Reliability of genomic predictions for feed efficiency traits based on different pig lines

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Introduction

In the majority of genomic predictions

A unique population split between a reference and a validation set

A genomic evaluation using genetically different reference and validation sets gives:

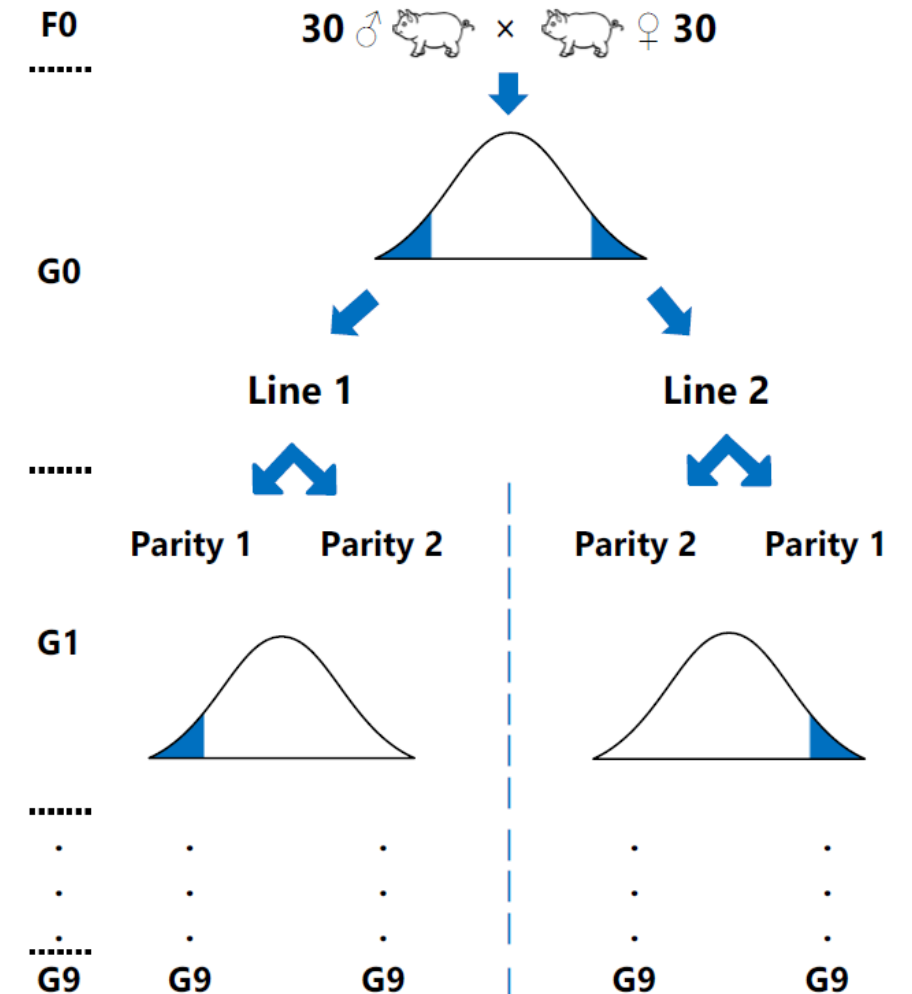more flexibility for the choice of reference sets in small populations

Aim of our study

A reference population comprising animals from two different lines

- Prediction of genomic breeding values (GBVs) throughout six different scenarios

- Five production traits

- Single-step genomic BLUP

Data structure

- Two divergent lines: **low RFI and high RFI**

- 9 generations of selection for Residual Feed Intake

- 4,143 animals with phenotypes

- SNP genotyping data (64K SNPs) of 1,600 animals

  - **RFI:** residual feed intake
  - **FCR:** feed conversion ratio
  - **DFI:** daily feed intake
 - **BFT:** back fat thickness
  - **ADG:** average daily gain

F0 .... 30 ♂ 🐷 × 🐷 ♀ 30

G0 Line 1 Line 2

.... Parity 1 Parity 2 Parity 2 Parity 1

G1

....
G9 G9 G9 G9 G9

Model

$$y = Xb + Z_1a + Z_2l + e$$

$$a \sim N(0, \mathbf{H} \otimes \mathbf{G0}), l \sim N(0, \mathbf{I} \otimes \mathbf{R_l}) \text{ and } e \sim N(0, \mathbf{I} \otimes \mathbf{R_e})$$

- **Bivariate analyses**
  - Trait 1: index (selection criterion)
  - Trait 2: other five traits

- **Software:**
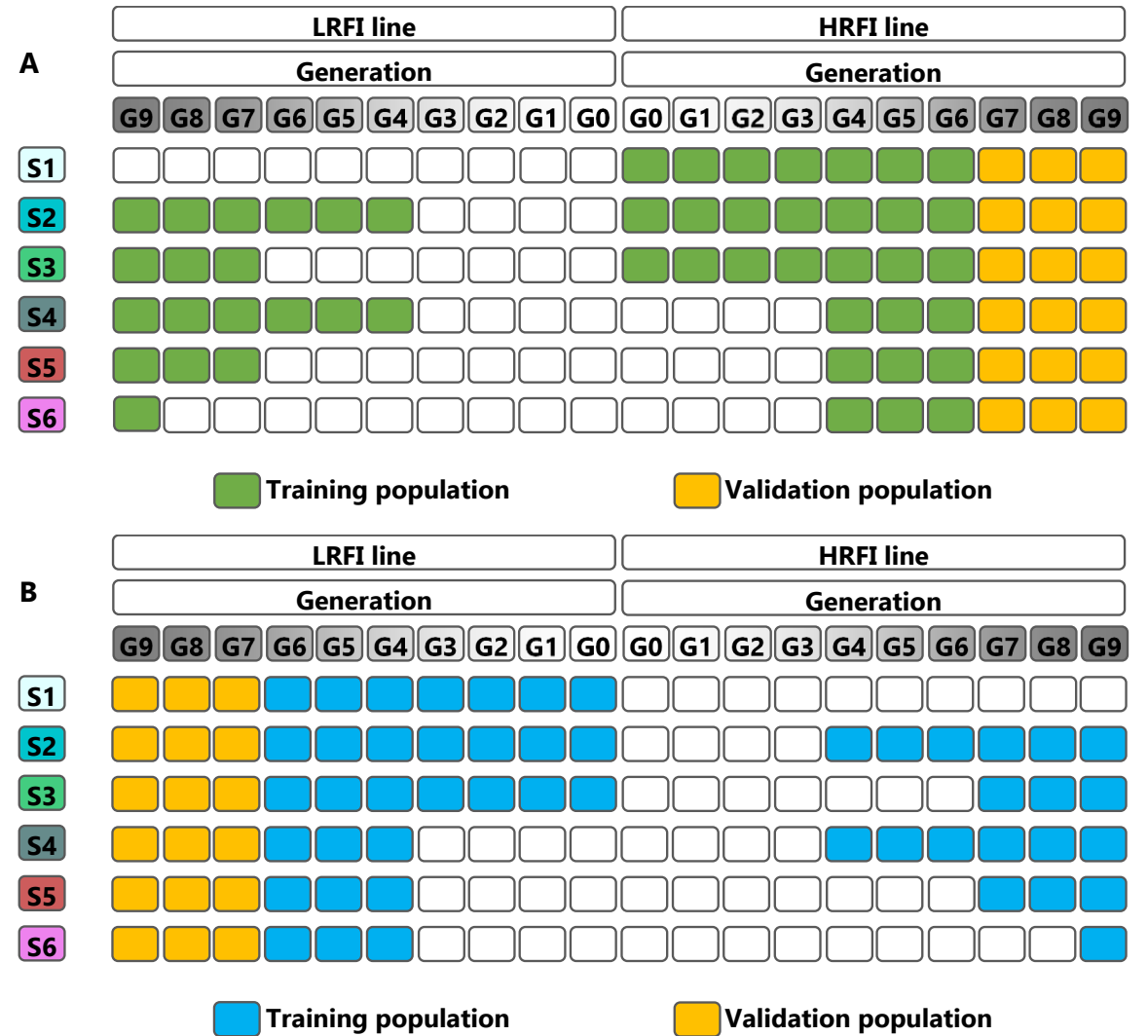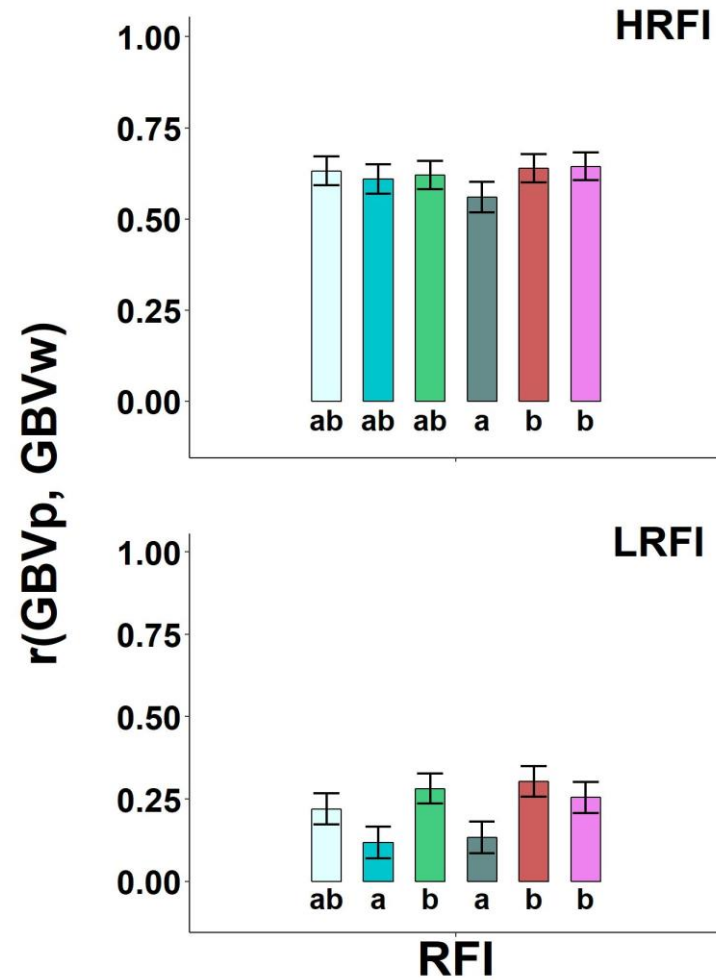 - AIREMLF90 (for BLUP)
  - BLUPF90 (for ssGBLUP)

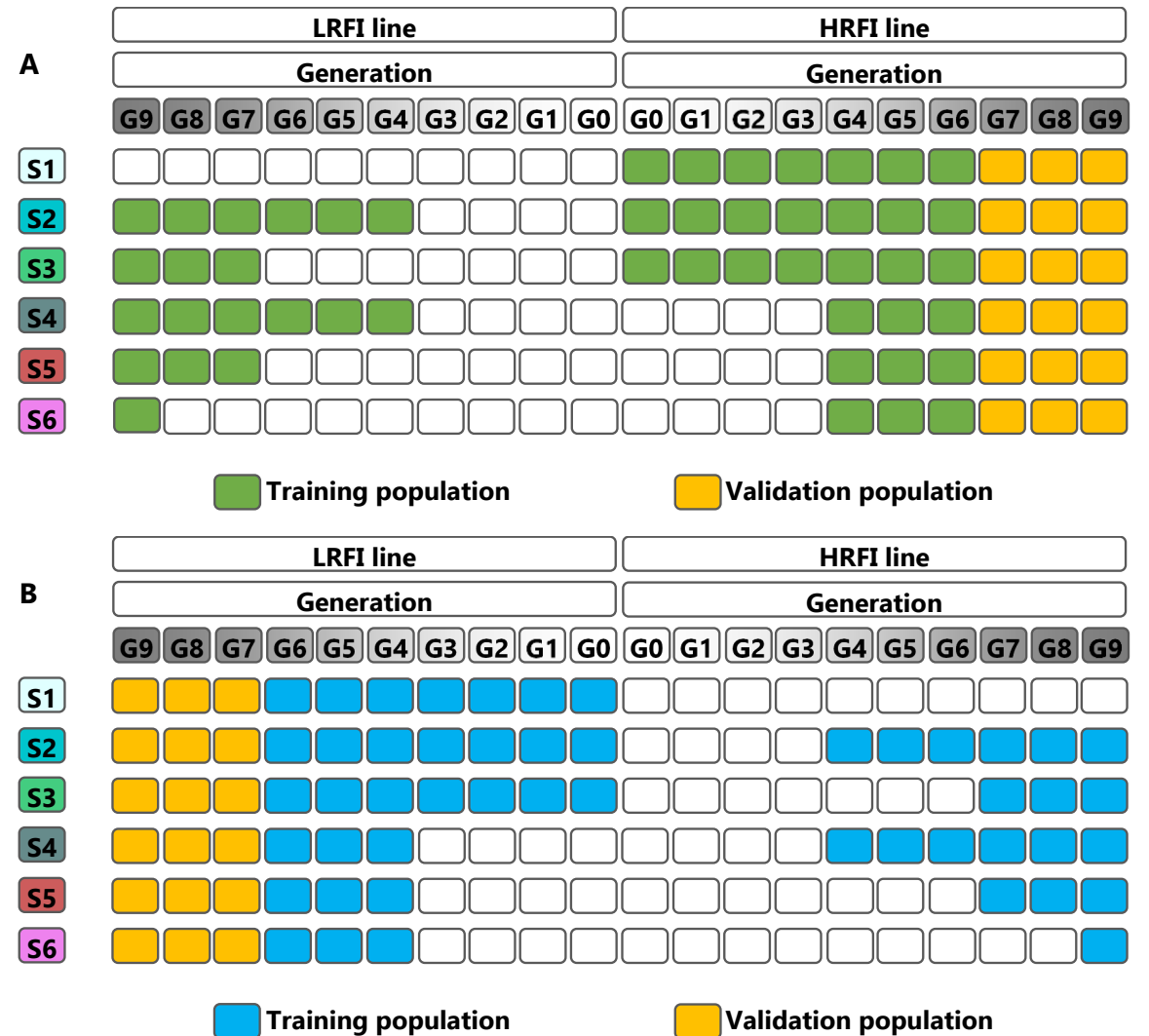# Design of scenarios to predict validation animals in HRFI and LRFI lines
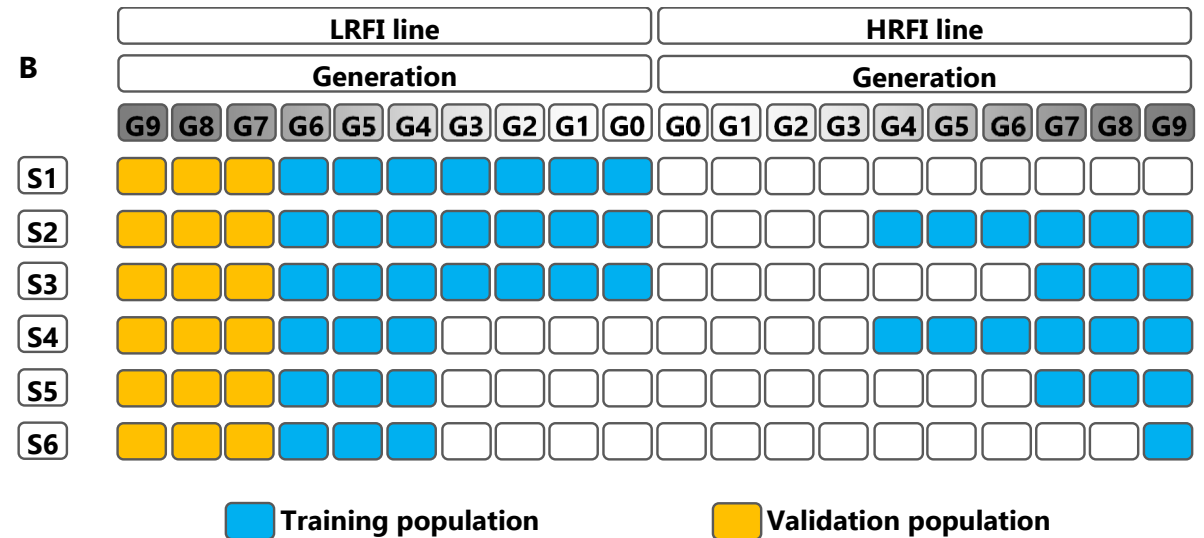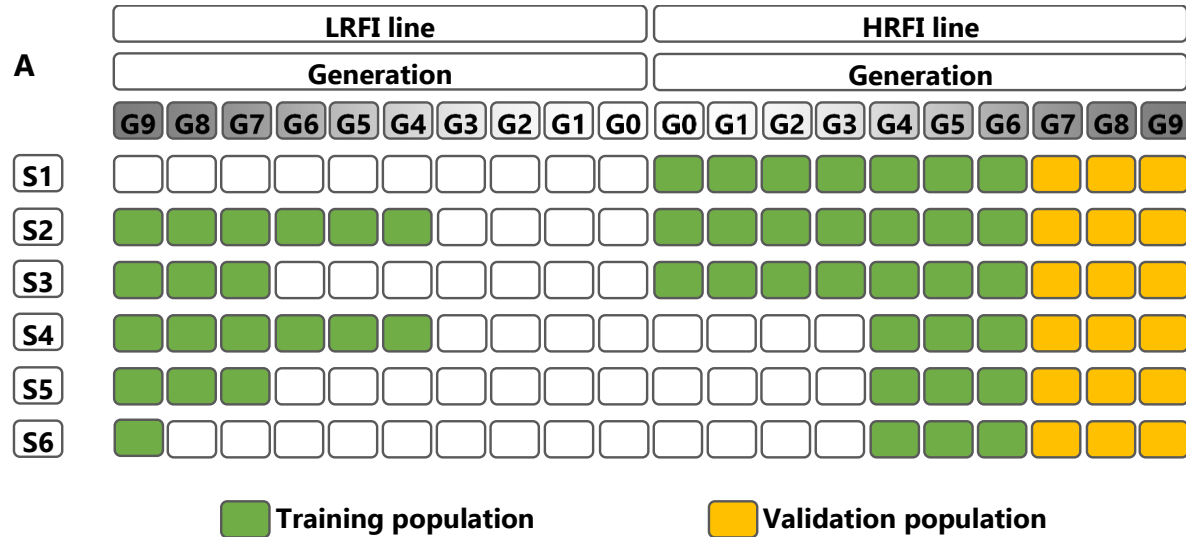
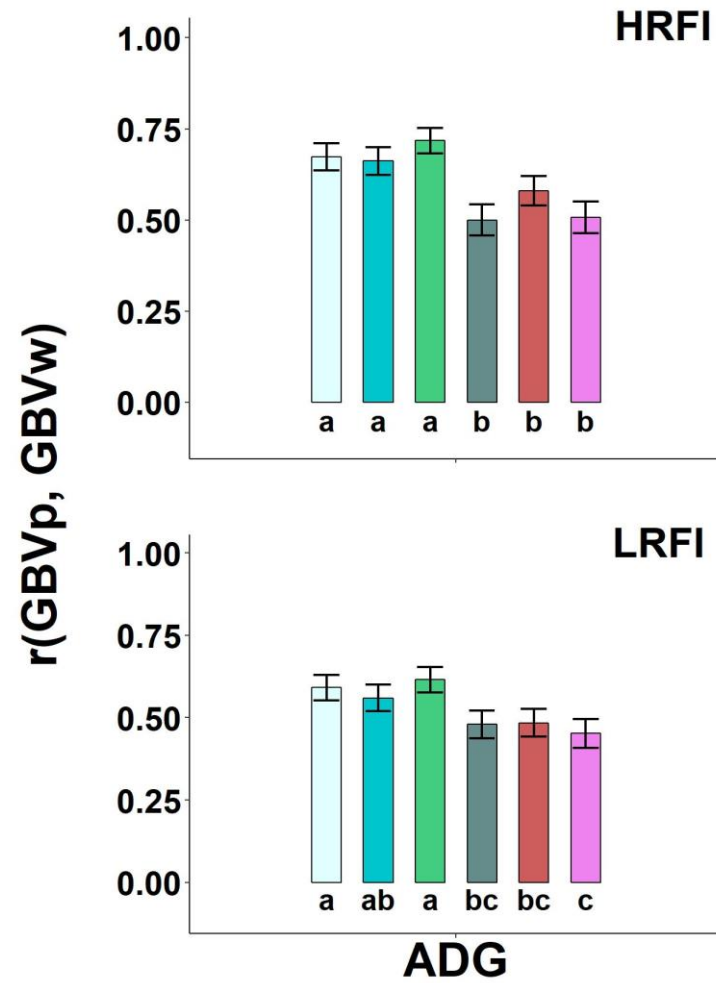## Number of animals in the training and validation sets to predict the HRFI or LRFI candidates

	HRFI		LRFI	
	Training	Validation	Training	Validation
S 1	403	399	400	433
S 2	1,055	399	1,009	433
S 3	802	399	802	433
S 4	863	399	829	433
S 5	610	399	622	433
S 6	403	399	400	433

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Accuracy of predictions and bias

Accuracy: *Correlation between GBV_p and GBV_w*

Bias: *Regression of GBV_w on GBV_p*

GBV_p: GBV obtained each scenario

GBV_w: GBV obtained for each line with whole information
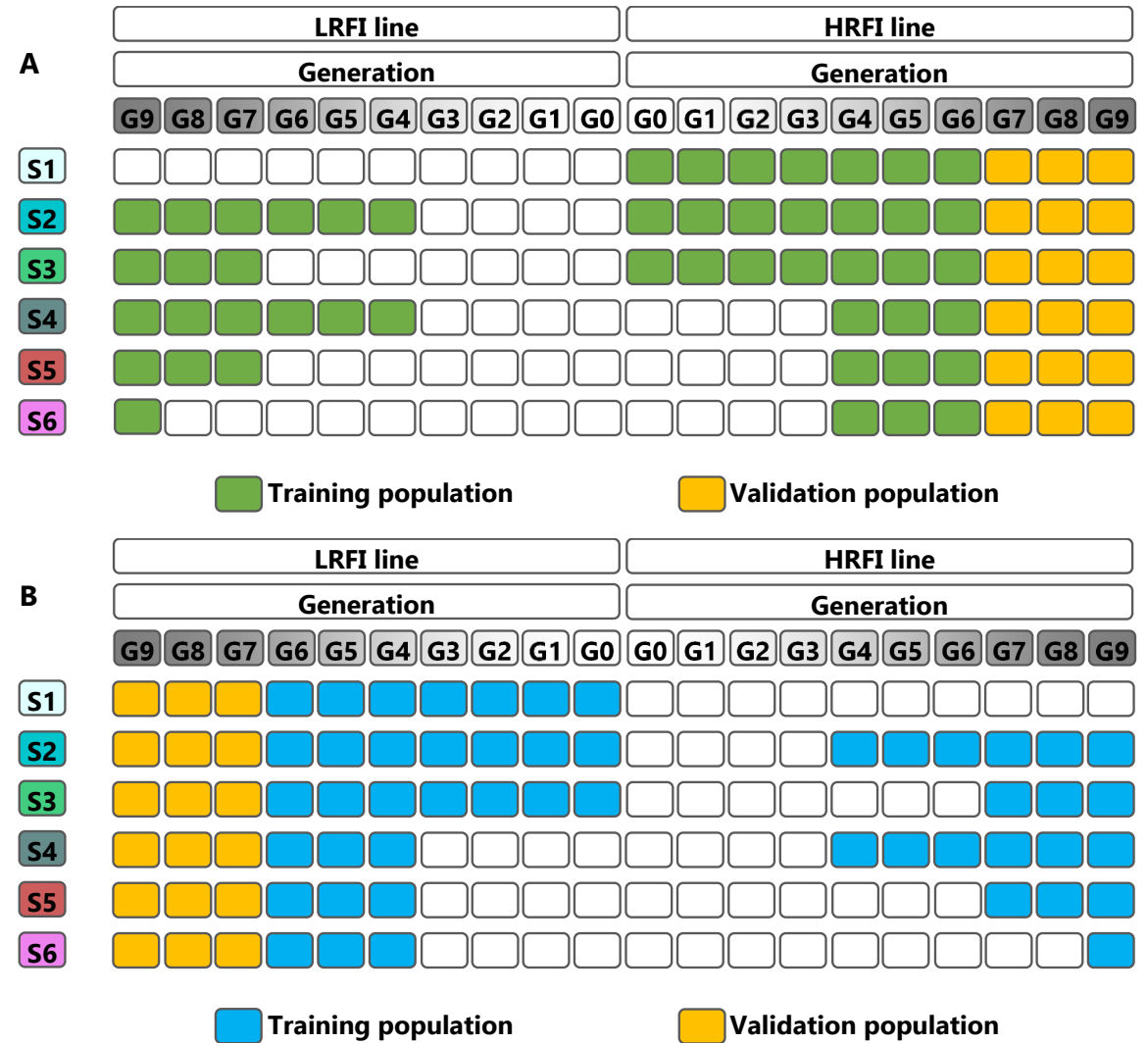
Legarra and Reverter - Genet Sel Evol (2018)
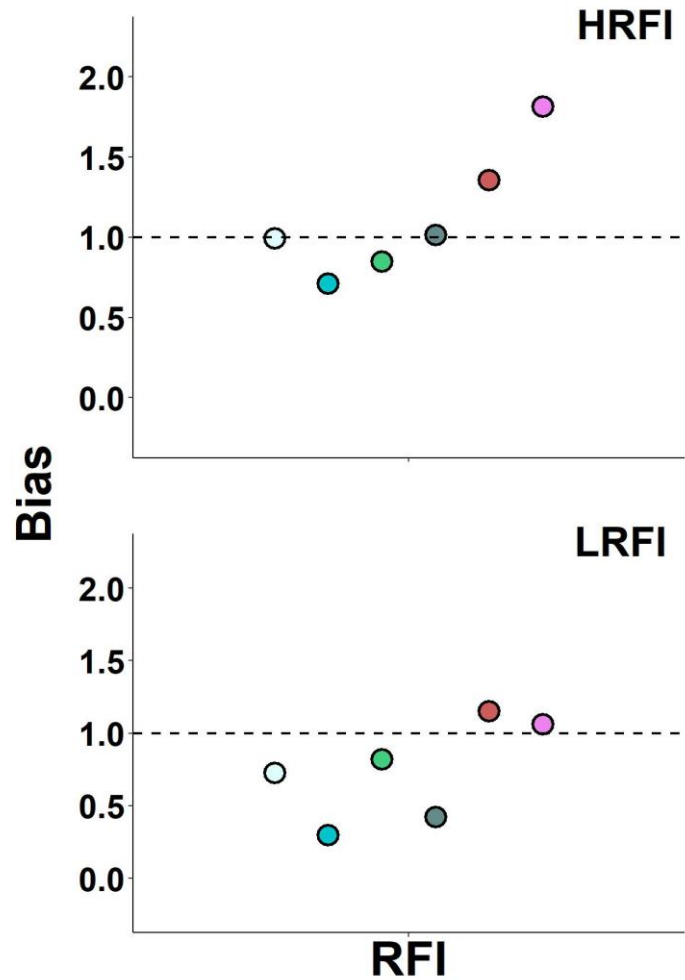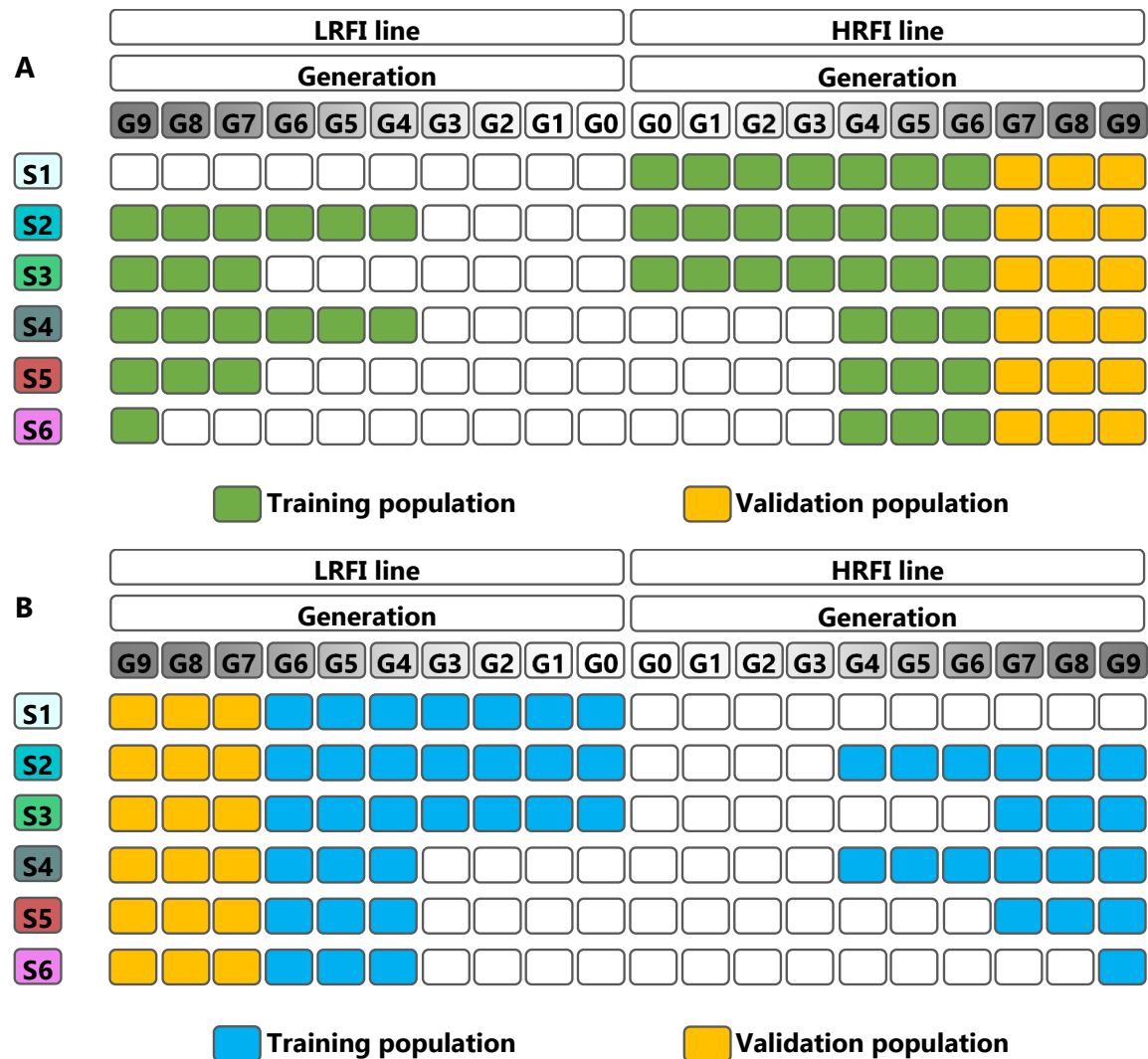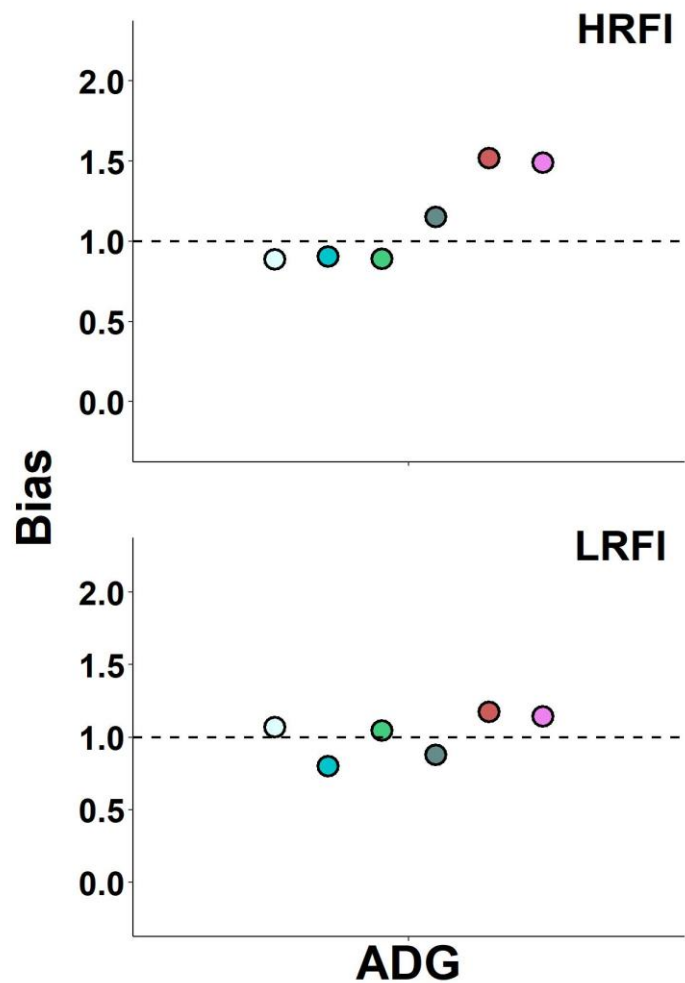
Prediction accuracy for RFI

Prediction accuracy for ADG

Bias of prediction for RFI

Bias of prediction for ADG

Conclusion

Genomic prediction using a training set comprising animals from lines selected for different traits:

- *Could be as accurate as genomic prediction using a unique population training set.*

- *More biased predictions were observed in these scenarios, so genetic gains would be difficult to predict.*

Recommendations

- *To initiate a genomic selection population when historical samples are missing*

- *When two lines are considered and costs should be limited*

- *Special care should be taken regarding the magnitude of the relationships within the pooled reference set*

Thanks for your attention