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Role of phenotypic plasticity in rapid adaptation in maize

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Introduction

Natural selection is one of the main mechanisms of evolution. It requires time to act. In the context of rapid changing environment, we may expect that plastic genotypes will be favoured.

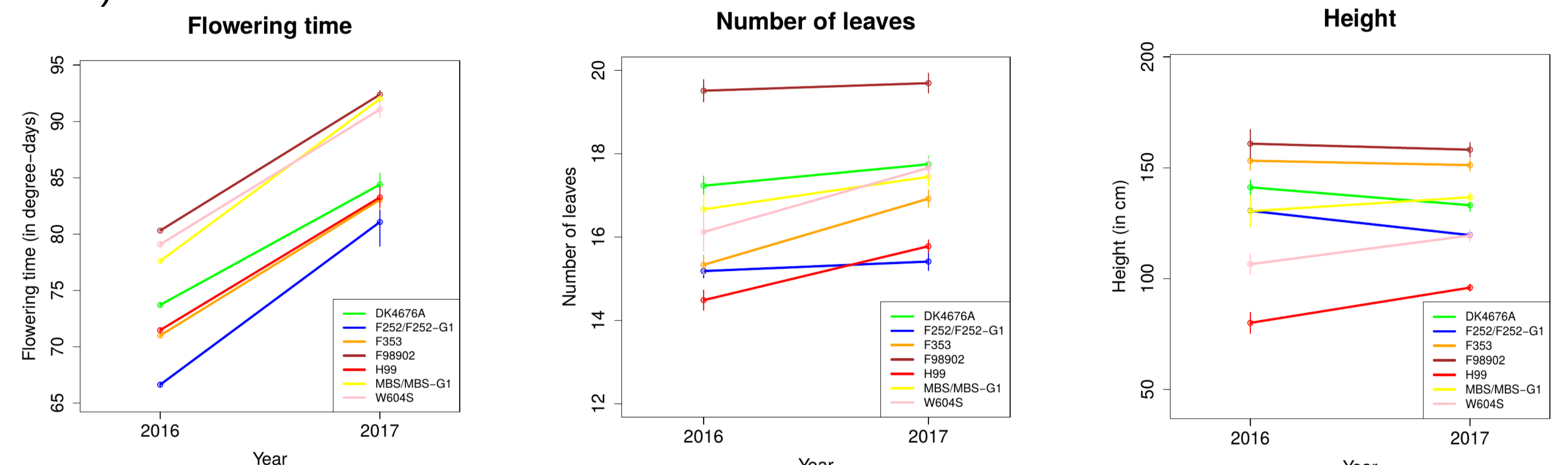
Phenotypic plasticity is the capacity for a organism to exhibit different phenotypes in response to environment. On the opposite, phenotypic traits are canalized when they are insensitive to the environmental conditions.

A given genotype can exhibit different levels of plasticity depending on the environments and the phenotypic traits that are considered.

Phenotypic plasticity can be considered as a trait on which selection potentially acts. It can also help natural selection through genetic assimilation.

Plasticity and GxE in maize lines

Growth and development phenotypes were evaluated on 7 maize lines in the field (Saclay, France) in 2016 and 2017.



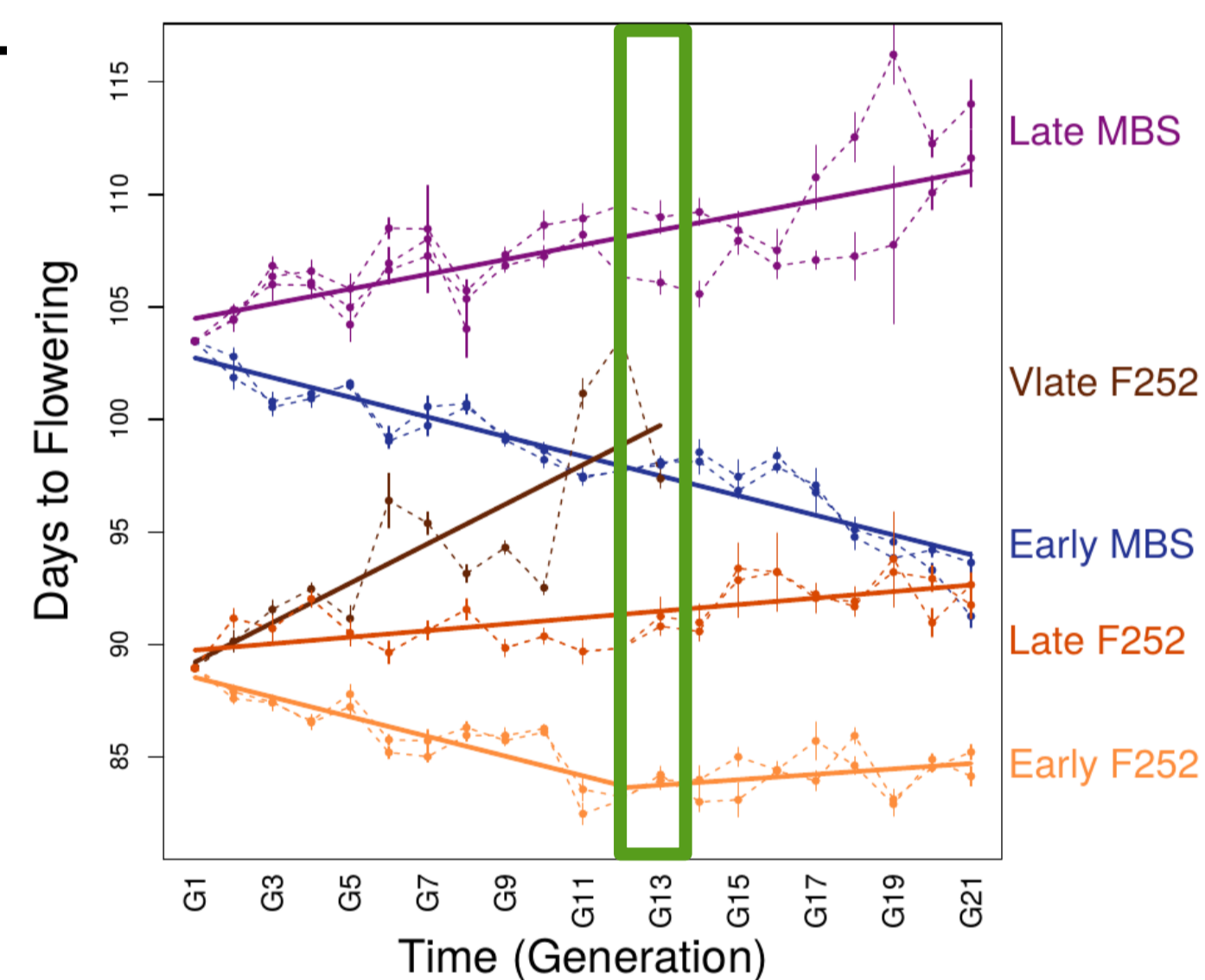
Flowering time is a plastic phenotype. The phenotypic plasticity of leaves number and height depends on the genotype => GxE

Differences in phenotypic plasticity between maize lines are the result of a medium-term adaptation. How does it contribute to short-term adaptation ?

Plant material

We used an original plant material resulting from two Divergent Selection Experiments (DSEs) for flowering time of maize. This material was developed over the last 20 years⁽¹⁾. Early- and Late-flowering populations, subsequently structured into families within populations were formed. A strong response to selection was observed over the 20 generations for flowering time.

In this work, we focused on 9 genotypes representing the generation G13 from the DSEs evaluated two consecutive years (2014 and 2015) in field experiments (Saclay's Plateau - France)

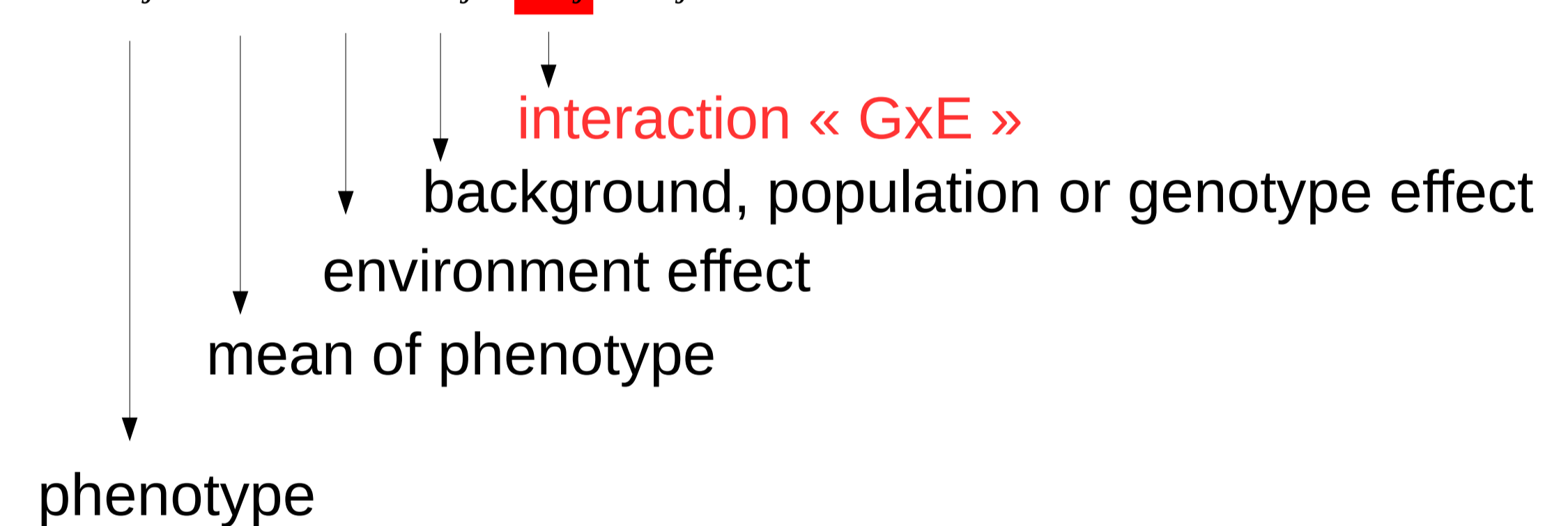


Method

We considered 4 phenotypes on **G13 genotypes of the DSEs** : flowering time, leaf number, height of the plant and slope of the phyllochron.

For each phenotype, the following model has been applied at 3 levels : the genetic background (F252/MBS), the population (early/late) within the genetic background and the genotype within the populations.

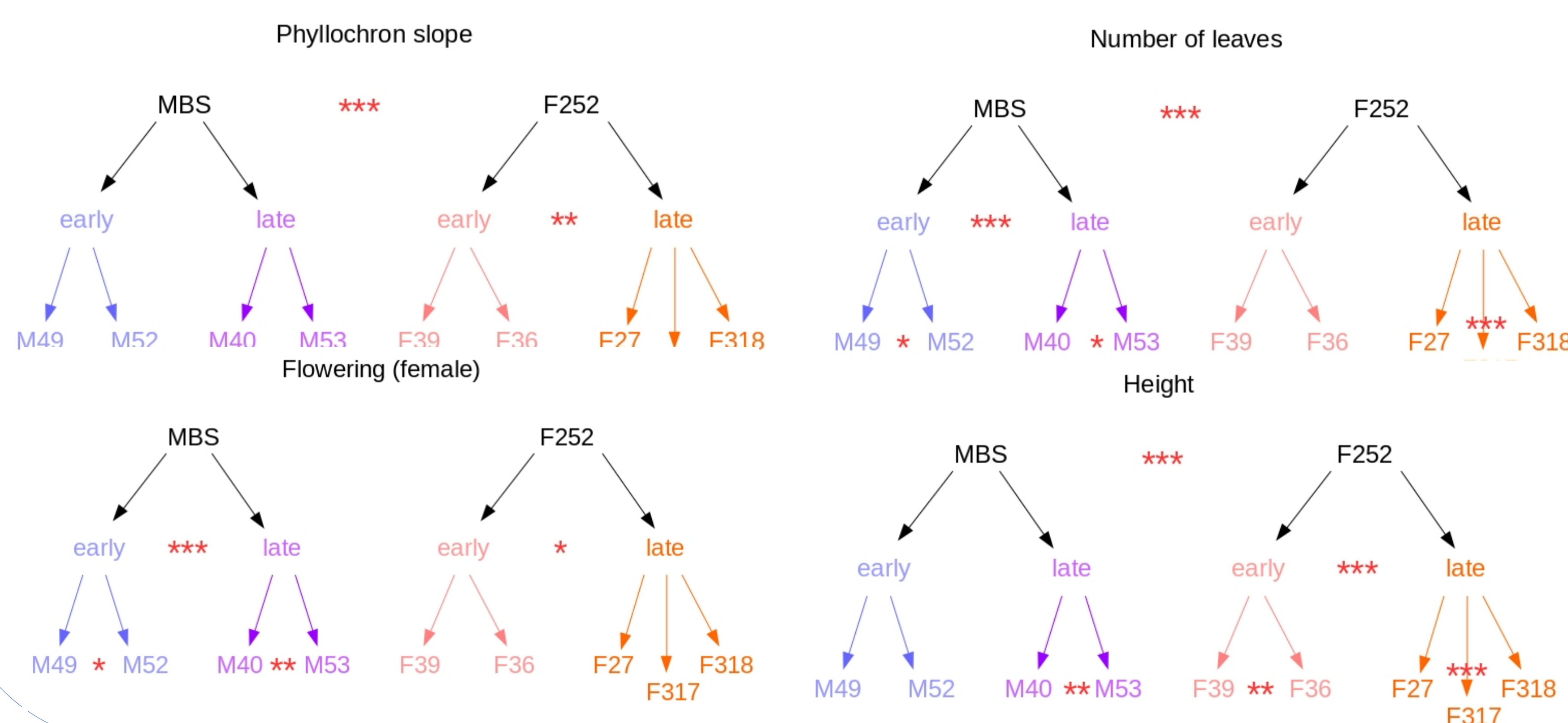
$$y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + \epsilon_{ijk}$$



We are particularly interested in the **interaction term**. It corresponds to a difference in plasticity inter background, family or genotype.

Significance of plasticity effect

Phyllochron slope, leaf number, flowering time and height have significant environment and genetic background effect (α and β effects). Pvalues for the significance of the GxE effect are indicated with * : $P > 0.05$ * ; $P \leq 0.01$ ** ; $P \leq 0.01$ ***



- Confirming previous results, we observe a plasticity that depends on the genetic background (MBS / F252) for most of the traits excepted for silk emergence (female flowering).

- Directional selection (early / late) impacted trait plasticity in specific genetic background and phenotypes (comparison early/late)
 - plasticity for height and phyllochron in F252 background
 - plasticity for leaves number and flowering time in MBS background

- We can also observe changes in plasticity in convergent selection (comparison of genotypes within populations)

References

(1) Durand E. et al., BMC Evol Biol. 2015

Conclusion and perspectives

By selecting for flowering time in maize, we observe changes in phenotypic plasticity (in specific phenotypes / genotypes combinations). It needs to be considered to study the convergence of phenotypes in genotypes that are subjected to the same selection pressure.

- How did this plasticity changes over the 20 generation of the DSEs ? This material offers potential to study the evolution of phenotypic plasticity under 20 generations of selection.
- Do we observe such plasticity at the molecular level ? Do we observe differences in the ratio plasticity/canalization depending on the integration level of the phenotype (molecular vs developmental phenotypes) ? To answer these questions, ongoing experiments collecting phenotypic data at several molecular levels and integrative phenotypes on several progenitors of the DSEs will be used. .