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Animal Production

# Application of a single-step SNP BLUP model to conformation traits of German Holsteins

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# I) A single-step SNP BLUP model (Liu & Goddard, 2014) via MiXBLUP and MiX99

- A multi-trait ssSNPBLUP model with MACE information integrated
  - The same multi-trait animal model, as for national conventional evaluation, for all 23 conformation traits
  - Phenotype records of national cows with a pre-adjustment for heterogeneous variances
  - Deregressed MACE EBV for all bulls in Interbull evaluation as new type of records
  - A pseudo-ID for each of the fixed effects for deregressed EBVs of all the bulls from MACE
    - Weight as difference in (animal-model-based) EDC between MACE and national evaluation
    - No adjustment in deregressed EBVs from national and MACE evaluation yet

- The ssSNPBLUP model with a RPG (30%) equal for all the conformation traits

- Pedigree of genotyped and non-genotyped animals contains more generations of animals
  - **Phantom parent groups** fitted via QP transformation (Vandenplas et al. 2021)
- Distances of candidates to reference population NOT considered: first, second or third generations

- A special implementation of ssSNPBLUP (Liu-Goddard) model in MiX99
  - Treating SNP markers as animals with no parents in pedigree (Mäntysaari et al. 2018, EuroGenetics May 2018)
  - SNP effect estimates to be divided by sqrt(2*sum(p*q))

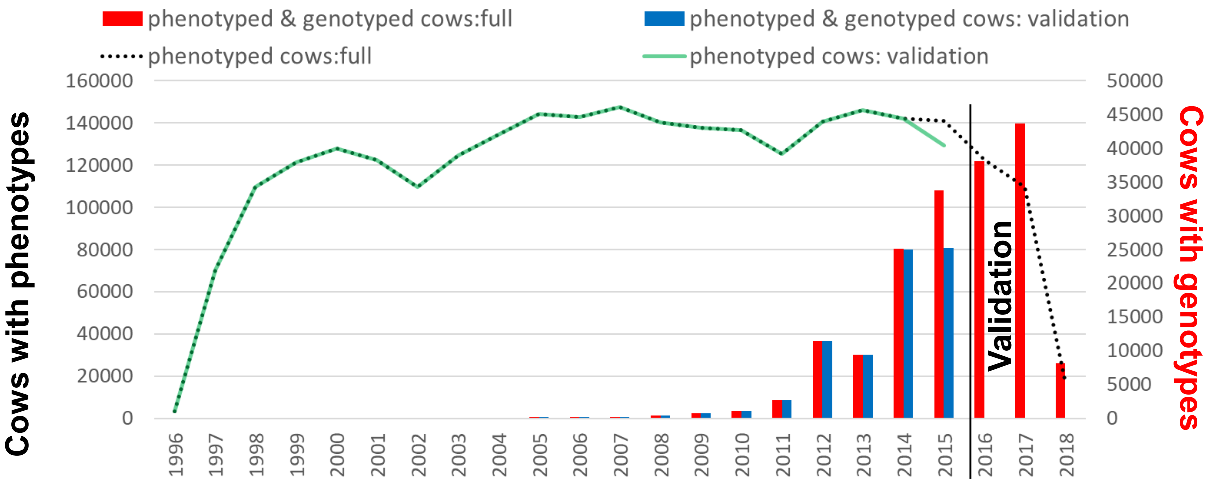
## II) Data materials and computational requirements

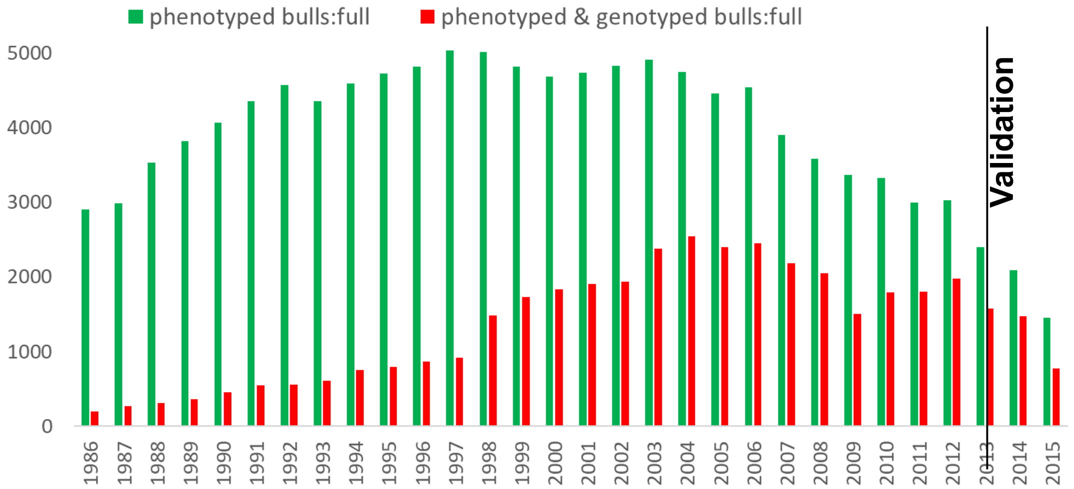
- Genotyped population of German Holsteins for routine genomic evaluation
  - 875,252 genotyped animals plus 1,635,584 ancestors → 2,510,836 animals in pedigree
- Phenotype data of national cows and international bulls for conformation traits from August 2020
  - Full data set (trait: stature)
    - 2,715,550 cows as in official conventional evaluation with all 23 conformation traits jointly
    - 118,552 bulls with deregressed MACE EBV added (ΔEDC >0), → 2,834,102 cows and bulls
  - Truncated data set (trait: stature)
    - 5,945 bulls born in 2013-2016 removed (3830 with genotypes)
    - 260,749 cows born in 2016-2018 and daughters of validation bulls removed
    - 2,567,408 bulls and cows for genomic evaluation
- Pedigree file for the single-step model evaluation
  - 9,012,965 animals in pedigree for the full evaluation and 138 phantom parent groups
- Computing requirements for a full evaluation by MiXBLUP / hpblup on a Linux server
  - Total # equations/effects: 217,423,347
  - 15 of a total of 48 cores were used
  - Total clock time: 49 hours (3387 rounds), peak memory usage VmPeak 65 Gb and VmHWM 39Gb

# II) A genomic validation study for the single-step and multi-step genomic model

- Due to a short history of cow genotyping, phenotypes of last three (birth) years of cows were removed
- Last three birth years of bulls from August 2020 MACE evaluation were deleted
- Daughters of validation bulls removed as well

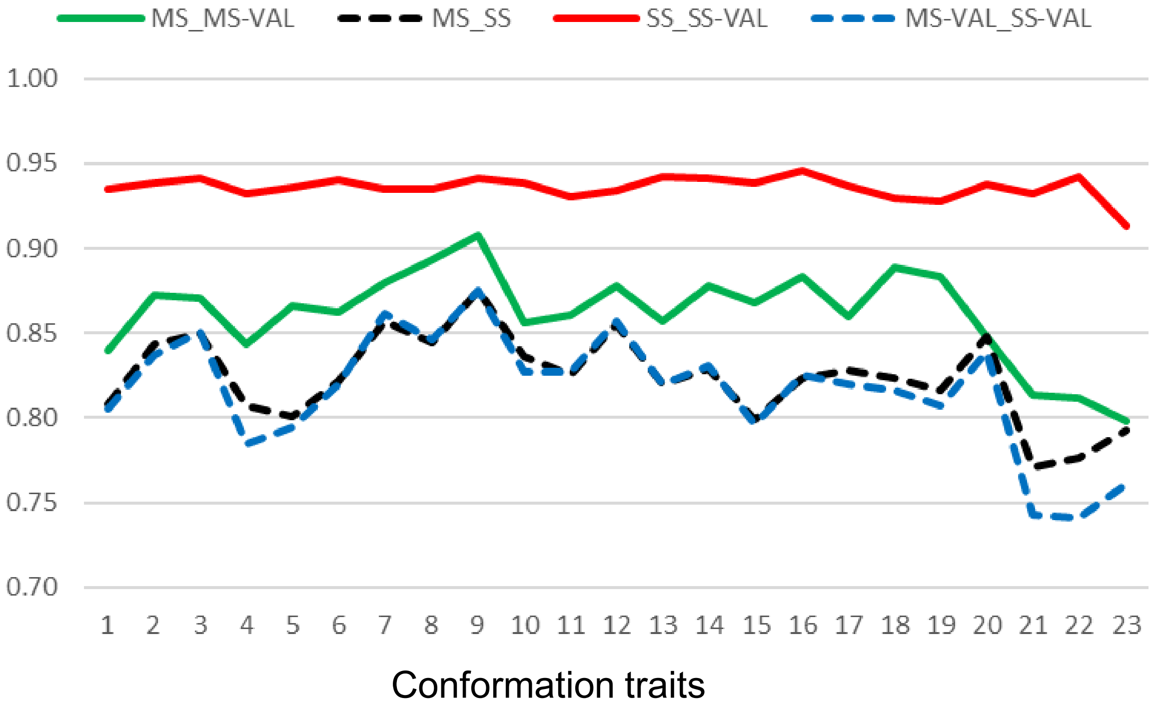
- Validation bulls defined as genotyped & phenotyped DEU bulls:
  - Born in between 2013 to 2016 (three years)
  - With daughters in ≥ 10 herds
  - Most daughters In DEU
  - A total of **798** DEU validation bulls



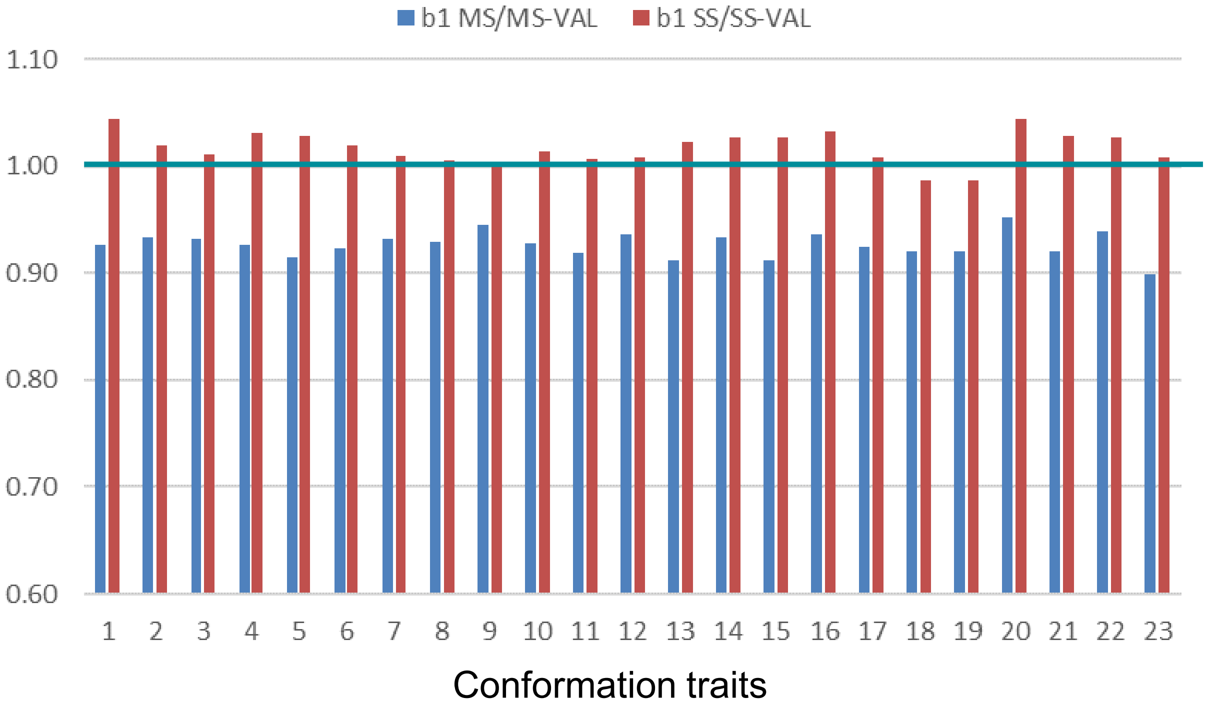


# II) Comparison of SNP effect estimates

Observed correlations between SNP effects for the full and truncated data sets

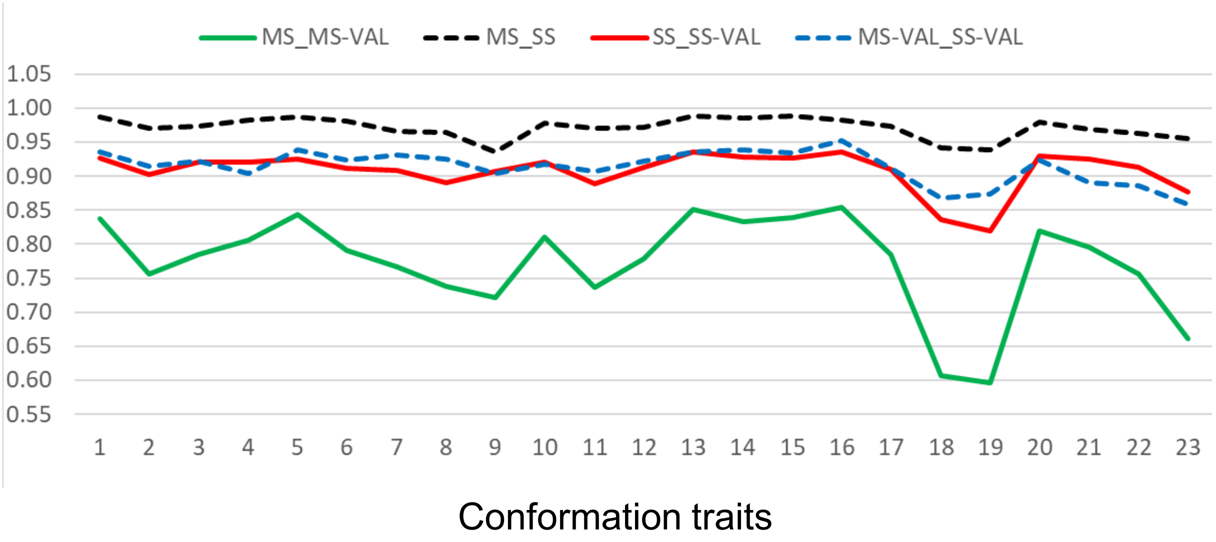


Regression of SNP effects of the full on SNP effects of truncated data sets

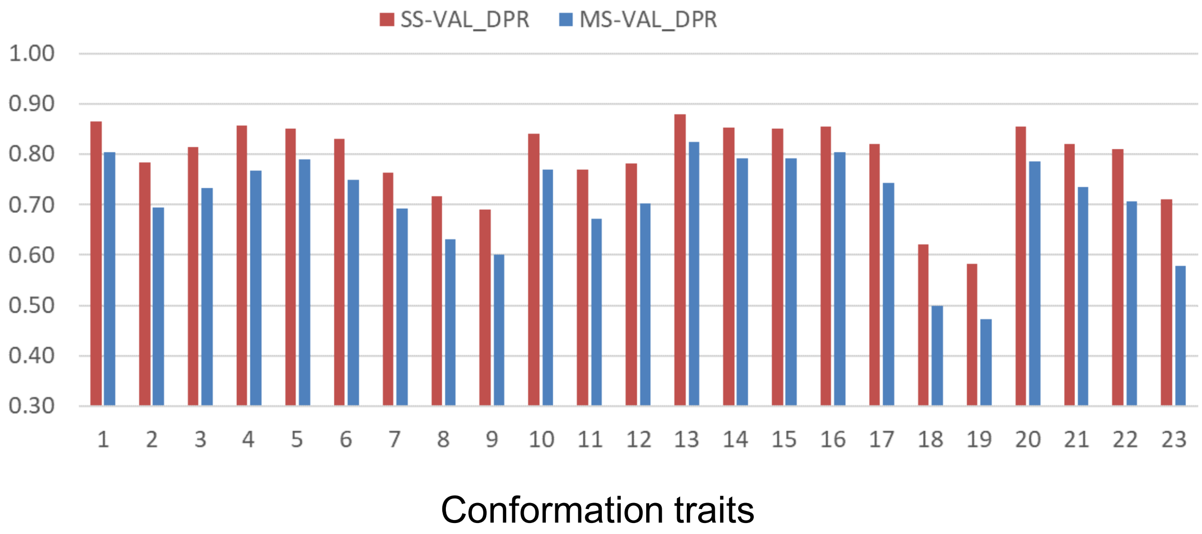


# II) Accuracy of genomic prediction: GEBV correlations for DEU validation bulls

Observed correlations between GEBVs of the full and truncated data sets

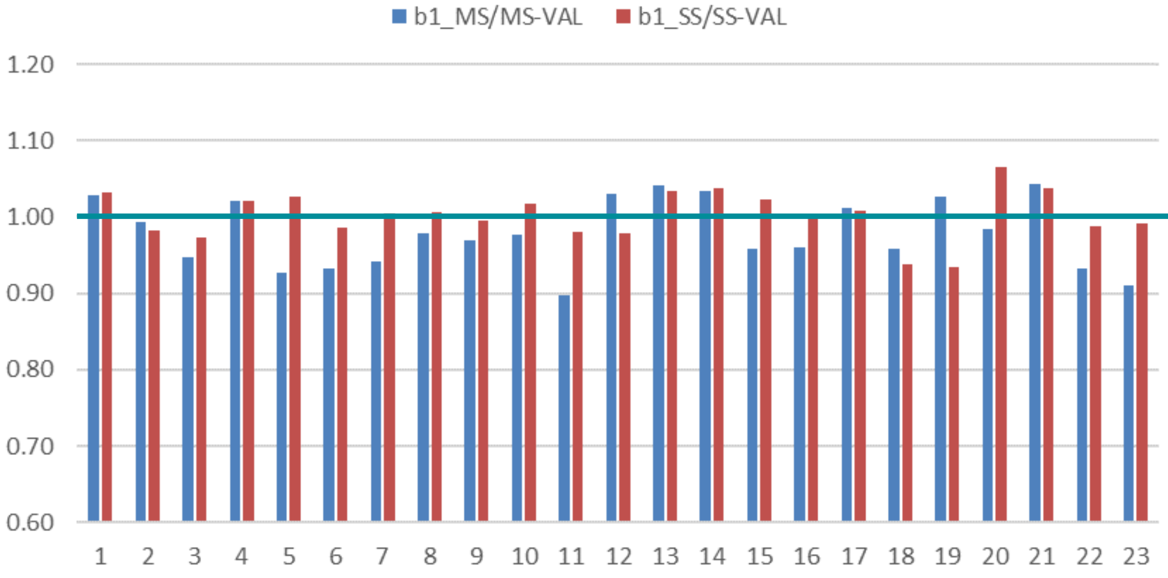


Observed correlations of GEBV of the truncated with deregressed EBV of full data sets



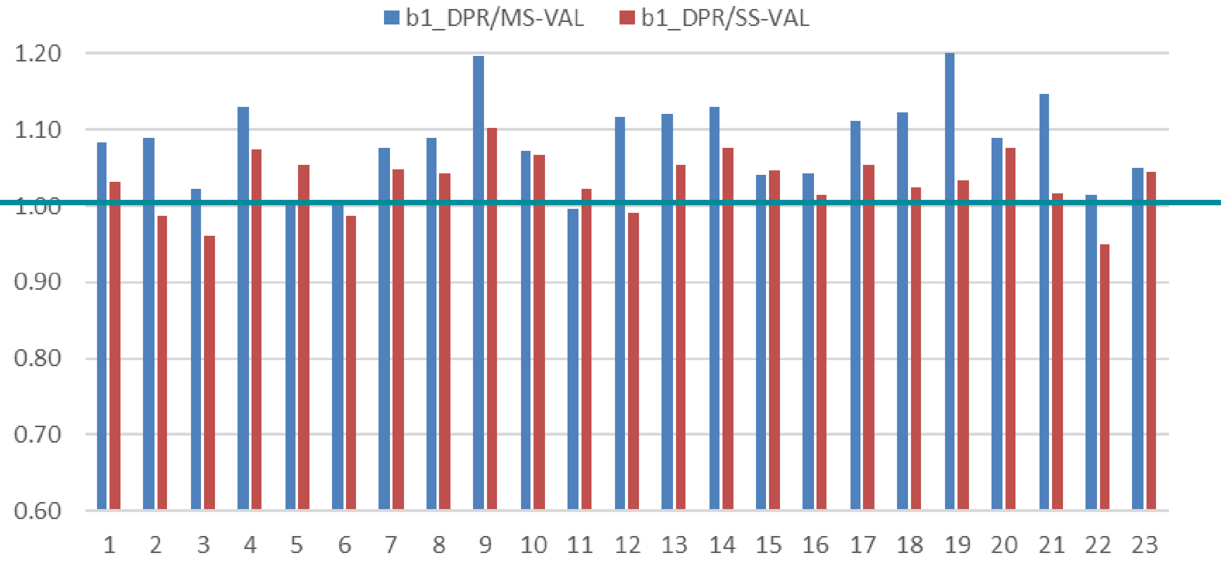
# II) Dispersion of genomic prediction: GEBV regressions for DEU validation bulls

Regression of GEBV of the full on GEBV of truncated data sets



Conformation traits

Regression of deregressed EBV of the full on GEBV of truncated data sets

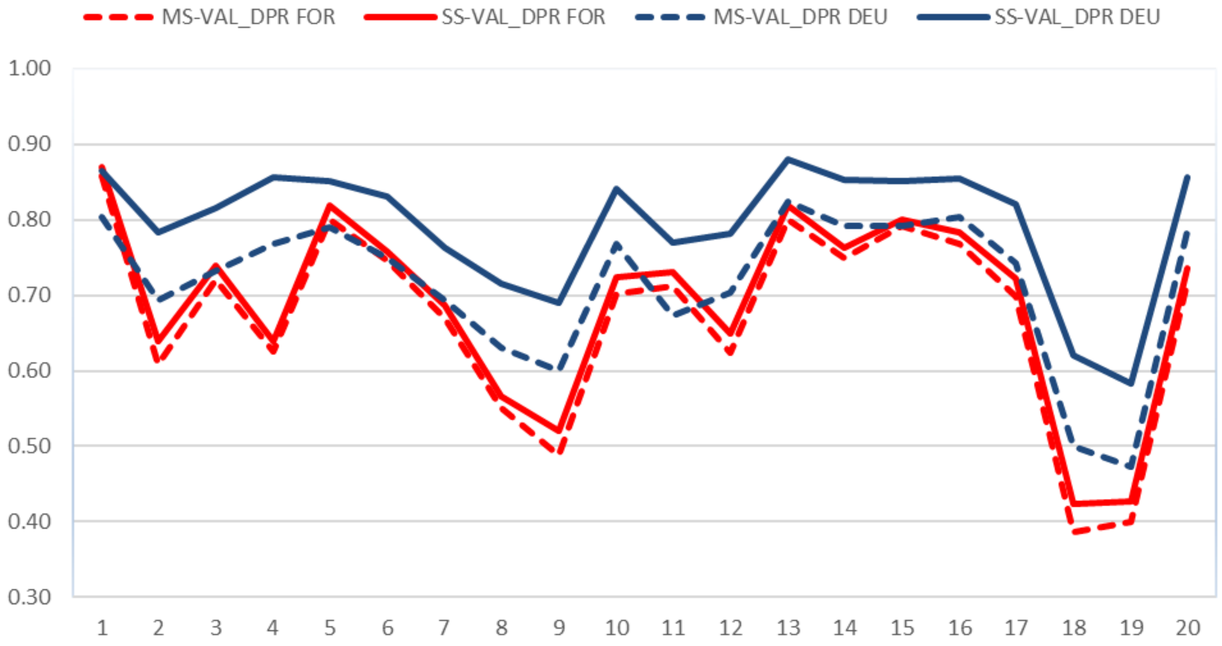


Conformation traits

# II) Accuracy of genomic prediction: GEBV correlations for foreign validation bulls with no daughters in DEU

- Larger difference in GEBV correlations between the 2 models for DEU than FOR bulls
- Foreign validation bulls have lower accuracy than DEU validation bulls

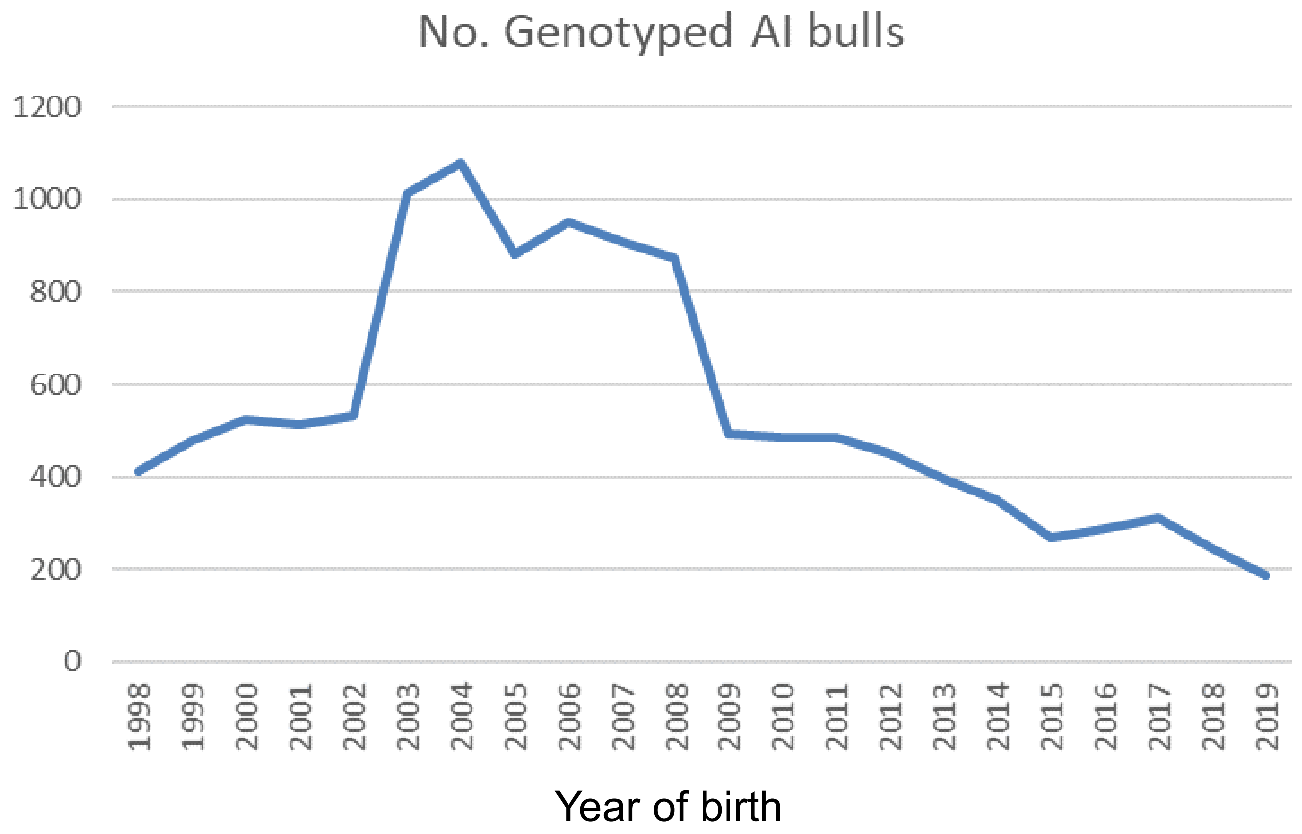
Observed correlations of GEBV of the truncated with deregressed EBV of full data sets



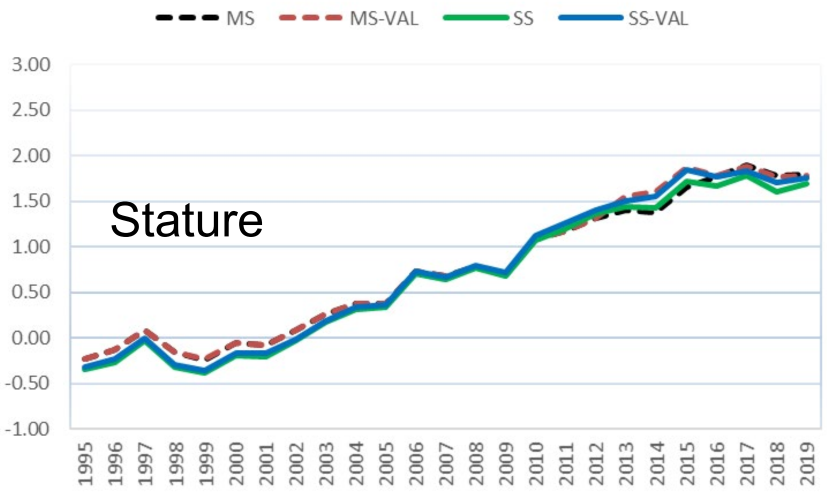
Conformation traits

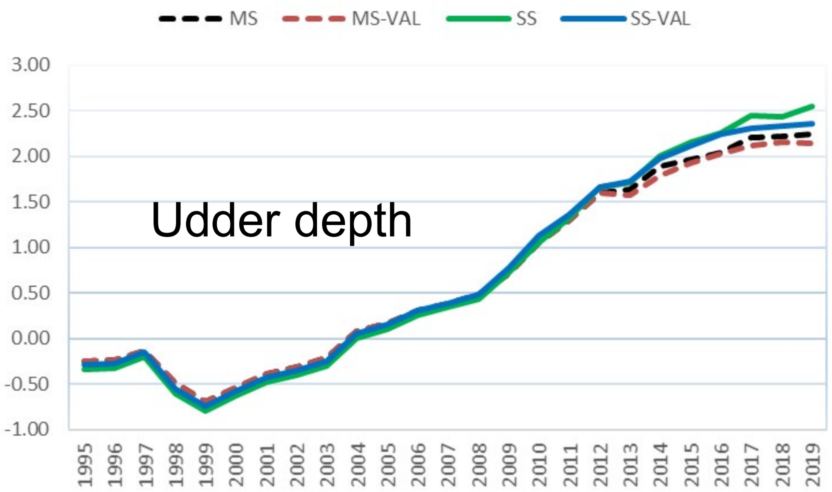
No. foreign validation bulls: 2964

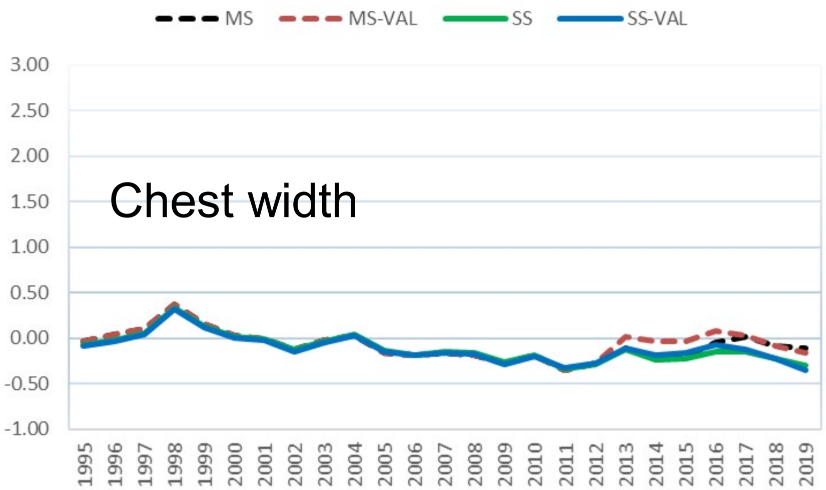
# III) Genotyped German Holstein AI bulls

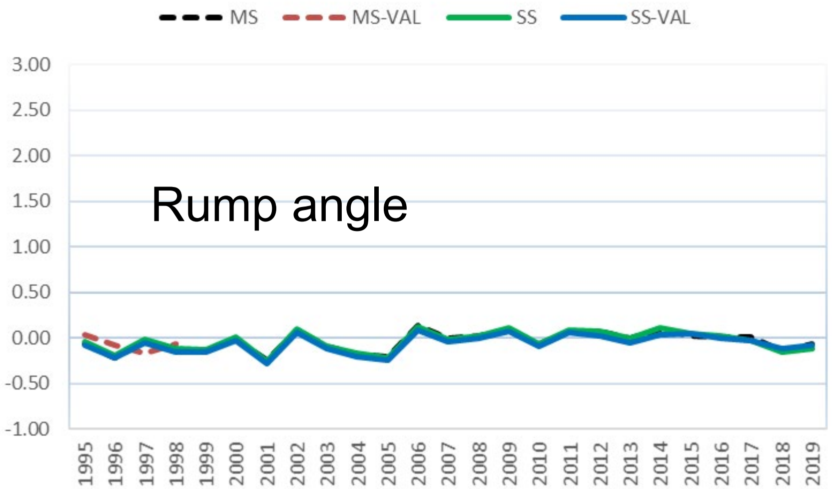


# III) Genotyped German Holstein AI bulls: Genetic trends in GEBV

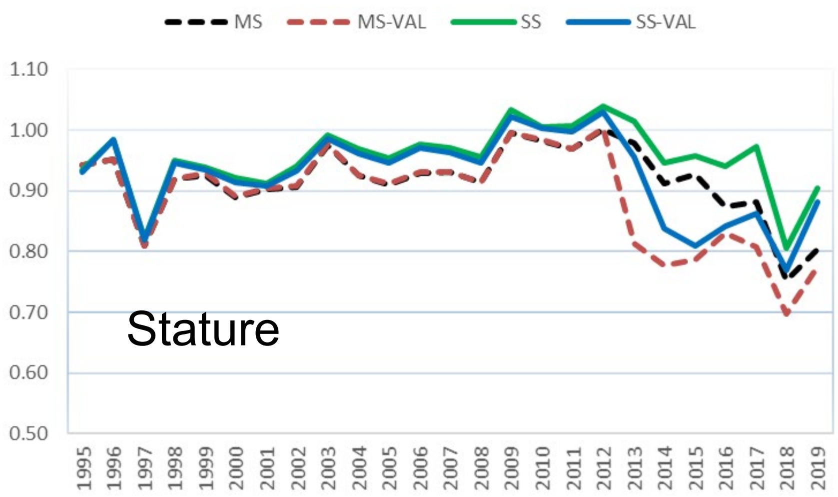


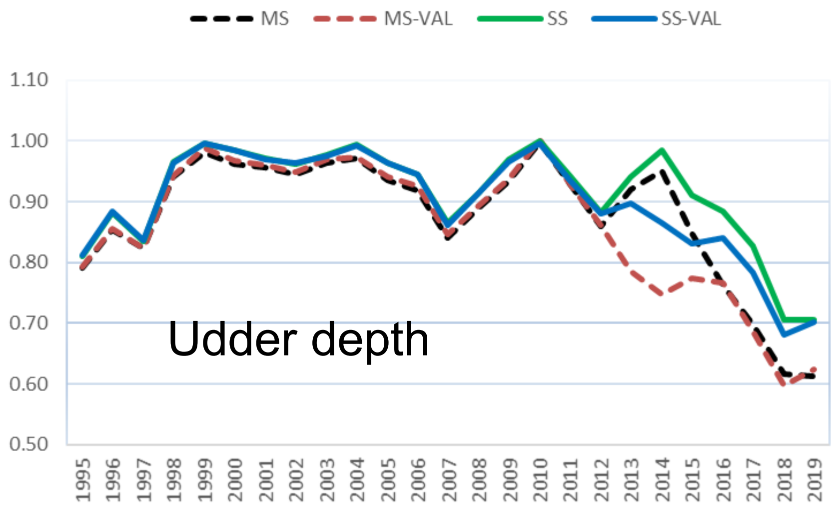


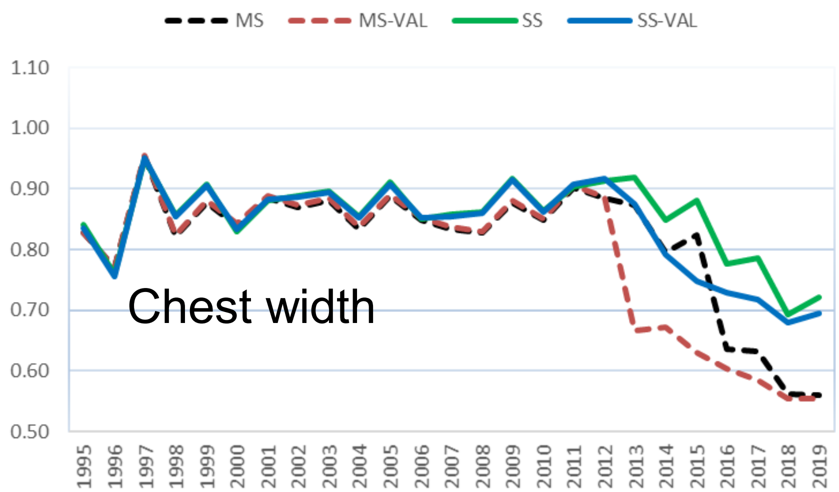


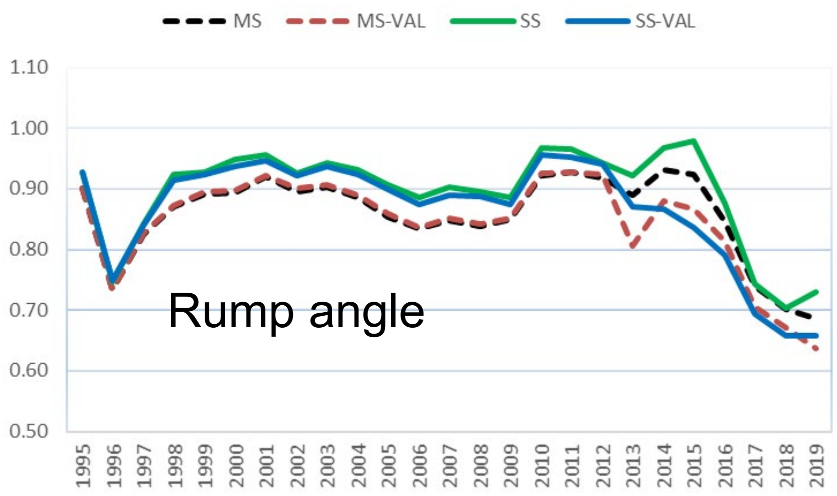


# III) Genotyped German Holstein AI bulls: Standard deviations of GEBV

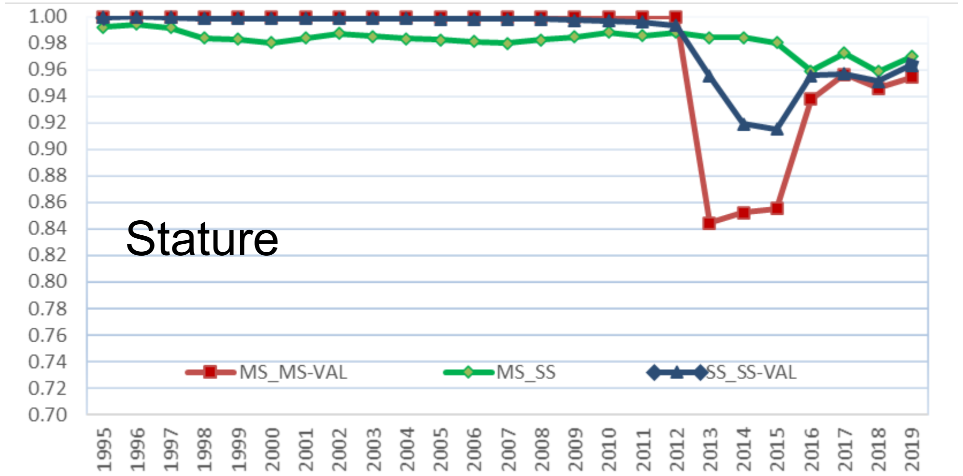


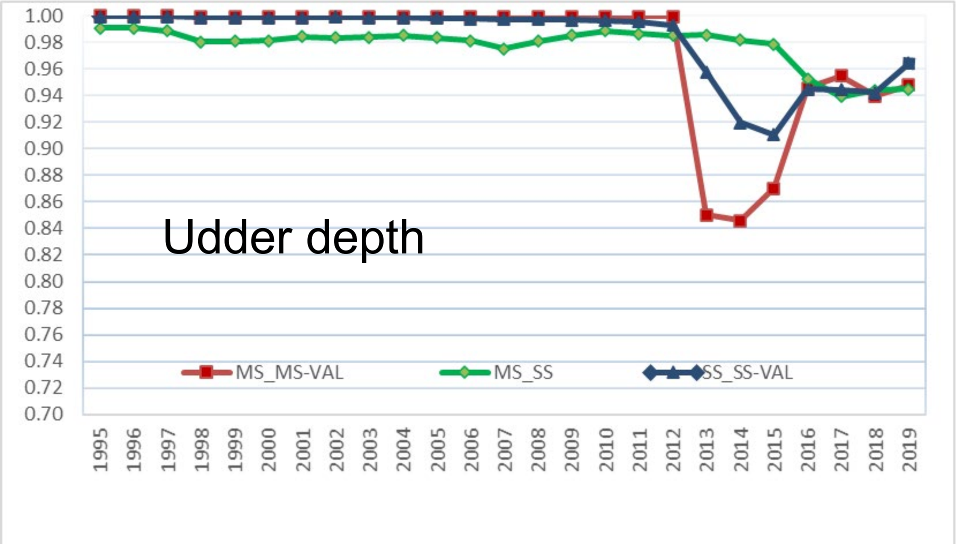


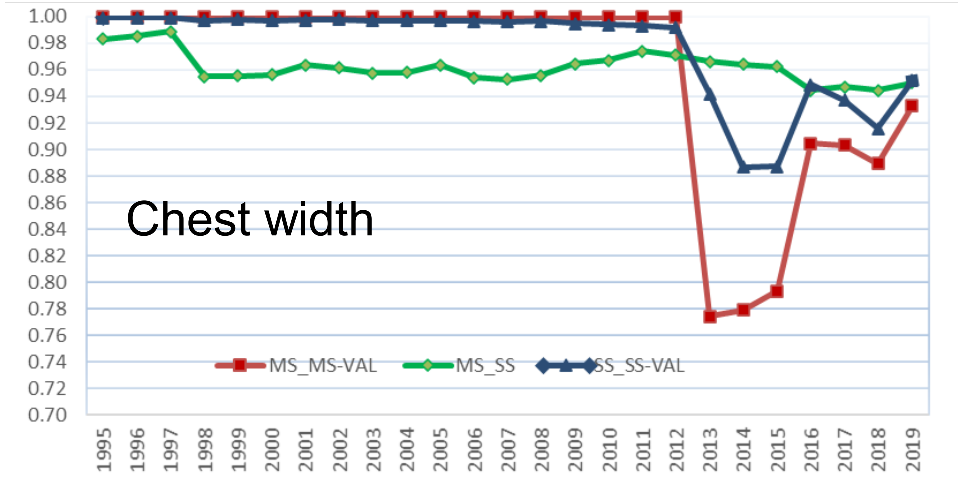


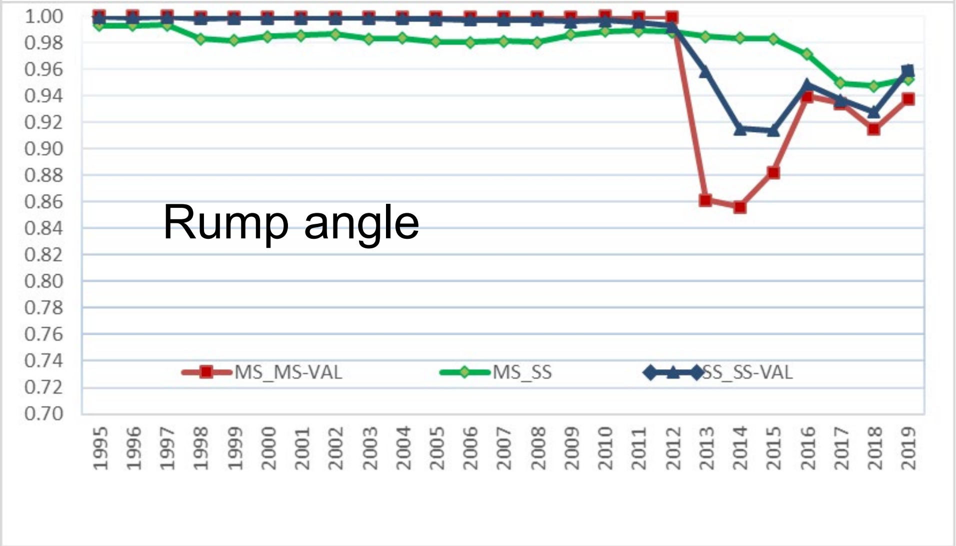


# III) Genotyped German Holstein AI bulls: Observed GEBV correlations between two evaluations









## Summary and conclusions (I)

- Deregressed bull MACE evaluation was integrated as additional phenotype data
- The ssSNPBLUP model compared to the current multi-step genomic model via validation
  - Higher accuracy, greater GEBV variance
  - Regression of GEBV of current on early evaluation more closer to 1
  - Regression of deregressed EBV on early GEBV do not differ much from 1
- For youngest genomic AI bulls or validation bulls GEBV correlation between the two models: ~0.95
- No major concern about over-prediction of young animals by the single-step model for the type traits

- Further developments
  - Calculation of conformation indices for routine implementation
  - Meta-founders to be investigated
  - Distance of young animals to reference population to be considered: first, second or third generation

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