



# The heterogeneity in convergence behaviour of a single step SNP-BLUP model across effects and animal groups

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## Goal

- Most implementations used the preconditioned conjugate gradient method (PCG) to solve large system of equations. The goal of our study was, the examination of:
- differences in the model convergence depending on the number of individuals considered in the evaluation,
  - The convergence rate for different components of the model.

## Material

- Phenotype:
  - 1,098,611 cows with phenotype,
  - 141,397 bulls with MACE DRPs.
- Genotype:
  - 134,960 individuals with 46,118 SNPs.
- Pedigree:
  - FULL – 8,461,877 individuals,
  - 5GEN – 1,555,995 individuals.

## Methods

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{W}\mathbf{a} + \mathbf{e}$$

- $\mathbf{y}$  – phenotypes,
- $\boldsymbol{\beta}$  – fixed effects,
- $\mathbf{a}$  – breeding values,
- $\mathbf{a} = \mathbf{Z}\mathbf{g} + \mathbf{u}$ ,
- $\mathbf{g}$  – random SNP effects,
- $\mathbf{u}$  – random additive polygenic effects,
- $\mathbf{e}$  – residuals.

## Conclusions

- The same convergence rate for all parameters of single step SNP-BLUP model,
- GEV of the genotyped animals with phenotype data reached the final solutions with the least number of iterations, whereas the nongenotyped animals without own phenotype records required the highest number of rounds of iterations to reach their final solutions,
- The SNP effects converged the fastest, whereas the genetic groups had the lowest rate of convergence,
- The depth of pedigree markedly influences the rate of convergence, with fewer generations in pedigree leading to faster convergence.

## Convergence

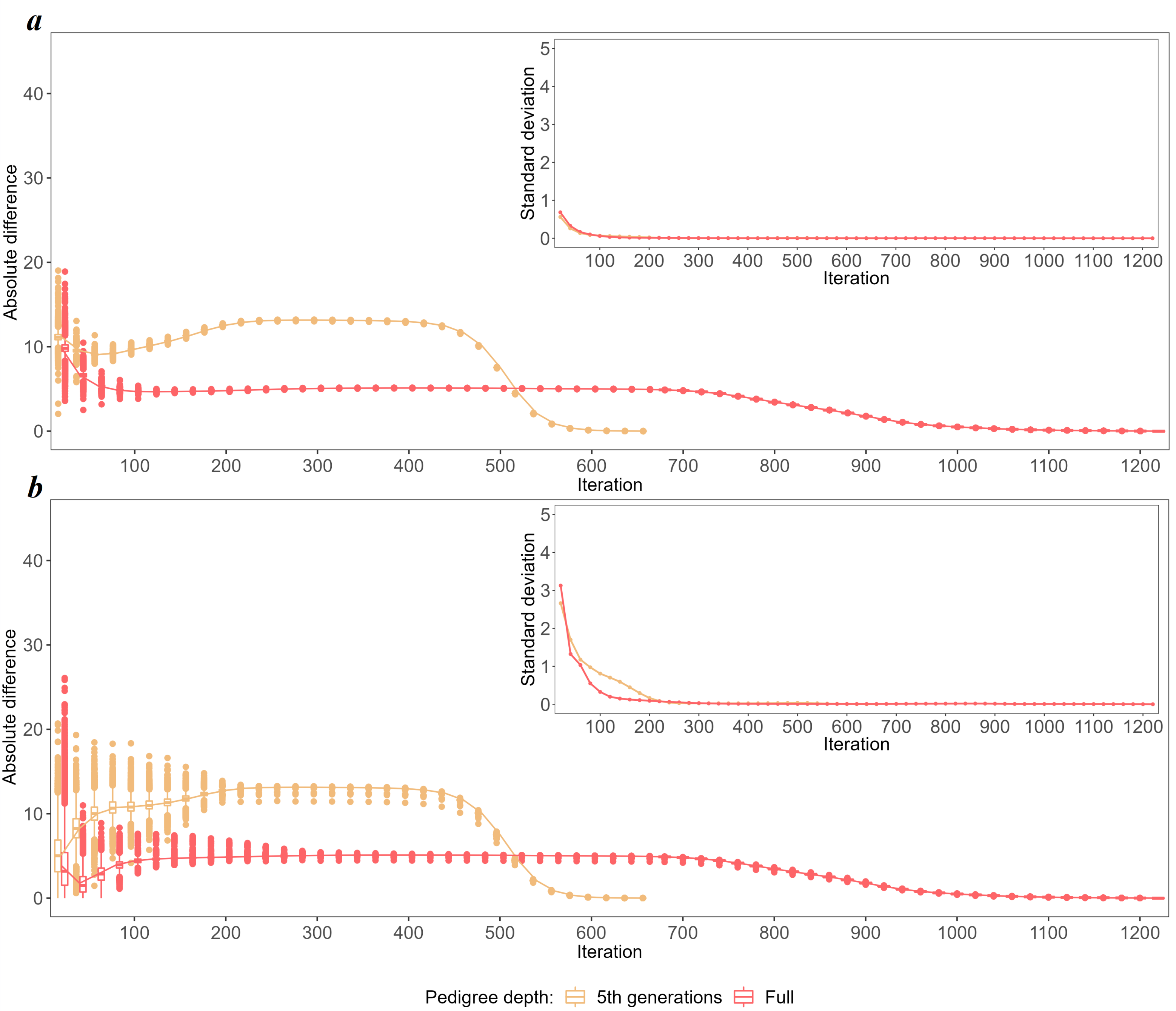
Two-level PCG:

$$\mathbf{P}^{-1}\mathbf{M}^{-1}\mathbf{C}\mathbf{x} = \mathbf{P}^{-1}\mathbf{M}^{-1}\mathbf{b}$$

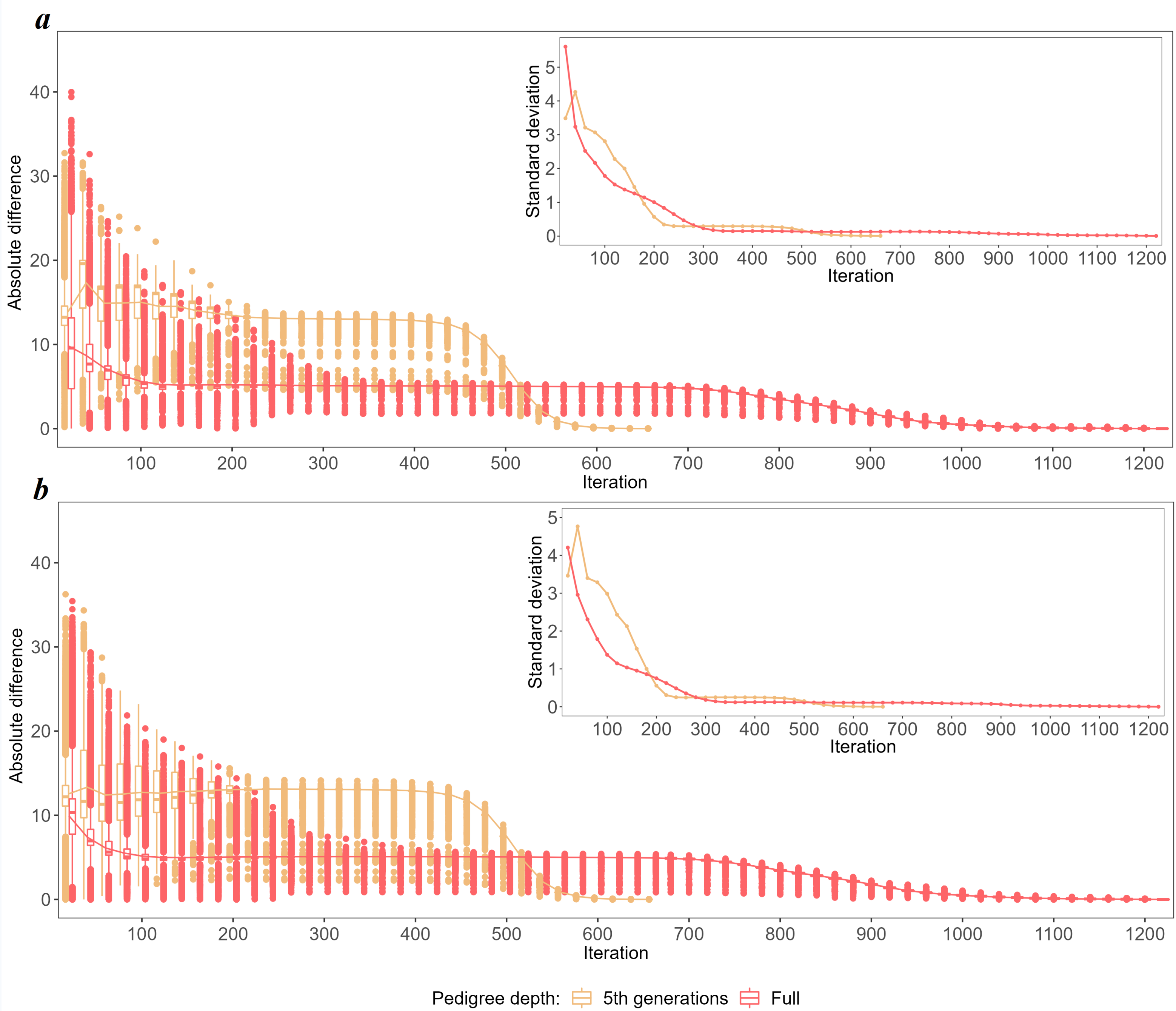
- $\mathbf{C}$  – coefficient matrix from MME,
- $\mathbf{x}^T = [\boldsymbol{\beta}^T \mathbf{g}^T \mathbf{u}^T]$ ,
- $\mathbf{b}$  – the RHS of MME,
- $\mathbf{M}, \mathbf{P}$  – preconditioning matrices.

Estimation with MiXBLUP.

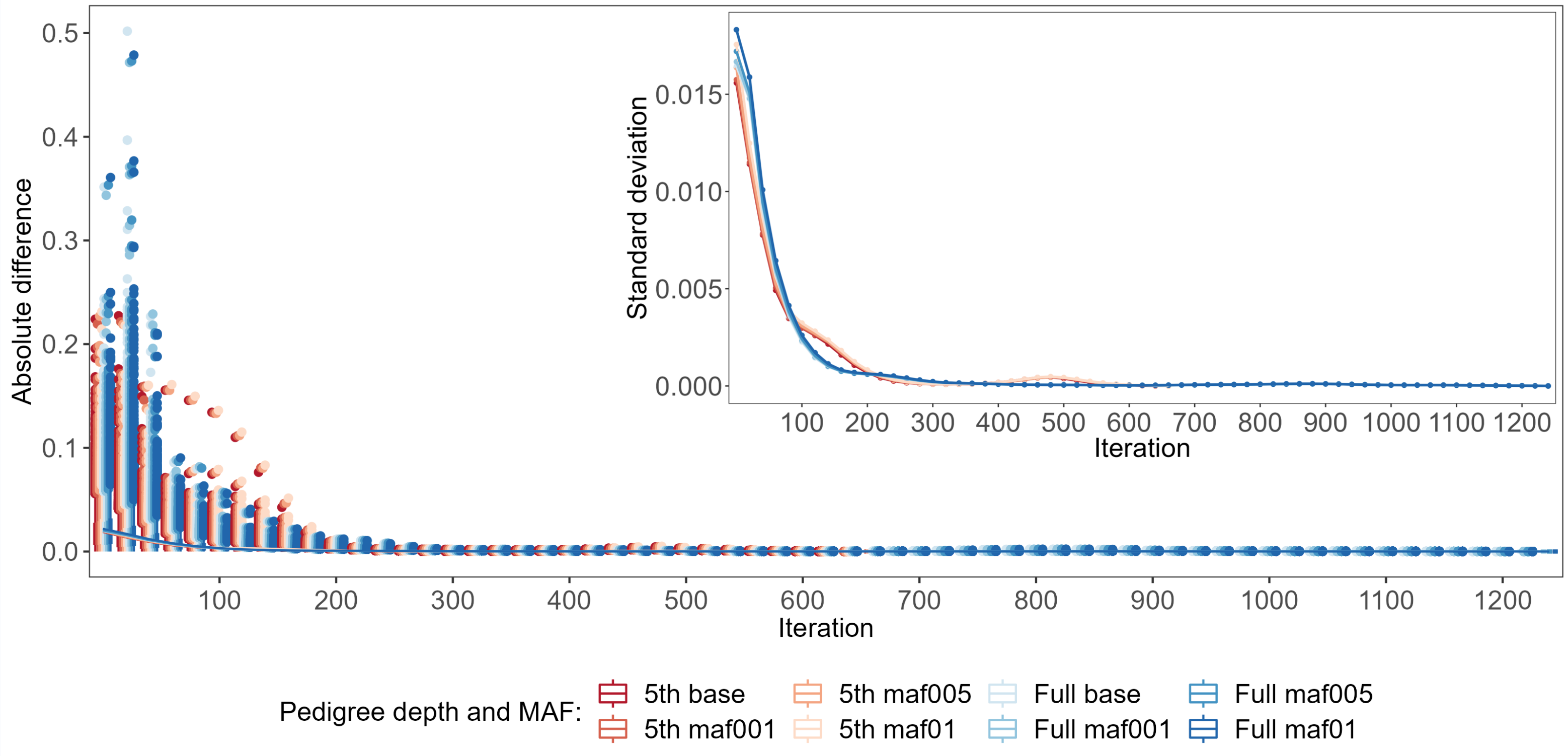
## Results



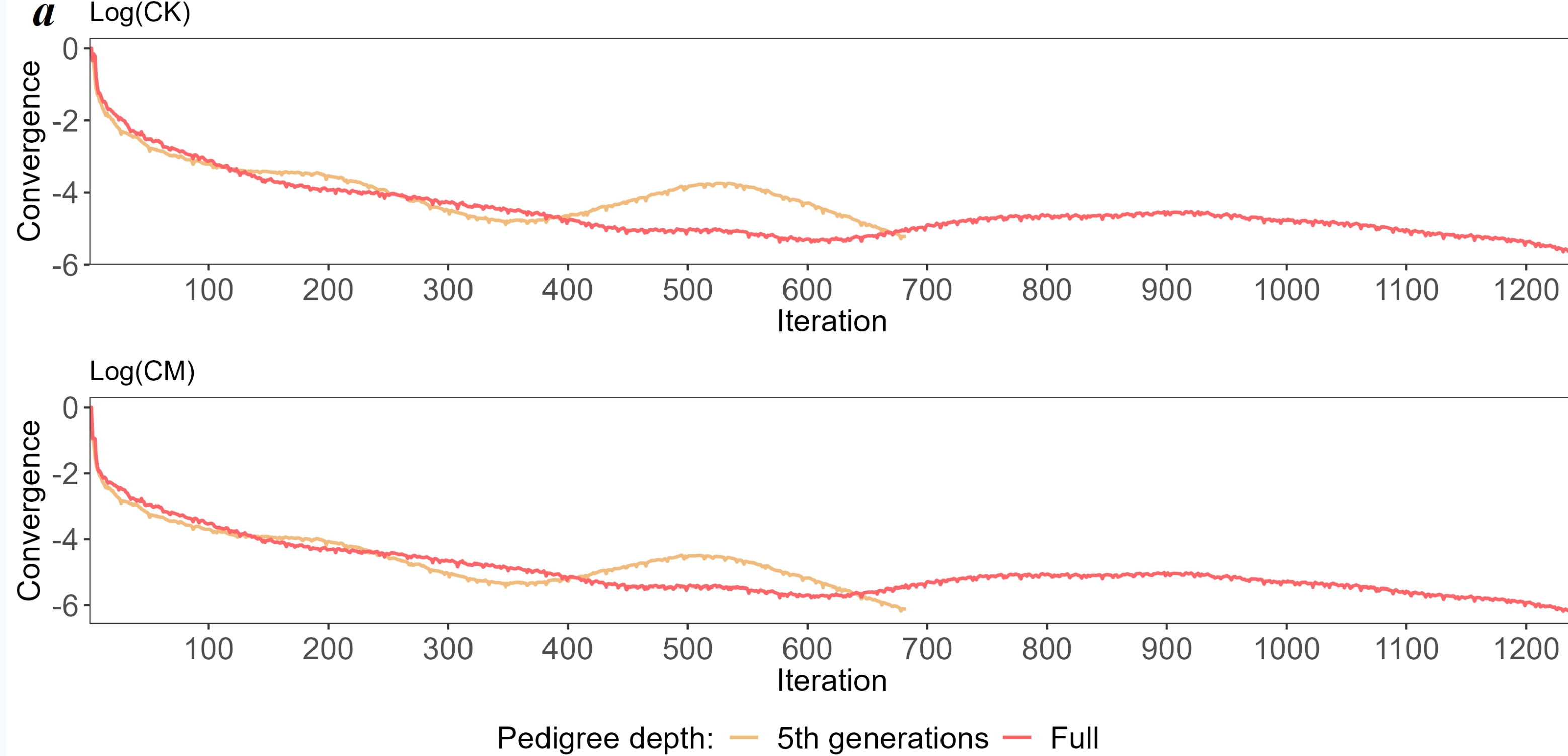
Average absolute difference in EBV for animals with phenotypes and genotype. **A** bulls, **B** cows.



Average absolute difference in EBV for ungenotyped animals without phenotypes. **A** bulls **B** cows.



Average absolute difference in the estimates of SNP effects for different SNP preselection criteria based on the MAF threshold.



The convergence criteria (CK, CM) of PCG along the optimisation process.