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

Trine Andersen, Ulrik Sander Nielsen,
Jukka Pösö, Elisenda Rius-Vilarrasa,
Esa Mäntysaari & Gert Pedersen Aamand

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

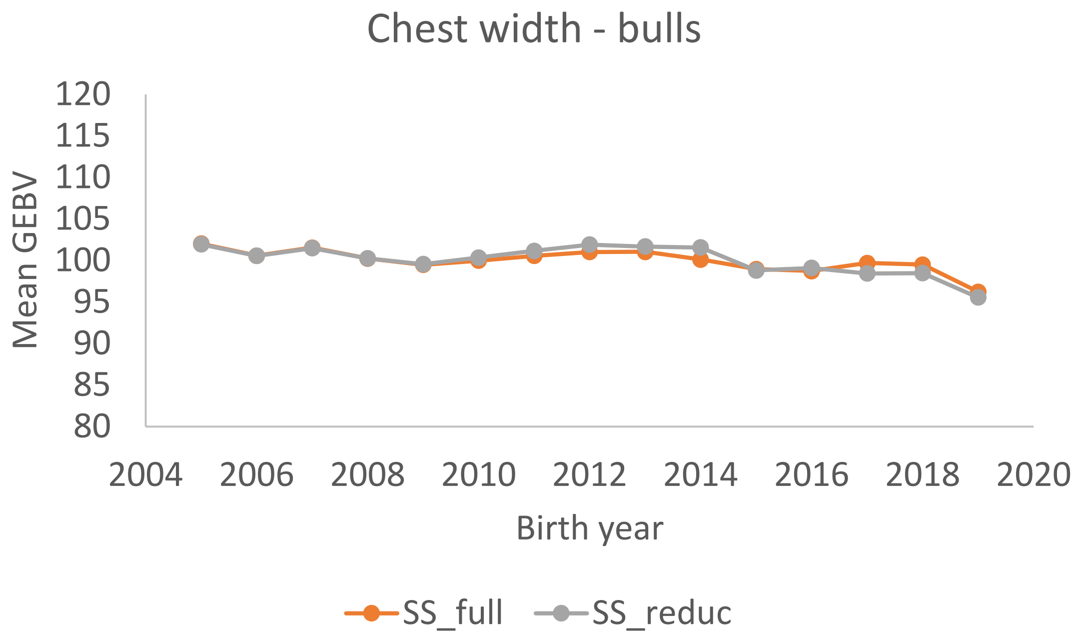
- Records of 1. -3. lactation
- Traditional multi trait model (EBV)
- Twostep SNP-BLUP model (GEBV)

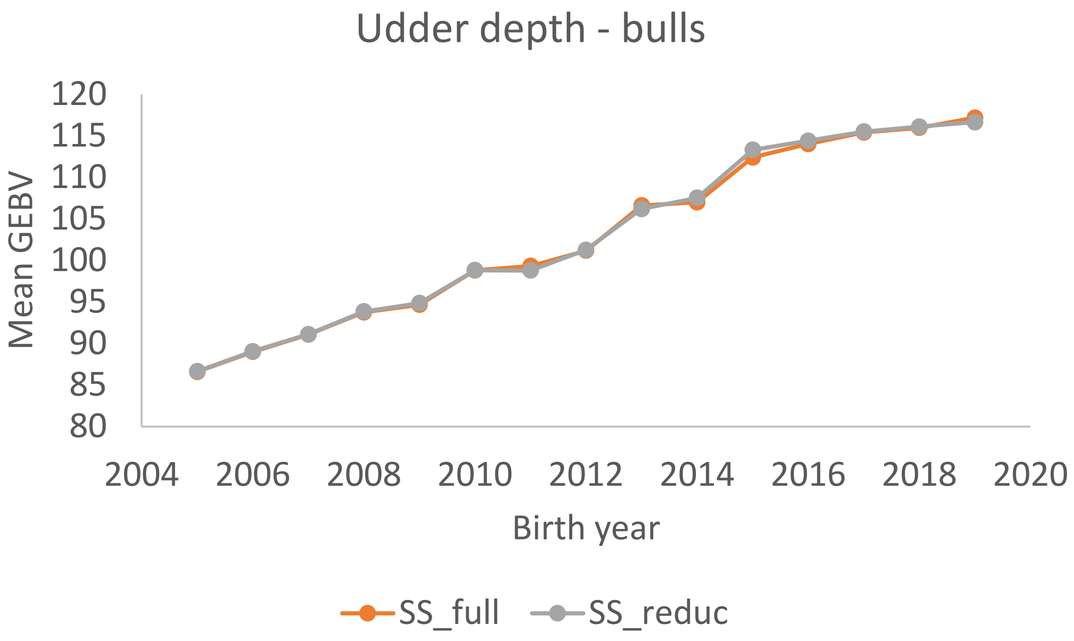
  with 10% polygenic effect

GEBV for single-step full vs reduced for AI bulls

Polygenic effect 30%

Similar genetic trend for single-step full and reduced

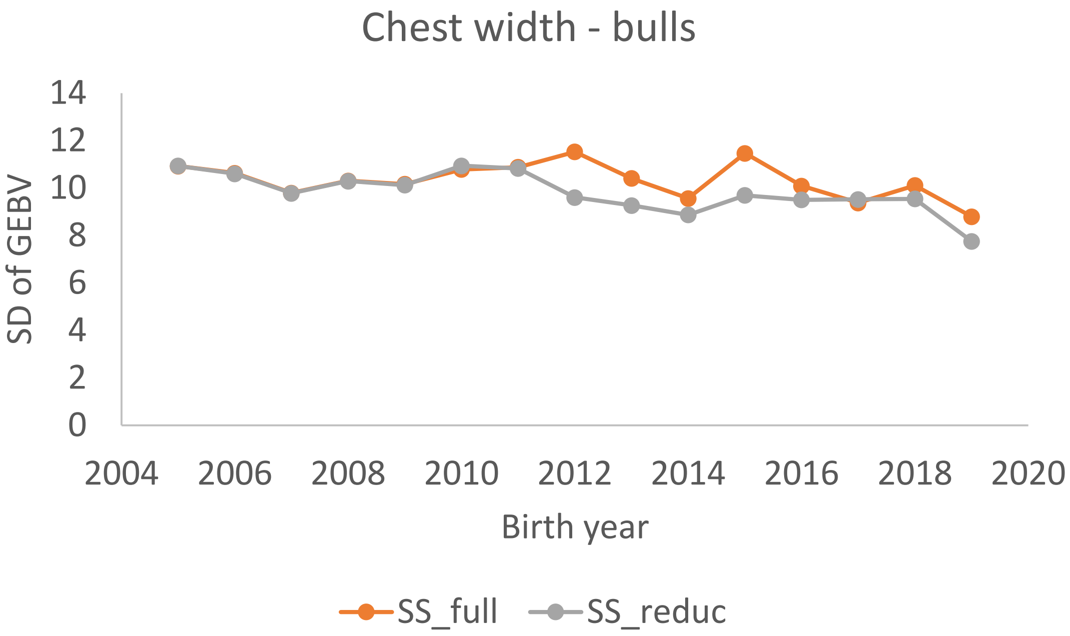


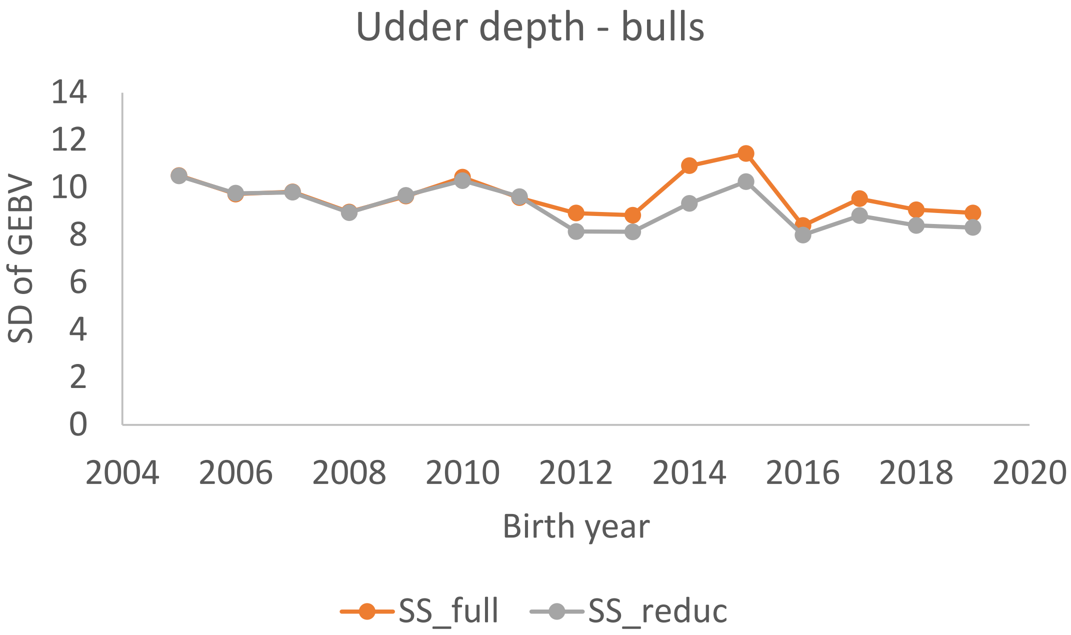


Birth year	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019
N	334	383	334	293	269	226	167	172	120	104	80	66	65	89	42

SD of GEBV full and reduced for AI bulls
Polygenic effect 30%

Similar standard deviation for single step full and reduced





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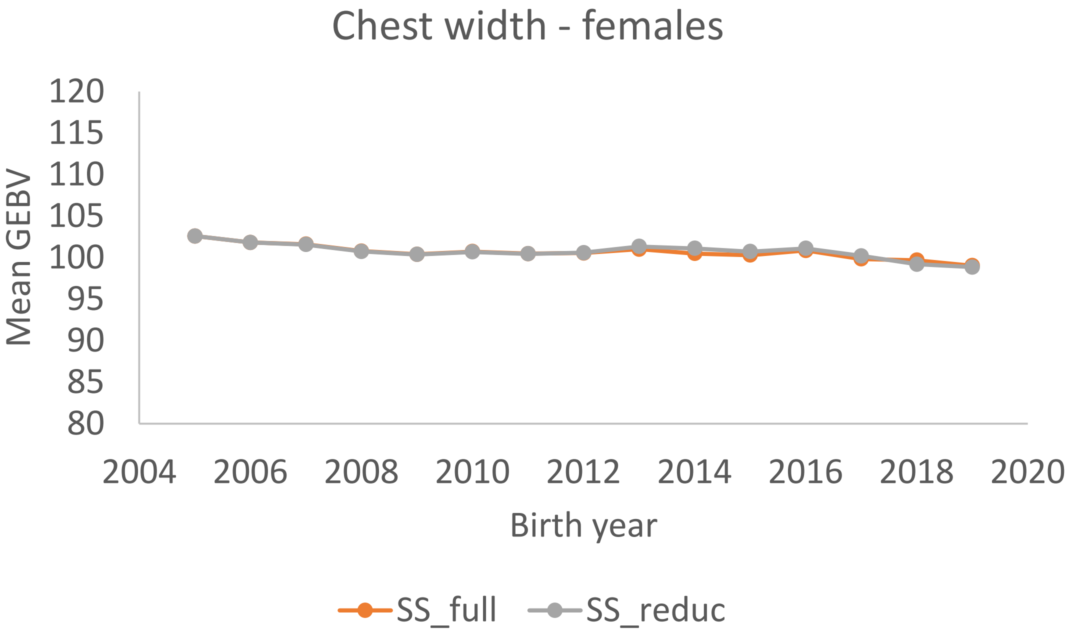
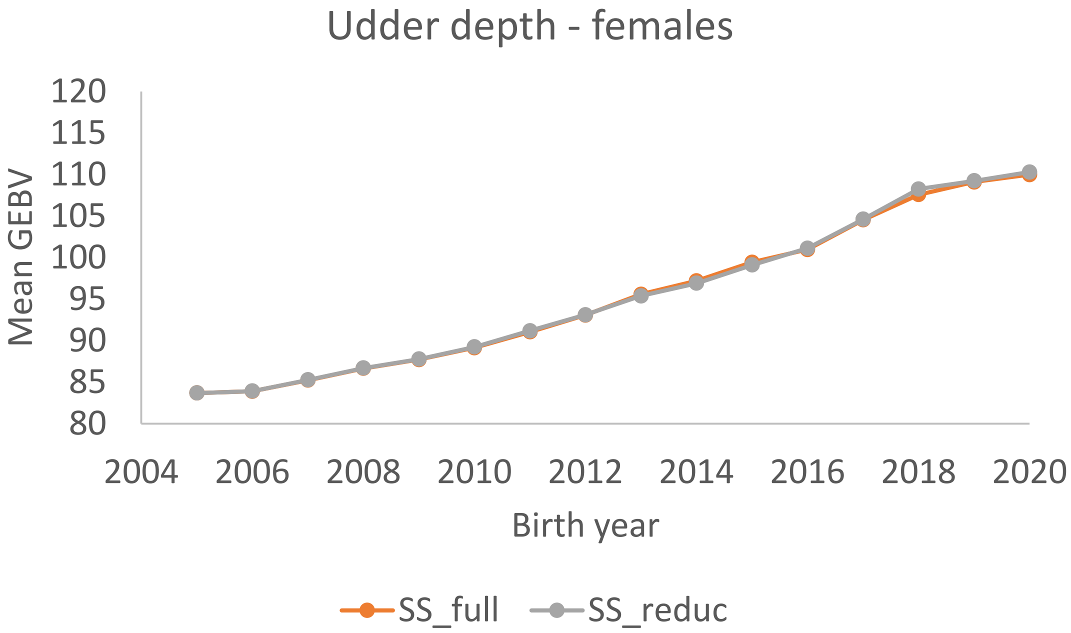
GEBV for single-step full vs reduced for females

Polygenic effect 30%

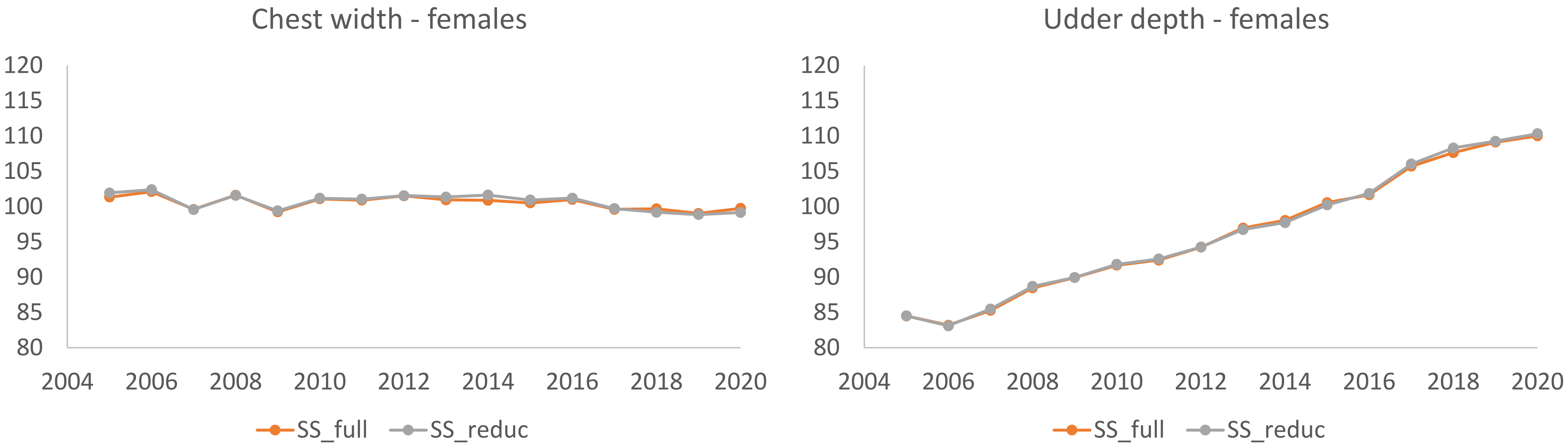


Chest width - females



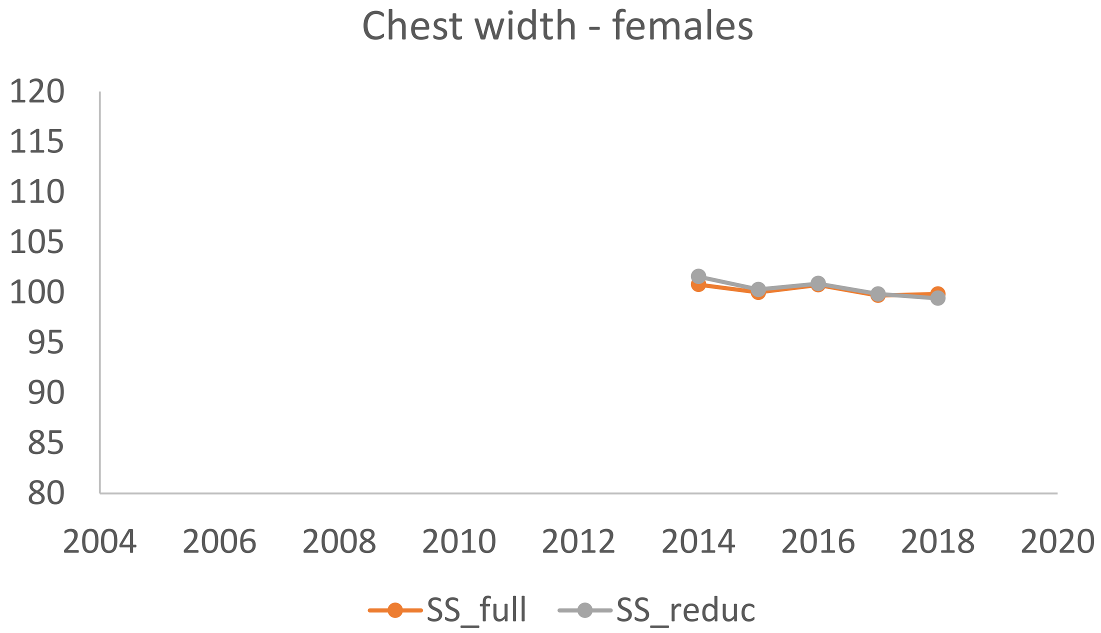
Udder depth - females

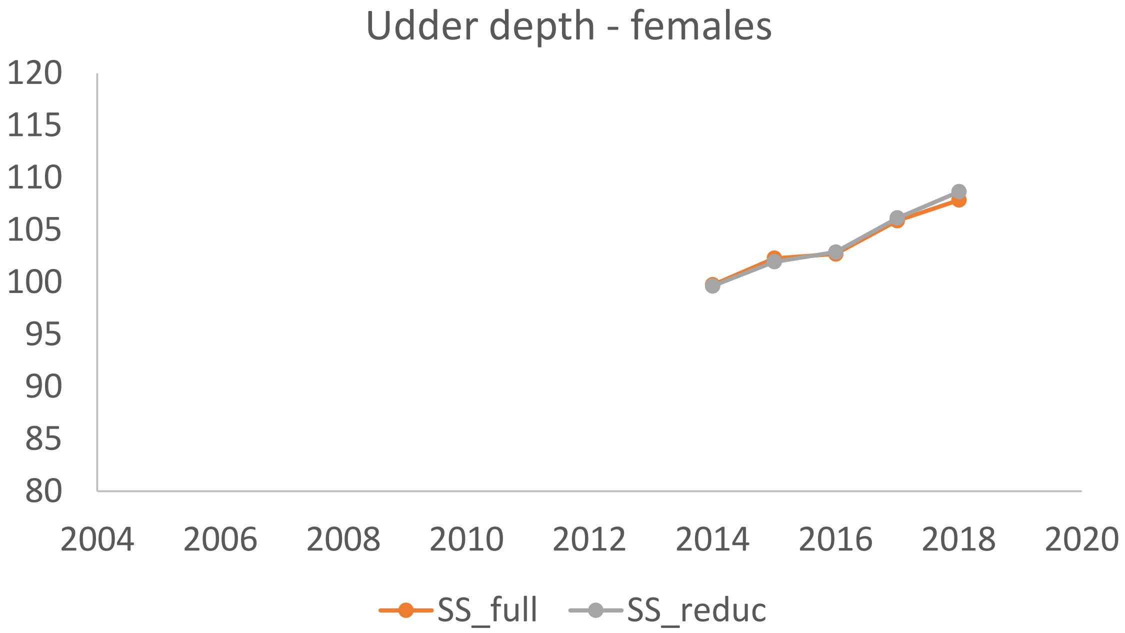
Genotyped females
no phenotypes in full, no phenotypes in reduc



Genotyped females phenotypes in full, no phenotypes in reduc

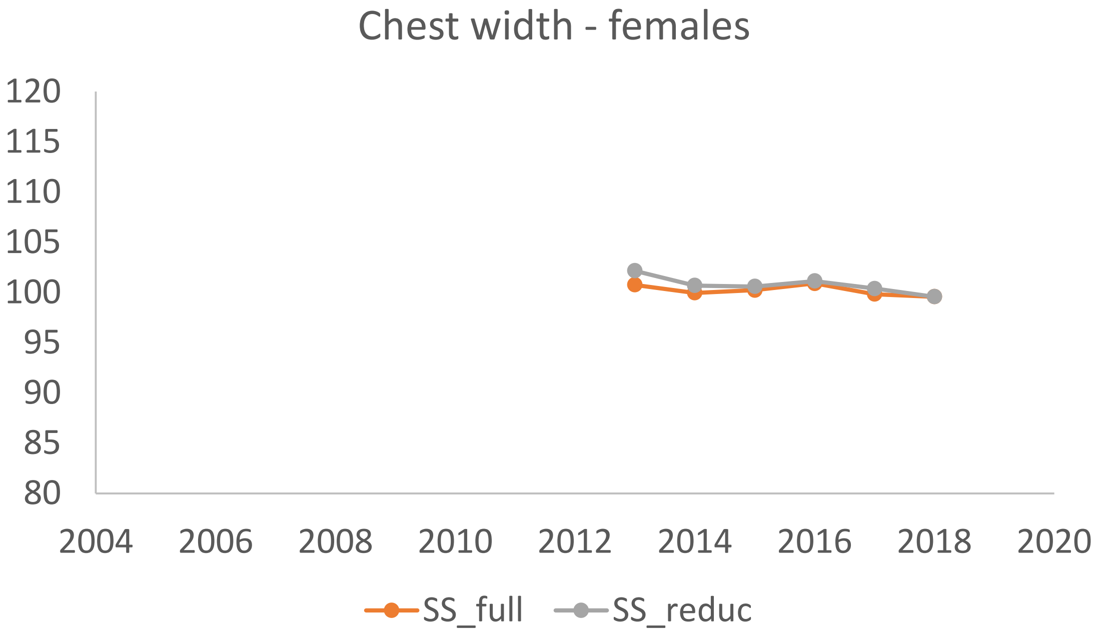
Getting a phenotype do not affect the mean GEBV for genotyped females

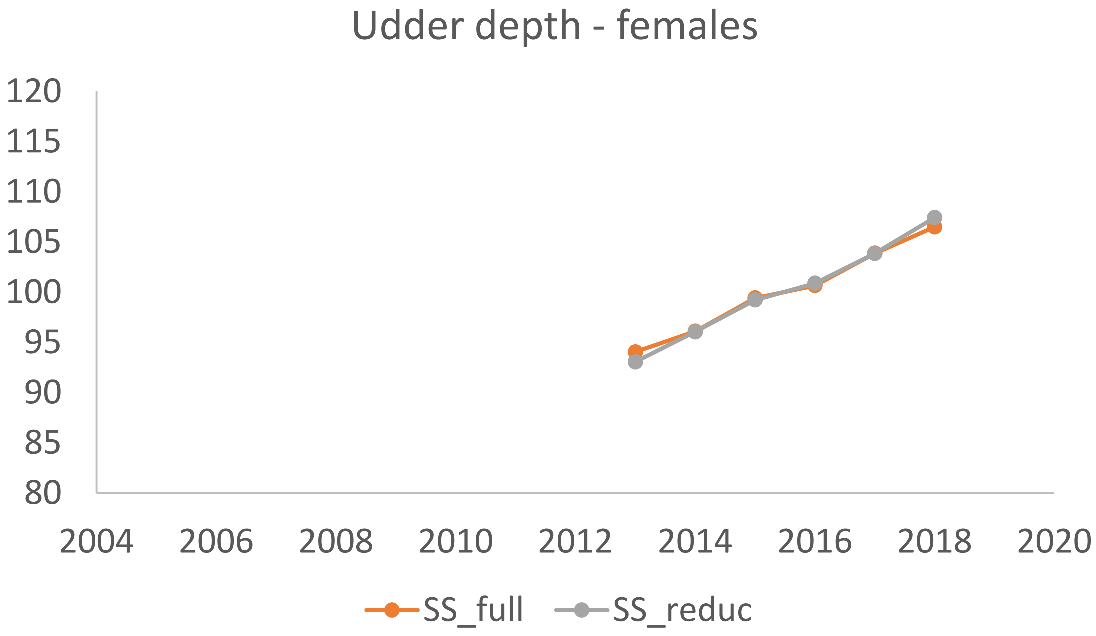

Chest width - females


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





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	R²
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 ≈ b2

- Divide bulls by number of daughters

- For bulls with 10-45 daughters
  the b1 ≈ b2 for Pol30%
  the b1 ≠ b2 for Pol10%

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

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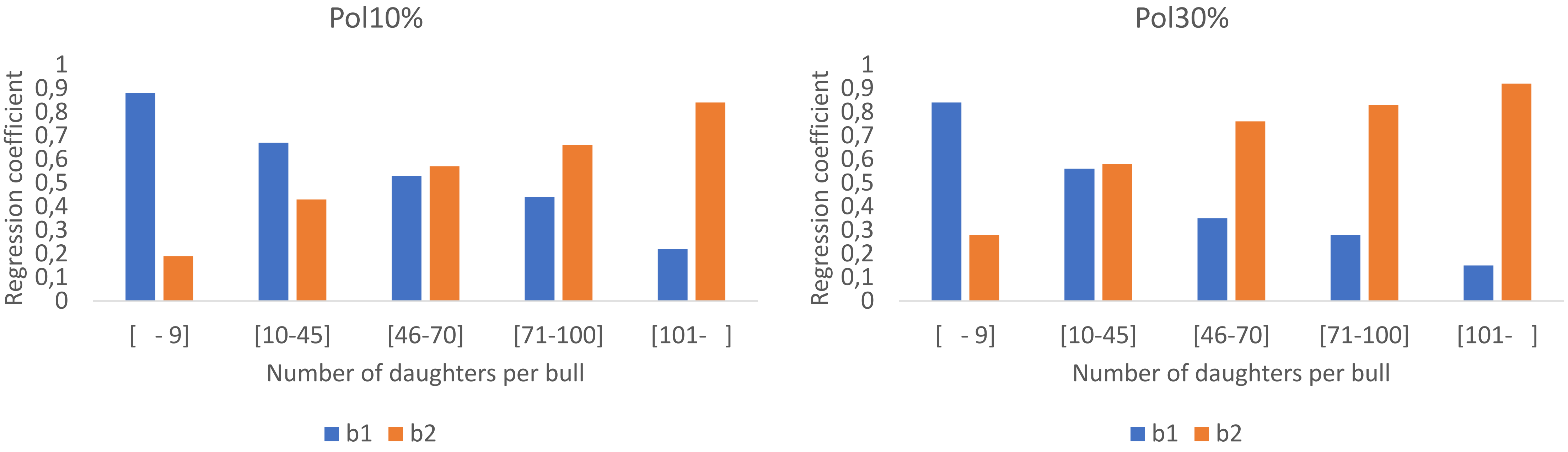
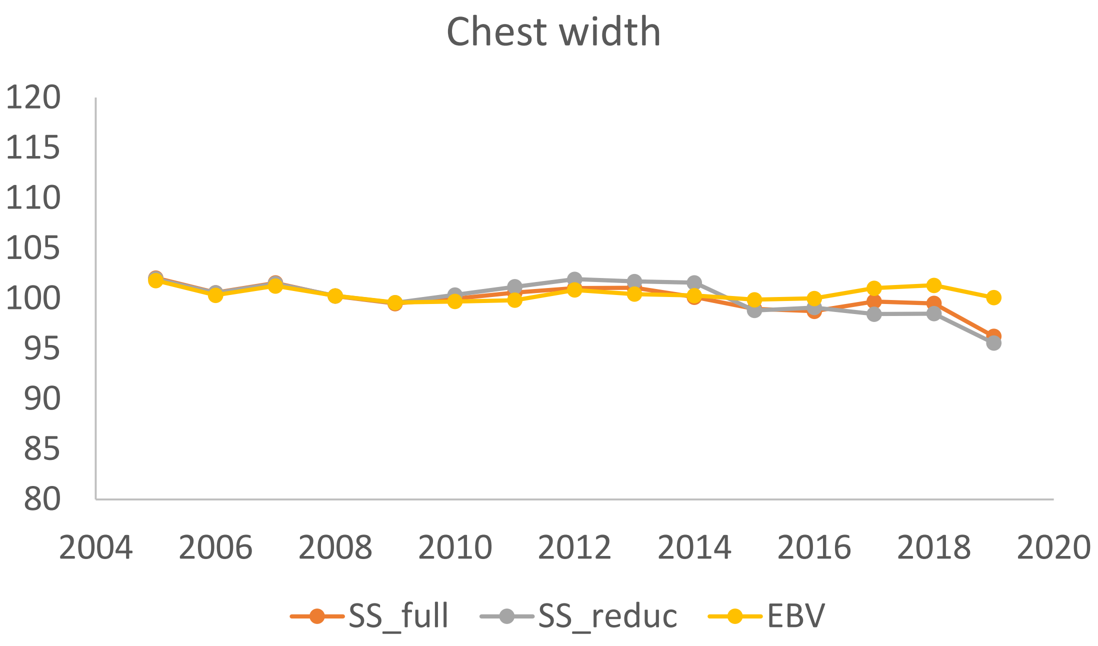
SS_full = b1*SS_reduc + b2*EBV

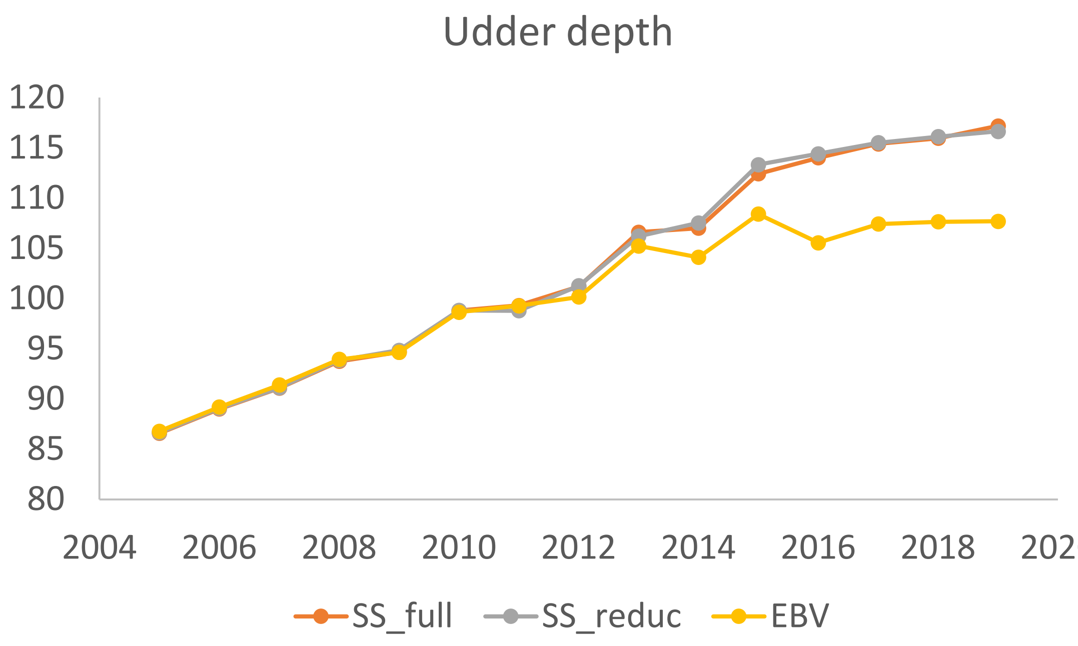
Udder depth



Single-step GEBV vs traditional EBV for AI bulls

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





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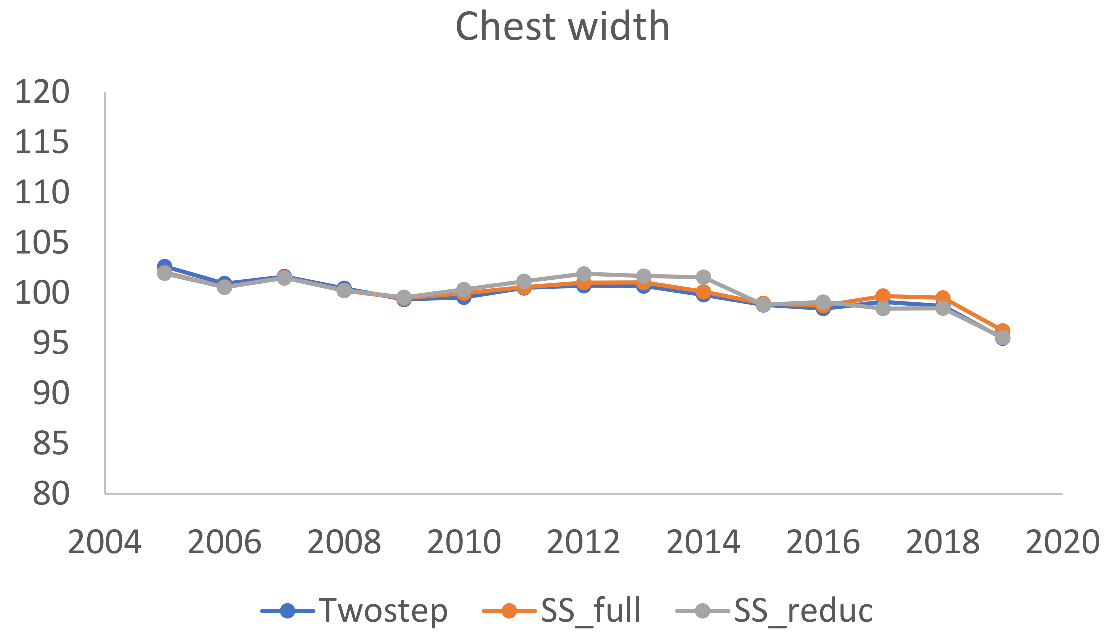
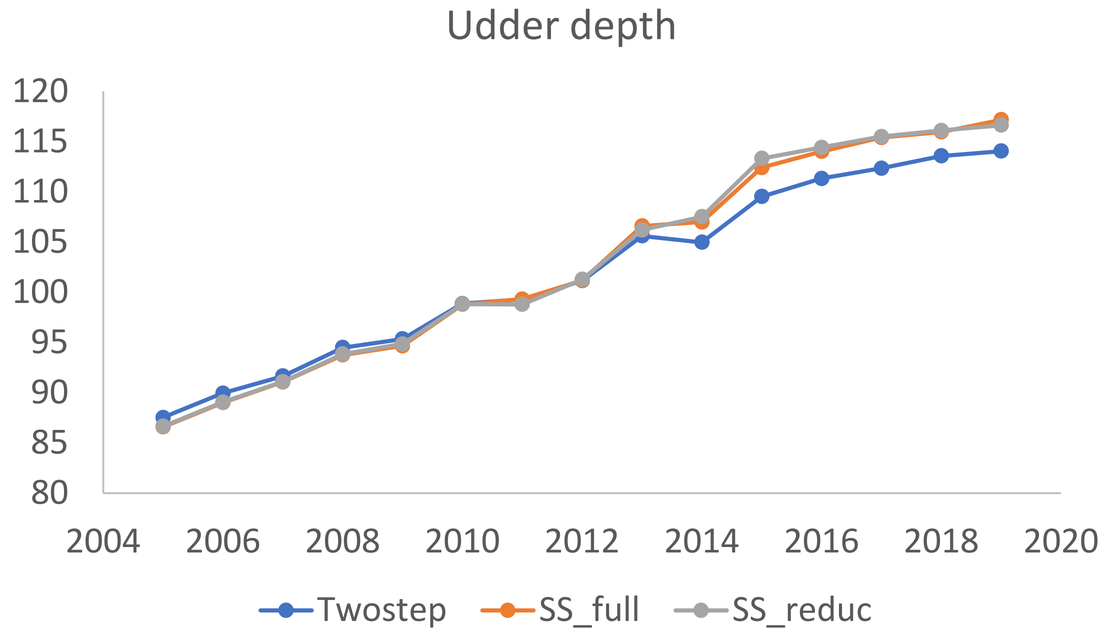
Single-step vs two-step for bulls

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


Chest width


Udder depth

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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