

# Animal models constructed with hybrid relatedness matrix vs incomplete pedigree in *Fagus sylvatica*

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## Context and aims

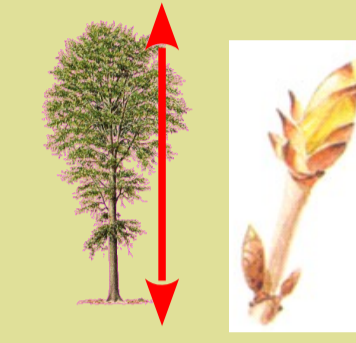
To alleviate the effort associated with generating offspring with complete pedigree information, simplified protocols with incomplete pedigrees have been adopted, like open-pollinated schemes. This solution accept untestable assumptions related to the genetic constitution of the families, the numbers of male parents involved and their contributions. Today, molecular markers provide an alternative way to construct animal models via reconstructed pedigrees or relatedness matrix. However, for some species phenotypic informations are still easier to obtain than molecular informations.

This study aims at judging the estimation errors caused by simplifying assumptions in classical breeding experimentations, and at investigating the efforts that should be allocated to obtain respectively phenotypic and information in quantitative genetic studies in wild population.

## Material

• **Study species** : *Fagus sylvatica*, a monoecious, wind-pollinated, highly outcrossed European tree species

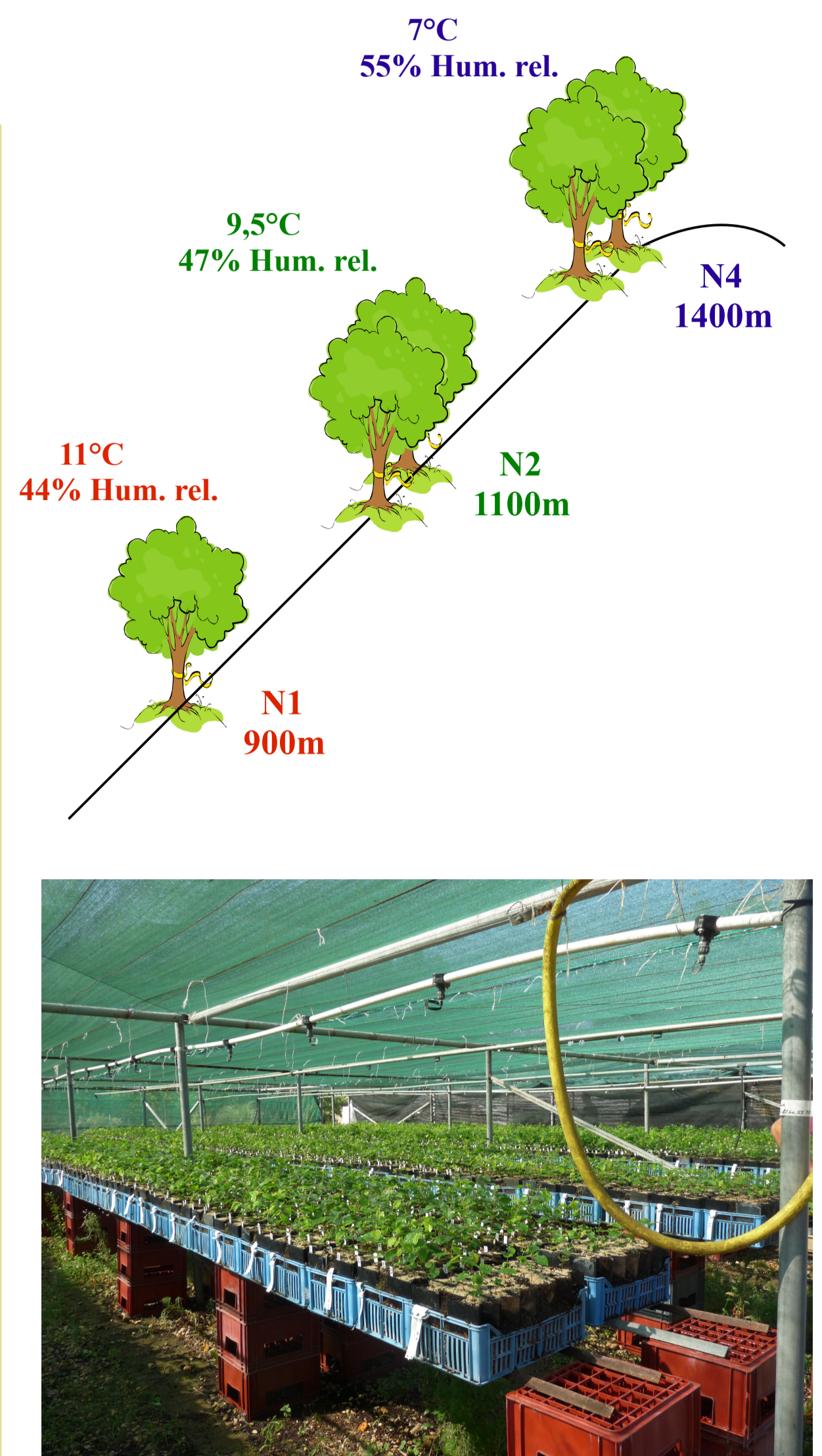
• **60 maternal progenies** (100 individuals per family) from 3 wild populations on an altitudinal gradient in the South East of France, transferred in a common garden



• Putatively adaptative and performance traits measured on **6000** seedlings : height increment and budburst phenology



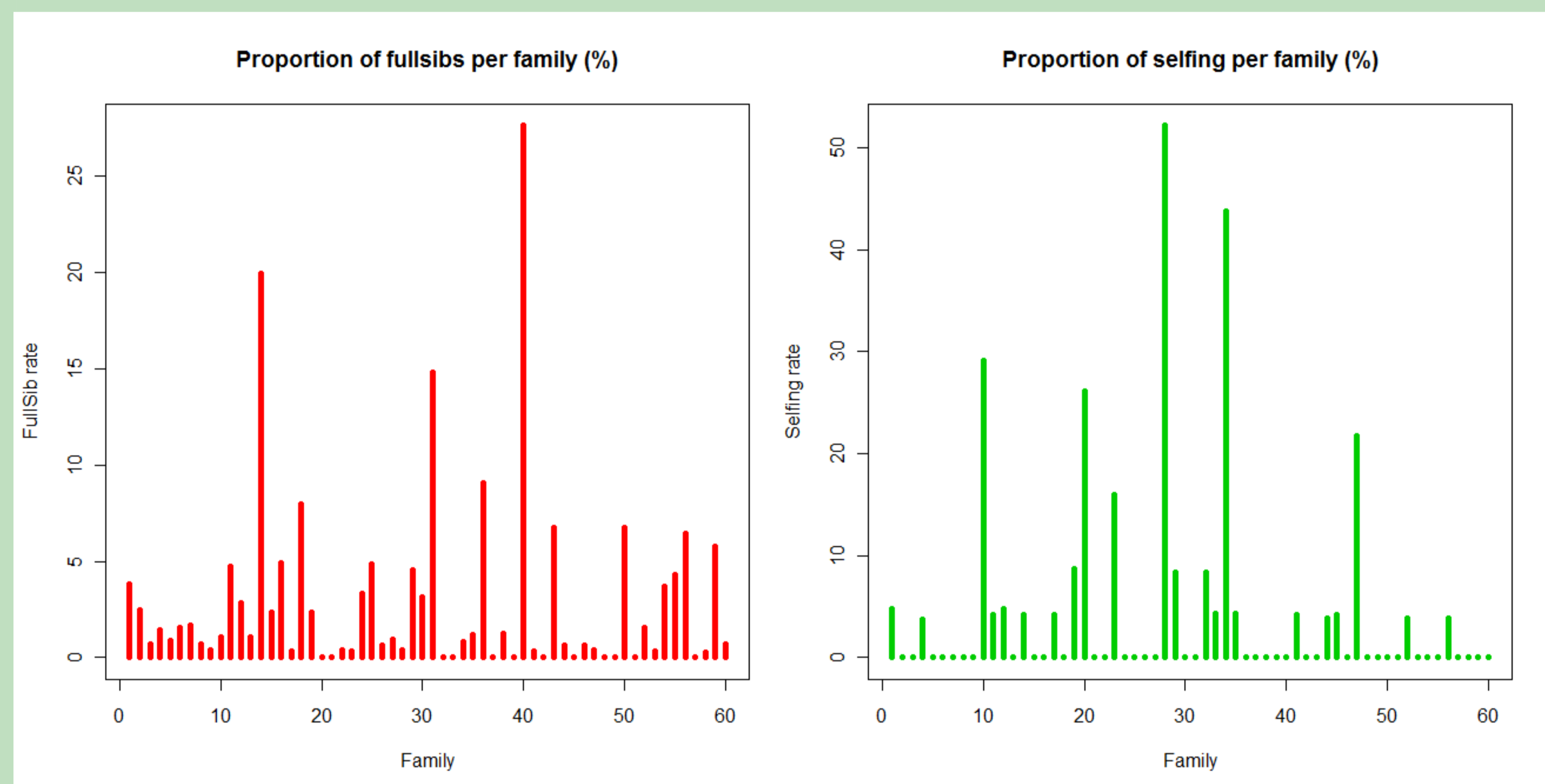
• A subset of **625** offspring and all their mothers and putative fathers genotyped at 13 microsatellite markers



## Methods and results

### a) Results of mating pattern analysis

Cervus analysis with n potential father in each population....and we found x real pollen donor...

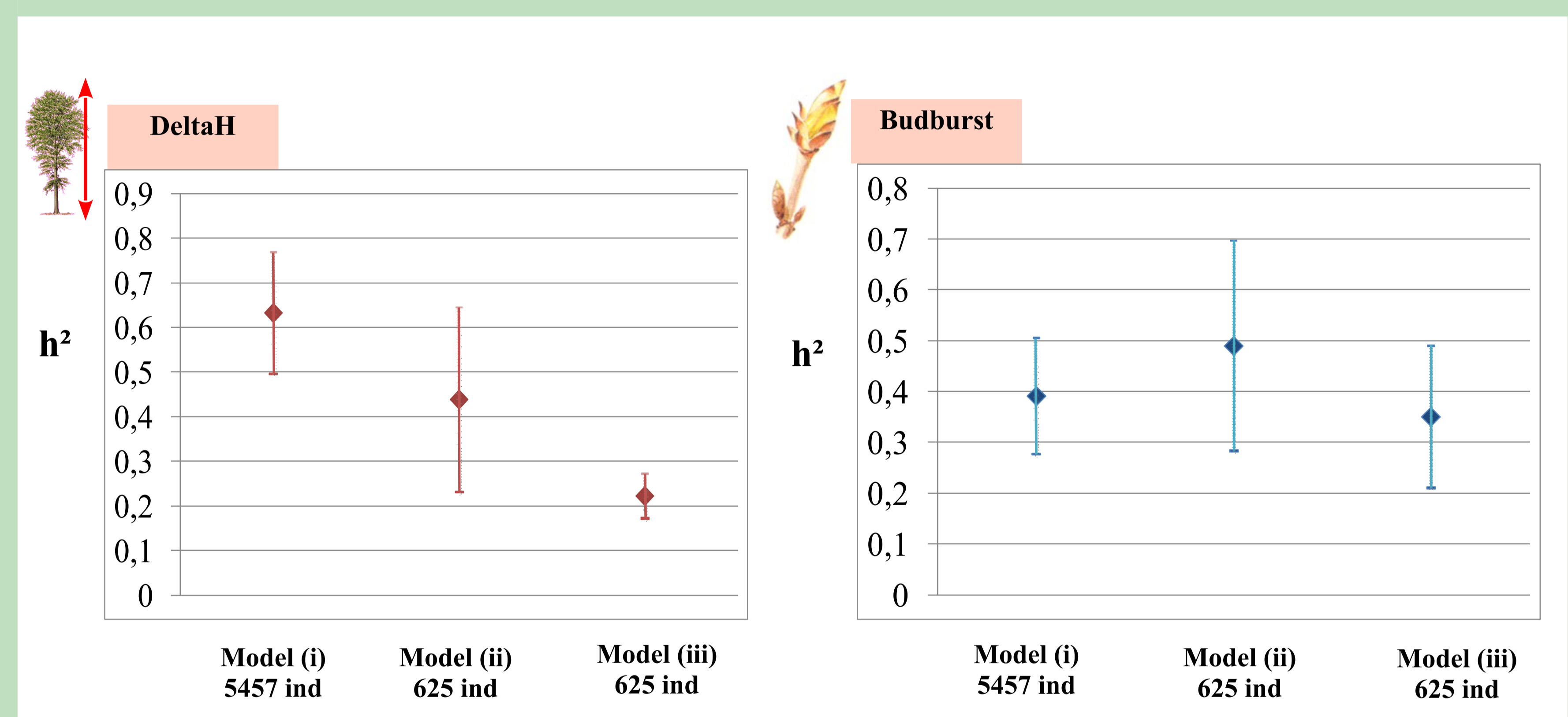


- High heterogeneity of matings systems among mother-trees
- High rates of full sibs and selfing in some families = assumption of maternal half sibs families violated

### b) Quantitative genetics analysis

The VA and h<sup>2</sup> of the traits were estimated :

- (i) using the 6000 phenotyped seedlings, and assuming that they were all half-sibs
- (ii) using the sub-sample of 625 individuals, still assuming that they were all half-sibs
- (iii) using the same sub-sample and accounting for the paternal relatedness between individuals inferred by Cervus analysis



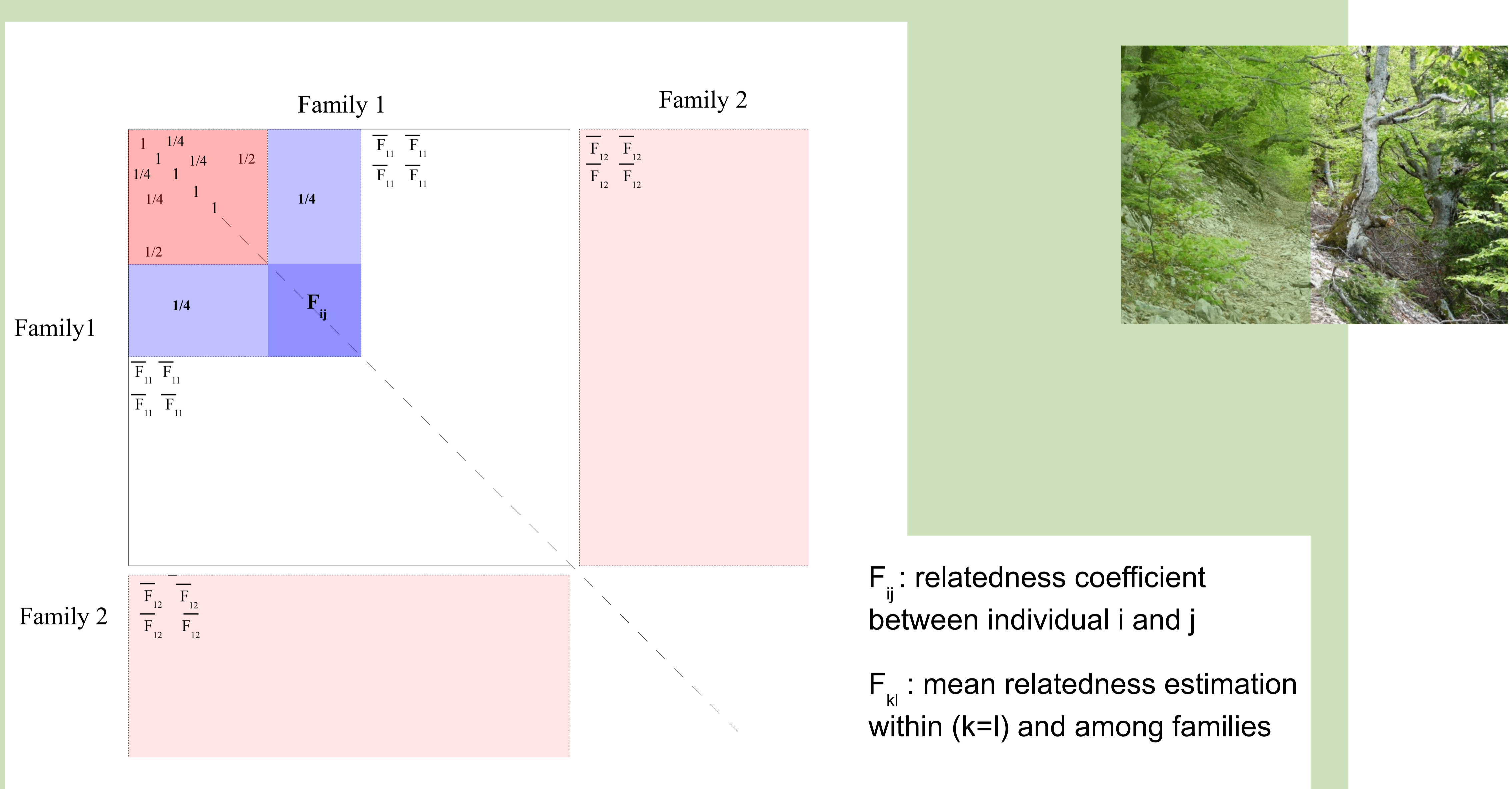
## Discussion

Accounting for complex kinship structure markedly changed VA and h<sup>2</sup> estimates : for the different studied traits, the estimates of h<sup>2</sup> varied between 0.22 and 0.45 when using paternal information, versus h<sup>2</sup> between 0.39 and 0.63 assuming only maternal half-sibs.

The best quantitative genetics model is an intermediate between the models (i) and (iii), i.e. the model which include the most genetic and phenotypic information. However, genetic data are rarely available on sampled of this size.

We can optimize the use of genetic information in creating a **hybrid relatedness matrix** which should contain : information from paternity assignments (complete pedigree), relatedness estimated from markers (F<sub>ij</sub>) and mean relatedness estimations within and between families. This last point should allow to consider that the paternal contributions to the fertilization are skewed and that mother-tree can be pollinated by only a few male-trees.

## Hybrid Matrix



## Conclusion

- ✓ Mating pattern is highly variable among families
- ✓ Quantitative genetics simplified protocols can lead to wrong interpretations since genetic effects can be confuse with maternal effects
- ✓ Accounting for paternal relatedness among individuals greatly affect the estimation of VA and h<sup>2</sup>
- ✓ The relevance of constructing a « hybrid » relatedness matrix incorporating several sources of available information (incomplete pedigree, paternity assignments, relatedness estimated from markers) instead of using simplifying assumptions, will be tested by simulation approach