

Detecting effective starting point of genomic selection by divergent trends from BLUP and ssGBLUP

Ignacy Misztal, Rostam Abdollahi-Arpanahi, Daniela Lourenco,
University of Georgia
USA



The University of Georgia



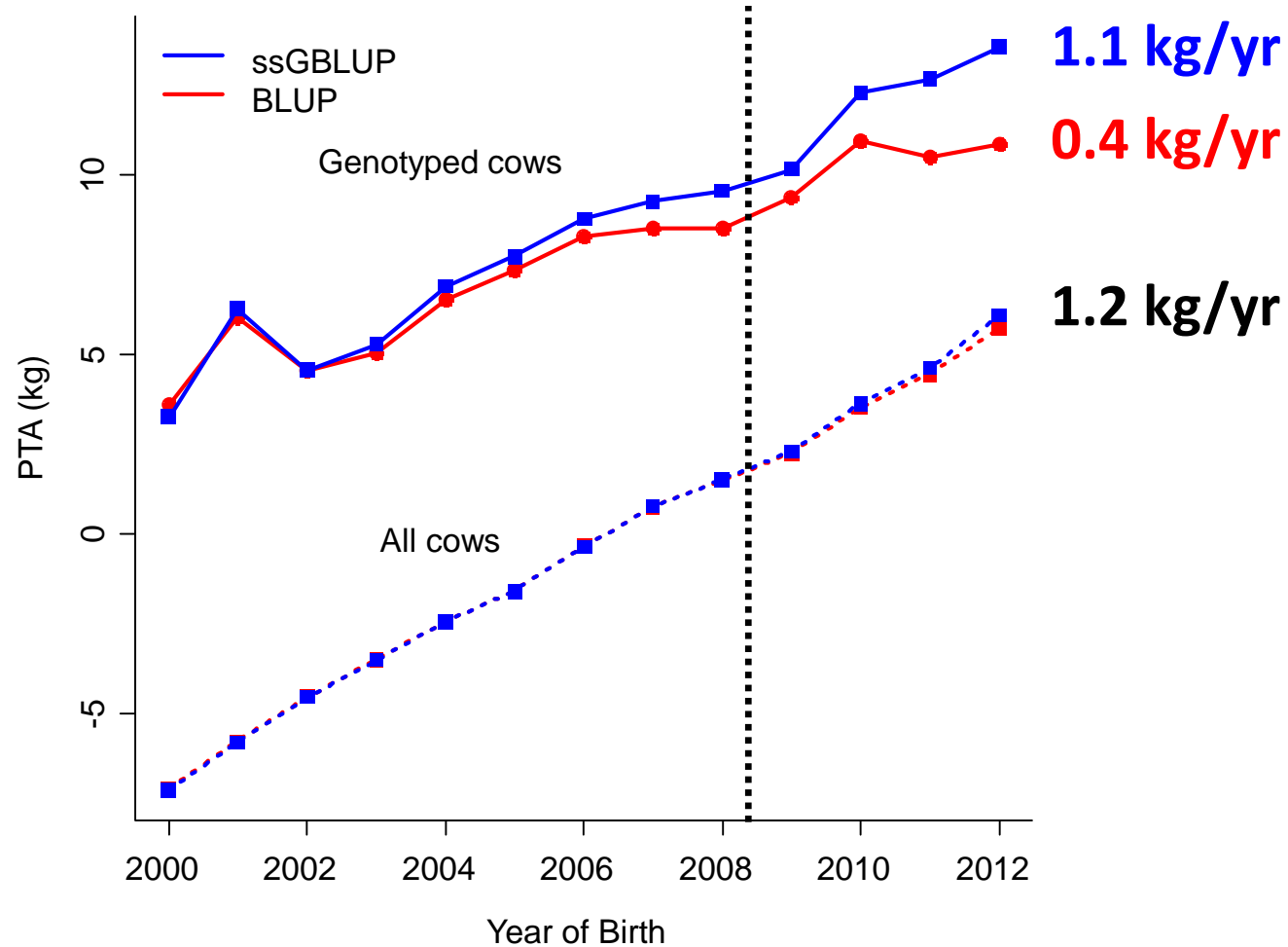
Genotyping and genetic progress

- Extensive genotyping
- Genomic evaluation
- Various models and quality control
- Importation of “genetic progress”

- Effects of genomic preselection and selective genotyping

- Is genomic selection effective for specific organization?

Trends for Holstein cows with ssGBLUP and BLUP



Goals

- Can differences in trends of ssGBLUP and BLUP identify onset of genomic selection?
- Find the theory
 - Past work: Patry and Ducrocq (2012), Tyriseva et al. (2018)
- Validate with field data sets

BLUP: $EBV = w_1^c PA^c + w_2^c YD^c + w_3^c PC^c$

ssGBLUP: $GEBV = w_1^g PA^g + w_2^g YD^g + w_3^g PC^g + w_4 GI$

If positive selection

+ genomic selection effective: $avg(GEBV) > avg(EBV)$

PA =parent average YD = yield deviation. PC = progeny contribution GI = genomic index

Realized Mendelian Sampling: $RMS_i = (G)EBV_i - PA_i$

If all progeny genotyped $E(RMS_{BLUP}) \approx 0$

$$E(RMS_{SSGBLUP}) \approx 0$$

If selective genotyping, for “best” animals: $E(RMS_{BLUP}) > 0$

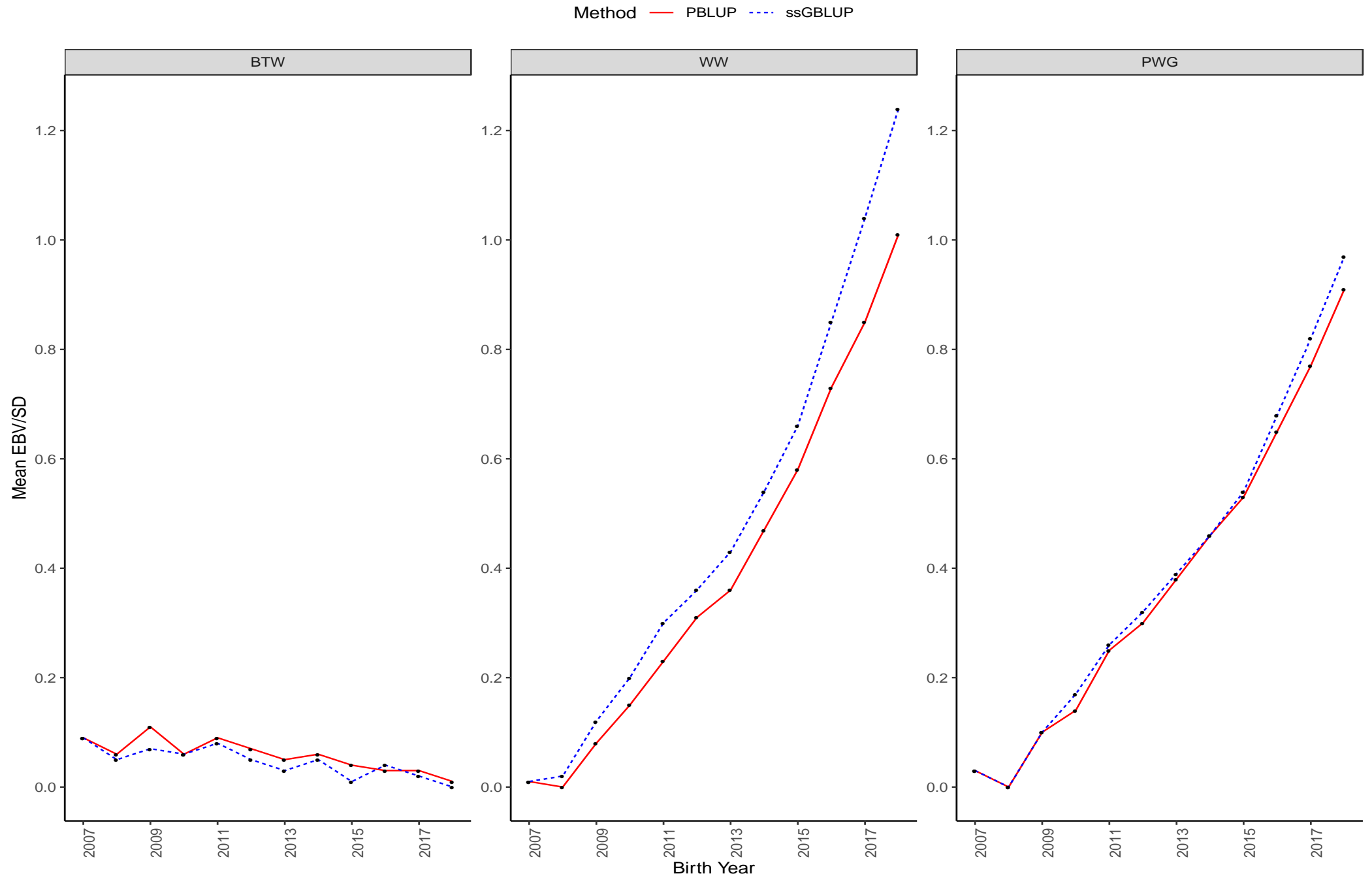
$$E(RMS_{SSGBLUP}) > 0$$

$$E(RMS_{SSGBLUP}) > E(RMS_{BLUP})$$

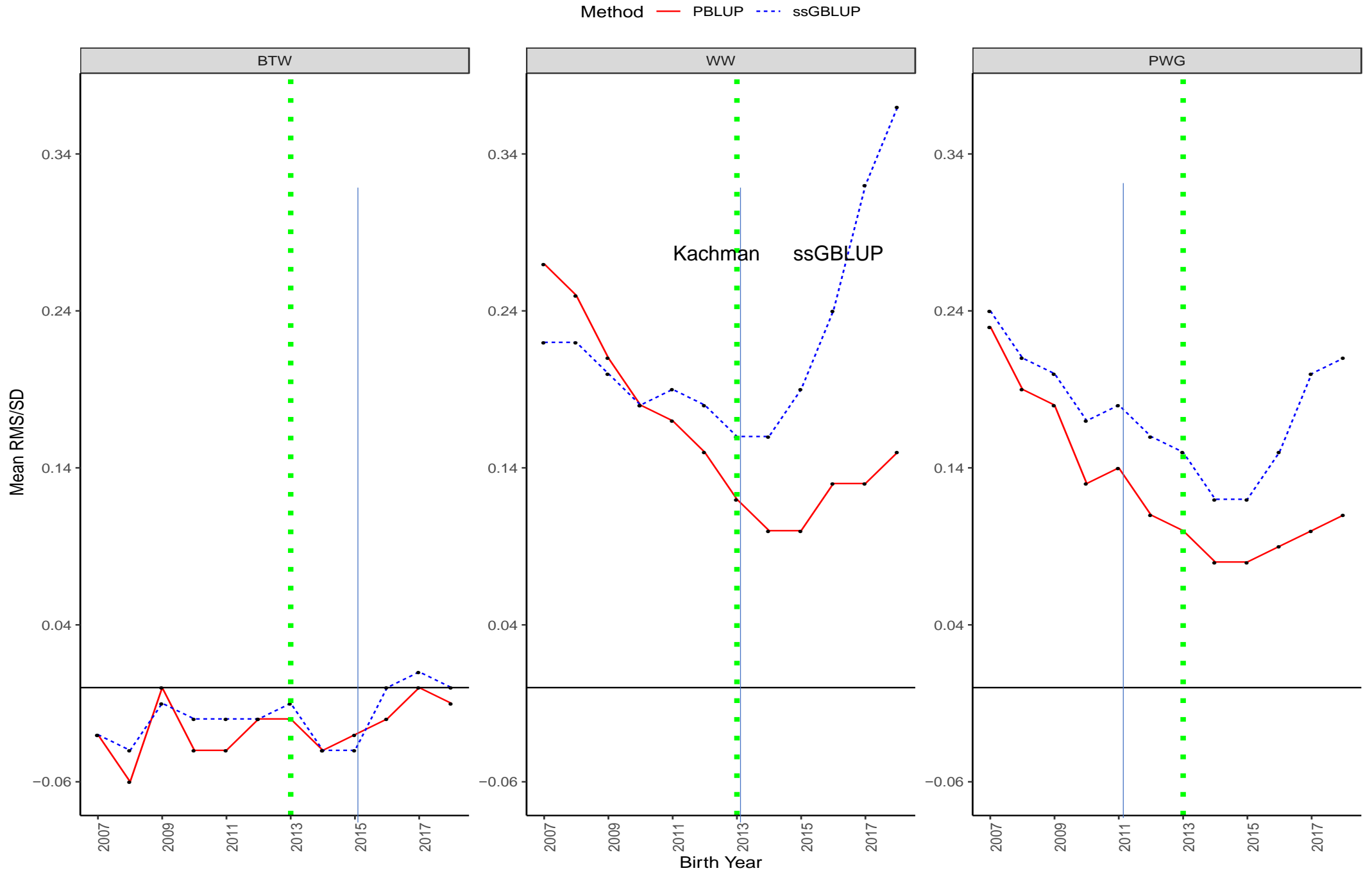
US Angus national data

- 11M animals
 - 9M records for birth weight and weaning weight
 - 4M records for yearling weight
 - 842k genotyped
-
- Results in genetic SD

(G)EBV trends



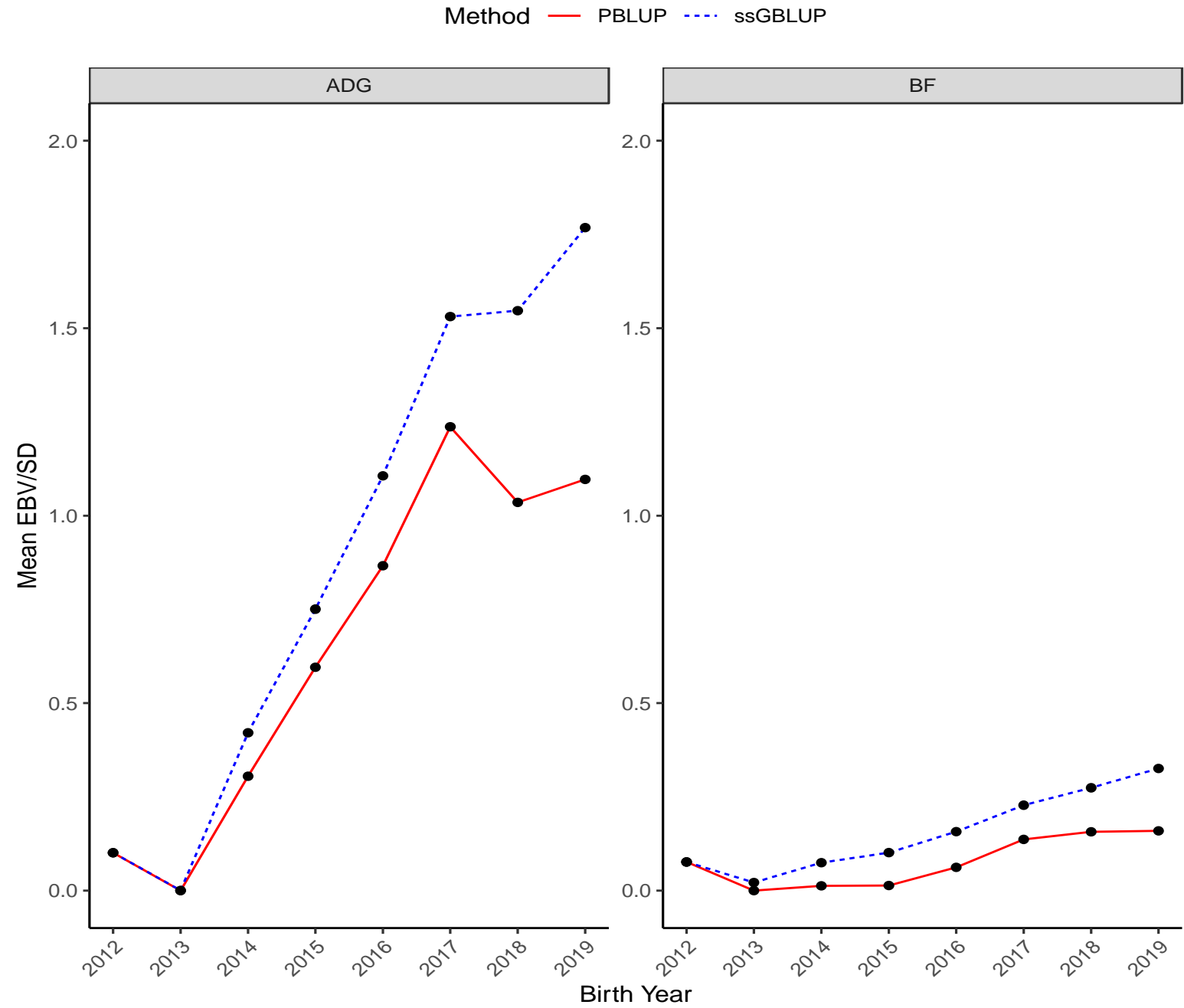
Mendelian sampling trends



Pig data

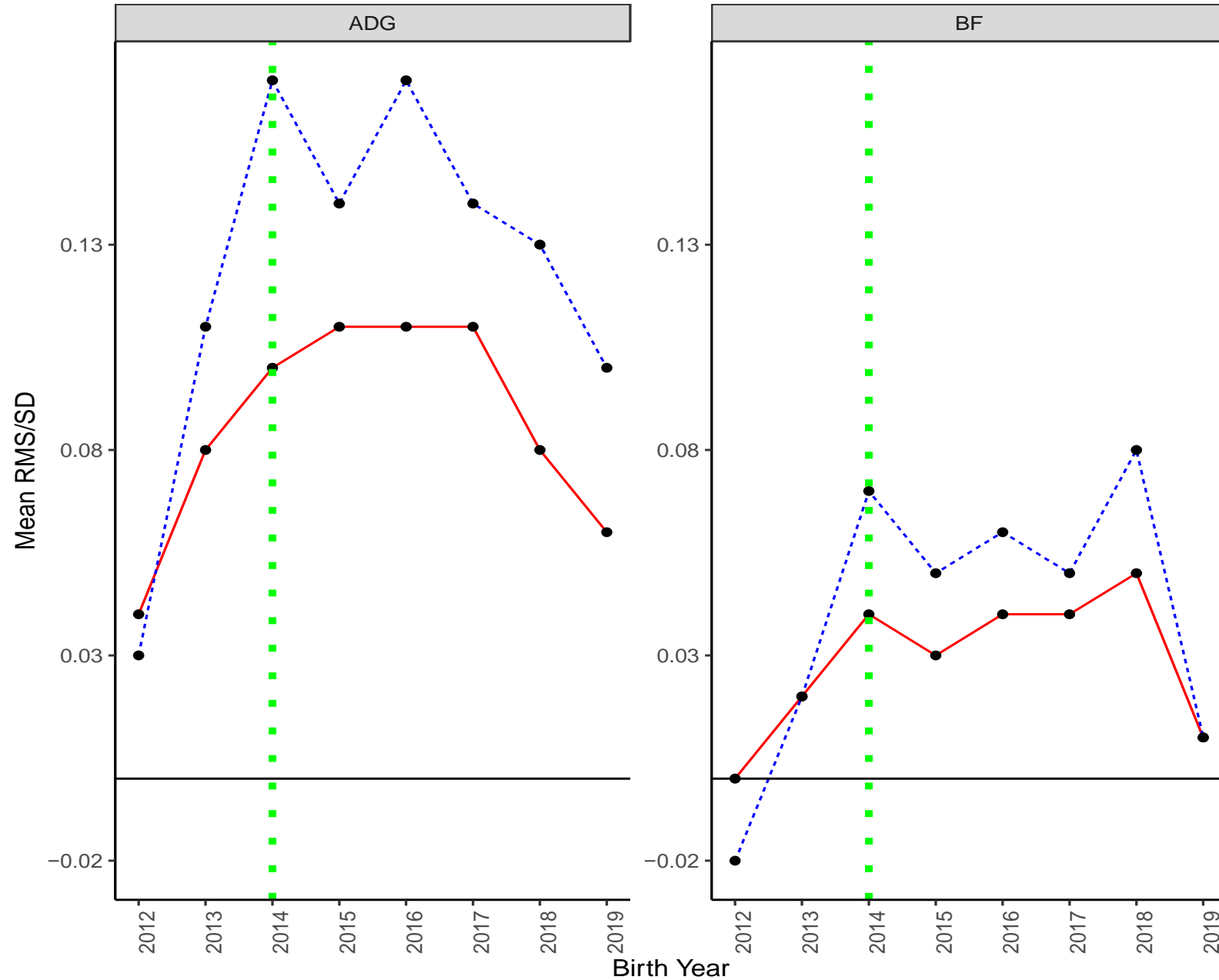
- 1.3M animals
- > 0.8M records for body weight and backfat
- 116k genotyped

(GEBV) trends



Mendelian sampling trends

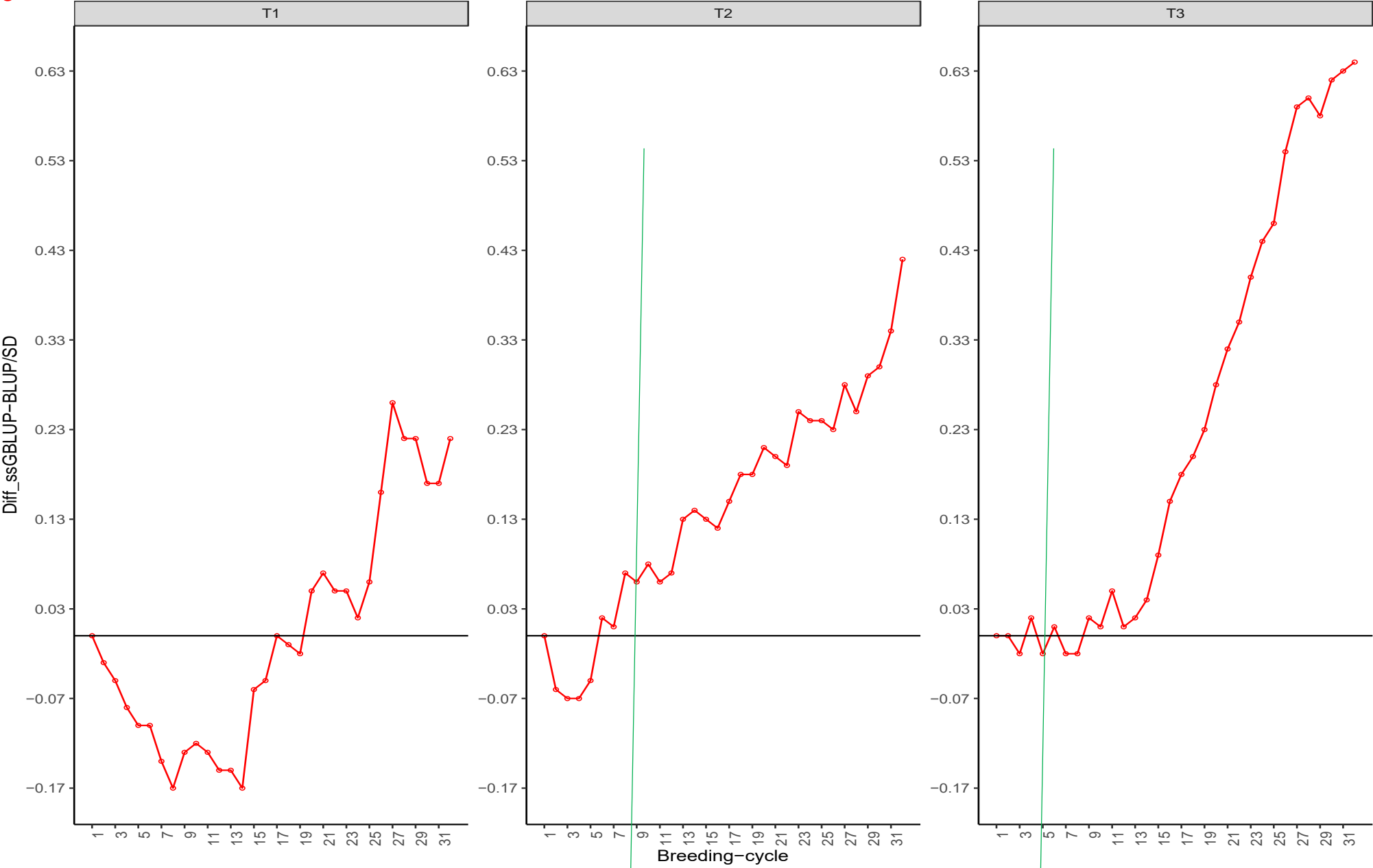
Method — PBLUP — ssGBLUP



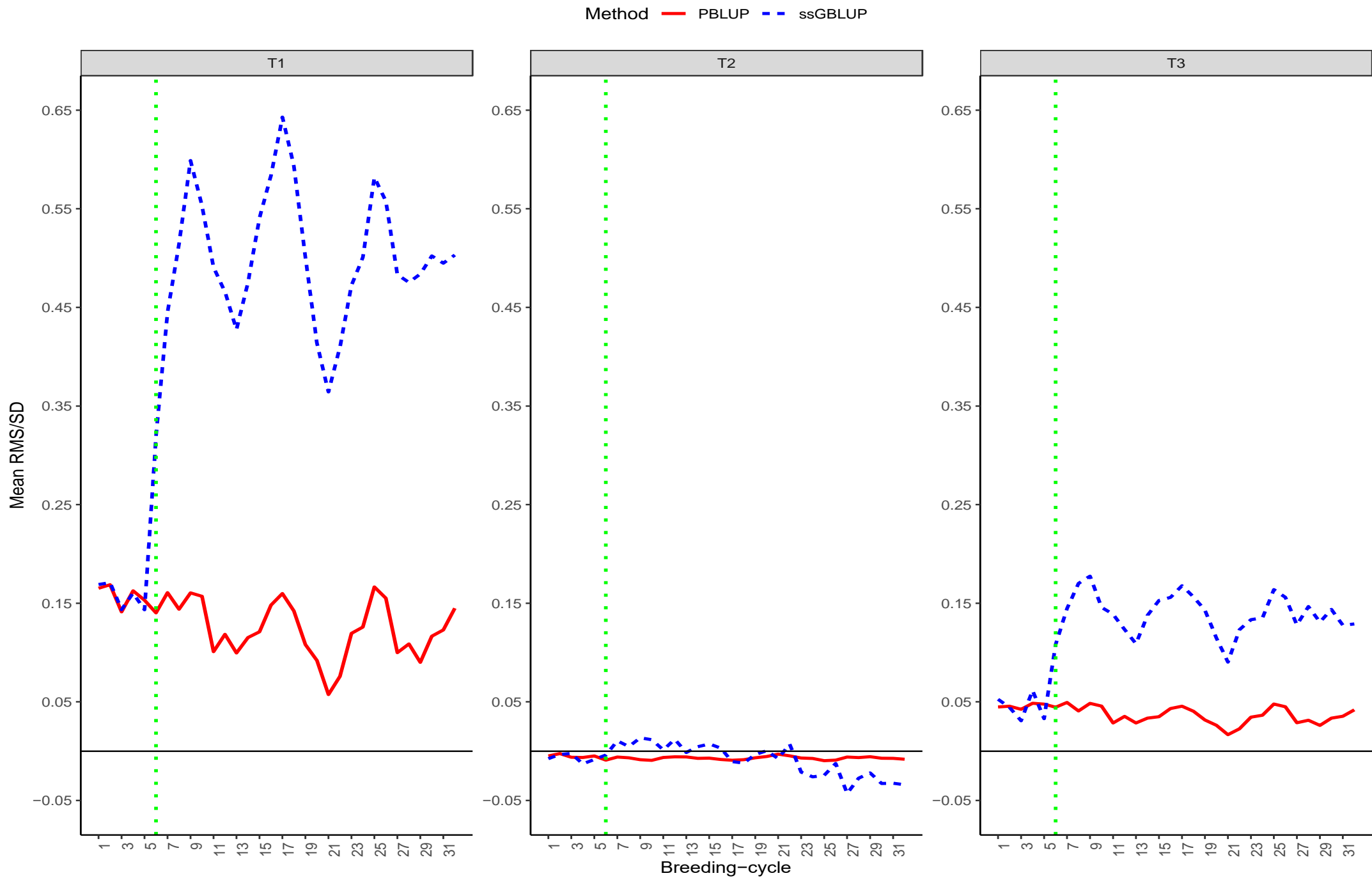
Broiler data set

- 1.2M animals
- 1M records for trait 1
- > 200k records for traits 2 and 3
- 154k genotyped

Trends of difference of GEBV and EBV



Mendelian sampling trends



Conclusions

- Genomic selection generally starts with divergence of BLUP and ssGBLUP trends
 - Some divergence if best animals genotyped retroactively
 - Affected by correlated traits
- Realized Mendelian sampling positive if selective genotyping even without genomic selection
- Results in agreement with practices at specific organizations

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