Modeling unknown parents in single-step GBLUP: Metafounders vs. unknown parent groups in a simulated cattle population

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EAAP, Florence, 2024-09-04

What is the aim of the study?

ssGBLUP for German-Austrian-Czech Fleckvieh population since April 2021

potential next step in the national evaluation: **metafounder (MF)**

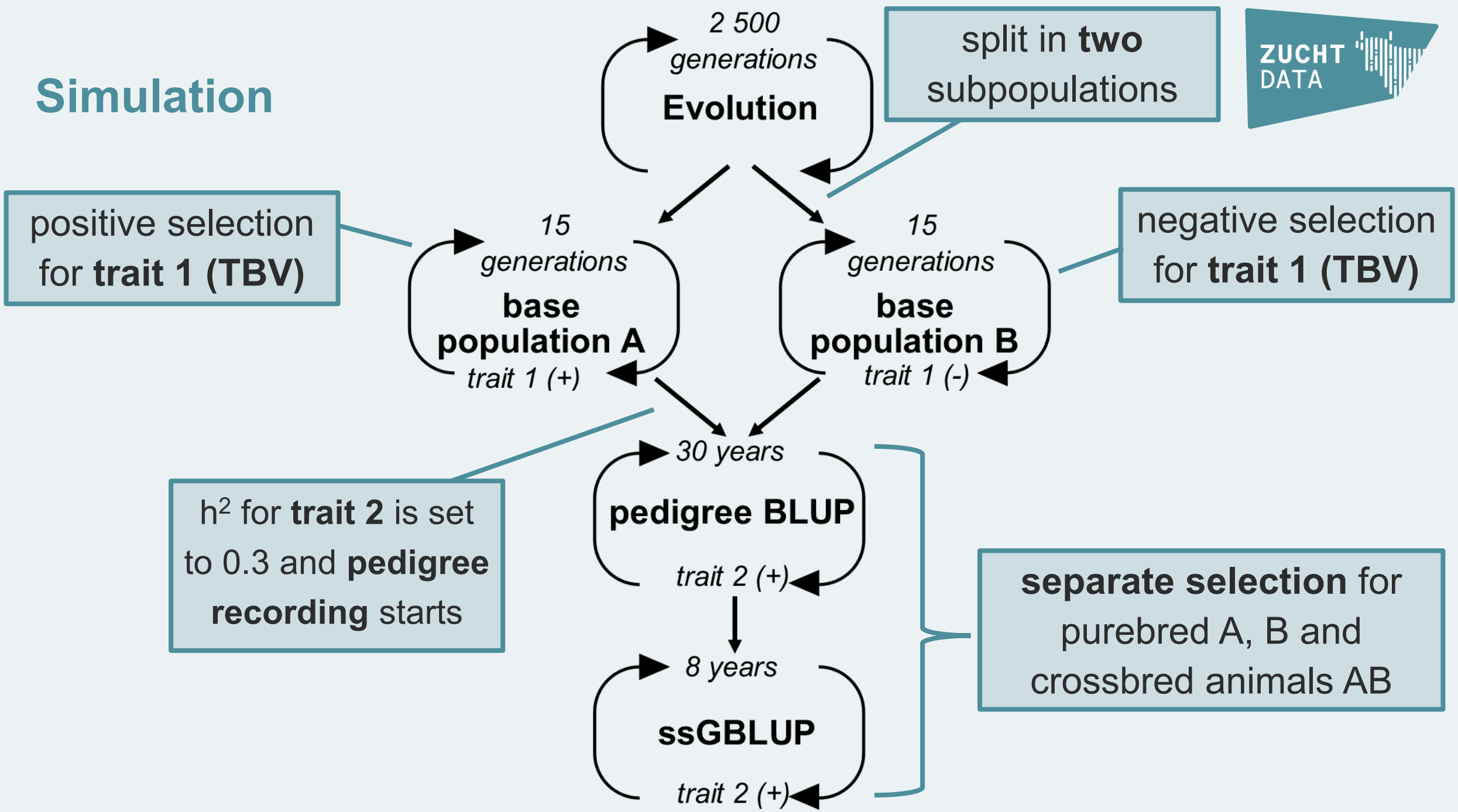
➔ simulation study to test and investigate multiple aspects

Article in Journal of Dairy Science (https://doi.org/10.3168/jds.2024-24891, in press)

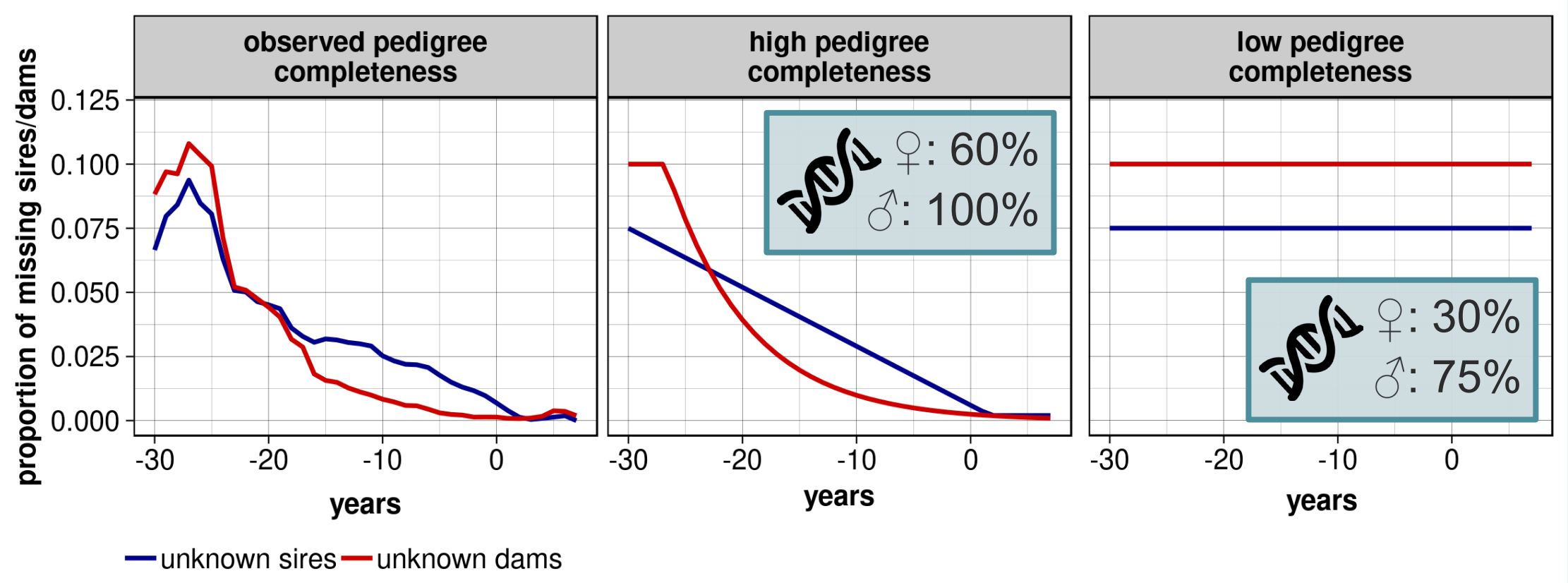
Content of this presentation:

- validation statistics for genetic evaluations with and without unknown parent groups (UPG) and MF
- method to estimate pedigree for animals with unknown parents
- expected effects of MF in routine validation (linear regression , LR)

Simulation


2 500
generations
Evolution
split in **two** subpopulations
positive selection for **trait 1 (TBV)**
15
generations
base population A
trait 1 (+)
15
generations
base population B
trait 1 (-)
negative selection for **trait 1 (TBV)**
h^2 for **trait 2** is set to 0.3 and **pedigree recording** starts
30 years
pedigree BLUP
trait 2 (+)
8 years
ssGBLUP
trait 2 (+)
separate selection for purebred A, B and crossbred animals AB

Pedigree completeness - scenarios



Classification of UPG/MF

- **Full pedigree:**
  - true full pedigree without missing parents
  - 2 UPG or MF for the two subpopulations in the pedigree base

- **True missing pedigree:**
  - unknown pedigrees
  - classification based on *true* subpopulation, true age, and true sex

- **Estimated missing pedigree:**
  - simulate a real situation
  - classification based on *estimated* subpopulation, estimated age and sex

Genetic evaluations

for all ssGBLUP G was computed with APY

evaluation	abbreviation	UPG in		MF
		A	G	
ssGBLUP without UPG	**no_UPG**	✗	✗	✗
ssGBLUP with UPG in A	**UPG_alteredQP**	✓	✗	✗
ssGBLUP with UPG	**UPG_fullQP**	✓	✓	✗
ssGBLUP with MF and true Γ	**MF_true**	✗	✗	✓

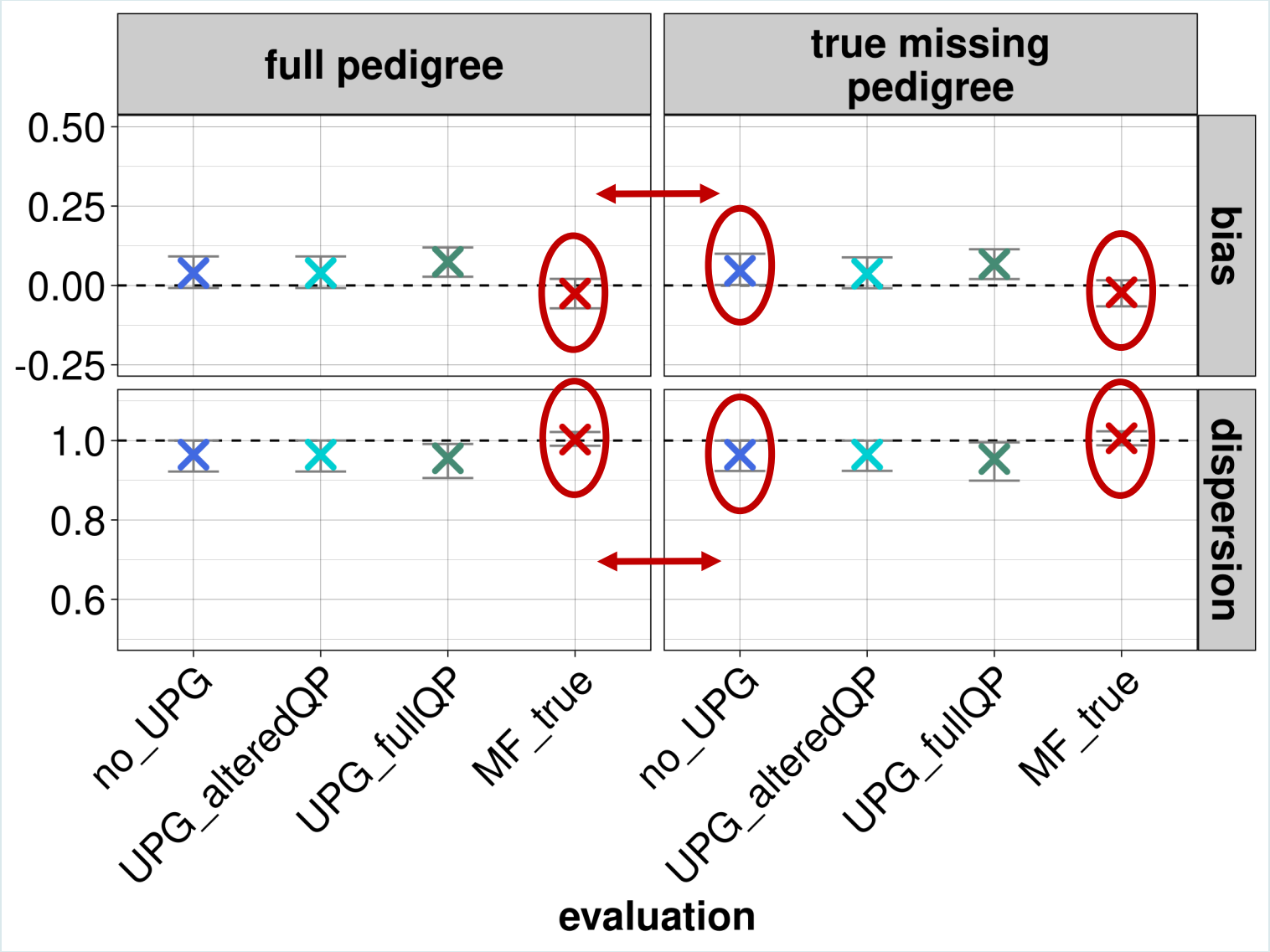
Comparison of evaluations: high pedigree completeness

low proportions of unknown parents and high genotyping rate

➔ effects from MF/UPG on GEBVs are very small

less bias and dispersion with MF

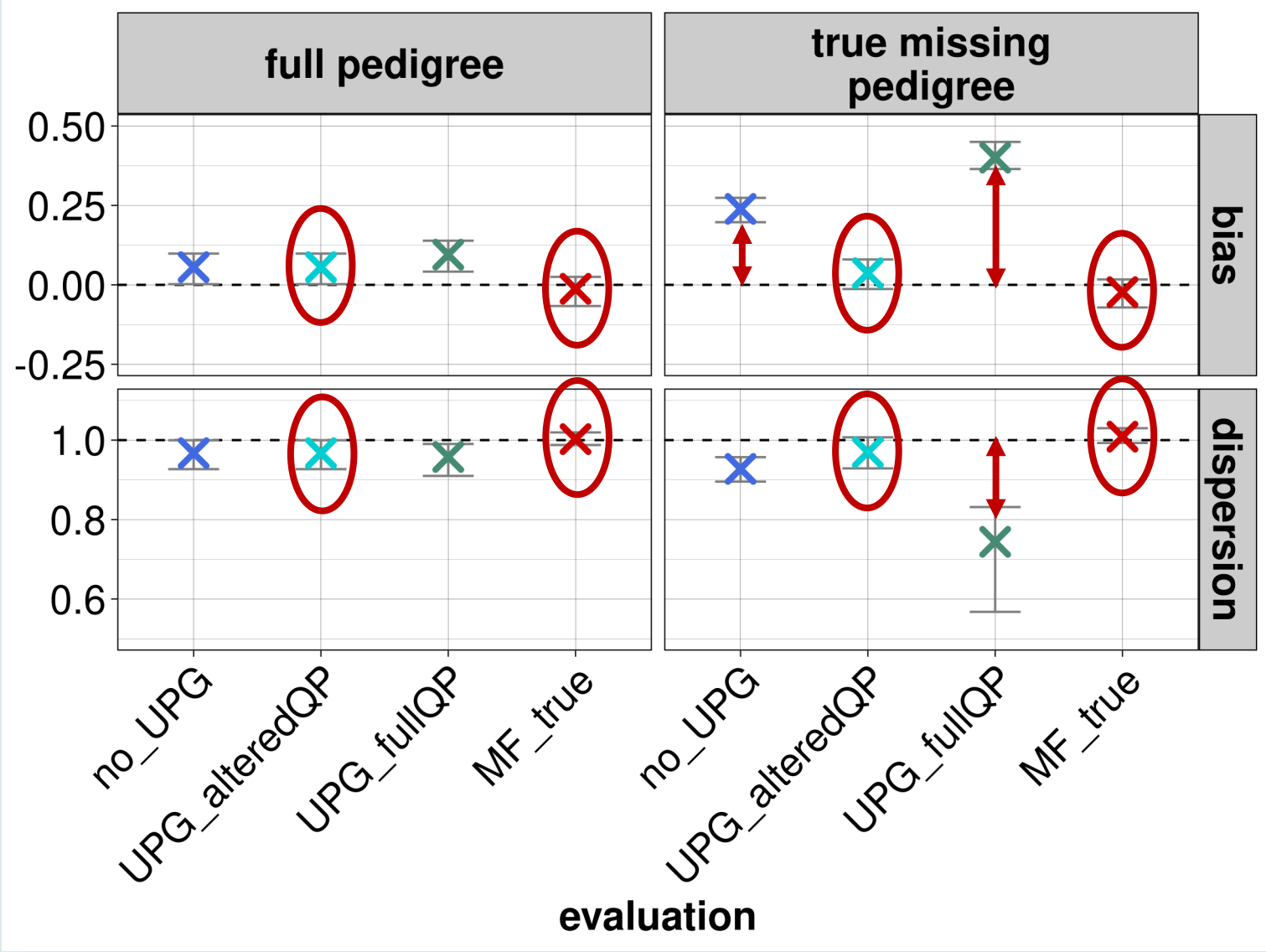
➔ positive effects from better alignment of A and G



Comparison of evaluations: low pedigree completeness

clear differences for no_UPG and UPG_fullQP between full and missing pedigree

UPG_fullQP: double counting (relationships in G are already complete)

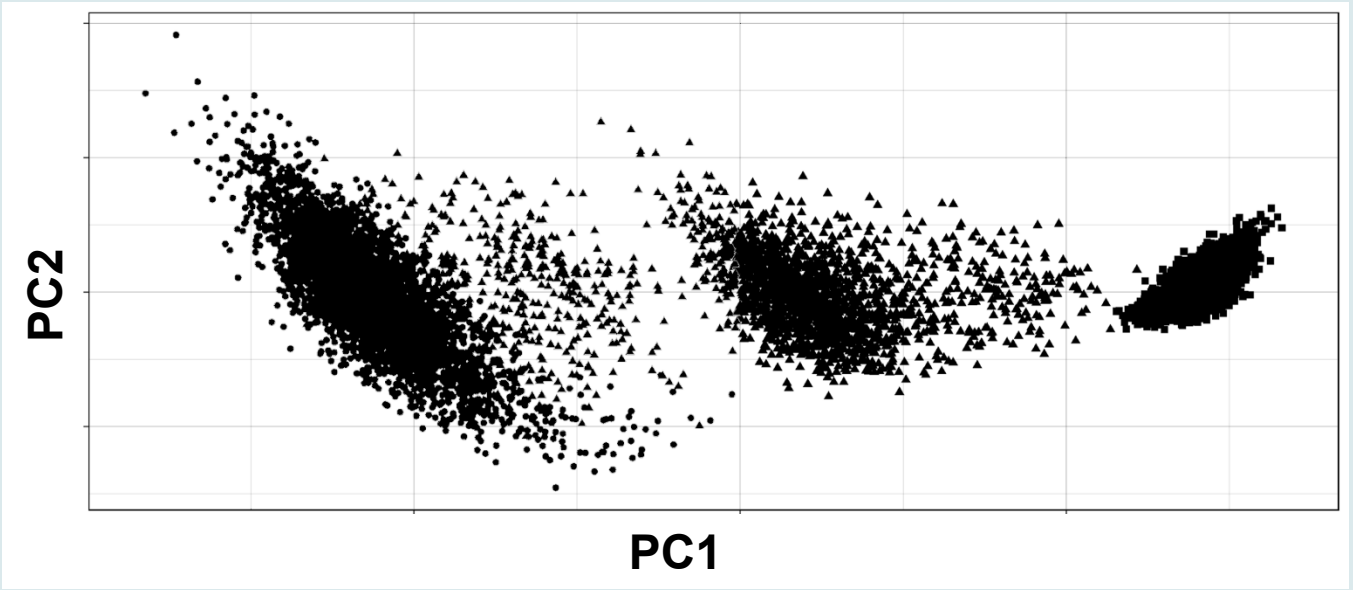


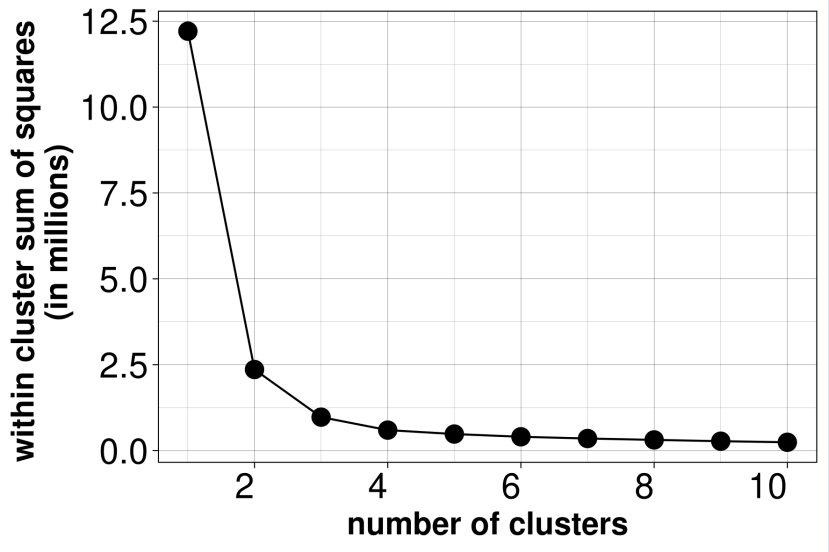
Estimation of pedigree

10,000 random genotyped animals and PCA on genotypes

K-means clustering with first 2 PC for n=1, …, 10

determine optimal n based on “within cluster sum of squares”



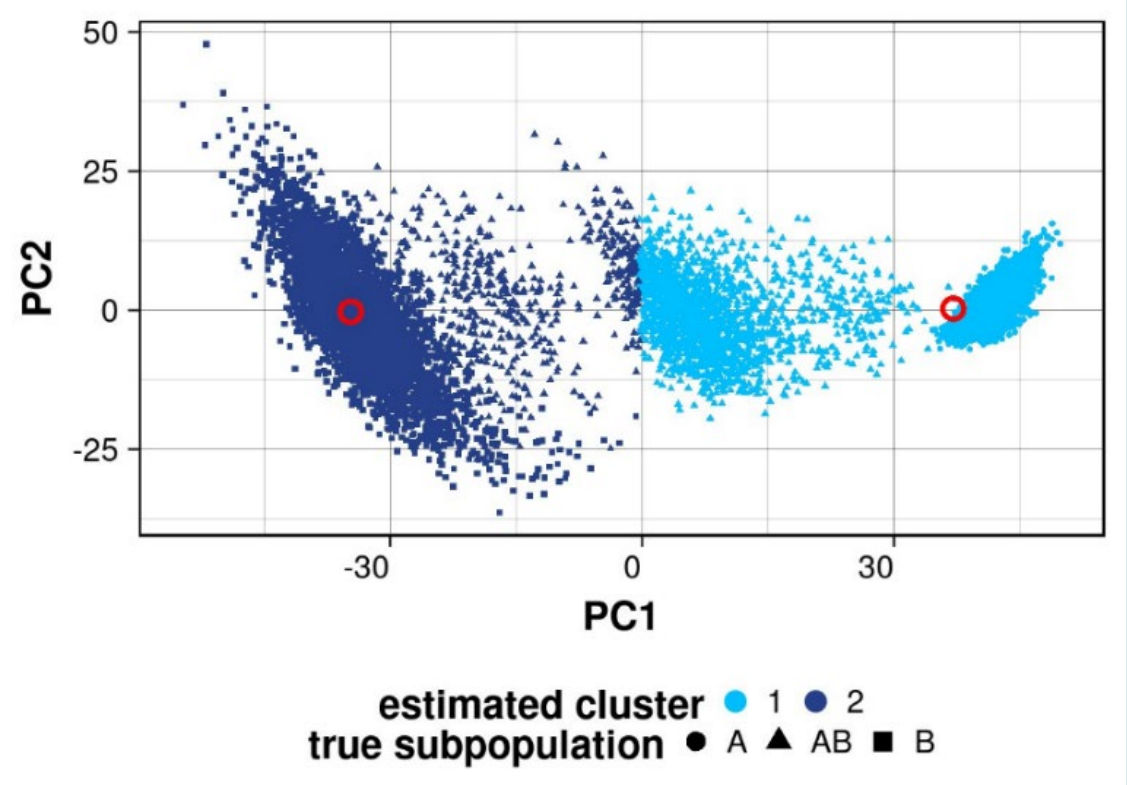


Estimation of pedigree

allele frequencies for cluster centers

GBC for genotyped animals based on allele frequencies and linear regression (He et al. 2018)

GBC for all animals from ssGBLUP where GBC are traits with h^2=0.999



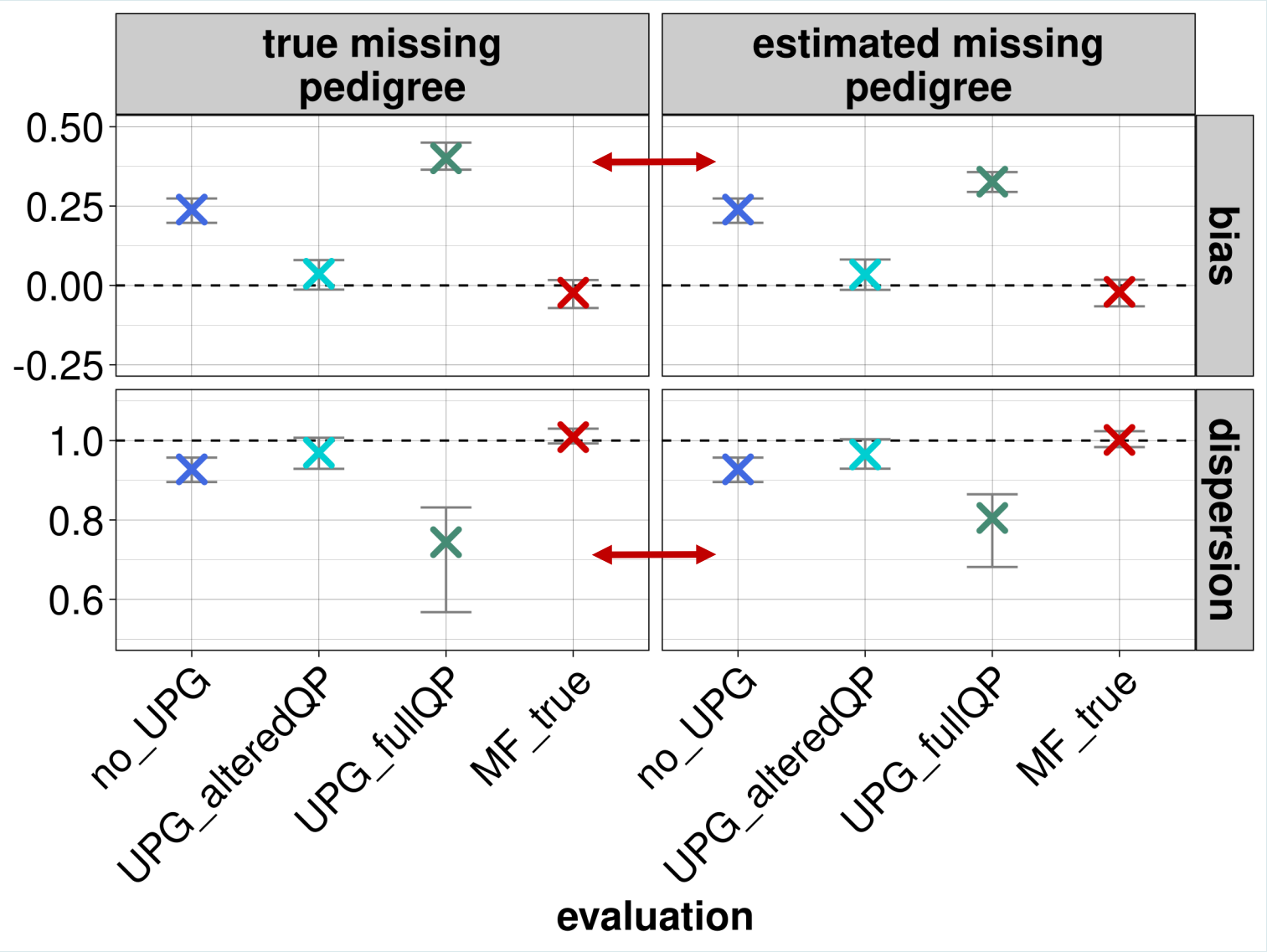
genotyped	estim. A	estim. AB	estim. B
true A	99.64%	0.36%	0%
true AB	19.71%	78.59%	1.69%
true B	0%	0%	100%

Estimation of pedigree: low pedigree completeness

although allocation is not fully correct:

➔no negative effects on validation statistics

➔classification used in this study reflects the essential population structures

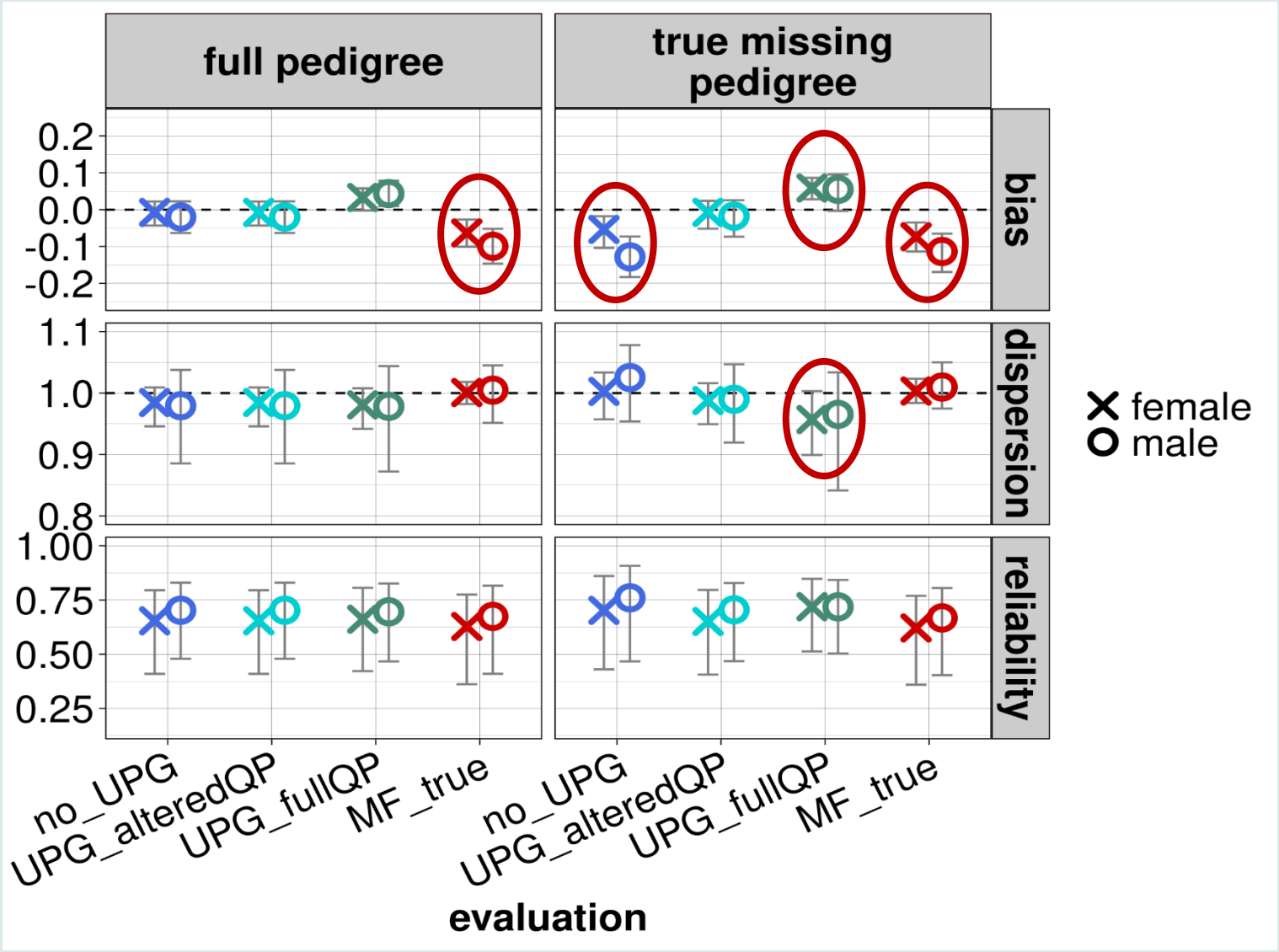


LR validation: low pedigree completeness

no big differences between the evaluations

bias and dispersion of no_UPG and UPG_fullQP is not detected

small „wrong“ bias for MF_true



Conclusions

➔ MF have positive effects on bias and dispersion

➔ wrong consideration of UPG can lead to extreme bias and dispersion (in (sub)populations with many unknown pedigrees)

➔ used classification of unknown parents, reflects the essential population structures in this study

➔ validation with LR seems to be of limited use to assess the benefits of MF in this study

ZUCHT DATA

J. Dairy Sci. TBC:1–23 JDS24891
https://doi.org/10.3168/jds.2024-24891

Exploring unknown parent groups and metafounders in single-step genomic best linear unbiased prediction: Insights from a simulated cattle population

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Thank you for your attention!