



# Molecular evolution within and between populations of *Arabidopsis thaliana*: the FRIGIDA gene

Valérie Le Corre, Lucile Jacquens, Fabrice Roux

## ► To cite this version:

Valérie Le Corre, Lucile Jacquens, Fabrice Roux. Molecular evolution within and between populations of *Arabidopsis thaliana*: the FRIGIDA gene. IXth Congress of the European Society for Evolutionary Biology, Aug 2003, Leeds, United Kingdom. hal-03579947

**HAL Id: hal-03579947**

**<https://hal.science/hal-03579947>**

Submitted on 18 Feb 2022

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



# Molecular evolution within and between populations of *Arabidopsis thaliana*: the *FRIGIDA* gene



Valérie Le Corre, Lucile Jacquens and Fabrice Roux

UMR Biologie et Gestion des adventices, INRA, BV 86510, 21065 Dijon Cedex, France

lecorre@dijon.inra.fr

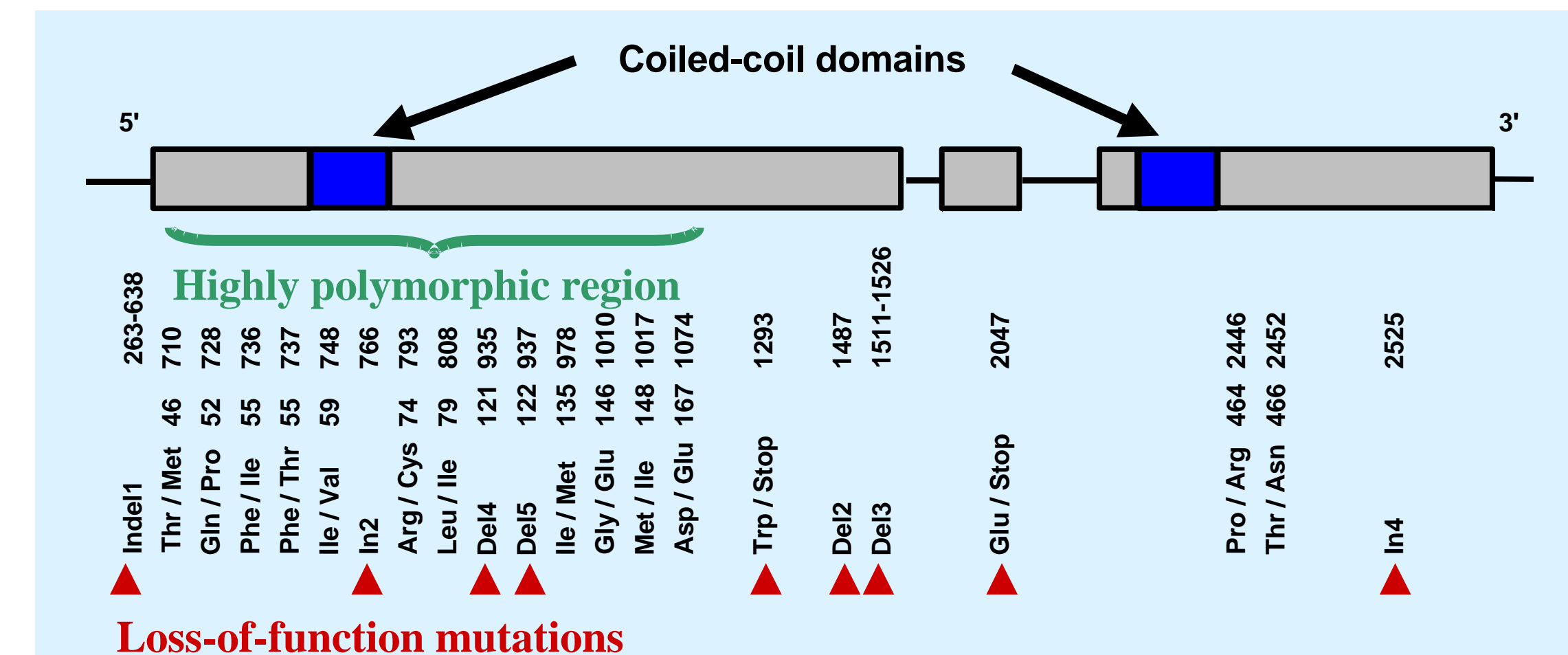
## INTRODUCTION

*Frigida* is a major gene controlling flowering time in *Arabidopsis thaliana* (Johansson *et al.*, 2000). It increases the expression level of *FLC*, a central regulatory gene that inhibits the transition to flowering. Ecotypes that carry a functional copy of *Frigida* are therefore late-flowering in the absence of vernalization.

Nucleotide variation at *Frigida* is characterised by :

- extensive non-synonymous variation in the first exon,
- several loss-of-function mutations throughout the gene.

This suggests that *Frigida* is a target for natural selection (Le Corre *et al.*, 2002).



In the present study, we compare variation at *Frigida* within and between 12 populations of *A. thaliana* with variation at neutral markers and quantitative variation for bolting time. Fine-scale spatial patterns of variation are described for two additional, large, polymorphic populations.

## MATERIAL AND METHODS

**Population samples:** 14 natural *A. thaliana* populations from various locations in France. Seeds were collected on 4 to 16 random plants per population, except for 2 locations (TOU, MIB), where more than 100 plants regularly spaced on a linear transect were harvested.

**Variation at *Frigida*:** a 387 bp fragment corresponding to the highly polymorphic region in exon I was sequenced in 4 to 8 individuals per population. Nine loss-of-function mutations were detected using either sequencing or allele-specific PCR assays.

**Variation at markers:** 6 CAPS (Cleaved Amplified Polymorphic Sequences) markers, distributed on all 5 chromosomes.

**Variation for bolting time:** measured in a random bloc experiment with 4 individuals per selfed family (4 to 16 families per population).

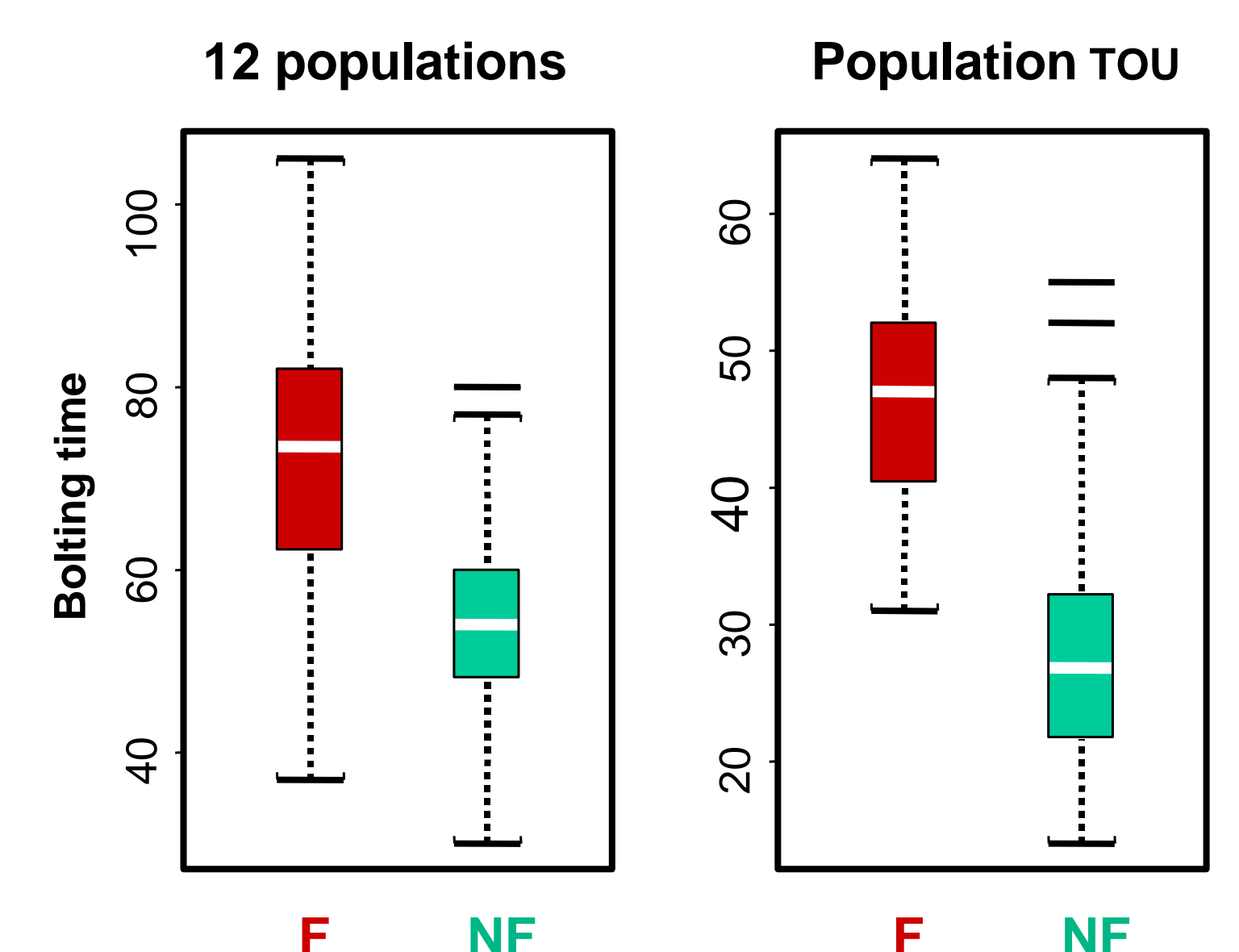
## RESULTS

### Within and between-population variability:

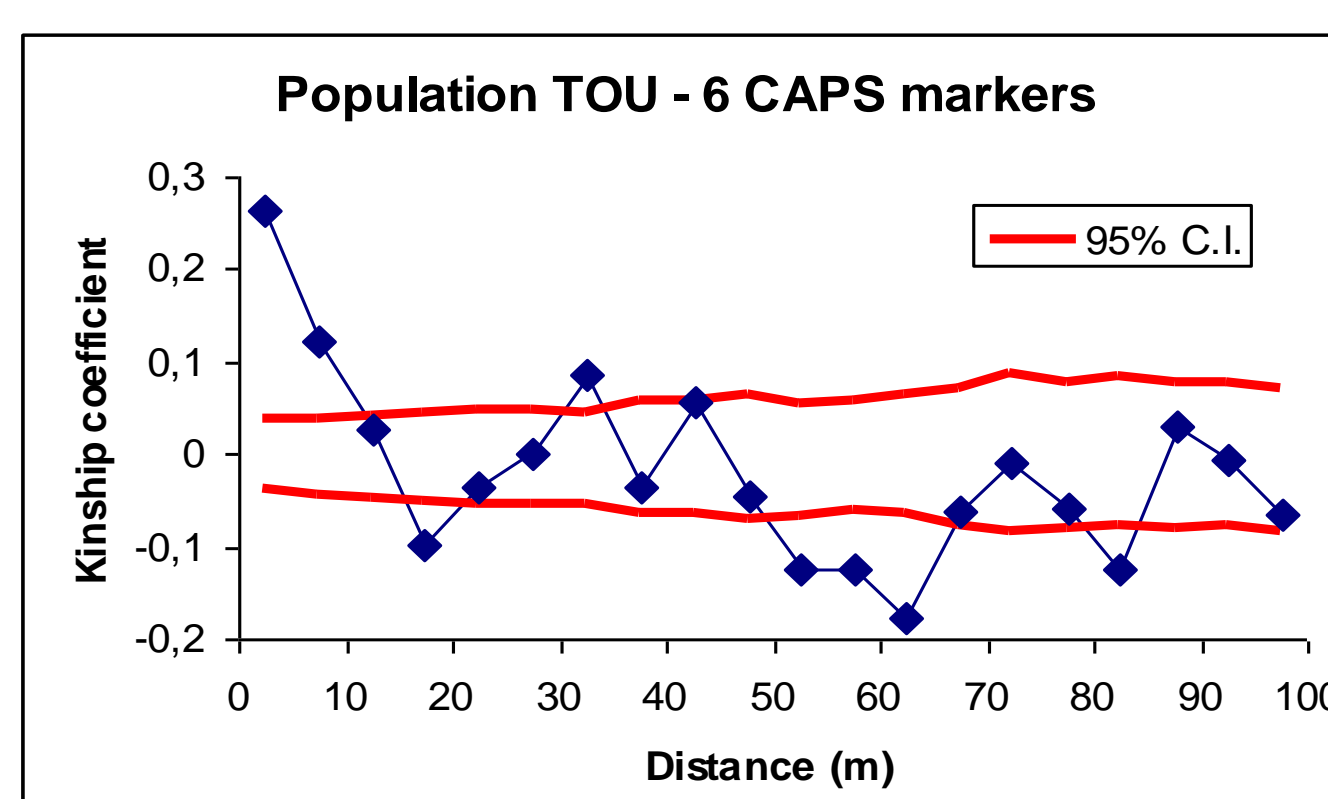
- Similar patterns are observed for CAPS markers, sequence of the 1st exon of *Frigida* and Bolting time
- Low-variability populations (A) and highly variable ones (B) are both observed
- Genetic differentiation between population is highest for the frequency of non-functional (NF) *Frigida* alleles

Population	CAPS	Frigida		Bolting time
	Hs	Nucleotide diversity	Frequency of NF alleles	Heritability
CLE	0.000	0	1	0
MAR2	0.000	0	1	0.033
FET	0.000	0	0	0.127
PYL	0.000	0	1	0.281 *
CLA	0.113	0	0	0
ALL2	0.159	0.00468	0.600	0.525 **
ROM	0.267	0.00416	0	0.721 ***
VOU	0.271	0.00698	0.714	0.686 ***
CUR	0.295	0.00334	0	0.691 ***
PAR	0.424	0.00195	0.875	0.741 ***
LAC	0.425	0.00445	1	0.74 ***
ALL1	0.445	0.00417	0	0.947 ***
TOU	0.398	0.00563	0.710	0.807 ***
MIB	0.406	- (no data)	1	0.811 ***
$F_{ST}$ :		0.598	0.592	0.820
95% C.I.		(0.531 - 0.679)		(0.617 - 0.817)

Non-functional (NF) *Frigida* alleles are associated with early-flowering.

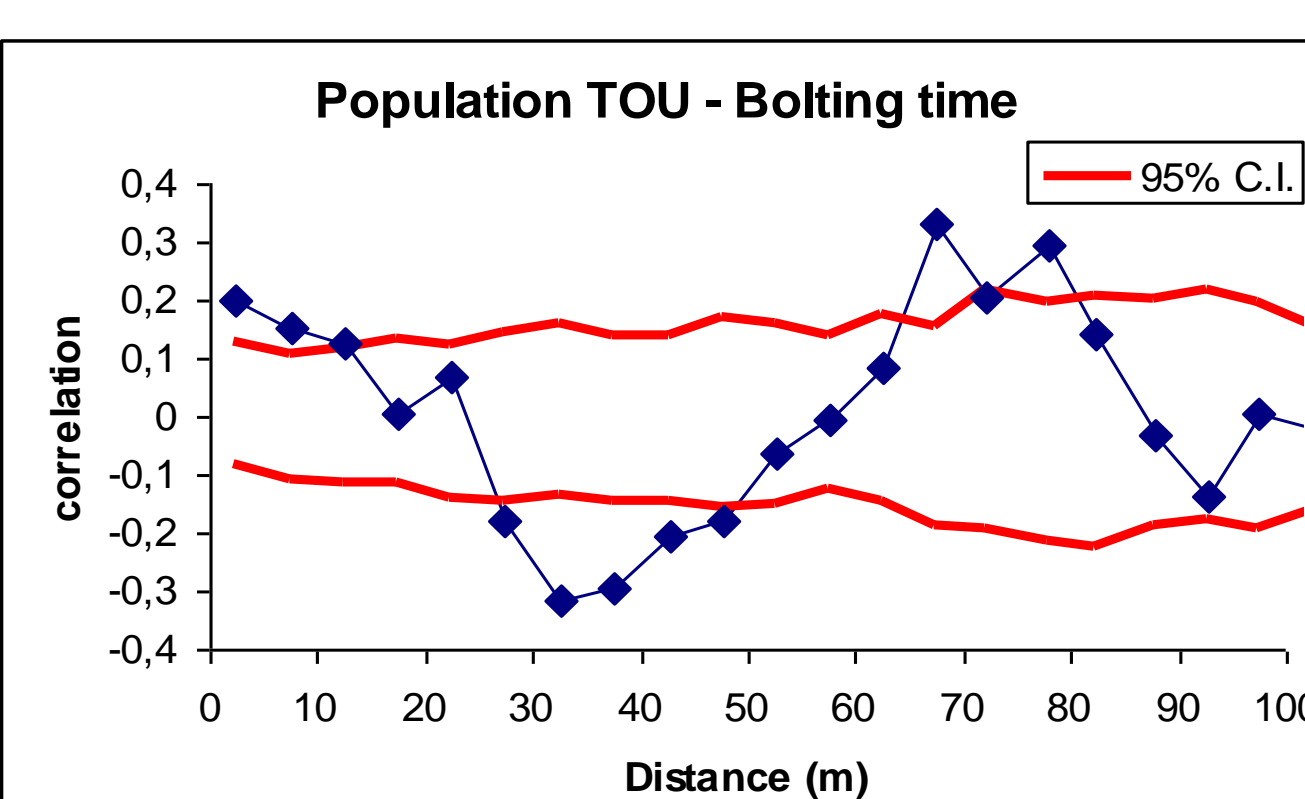
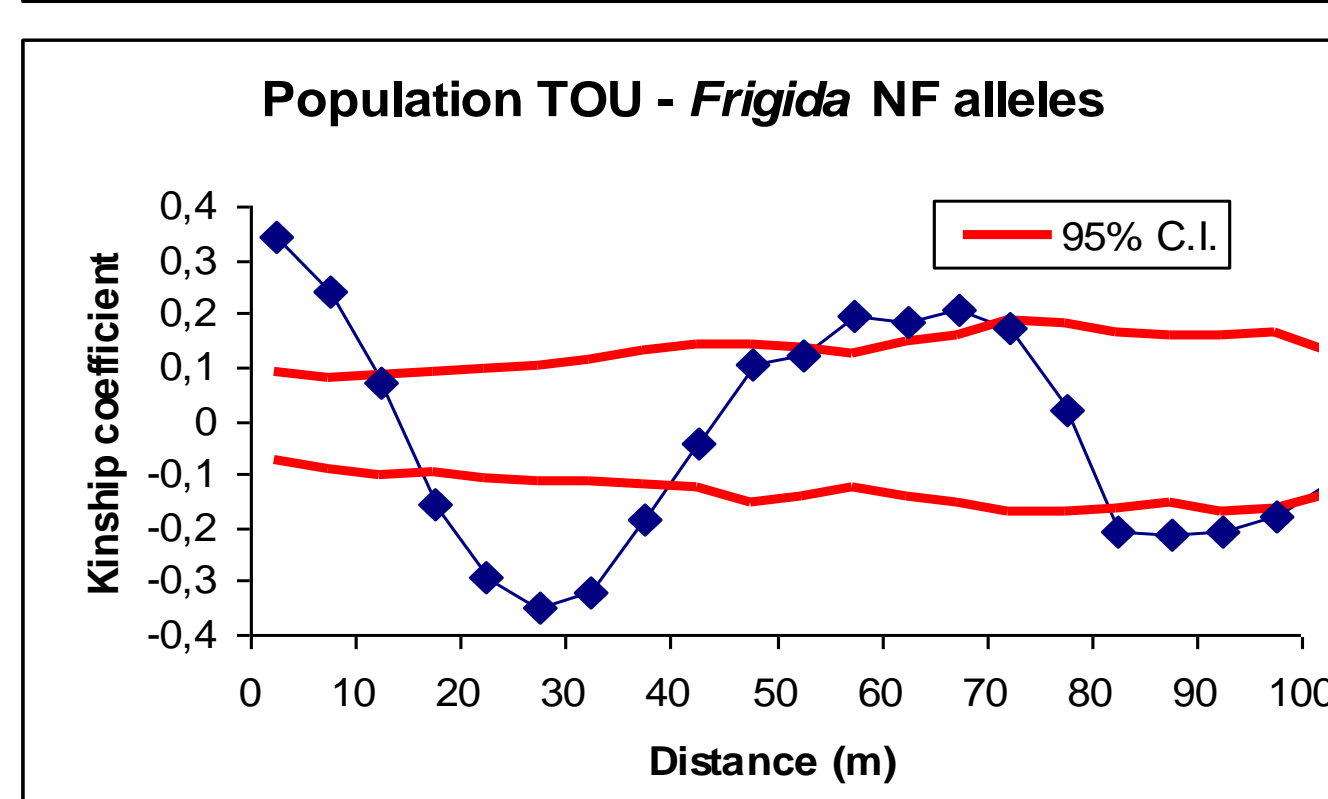


### Fine-scale spatial structure of genetic variability

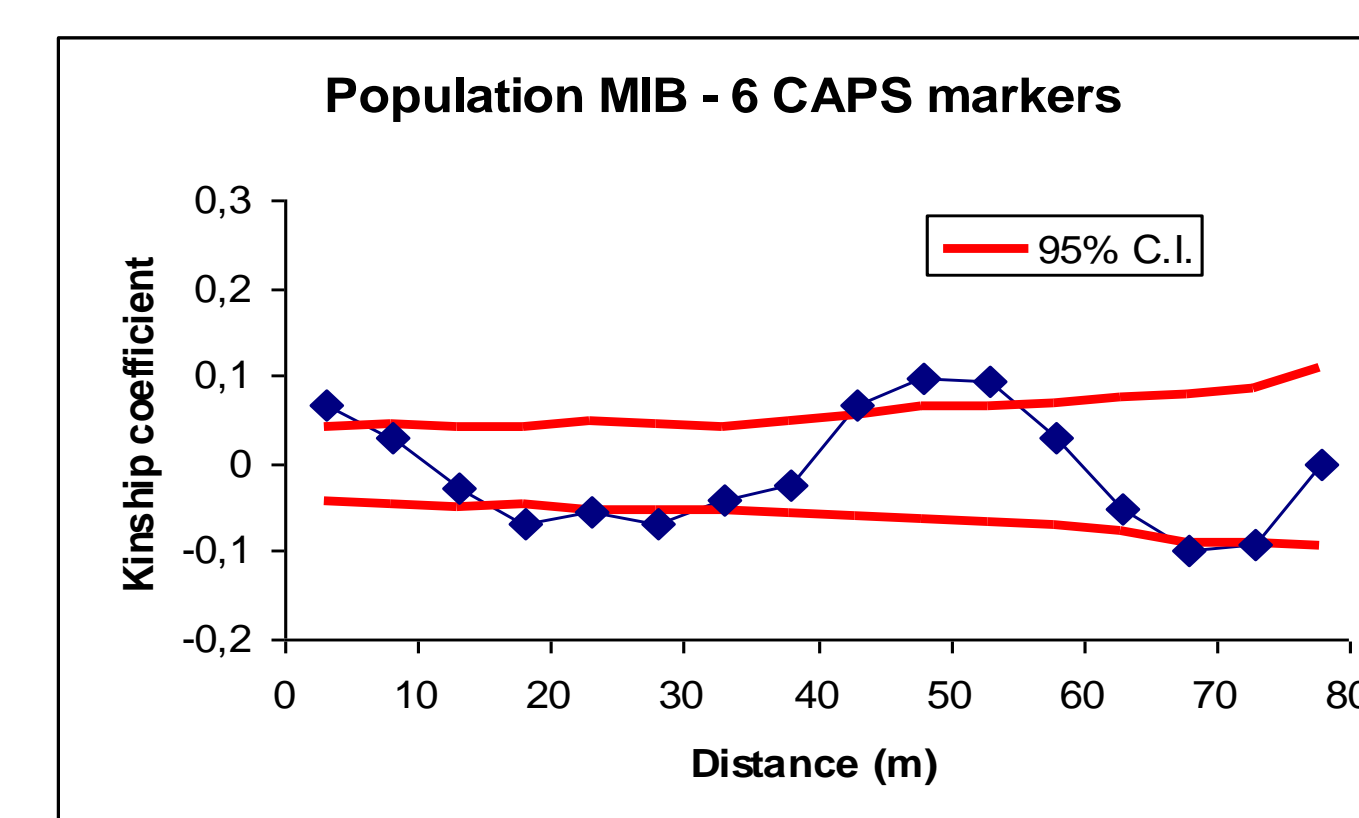


Population TOU:

- Variation at CAPS is consistent with isolation by distance; the standard deviation of gene dispersal distance estimated from the linear decrease of kinship with distance (Hardy and Vekemans, 1999) is between 1 and 2 m.

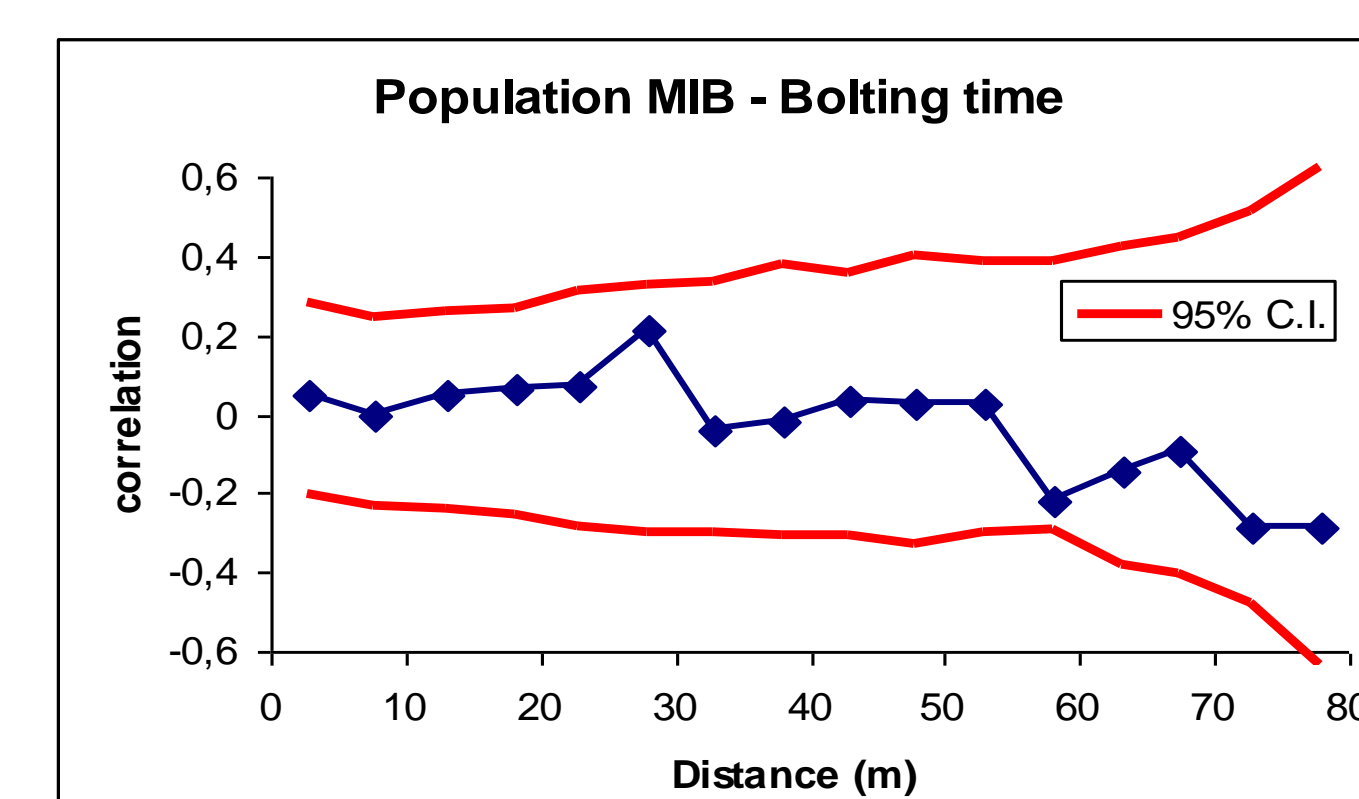


- NF alleles at *Frigida* and bolting time show similar, patchy variation, with a patch size of about 30 m.



Population MIB:

- Variation at CAPS is rather patchy, but not clear



- No spatial structure is observed for bolting time

## CONCLUSION

- “Neutral” variation : Large population to population variation in genetic diversity is consistent with metapopulation dynamics in a self-fertilizing species (Brown and Schoen, 1991). Isolation by distance may also maintain polymorphism in some populations (more likely those large and anciently founded).
- *Frigida* and bolting time : amino-acid variation at the 1st exon of *Frigida* was consistent with neutral variation. By contrast, local positive selection for flowering time probably drives the population frequency of F versus NF alleles at *Frigida*. Patchy patterns of variation suggest that adaptation to micro-scale environmental variation is perhaps also involved within some large populations.