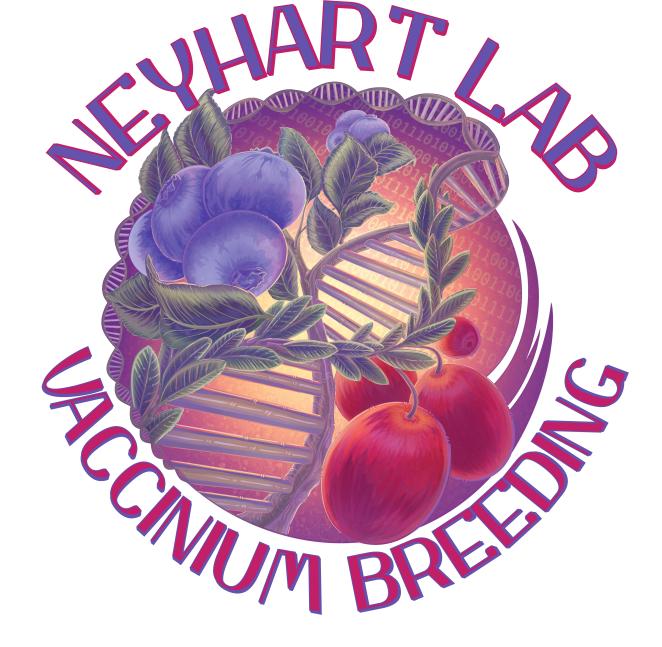


# Stage-wise analysis of multi-year phenotypic data for cranberry genotypic evaluation

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## Takeaways

- Analyzing multi-environment trial data for perennial crops (e.g. cranberry) must account for serial correlations caused by repeated measures
- Genetic correlations between years were high for four cranberry traits
- Accounting for serial correlations led to better model fit and higher prediction accuracy

## 1. Introduction

Optimal analysis of multi-environment trials (METs) can aid in identifying superior genotypes in breeding programs<sup>1</sup>.

Stage-wise analysis is common for analyzing data from METs of annual crops<sup>2</sup>.

MET data for perennial crops like cranberry (*Vaccinium macrocarpon* Ait.) presents statistical challenges:

- Unbalanced data:** not all genotype-environment combinations are observed
- Serial correlation from repeated measures:** plots, blocks, and genotypes are not randomized (and are thus correlated) across years<sup>3</sup>

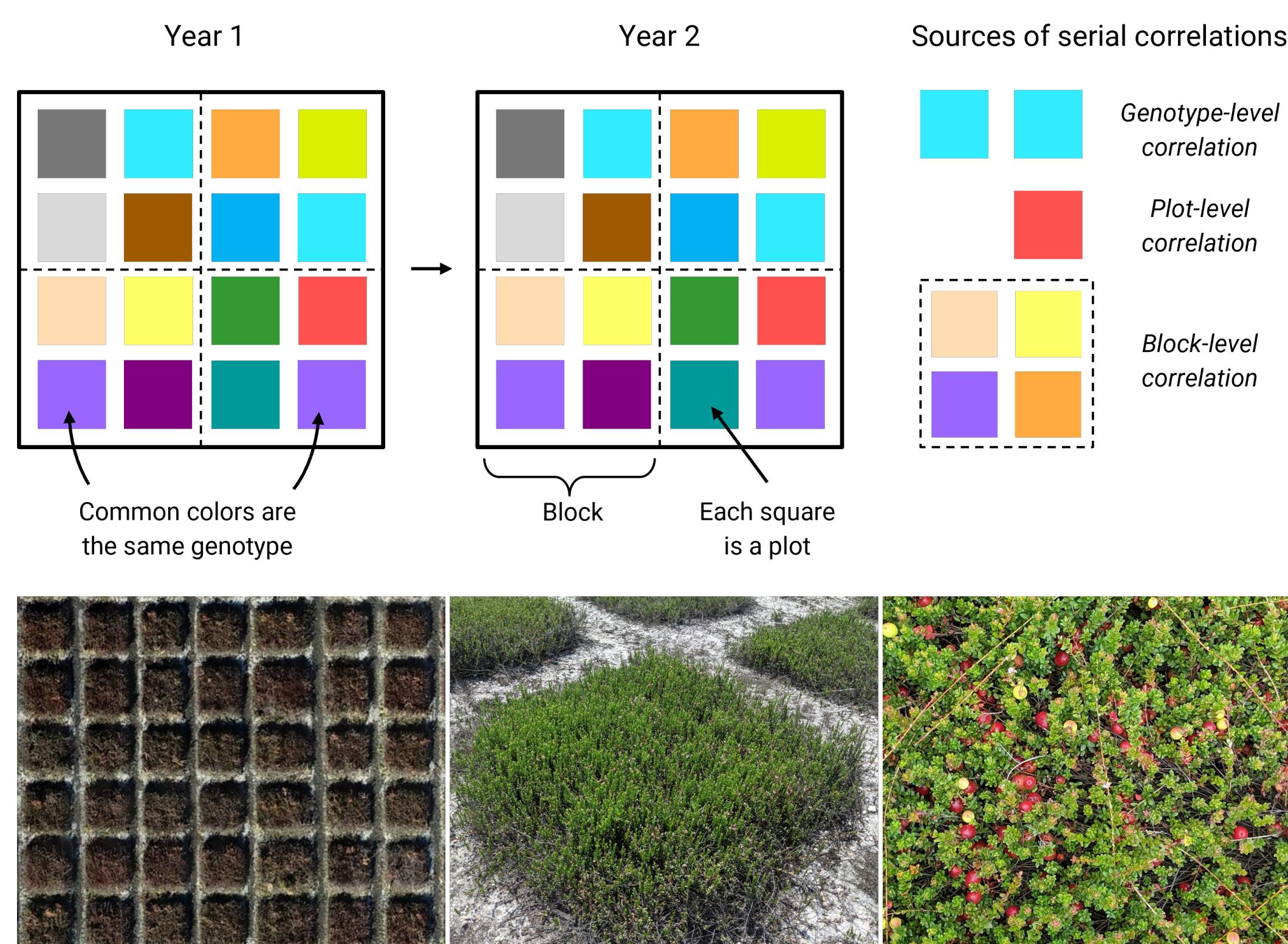


Figure 1: Fruit of the zoom (in): a bed, plot, and fruit from cranberry breeding trials

## Objectives:

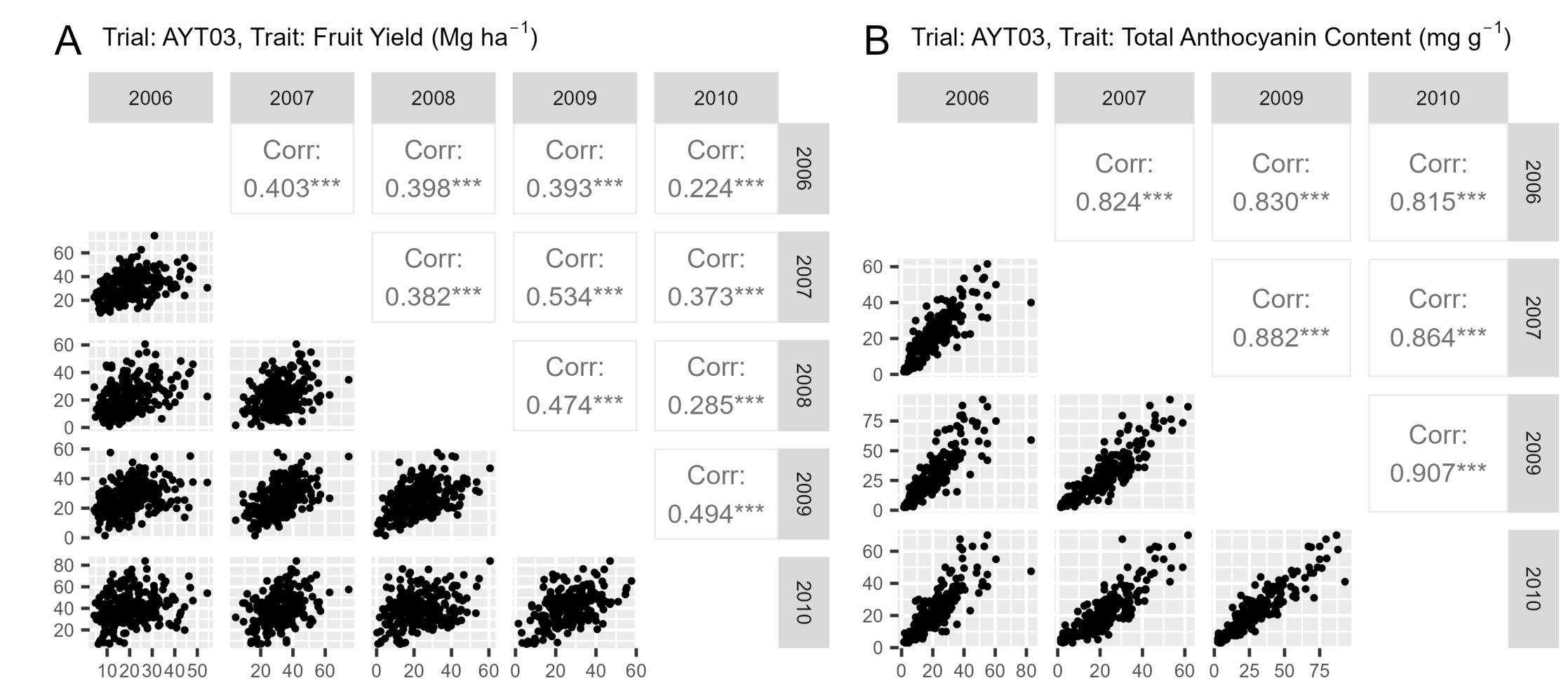
- Identify the best two-stage models for analyzing data from cranberry METs.
- Compare the ability of models to predict genotypic performance for multiple traits in future years.

## 2. Phenotypic Data and Stage 1 Analysis

We analyzed phenotypic data for four traits in two multi-year cranberry evaluation trials:

Trial	Year Planted	Plots	Genotypes	Reps	Years Harvested
AYT03	2003	240	80	3	5
AYT13	2013	60	30	2	6
Trait	Abbrv.	Description			
Fruit Weight	FW	Average mass (g) of individual fruit			
Fruit Yield	FY	Total yield of fruit (Mg) per unit area (ha)			
Total Anthocyanin Content	TAC	Level of anthocyanins (mg) per mass (g) of fruit			
Percent Rot	PFR	Percentage (%) of rotted fruit in a harvested sample			

Breeding plots are not randomized each year, which induces correlations



## 3. Stage 2 Analysis

In Stage 2, genotype-harvest year BLUPs are predicted using a model:

$$\text{BLUE}[G_{ij}] = y_{ij} = H_j + g(H)_{ij} + s_{ij}$$

$y_{ij}$ : BLUE of the genotype-harvest mean

$H_j$ : fixed effect of harvest year

$g(H)_{ij}$ : BLUP of genotype in harvest year [ $g(H)_{ij} \sim N(0, G)$ ]

$s_{ij}$ : residual error

Genetic correlations were high between harvest years (upper-right triangle in the below G matrices):

FY, CORH						
(03)	(04)	(05)	(06)	(07)		
1.5e+03	0.814	0.814	0.814	0.814		
1.72e+03	2.97e+03	0.814	0.814	0.814		
1.69e+03	2.38e+03	2.88e+03	0.814	0.814		
1.95e+03	2.75e+03	2.71e+03	3.85e+03	0.814		
2.64e+03	3.72e+03	3.66e+03	4.23e+03	7.03e+03		

FW, AR1H						
(03)	(04)	(05)	(06)	(07)		
0.0885	0.98	0.96	0.941	0.922		
0.0851	0.0853	0.98	0.96	0.941		
0.066	0.0661	0.0534	0.98	0.96		
0.0851	0.0852	0.0688	0.0923	0.98		
0.0864	0.0865	0.0699	0.0938	0.0992		

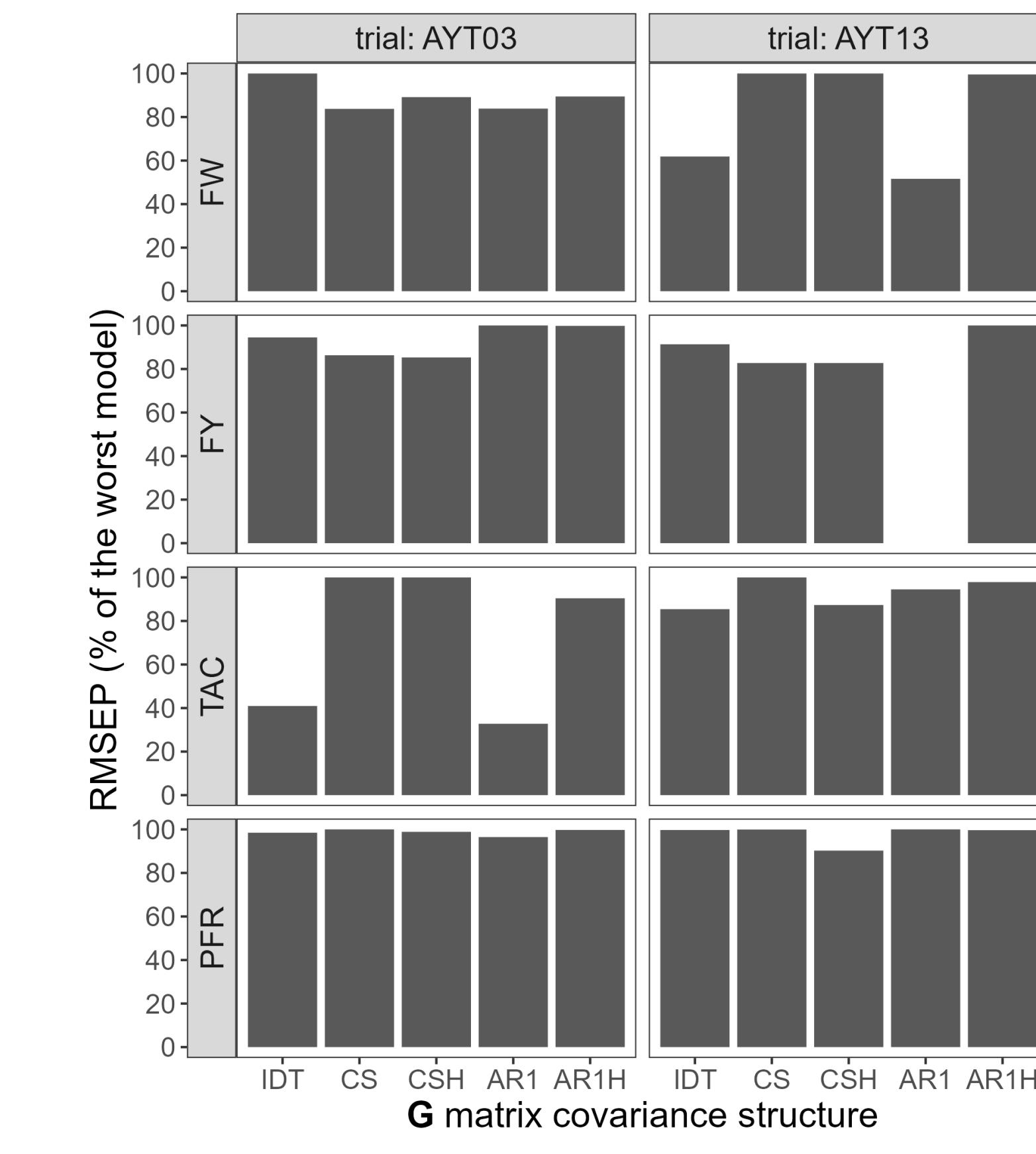
TAC, AR1H						
(03)	(04)	(05)	(06)	(07)		
109	0.98	0.96	0.941	0.922		
101	97.8	0.98	0.96	0.941		
2.71	2.63	0.0734	0.98	0.96		
154	149	4.18	248	0.98		
109	106	2.95	175	129		

PFR, AR1H						
(03)	(04)	(05)	(06)	(07)		
4.83	0.787	0.62	0.488	0.384		
8.52	24.3	0.787	0.62	0.488		
0.0825	0.235	0.00367	0.787	0.62		
4.66	13.3	0.207	18.9	0.787		
7.73	22	0.344	31.3	8.8		

### Cross-validation:

- Phenotypes in later years were masked
- Phenotypes in early years were used in prediction
- Models that include serial correlations were often most accurate



## 4. Next Steps

- Compare serial correlation models in genomic prediction
- Evaluate sparse phenotyping designs
- Develop improved perennial breeding trial experimental designs

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## References

- Bernardo, R. 2010. *Breeding for Quantitative Traits in Plants*. Stemma Press, Woodbury, Minnesota.
- Smith, A. B., L. M. Borg, B. J. Gogel, et al. 2019. *J. Agric. Biol. Environ. Stat.*, 24(4):573–588.
- Piepho, H.-P. and T. Eckl. 2013. *Grass Forage Sci.*, 69(3):431–440.
- Endelman, J. B. 2023. *Theor. Appl. Genet.*, 136(4):65.