	
1. NAV pedigree file	Information from all three countries – only new animals needed
2. Check of pedigree	Has to be solved in the future pedigree assignment program
3. Genotypes from GenoSkan	
4. Imputing (FImpute)	Check of pedigree done here as well can handle that part until step 2 is solved
5. GBLUP/SNP BLUP	
6. Blending	
7. Publication	

More frequent genomic prediction

- Requirement for weekly evaluations
  - More automatic
  - Establish a simple warning/error detecting system
  - Maybe need for more computer capacity

or

  - SNP BLUP (require GMACE test run – sept 2015)

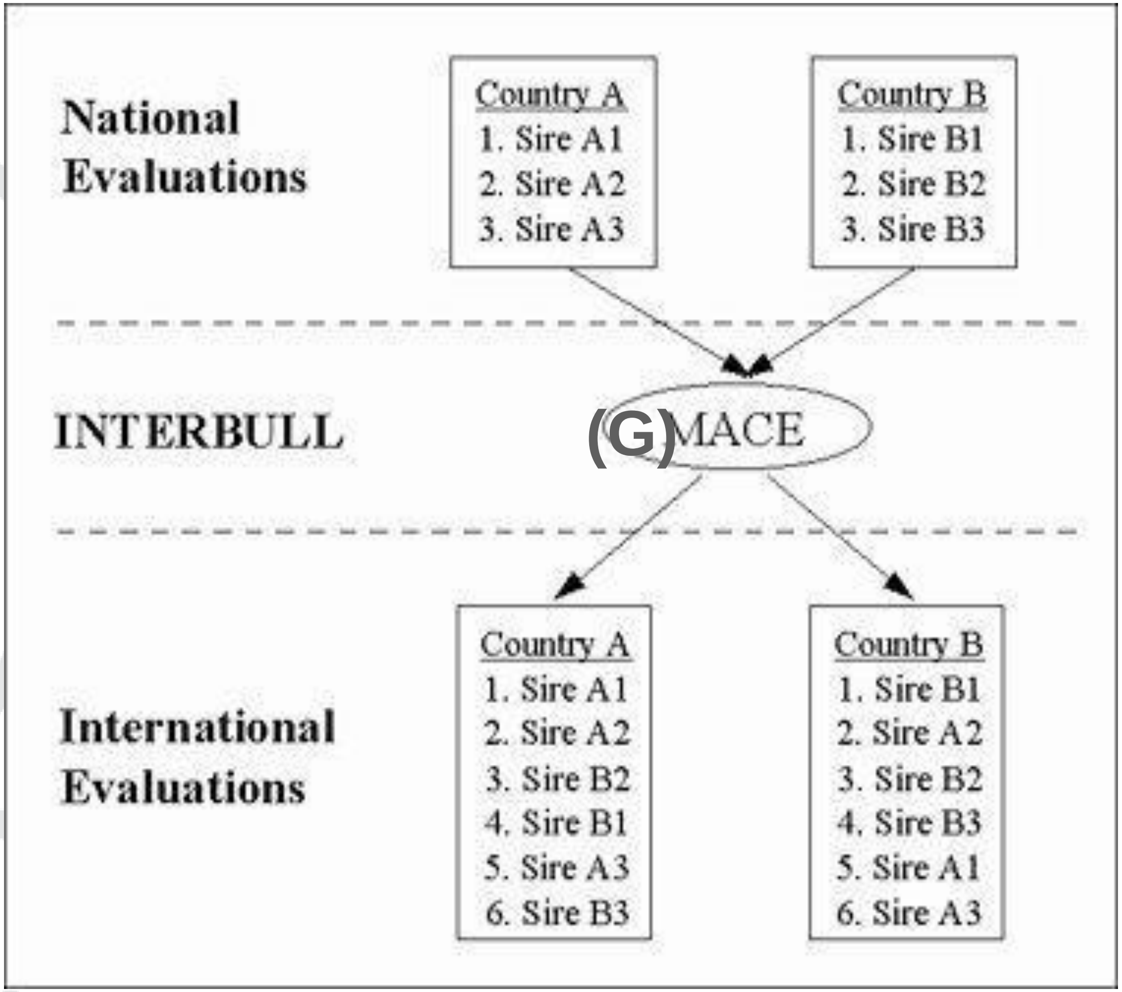
Work ongoing

- Kevin Byskov and Martha Bo Almskou in cooperation with Timmy Gregers Madsen, AU built stepwise a system up.
- Aim to introduce more frequent evaluation during 2015

Applied research focus 2015

- One step (MTT)
  - Simultaneously use of phenotypes and genotypes in evaluation
  - More optimal use of data
- Use of extra SNPs added on LD (AU)
  - Include information that some SNPs carry more information than other SNPs

(G)MACE



MACE use national EBVs based on phenotypes

GMACE use national GEBVs based on genotypes

MACE versus GMACE

- Breeding values from MACE and GMACE are expressed on the same scale and comparable on each country scale
- All bulls included in GMACE are expressed on all participating countries scale also scales for countries only participating in MACE.

What has to be published from GMACE?

All countries participating in MACE have to publish:

- **International EBVs for <u>all Interbull traits</u>**
- **Interbull EBVs can be EBVs from MACE or GEBV from GMACE**

Which countries participate in GMACE?

- December routine
  - Australia, Belgium, Canada (not Semex bulls), Germany, DFS, France, England, Italy, Holland, Poland

Groups of countries (e.g. NLD, FRA, DEU and DFS) exchange genotypes for young AI bulls

- A bull with a genotype in more countries get an GEBV with the same reliability as national bulls on all country scales within the exchange group. *(equivalent to a situation that a bull has daughters in all countries – no conversion by use of genetic correlation)*

and

- A slightly higher reliability on 3rd country scales than if information from GMACE is coming from one country only.

Y-index - MACE and GMACE

	MACE bulls born after 2007	GMACE bulls born >2010
Australia	97,5	106,0
Canada	101,1	110,9 (without Semex)
Germany	101,3	111,4
DFS	104,7	111,3
France	104,3	109,2
England	101,1	109,6
Italia	97,4	107,2
Holland	103,9	111,6

Udder health - MACE and GMACE

	MACE bulls born after 2007	GMACE bulls born >2010
Australia	96,9	-
Canada	94,4	109,4 (without Semex)
Germany	95,8	110,1
DFS	101,5	110,8
France	95,1	110,7
England	96,6	109,3
Italia	95,7	108,2
Holland	97,0	110,4

Interbull GMACE

- Focus on top lists
  - Proportion of top bulls primary depending on average and number of tested bulls.
  - Results see NAV interbull search tool