

Using a single-step SNP BLUP maternal-effect model for calving trait genomic evaluation in German Holsteins

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I) Different modelling of genetic effects in national and MACE evaluations

- German genetic evaluation model for calving data of national cows or calves
 - A direct-maternal effect model for calving ease and stillbirth (**a 2-effect model**) in first 3 parities
 - Calving ease (CE) and stillbirth (SB) as correlated traits
 - Genetic effects for national data: 2 traits x 3 parities x 2 effects = 12
 - **First parity direct and maternal effects** as official breeding values, defined as **MACE traits**

- MACE uses a **1-effect model** separately for direct and maternal effects of either CE or SB
 - Four **separate** MACE evaluations differ in participating countries and number of bulls
 - We do not discard any deregressed MACE EBV of maternal / direct effects

I) A single-step SNP BLUP model (Liu & Goddard) for calving traits

- A ssSNPBLUP maternal-effect model for calving traits with correlated MACE traits
 - 4 MACE evaluations (CEd, CEm, SBd, SBm) differ in participating countries and numbers of bulls
 - Weight as difference in (animal-model based) EDC between MACE and national evaluation
 - Adjustment in deregressed bull EBVs from national and MACE evaluation

- The ssSNPBLUP model with **30%** residual polygenic variance for all the calving traits

- A special implementation of the ssSNPBLUP (Liu-Goddard) model in MiX99



I) Phenotype and genotype data for the single-step test evaluation

- Genotyped population of German Holsteins for routine genomic evaluation **August 2021**
 - 1,003,041 genotyped Holstein animals including young candidates and culled animals

- Phenotype data of national cows or calves and international bulls for four MACE calving traits
 - Full data set of national calving with bull MACE data
 - 25,379,991 calving records/calves, 31,167,053 cows and calves with phenotype data
 - 112,076 bulls with deregressed MACE EBV added ($\Delta EDC > 0$)
 - 31,279,129 calves or cows or MACE bulls with phenotype data

- Pedigree file for the single-step evaluation
 - 38,150,805 animals in pedigree for the full evaluation and 90 phantom parent groups

- Total # of estimated effects: 615,848,330



I) The current multi-step genomic model

- **A mixed bull and cow reference population** for German Holsteins since 2019
- **A single-trait 1-effect genomic model** for the official (MACE) traits
- Data taken from **April 2021** genomic evaluation
 - 296,897 reference cows and 37,285 reference bulls (stillbirth maternal)
 - 203,439 reference cows and 35,780 reference bulls (stillbirth direct)
- Truncated data set for a genomic validation
 - Truncating cows or bulls using the current national conventional and MACE evaluations
 - Last 3 birth years of validation bulls (2014-2016) → 991 Holstein validation bulls
 - Last 2 years of cows plus daughters of the validation bulls removed



II) A genomic validation simulating a forward prediction

- Validation bulls defined following the rules of Interbull GEBV Test
 - Daughters or ≥ 50 calves in ≥ 10 herds in Germany for maternal or direct effects, respectively
 - EDC ≥ 20 for each trait separately
 - **Direct effects:** bulls born in 2015 through 2018; **maternal effects:** bulls born in 2013 through 2016

- Truncated national calving data based on calving date
 - Calving records in last four years removed

- Deregressed bull MACE EBV obtained from **August 2021**
 - Bull truncation by birth year, separately for direct and maternal genetic effects



II) Regression of GEBV of the full on truncated evaluation: validation bulls single-step and multi-step model

Single-step model with 30% residual polygenic variance

DEU validation bulls	No. bulls	b ₀	b ₁	R ²
Calving ease direct	1611	21.95	0.79	0.71
maternal	1710	10.09	0.89	0.75
Stillbirth direct	1618	26.82	0.70	0.57
maternal	1662	10.11	0.90	0.79

Multi-step model with 30% RPG, except 20% for SBm

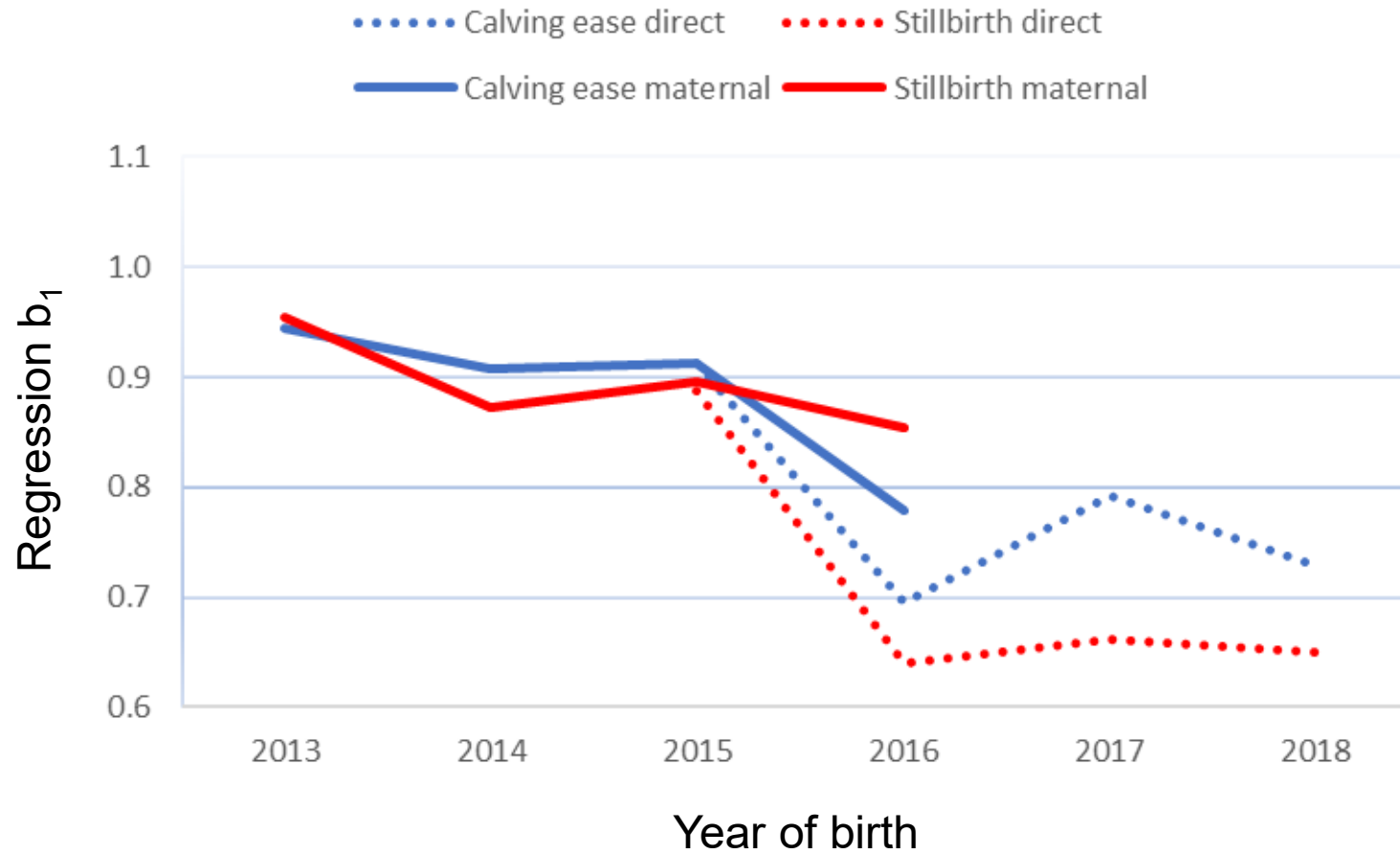
DEU validation bulls	No. bulls	b ₀	b ₁	R ²
Calving ease direct	1961	-3.74	1.04	0.54
maternal	955	-0.73	0.99	0.49
Stillbirth direct	1970	-2.85	1.02	0.38
maternal	935	8.33	0.91	0.55

Multi-step model: post-processing of genomic evaluation performed

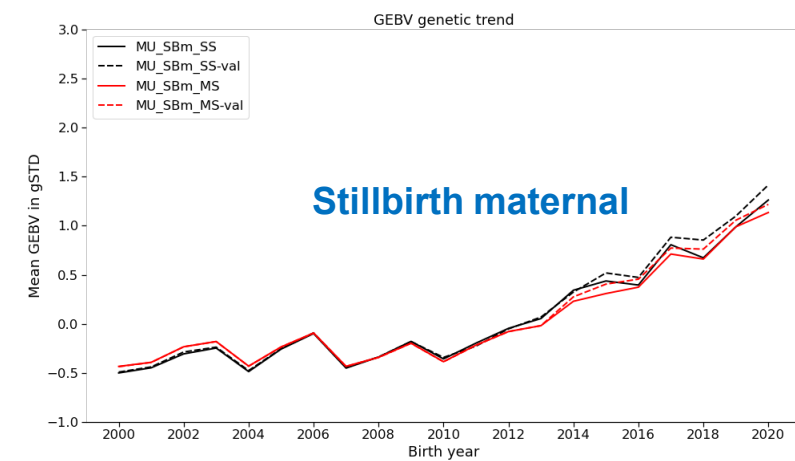
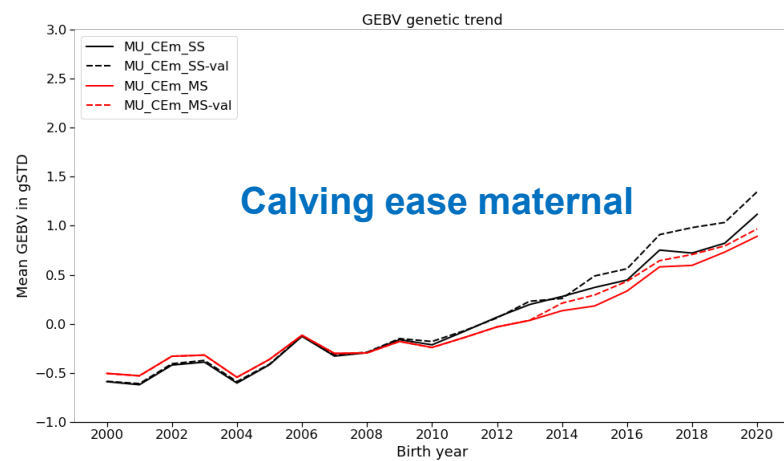
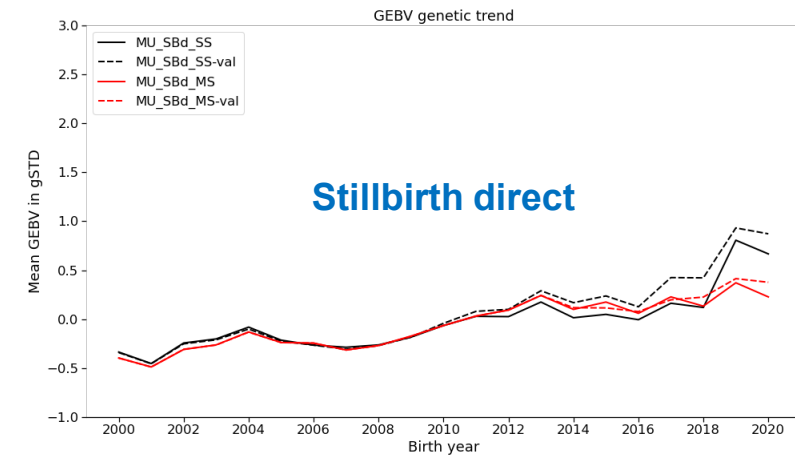
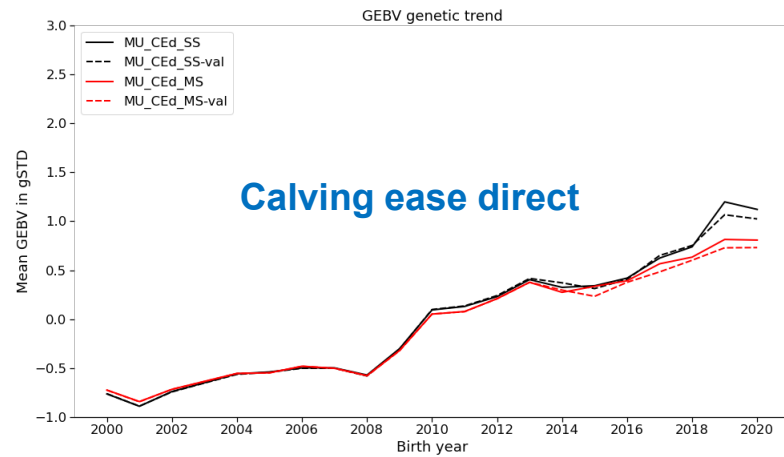


II) Validation regression coefficients stratified by birth year of validation bulls

30% RPG variance



III) Genotyped German Holstein AI bulls: Genetic trends in GEBV (30% residual polygenic variance)



VI) Summary and conclusions (1)

- A **1-effect model for MACE** complicated the integration of bull MACE data into the **2-effect national single-step evaluation**
 - Our modelling uses all four MACE traits (CEd, CEm, SBd, and SBm)
 - Largest difference between single-step and multi-step genomic models among all traits
- Single-step **SNP effect estimates** have less bias than the multi-step model
 - b_1 of single-step model are nearly 1
 - SNP correlations between the models range from 0.75 (SBd) to 0.85 (CEd)
 - Correlations of single-step SNP effects between the full and truncated data are 0.90 to 0.93
- Less satisfactory **validation results** for direct than maternal genetic effects, in particular stillbirth direct
 - b_1 for maternal effects around 0.9
 - Much lower b_1 for direct effects: 0.79 (CEd) and 0.70 (SBd)
 - More inflation for younger than older validation bulls, specially evident for direct genetic effects



VI) Summary and conclusions (2)

- Increasing RPG variance to **40%** improved only little in reducing overestimation
- A **bull reference population** did not improve the validation results either
- **Removing genotype data** of bulls born before 2005 did not reduce the inflation either
- Presentation at EAAP covering several test scenarios
 - Liu et al. EAAP session 14, 39770, oral presentation
- Post-processing GEBV of young candidates may be un-avoidable for calving traits



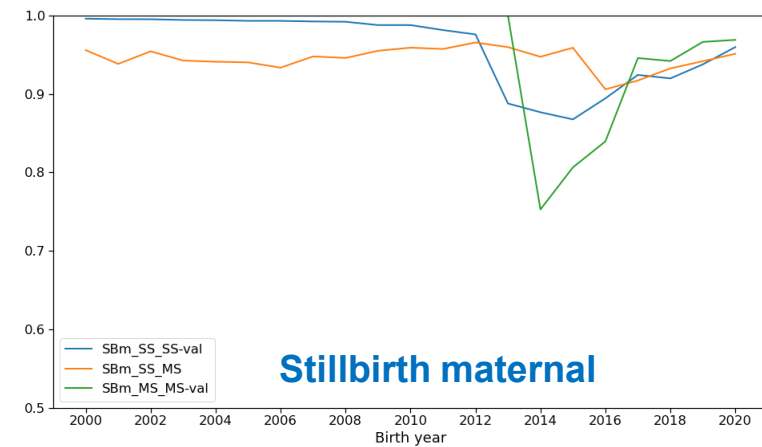
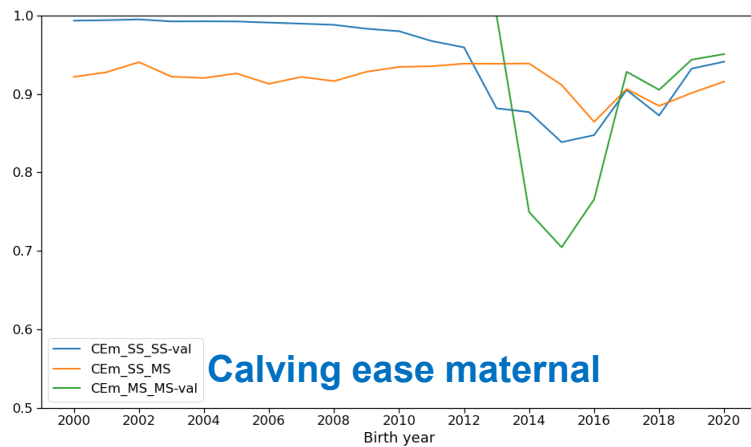
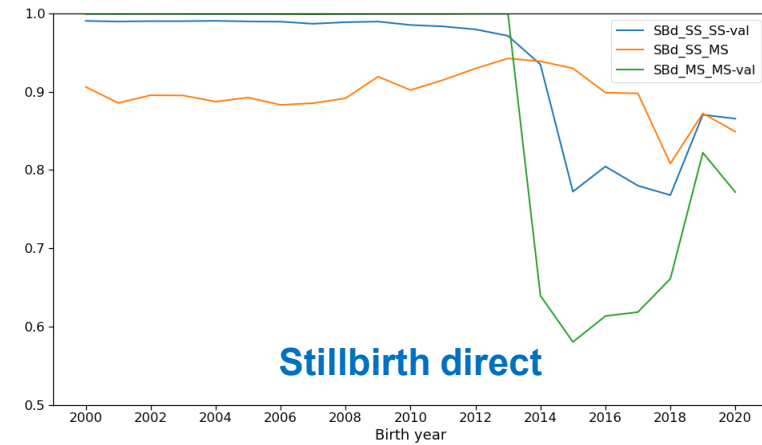
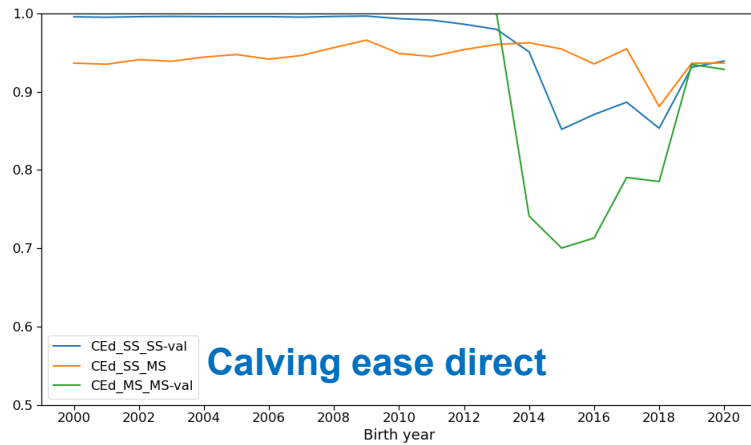
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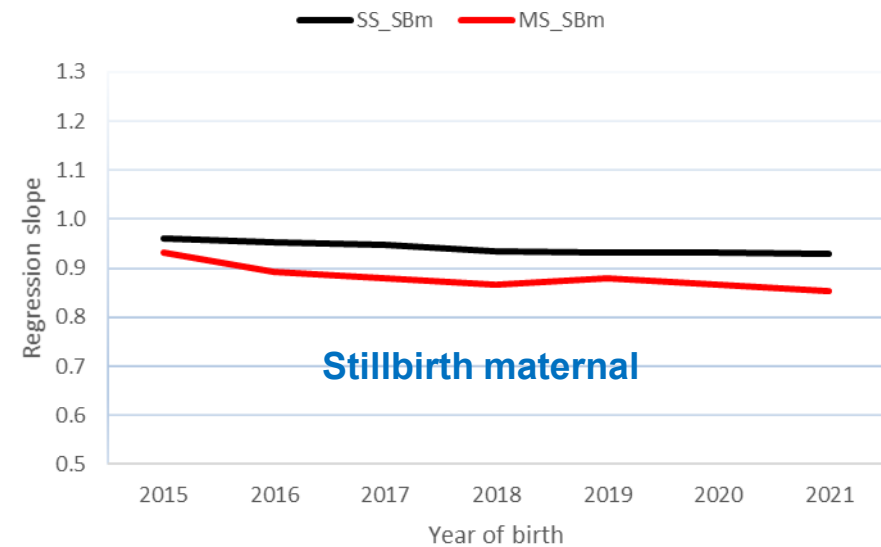
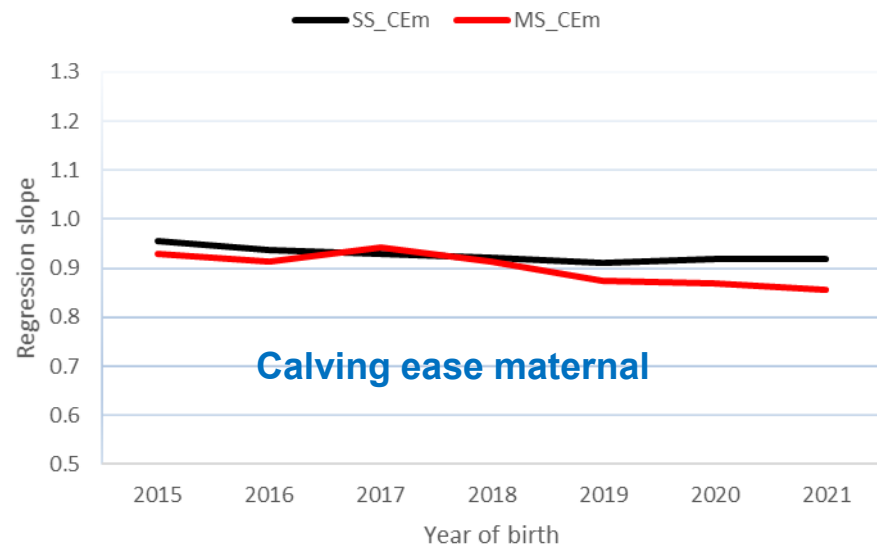
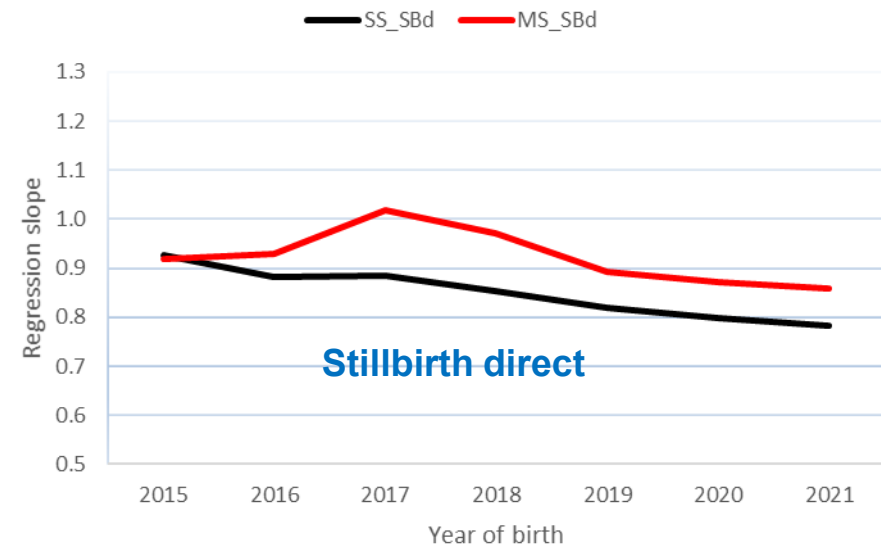
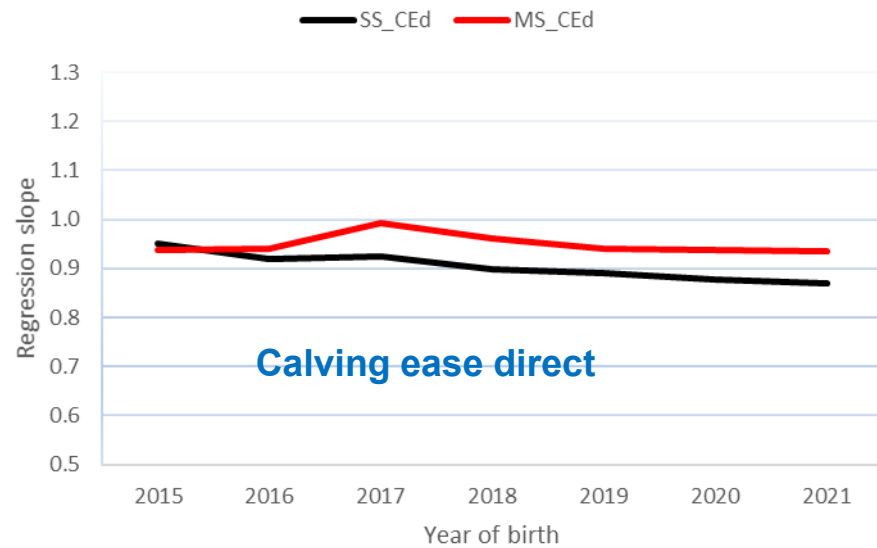
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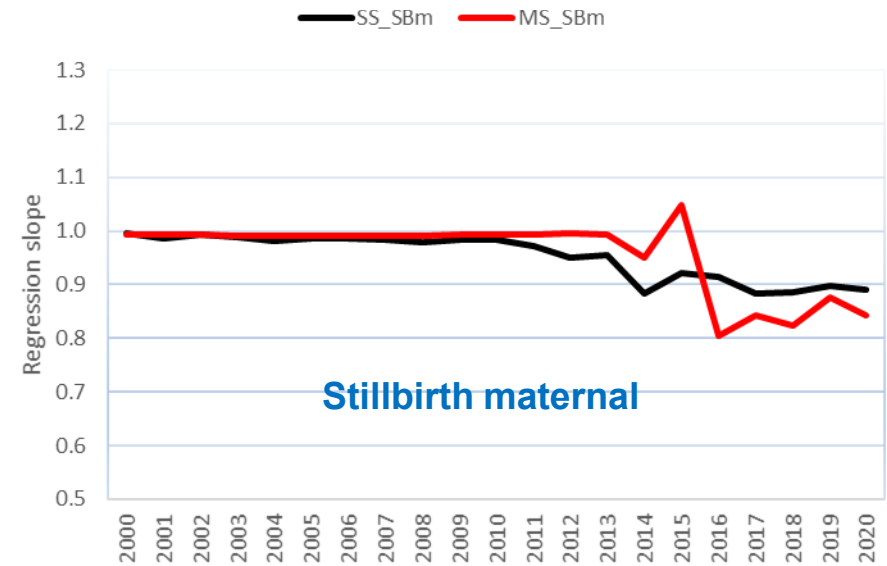
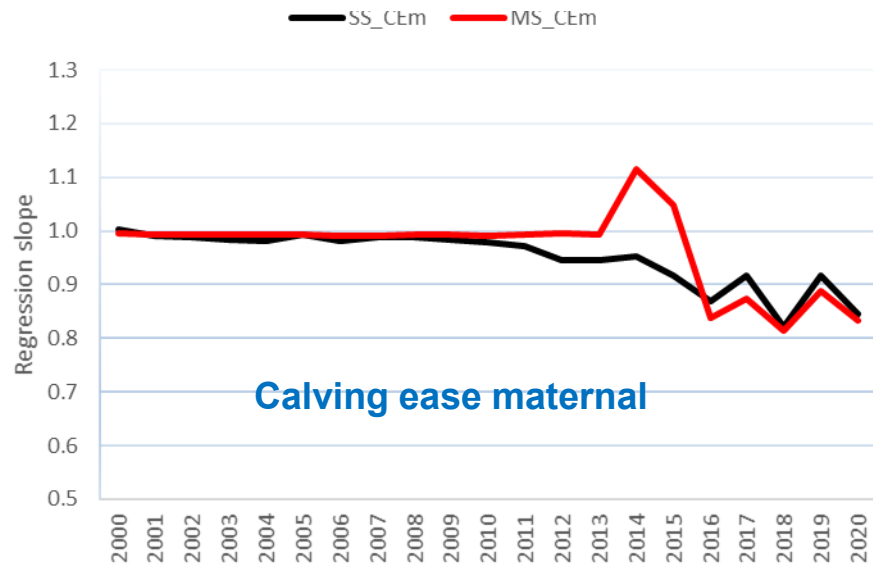
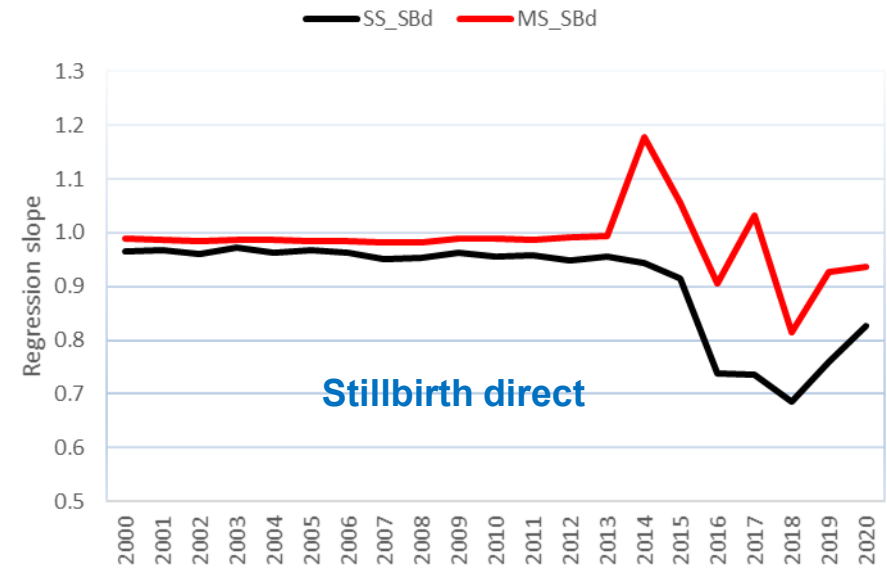
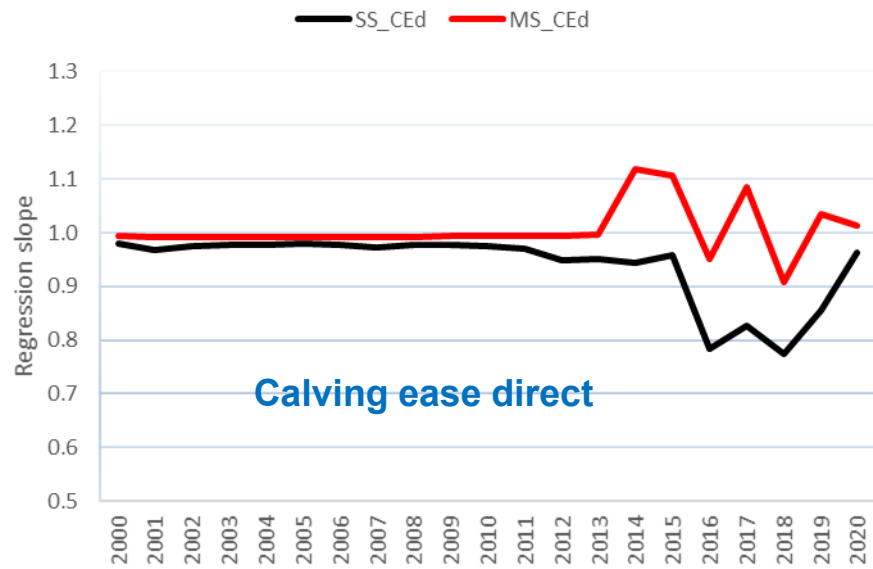
III) Genotyped German Holstein AI bulls: Observed GEBV correlations between the full and truncated evaluations (30% residual polygenic variance)



IV) Genotyped females: GEBV regression of the full on the truncated evaluations (30% residual polygenic variance)



III) Genotyped German Holstein AI bulls: GEBV regression of the full on the truncated evaluations (30% residual polygenic variance)



V) Genotyped male candidates: Observed GEBV correlations between two evaluations (30% residual polygenic variance)

