Sparse single-step genomic Best Linear Unbiased Prediction in crossbreeding schemes

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HENDRIX GENETICS

Cobb

TOPIGS

CRV

Single-step GBLUP

Unified BLUP procedure considering simultaneously genotyped and non-genotyped animals

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1} - \mathbf{A_{22}}^{-1} \end{bmatrix}$$

Inverse of the **pedigree-based** relationship matrix

Inverse of the **genomic-based** relationship matrix

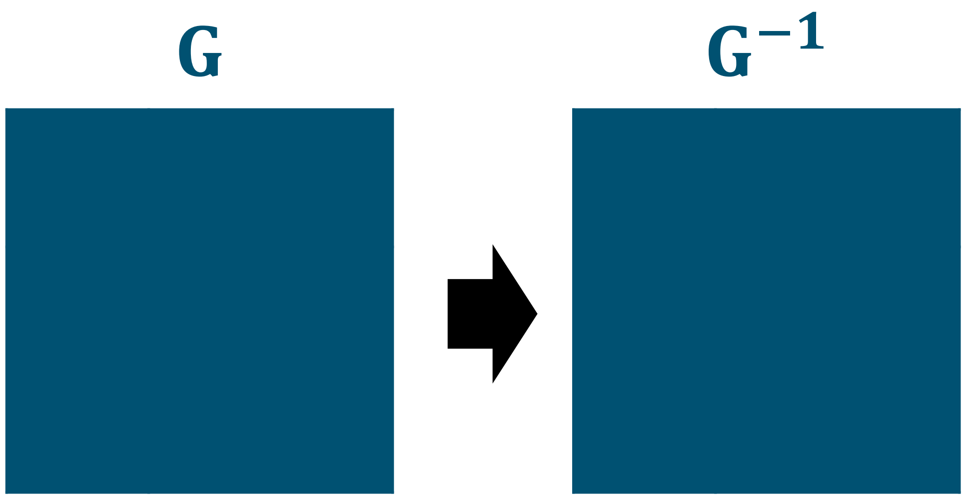
Inverse of the **pedigree-based** relationship matrix associated with **genotyped animals**

Creation and inversion of $\mathbf{G}$ and $\boldsymbol{A}_{22}$

ssGBLUP more and more implemented

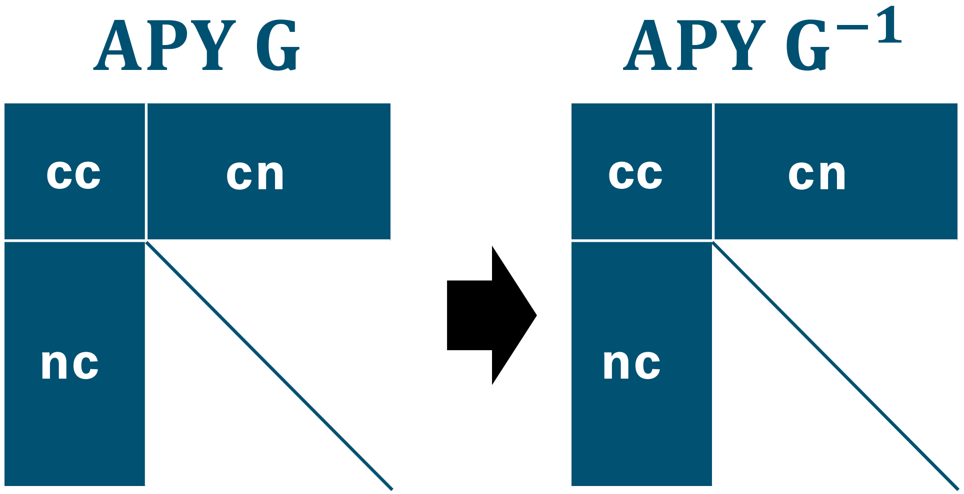
BUT

infeasible for > ~100,000 genotyped animals?



- **High computational costs**
- **High storage (dense $\mathbf{G}^{-1}$)**

Algorithm for Proven and Young animals



- **Core / non-core animals**
- **Lower computational costs**
- **Lower storage**

→ Limitations removed

Misztal et al., 2016

Aim

APY successfully tested with single-breed data

Applicable for crossbreeding schemes?

e.g., Fragomeni et al., 2015; Masuda et al, 2015; Ostersen et al., 2016

Simulation - pedigree

- 3 breeds (A, B, C)
  - Unrelated / Related
  - 10 discrete generations
    - 30 males – 6,250 females (Ne ~ 120)
- Crossbreds (BC and A(BC))
  - 30 males – 6,250 females from gen. 6 to 9
- Random matings
- Litter size: 2

Simulation - genotypes

- 89,000 genotypes randomly sampled
    - Generations 6 to 10

    - ~21,000 / breed
    - 10,000 BC
    - 16,000 A(BC)

    - 18 chromosomes - ~52,000 SNP

Simulation - phenotypes

- 126,000 phenotypes randomly sampled
    - 1 trait/breed composition
        - Polygenic effect: 5%

    - Generations 5 to 9

    - ~33,333 / breed
    - All genotyped BC and A(BC) = phenotyped

5-trait ssGBLUP

- **G** matrix
  - Allele frequencies across all animals
  - 5% polygenic

- Random core animals
  - A, B, C animals
  - A, B, C, BC, and A(BC) animals
  - Total: 4000 - 13,000 (15,000)

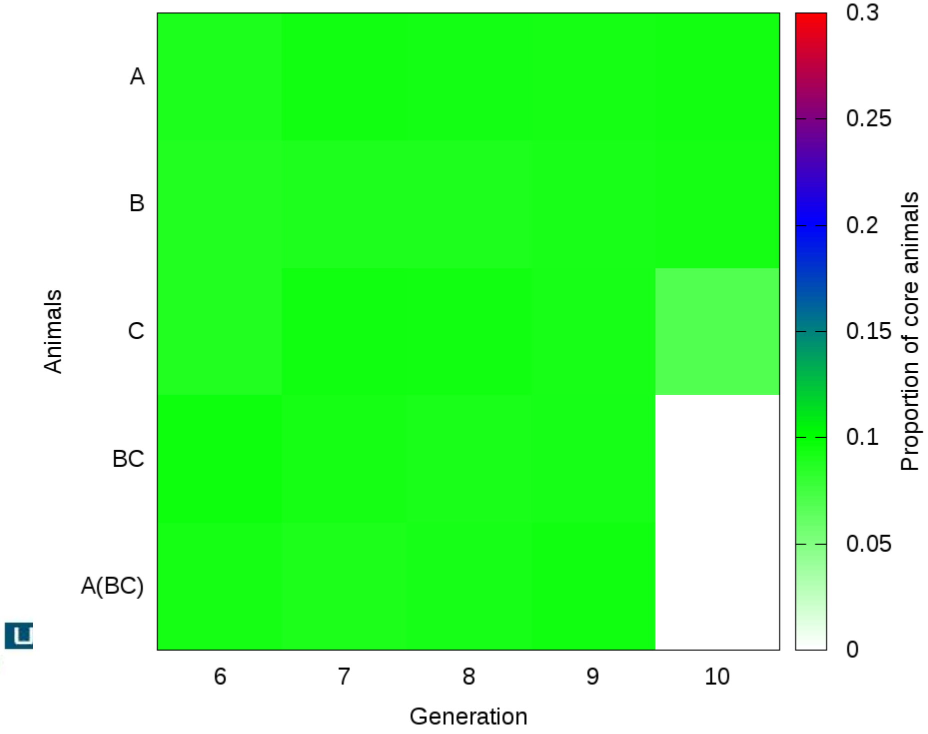
- 5 replicates

Core animals - representation

Due to properties of the genotype dataset

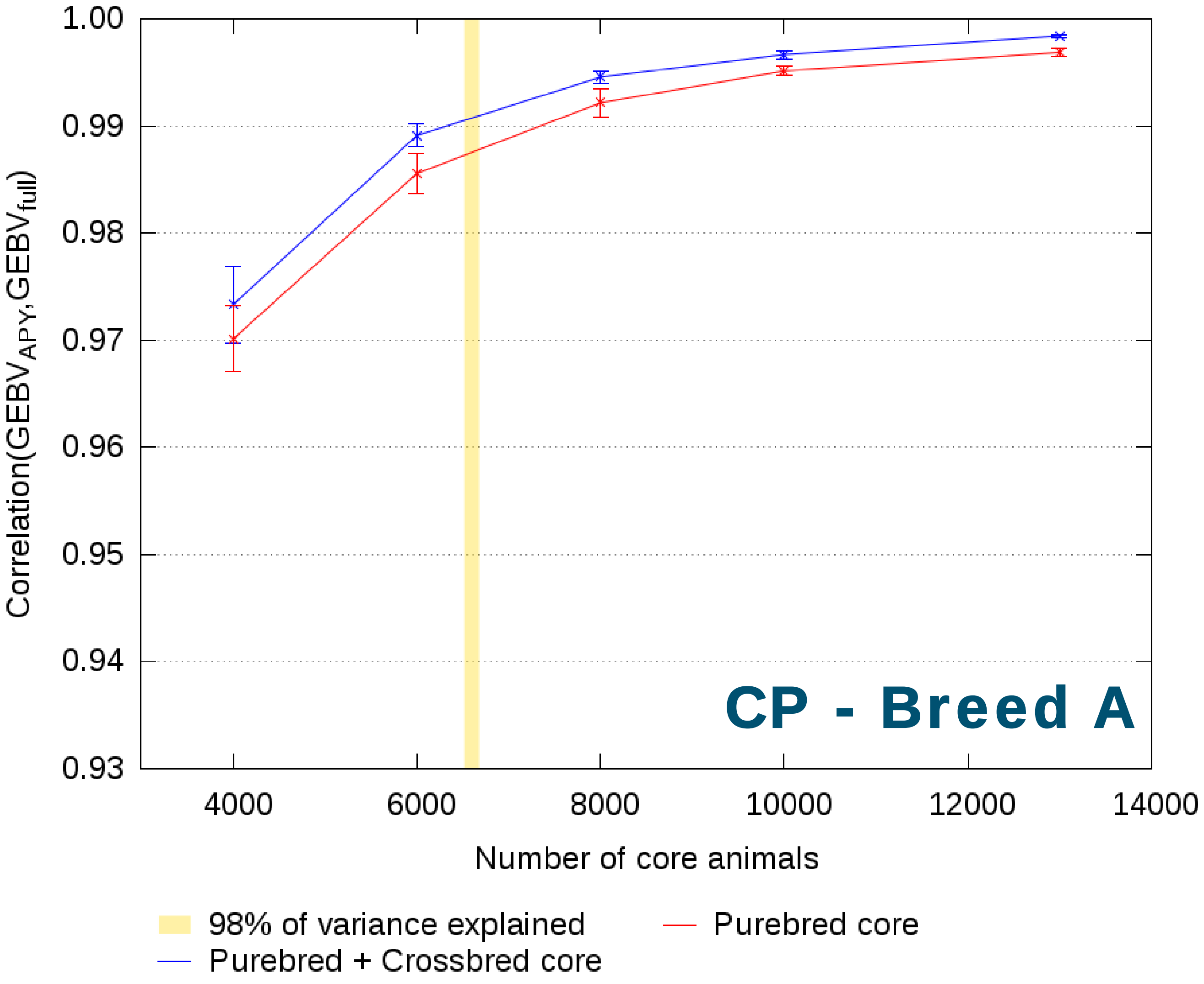
Similar representation of genotyped animals in

all generations (and all breed compositions)



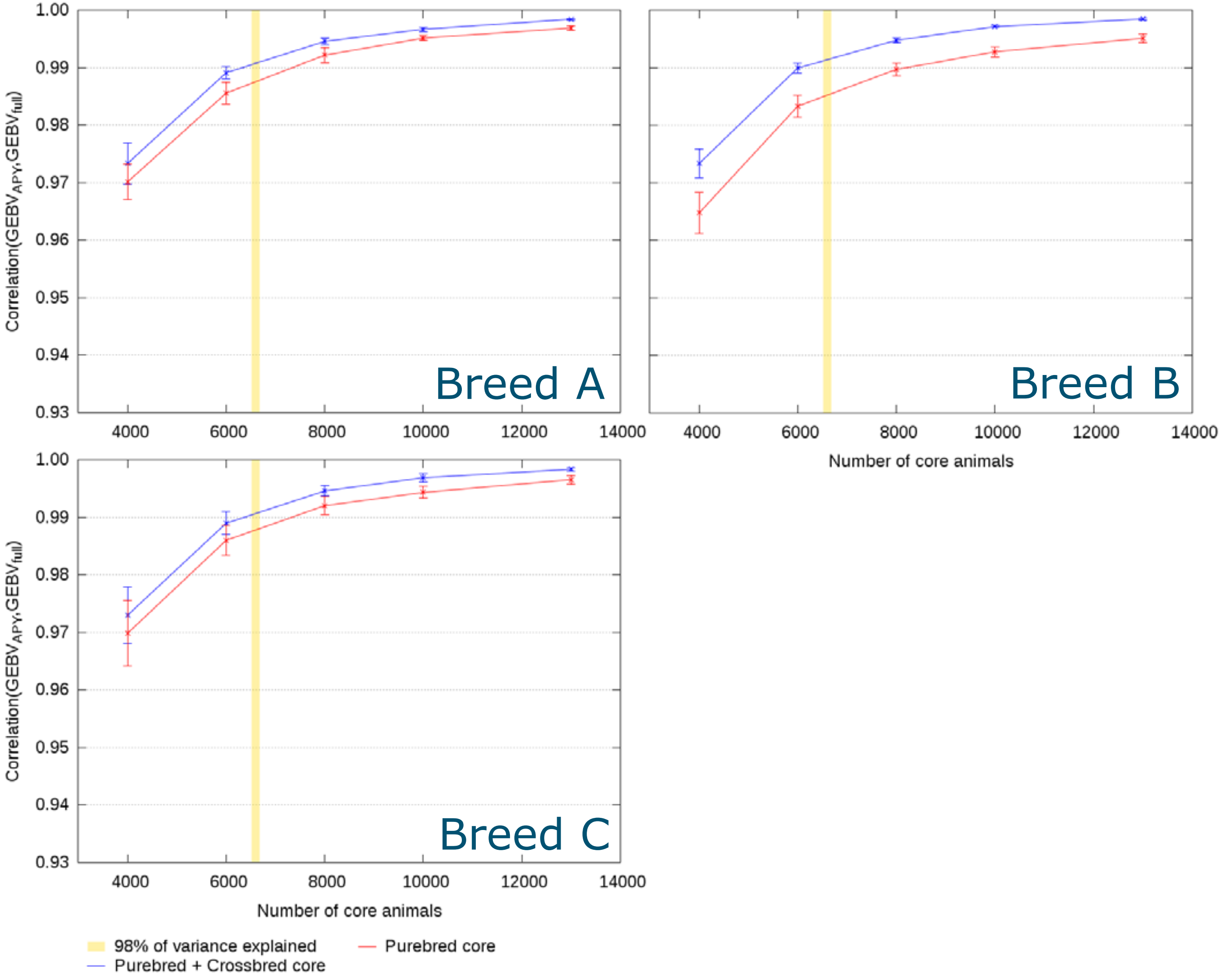
Validation – unrelated

Purebred animals (10th generation) without phenotype



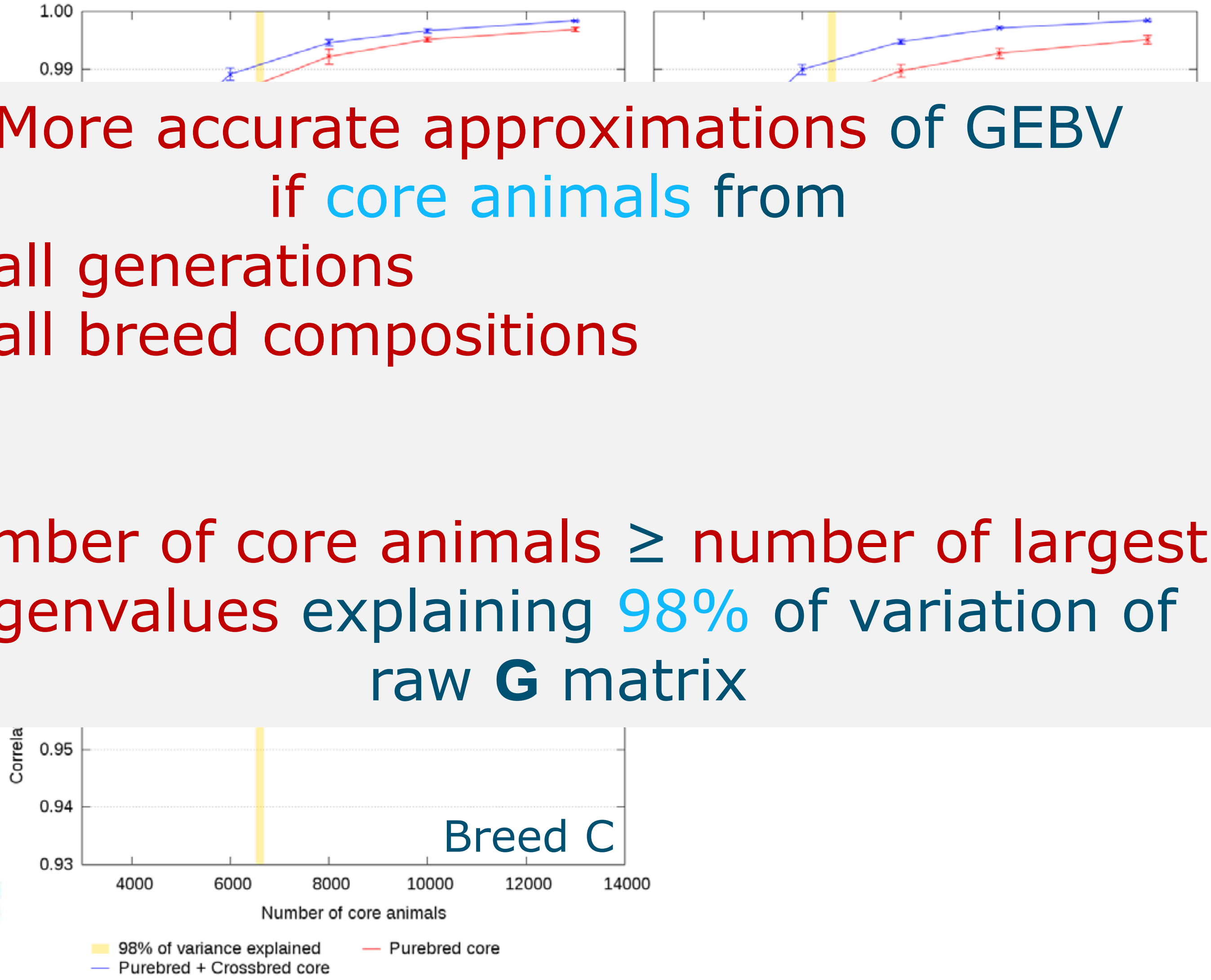
Validation – unrelated

Purebred animals (10th generation) without phenotype



Validation – unrelated

Purebred animals (10th generation) without phenotype



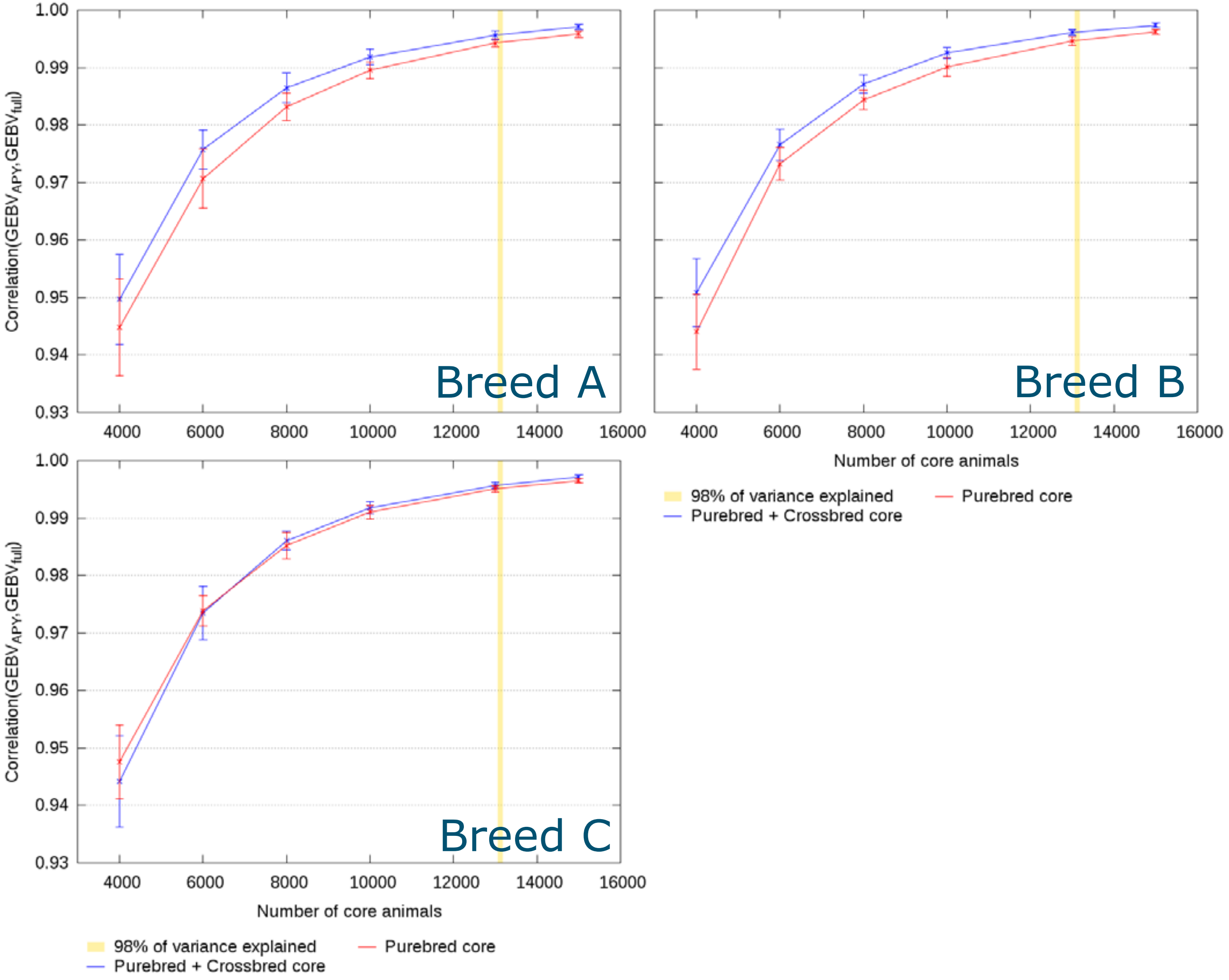
More accurate approximations of GEBV
if core animals from

- all generations
- all breed compositions

Number of core animals ≥ number of largest eigenvalues explaining 98% of variation of raw **G** matrix

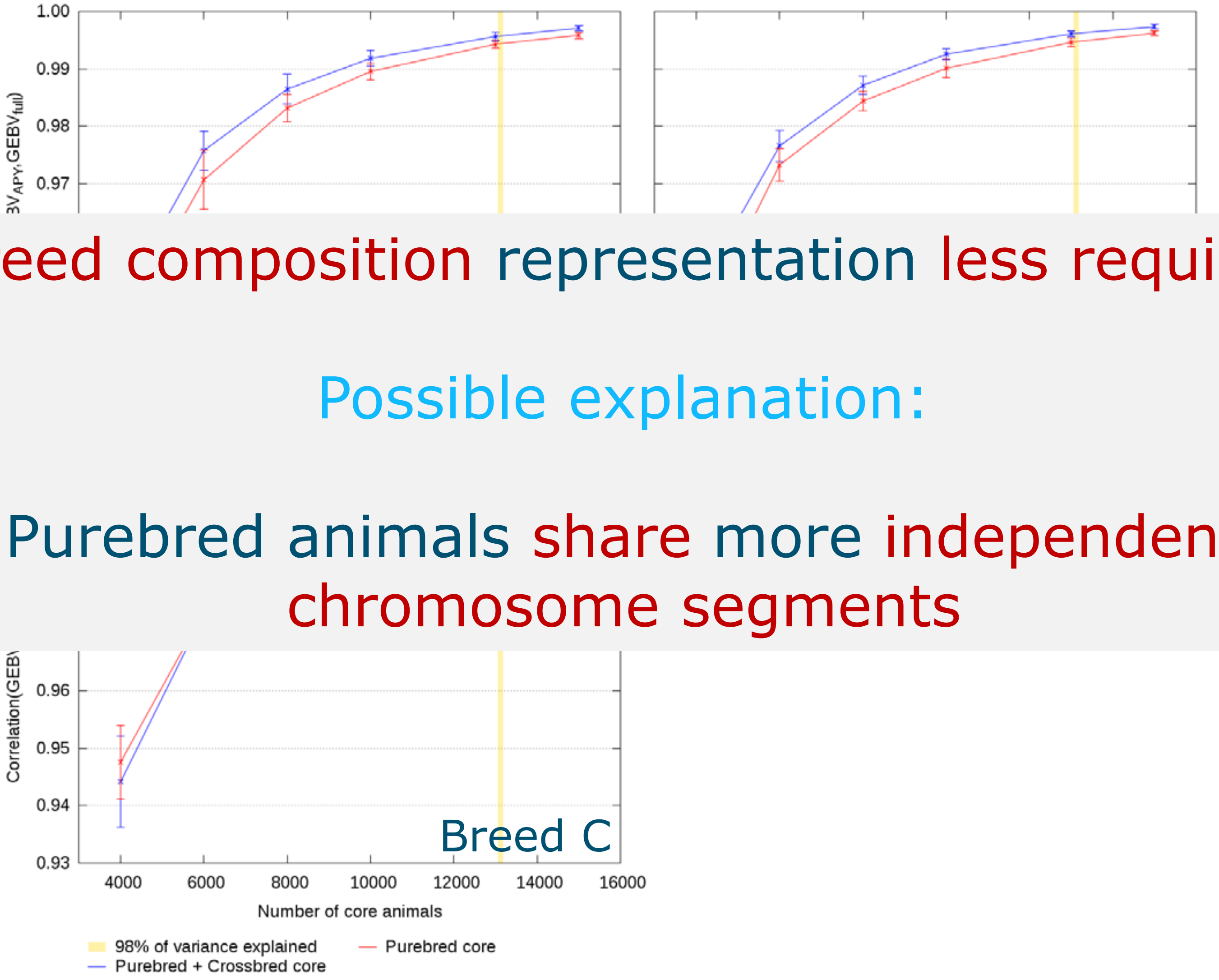
Validation – related

Purebred animals (10th generation) without phenotype



Validation – related

Purebred animals (10th generation) without phenotype



Breed composition representation less required

Possible explanation:

Purebred animals share more independent chromosome segments

Conclusions

- APY is applicable in (simulated) crossbreeding schemes
- Number of core animals
  - ≥ Number of largest eigenvalues explaining 98% of variation of raw **G** matrix
- Core animals must represent
  - all generations (Ostersen et al., 2016)
  - all breed compositions

Thank you!

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