

Using single-step genetic evaluation for type traits in the Nordic countries



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NAV



This presentation focus on

- Holstein cattle in Denmark, Finland & Sweden
- Two traits
 - Chest width - no genetic trend
 - Udder depth - significant positive trend
- Validate single-step results
- Comparison with current two-step and traditional EBV's



Single-step approach

Methods

- **Single step GTBLUP Model**
 - Same as ssGBLUP but with no explicit G-inverse
- **Blending of foreign information**
MACE EBV's deregressed and used as phenotypes with weights
- **Polygenic effect 30% (also tested 10%)**



Single-step approach

Data

- Chest width and udder depth
- 2,225,000 1. lactation records (official model has also later lact.)

Reference animals with genotypes

- 54,000 females
- 5,600 domestic AI bulls
- 50,000 foreign AI bulls (mainly Euro genomic bulls)



Two runs for the validation purpose

- **Full model**
All information included
- **Reduced model**
records of daughters of domestic AI bulls born after 2011 excluded



Current procedure for type traits

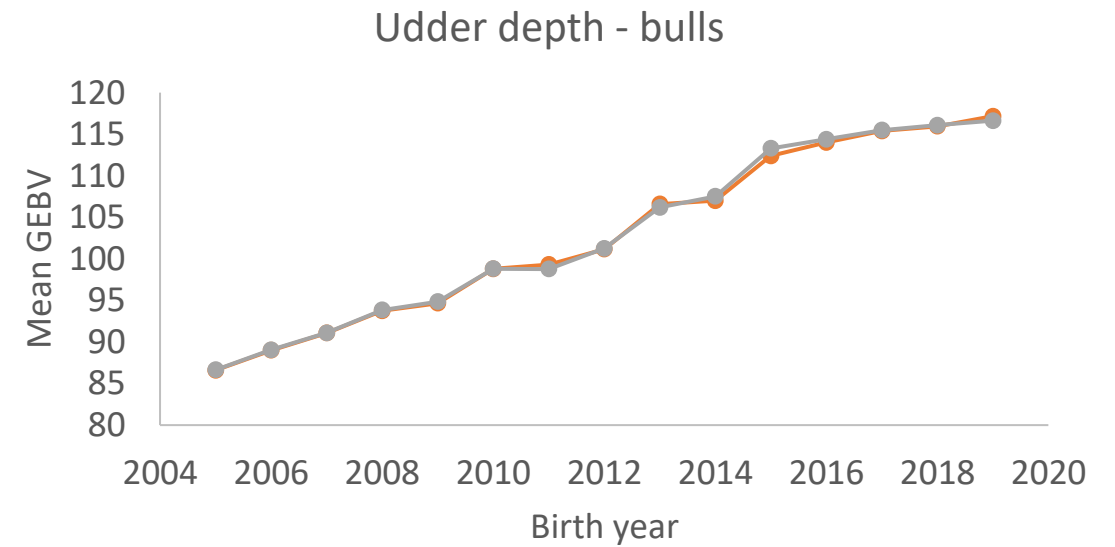
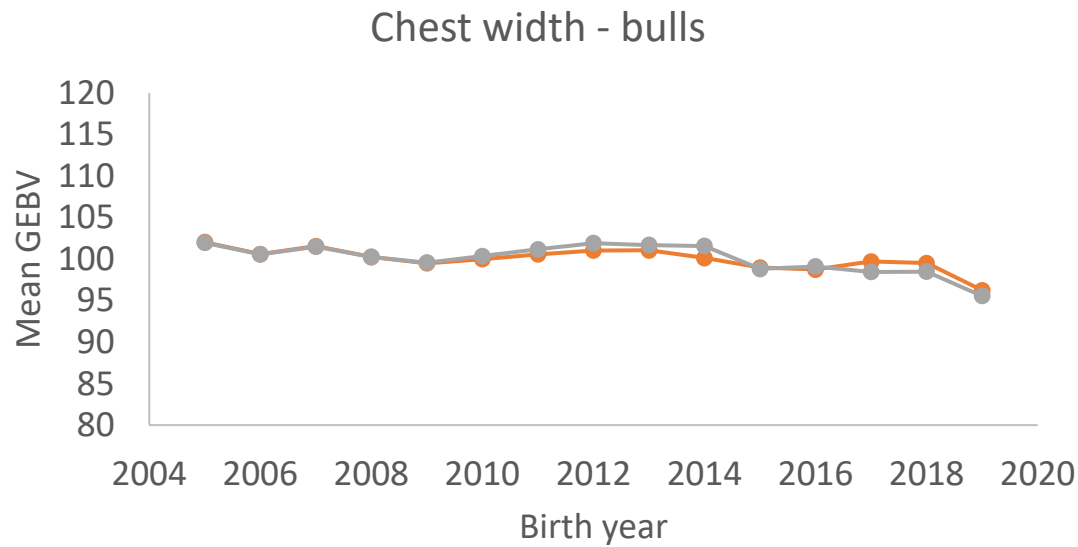
- Records of 1. -3. lactation
- Traditional multi trait model (EBV)
- Twostep SNP-BLUP model (GEBV)
with 10% polygenic effect



GEBV for single-step full vs reduced for AI bulls

Polygenic effect 30%

Similar genetic trend for single-step full and reduced



SS_full SS_reduc

SS_full SS_reduc



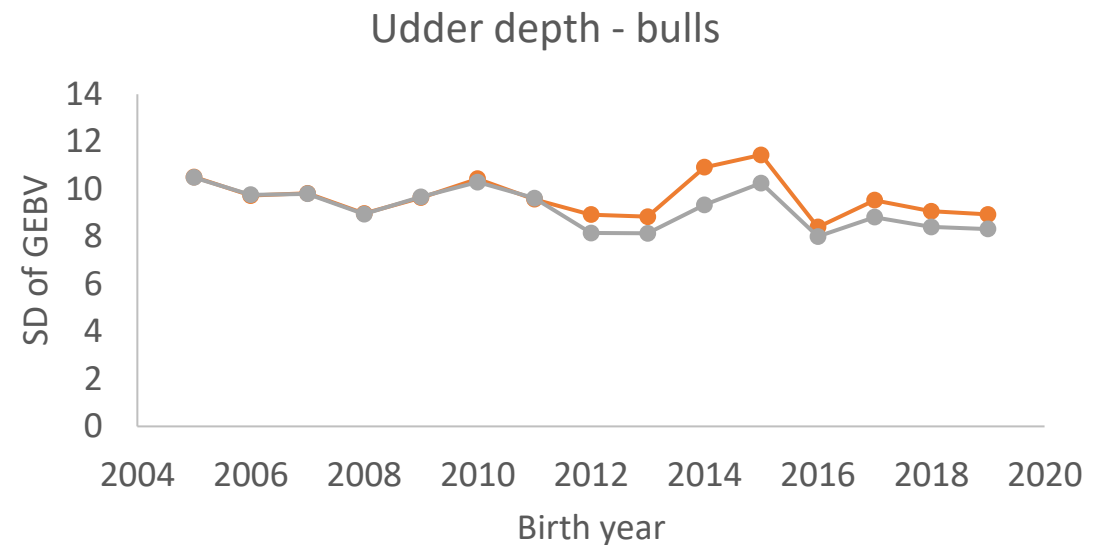
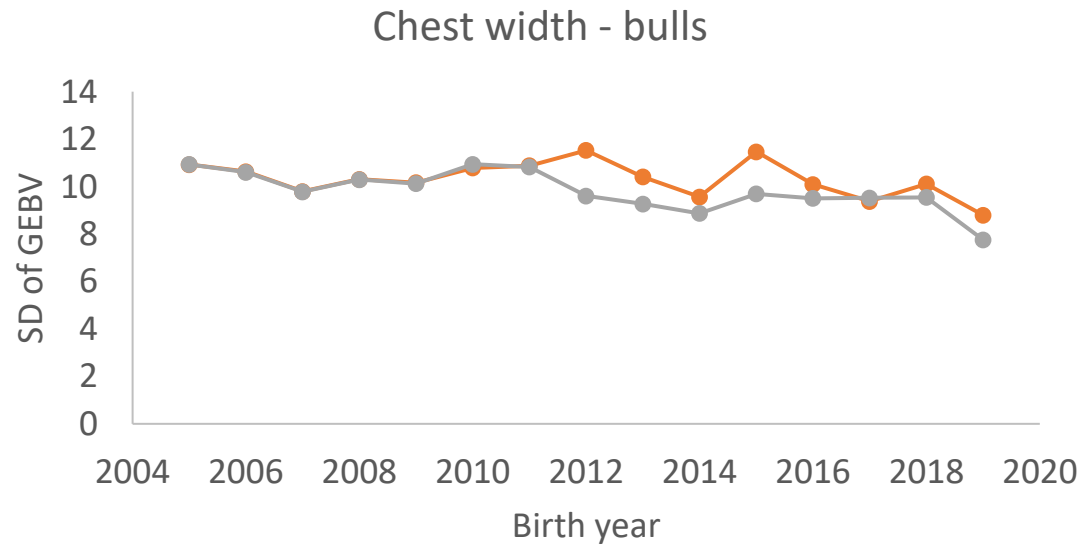
Birth year	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019
N	334	383	334	293	269	226	167	172	120	104	80	66	65	89	42



SD of GEBV full and reduced for AI bulls

Polygenic effect 30%

Similar standard deviation for single step full and reduced



—●— SS_full —●— SS_reduc

—●— SS_full —●— SS_reduc



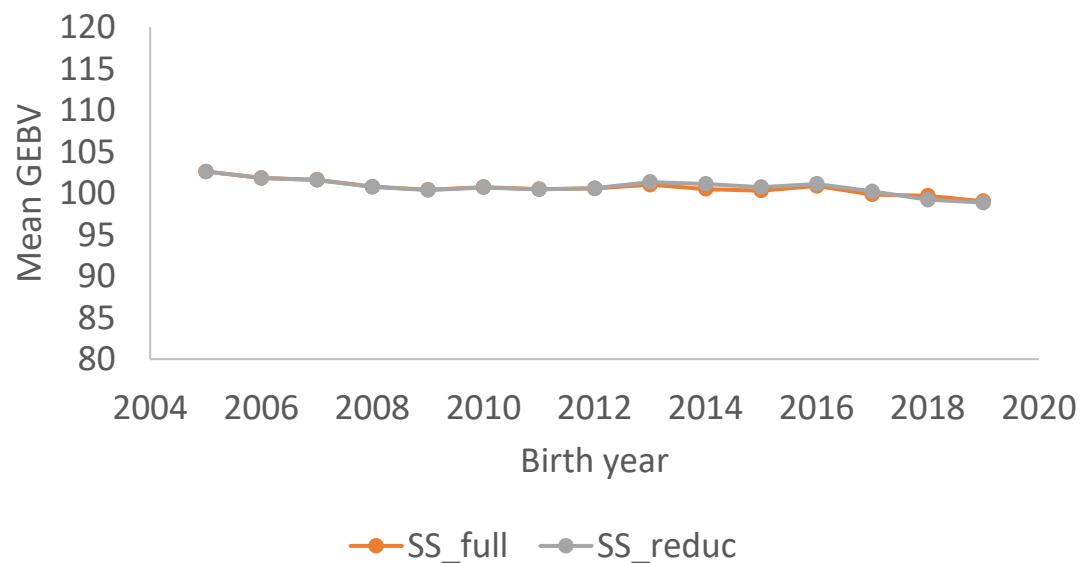
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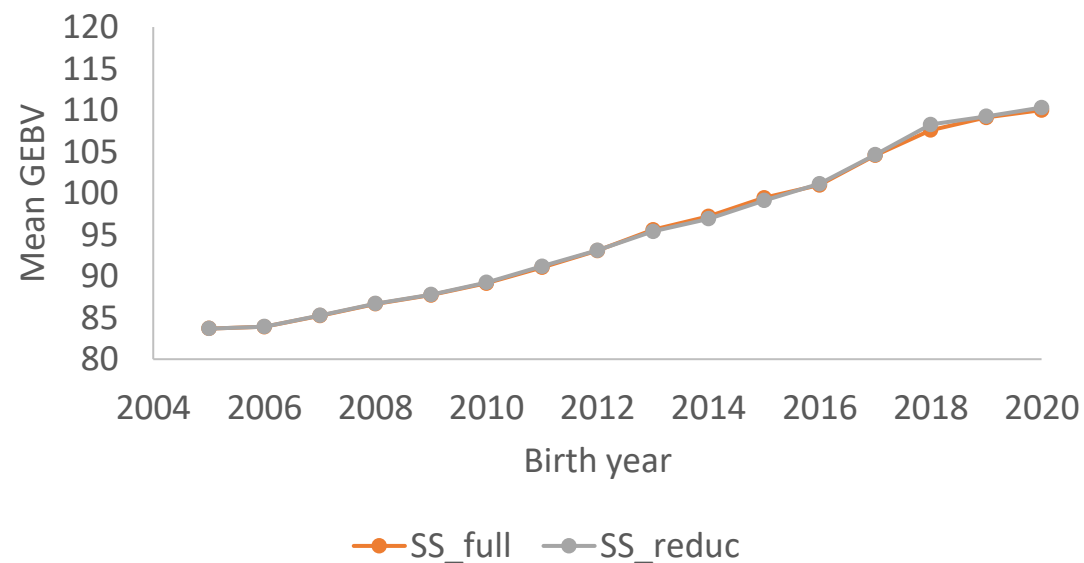
GEBV for single-step full vs reduced for females

Polygenic effect 30%

Chest width - females

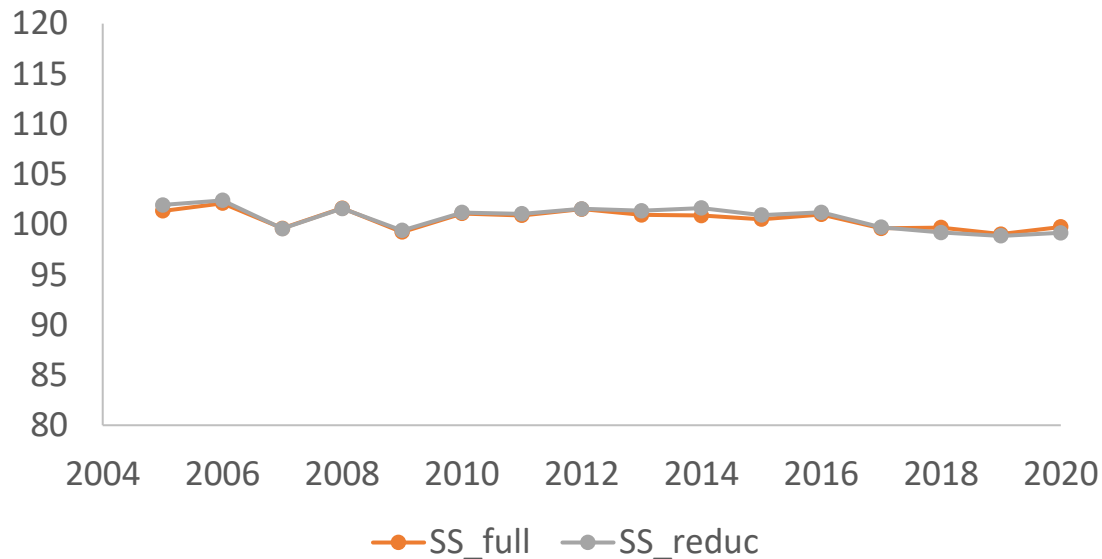


Udder depth - females

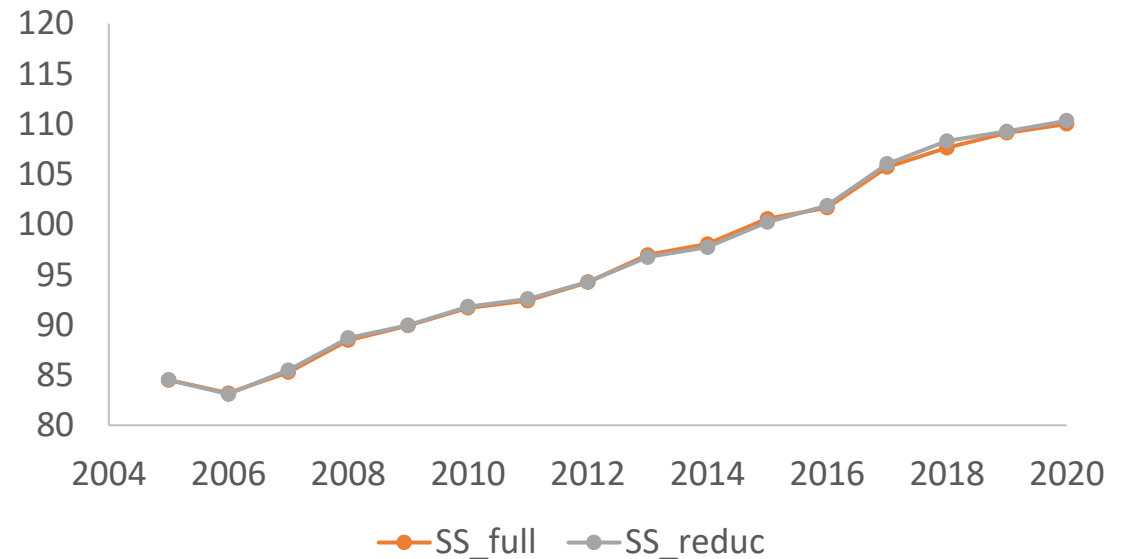


Genotyped females no phenotypes in full, no phenotypes in reduc

Chest width - females



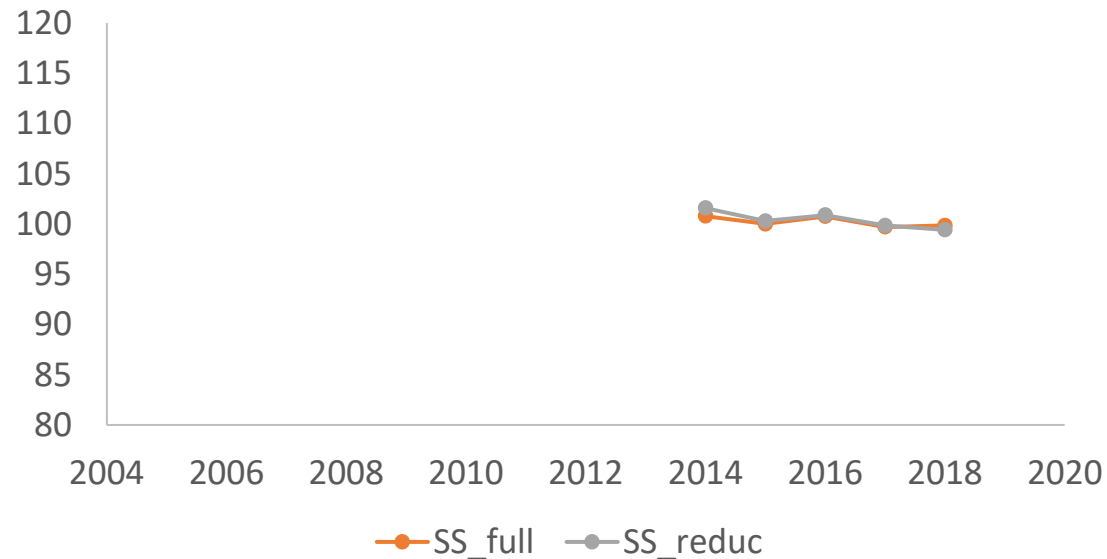
Udder depth - females



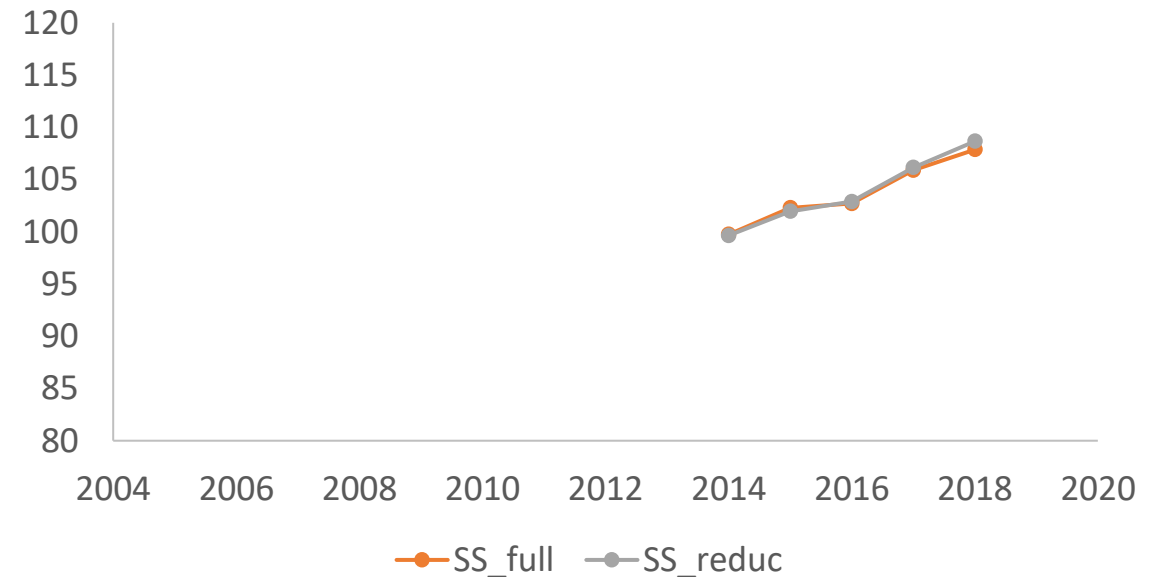
Genotyped females phenotypes in full, no phenotypes in reduc

Getting a phenotype do not affect the mean GEBV for genotyped females

Chest width - females



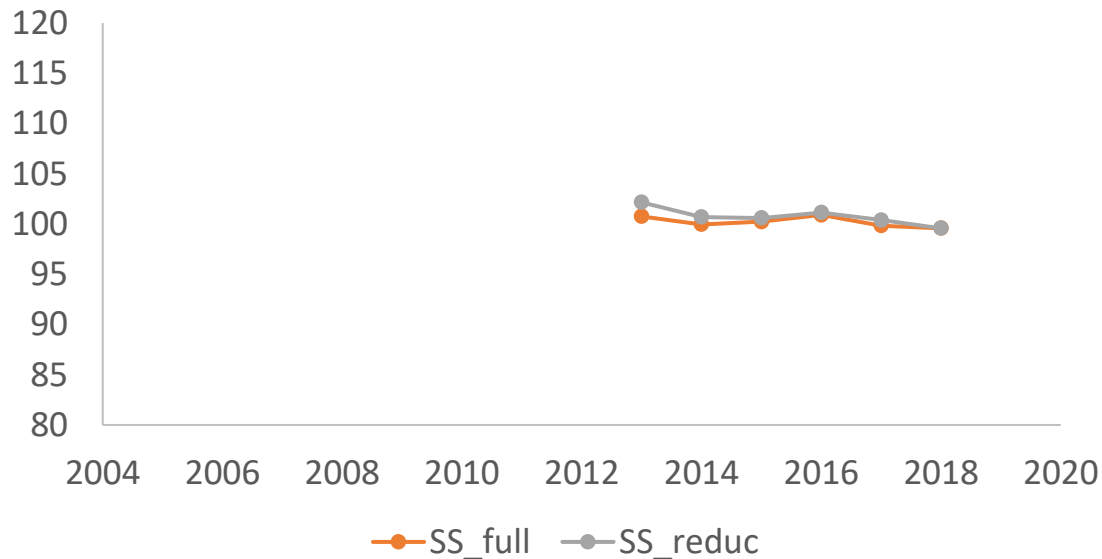
Udder depth - females



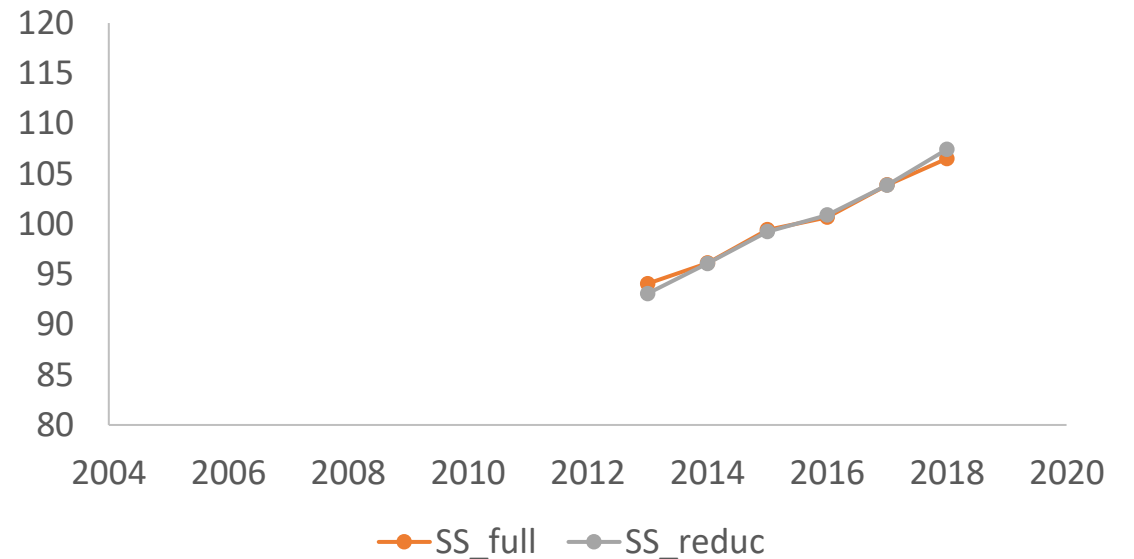
Non-genotyped females phenotypes in full, no phenotypes in reduc

Getting a phenotype do not affect the mean GEBV for non-genotyped females

Chest width - females



Udder depth - females



Interbull validation and Legarra Reverter regression for domestic bulls

- Born 2012-2015
- Total 363 bulls
- Regression coefficients (b1) close to 1

Udder depth

	Regression	b1	R ²
Interbull validation	Deregressed proof on SS_reduc	0.90	0.68
	Deregressed proof on pedigree index	0.78	0.16
Legarra Reverter Regression	SS_full on SS_reduc	0.99	0.80



10% or 30% of polygenic effect

- Nearly same genetic trend (mean GEBV and SD)

What is the balance between genomic and phenotypic information?

- Genomic prediction has ~70% reliability for udder depth
- Expect the same reliability for bulls with 10-40 daughters with phenotypes
- For this group of bulls, it is expected that genomic information will bring about half and progeny test will bring about half for the single-step GEBV's



10% or 30% of polygenic effect

- Regression
 $SS_{full} = b1 * SS_{reduc} + b2 * EBV$
Expect $b1 \approx b2$
- Divide bulls by number of daughters
- For bulls with 10-45 daughters
the $b1 \approx b2$ for Pol30%
the $b1 \neq b2$ for Pol10%

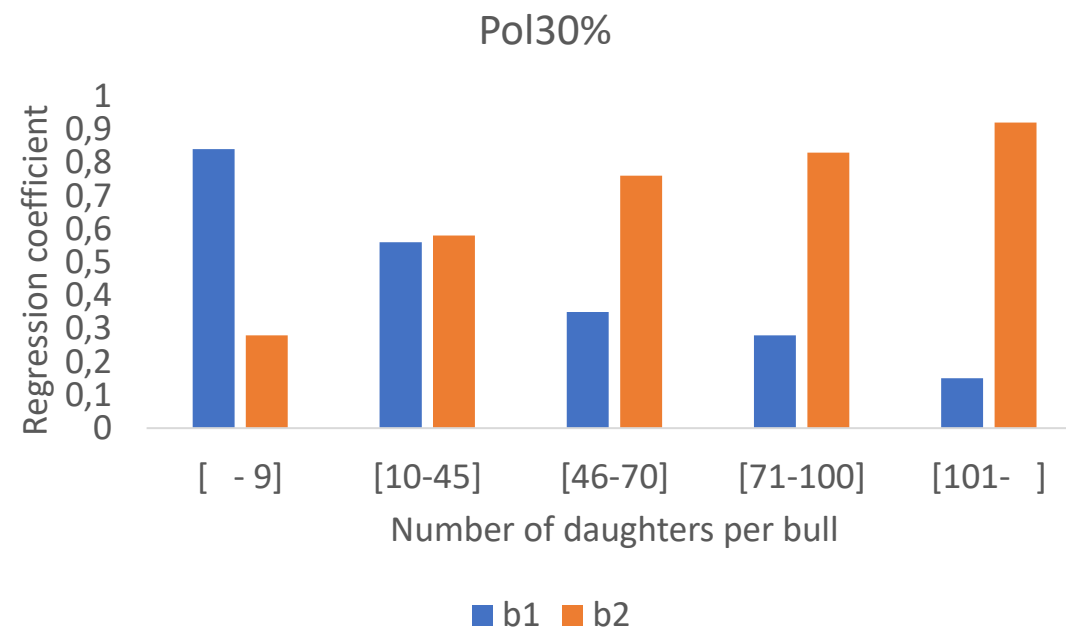
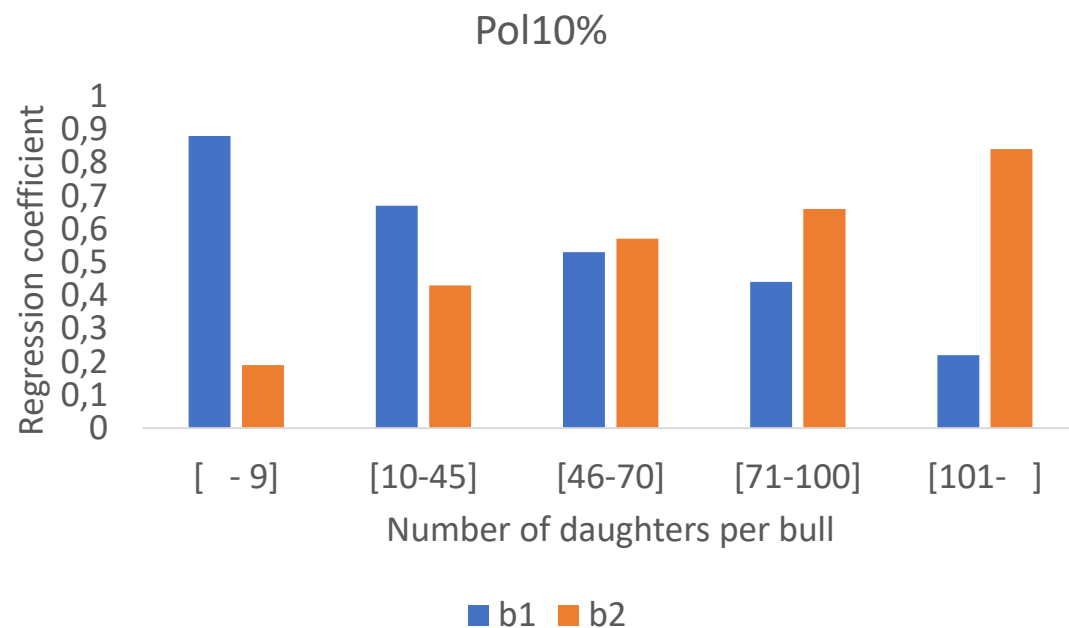
	Pol10		Pol30	
	b1	b2	b1	b2
[10-45]	0.67	0.43	0.56	0.58

..full figure on next slide



$$SS_{full} = b1 * SS_{reduc} + b2 * EBV$$

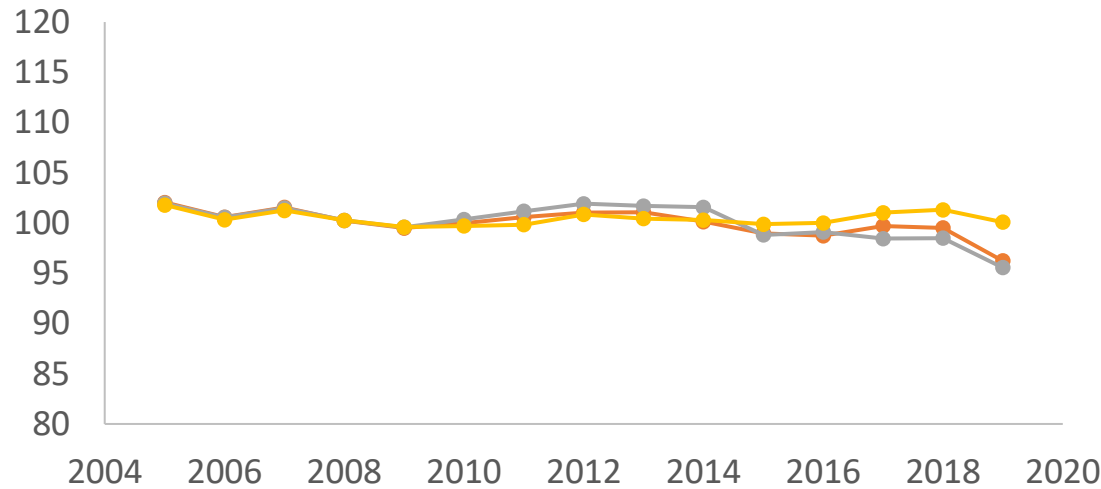
Udder depth



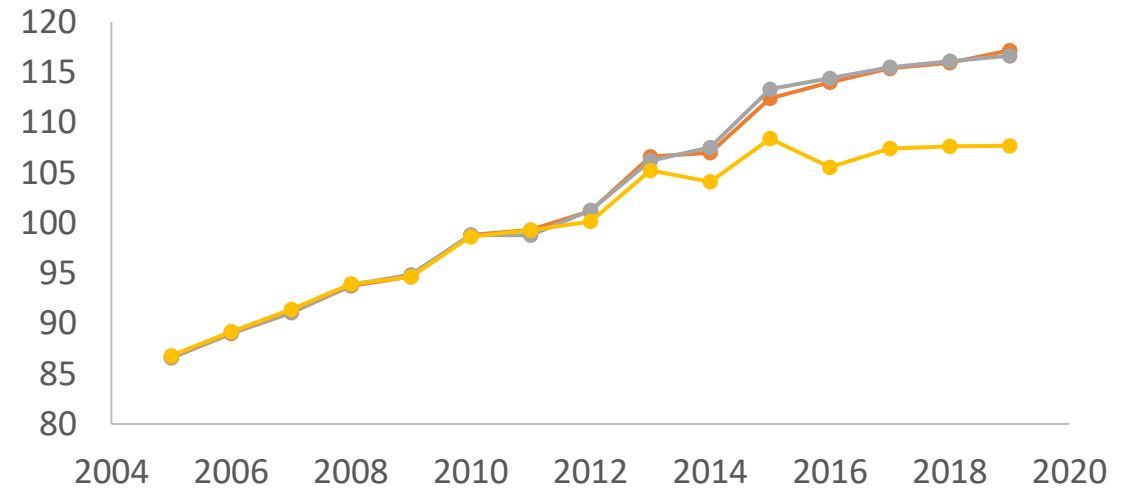
Single-step GEBV vs traditional EBV for AI bulls

For latest birth years the EBV's are lower than single-step for udder depth

Chest width



Udder depth



SS_full SS_reduc EBV

SS_full SS_reduc EBV



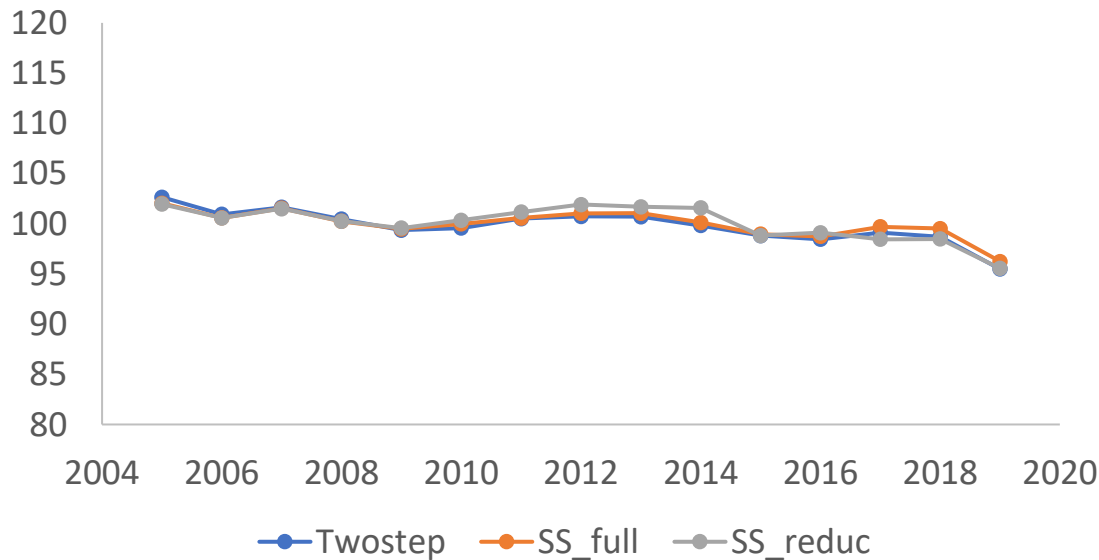
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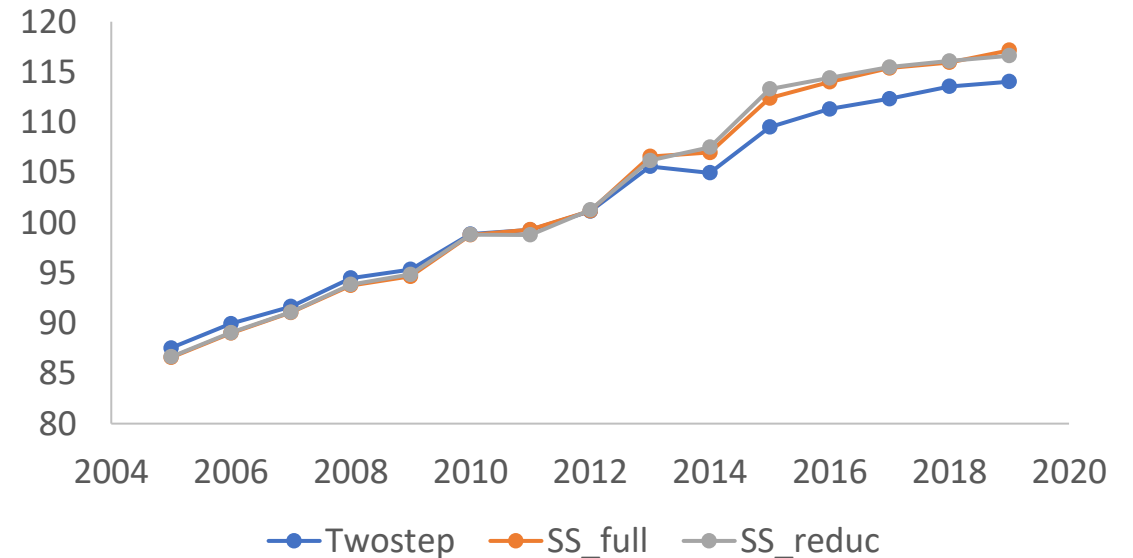
Single-step vs two-step for bulls

For latest birth years the two-step GEBV's are lower than single-step GEBV's for udder depth

Chest width



Udder depth



Correlations between single-step and two-step for candidate bulls

- Born 2019-2020
- 3978 candidate bulls
- High correlation

Udder depth

Pearson correlations between single-step and two-step

	SS_full	SS_reduc	Two-step
SS_full	1		
SS_reduc	0.97	1	
Two-step	0.97	0.95	1



Conclusion

Single-step for type traits polygenic effect 30%

- **Results as expected:**
 - **Genetic trend full and reduced data**
 - **Interbull validation and Legarra Reverter regression**

Comparison to EBV's and two-step

- **High correlations between single-step and current two-step results**

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