Quantifying the Drivers of Genetic Change in Plant Breeding

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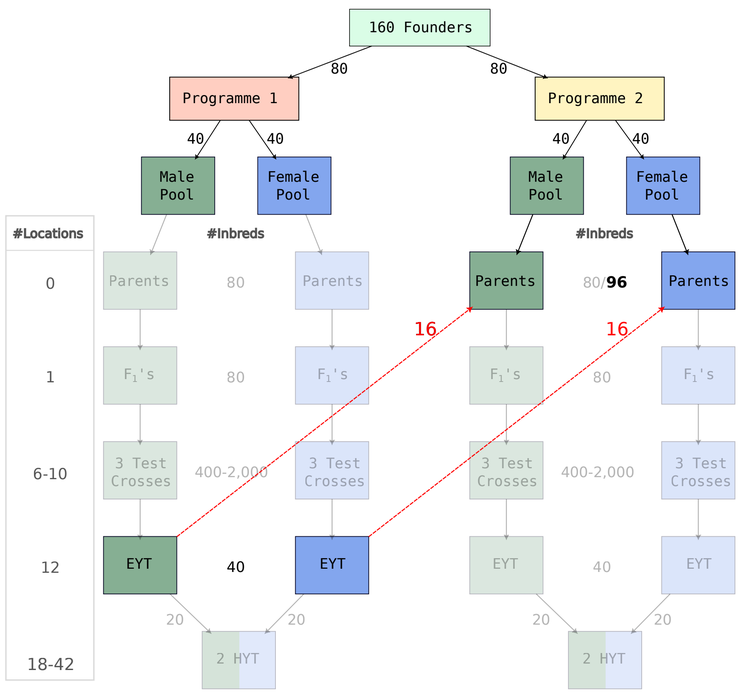
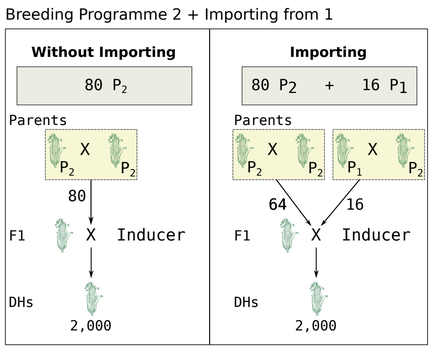
Introduction

It has long been recognized that genetic diversity is required in breeding programmes. It is crucial as a short- and long-term factor to improve genetic mean and maintain genetic variance at a reasonable level. However, there needs to be more research into how the germplasm exchange between breeding programmes contributes to each pool's genetic mean and variance over time and under different levels of genotype by environment interaction (GEI). Therefore, the objectives of this study are to i) simulate two parallel breeding programmes (BP_1 and BP_2), with gene flow from BP_1 to BP_2; ii) evaluate the contribution of genes originating from BP_1 and BP_2 to the genetic mean and variance in BP_2, and iii) evaluate the impact of GEI within and across programmes on the gene flow.

Simulation and Methods



- The breeding programmes are simulated using AlphaSimR with each QTL assigned additive and dominance genetic effects
- 16 individuals are imported from EYT in BP_1 to Parents in BP_2

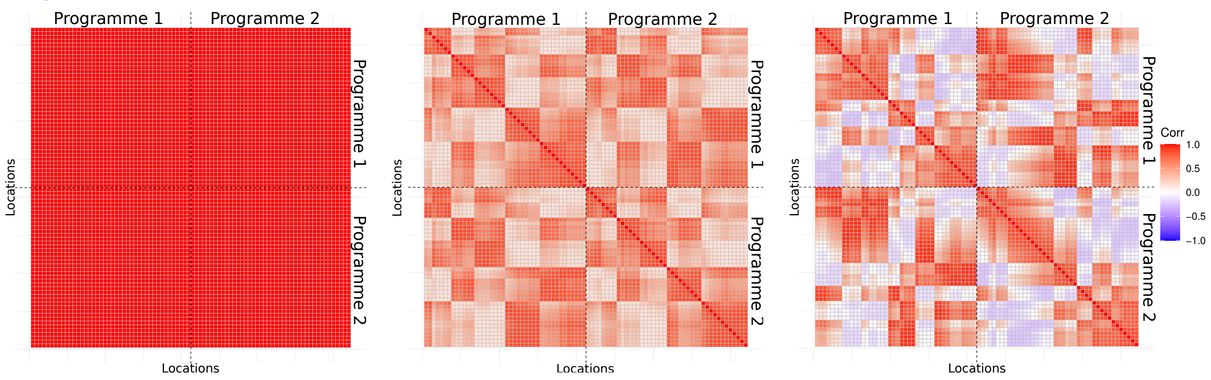


A single trait representing grain yield is simulated based on

$$\boldsymbol{y}_i = \mathbf{1}\mu + \boldsymbol{X}_i\boldsymbol{\beta} + \boldsymbol{a}_i + \boldsymbol{d}_i + \boldsymbol{e}_i$$
$$\boldsymbol{a}_i \sim N\left(\mathbf{0}, \boldsymbol{C}_A\sigma^2_A\right); \boldsymbol{d}_i \sim N\left(\mathbf{0}, \boldsymbol{C}_D\sigma^2_D\right); \boldsymbol{\epsilon}_i \sim N\left(\mathbf{0}, \boldsymbol{I}\sigma^2_\epsilon\right)$$

- Additive ($\boldsymbol{a}_i$) and dominance ($\boldsymbol{d}_i$) effects are simulated using, respectively, the correlation matrices $\boldsymbol{C}_A$ and $\boldsymbol{C}_D$.

To demonstrate the impact of GEI, we have defined respectively No, Low and High GEI scenarios:



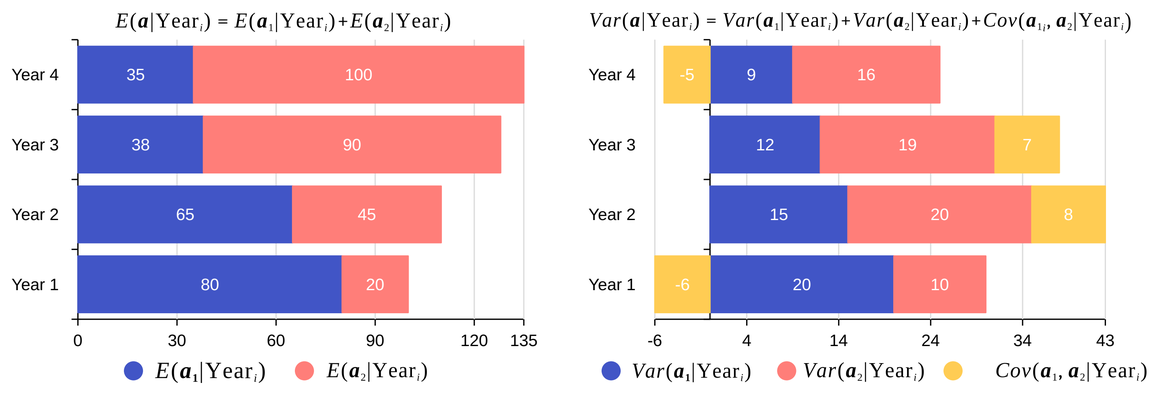
(a) No GEI (b) Low GEI (c) High GEI

Let $\bar{\boldsymbol{a}}$ be a vector of main additive genetic values assumed to be distributed as $\bar{\boldsymbol{a}} \mid \boldsymbol{A} \sim N\left(\mathbf{0}, \boldsymbol{A}\sigma^2_a\right)$, where $\sigma^2_a = \frac{1}{n_L}\sigma^2_A\left[1 + \frac{2}{n_L}\sum_{l=1}^{n_L-1}\sum_{l'=l+1}^{n_L}\rho_{l,l'}\right]$ with $\rho_{l,l'}$ being the additive genetic correlation between locations l and l'. As demonstrated by [1] and [2], we can use pedigree information to analyse the contribution of paths to changes in additive genetic mean and variance. Thus, the partition of additive genetic values by origin can be defined as:

$$\bar{\boldsymbol{a}} = (\boldsymbol{T}_1 + \boldsymbol{T}_2)\,\bar{\boldsymbol{w}} = \bar{\boldsymbol{a}}_1 + \bar{\boldsymbol{a}}_2, \quad (1)$$

where $\boldsymbol{T}_c = \boldsymbol{T}\boldsymbol{P}_c$, with $c = 1$ for origin in BP_1 and $c = 2$ for origin BP_2; $\boldsymbol{T}$ a triangular matrix of expected gene flow between ancestors and individuals; $\boldsymbol{P}_c$ a diagonal matrix containing ones or zeroes at the corresponding elements given germplasm origin; $\bar{\boldsymbol{w}} \sim N\left(\mathbf{0}, \boldsymbol{W}\sigma^2_a\right)$; and $\bar{\boldsymbol{a}}_1$ and $\bar{\boldsymbol{a}}_2$ represent the main contribution of germplasm origin from respectively BP_1 and BP_2.

Contributions can be summarised by conditioning the expectation and variance by any set of explanatory variables such as year, heterotic pool, stages, etc.

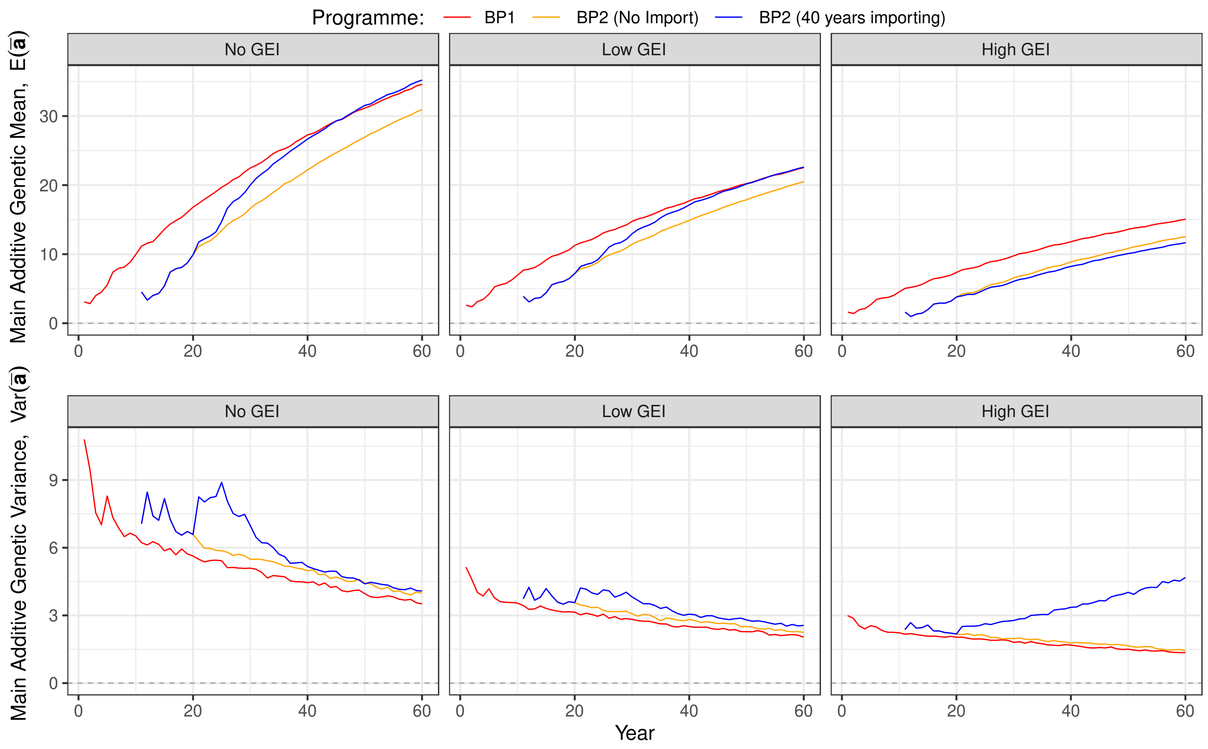


Final Remarks

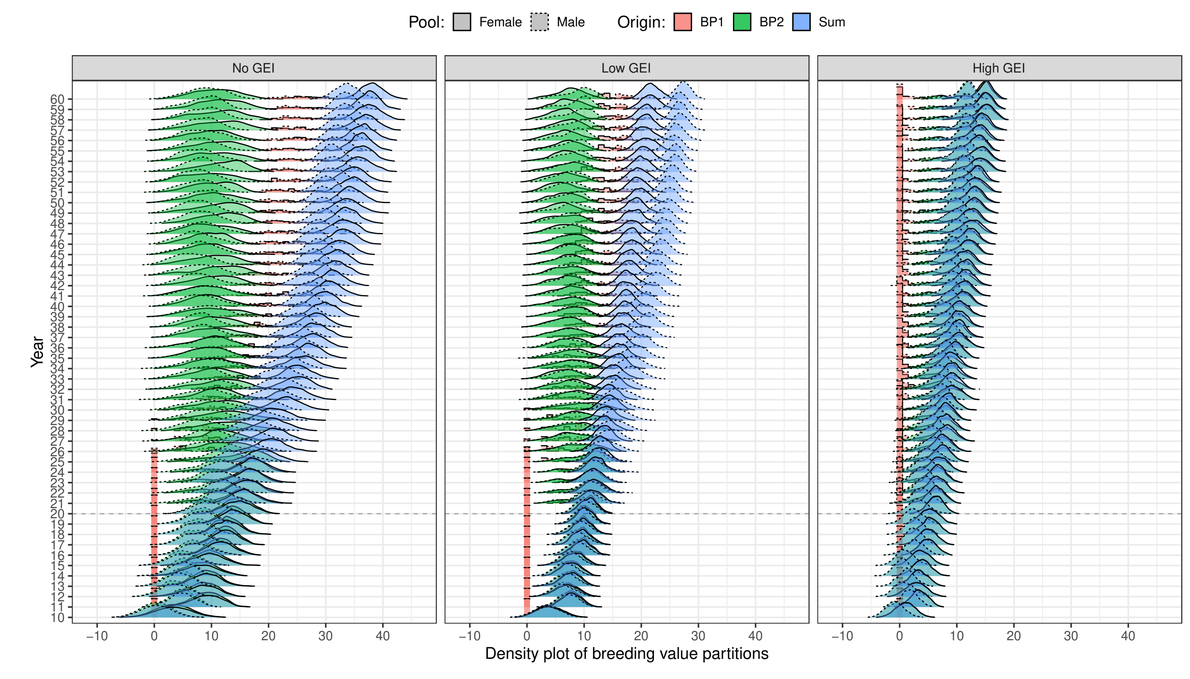
- Importing elite lines can increase genetic diversity in breeding populations, and combinations of yield-related alleles with minor effects across the genome can be distinct and maintained in populations of elite lines.
- Simulation of breeding programmes can be used as proof of concept and a powerful tool to test new environments and germplasm.
- By partitioning the additive genetic value by origin, we can further evaluate the impact of imported germplasm on additive genetic mean and variance changes. Understanding those mechanisms under different levels of GEI is essential to the breeder to manage imported germplasm.

Results and Discussion

- Under no and low GEI, the genetic mean of BP_2 (when importing from BP_1) increases until it reaches the mean of BP_1. In fact, the mean of BP_2 surpasses that of BP_1 after 40 years of import.
- Under high GEI, the genetic variance keeps increasing for BP_2 (when importing from BP_1), which is likely due to repeated introgression of poorly adapted germplasm. Such germplasm will be useful in new environments in BP_2 which match those in BP_1.



- There are differences in how imported germplasm affects heterotic pools, which is most related to the inheritance process of imported genes into BP_2 and can be visualized in the contribution of BP_2 given the pool.
- Increasing the amount of GEI within breeding programmes consistently reduces the genetic gain.



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