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# Tracking adaptation to environmental changes: selfing and detection of loci under selection

Miguel Navascués

► **To cite this version:**

Miguel Navascués. Tracking adaptation to environmental changes: selfing and detection of loci under selection. *Empirisme et Théorie en Écologie et Évolution*, Sep 2015, Gif-sur-Yvette, France. hal-02792415

**HAL Id: hal-02792415**

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Submitted on 3 Mar 2021

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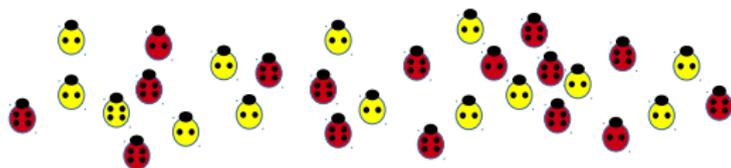
# Tracking adaptation to environmental changes: selfing and detection of loci under selection

Miguel Navascués

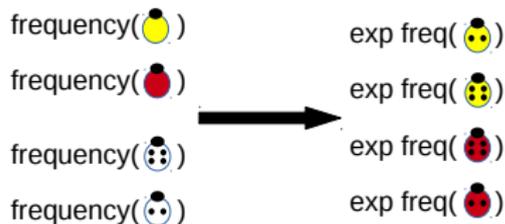
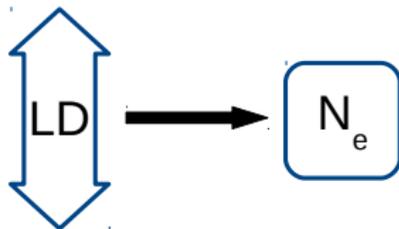
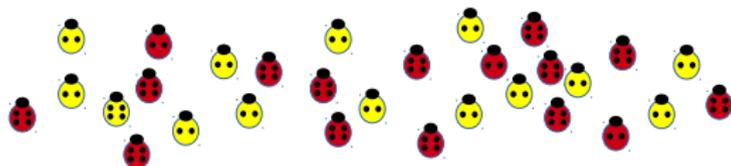
UMR CBGP (INRA Montpellier)  
Miguel.Navascues@supagro.inra.fr

30/06/2015

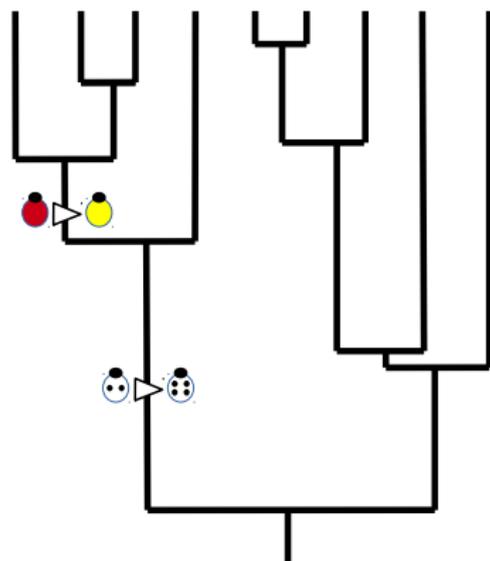
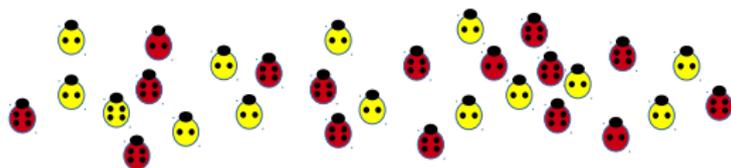
# Population genetics: sampling present generation



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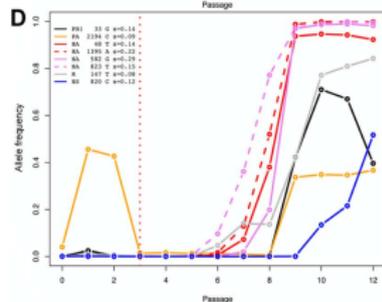
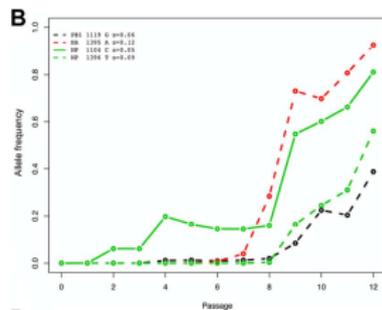
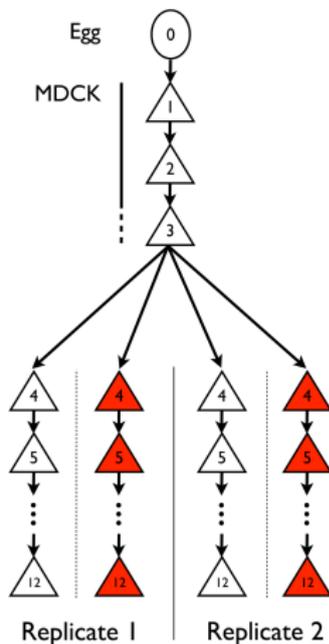


$$\Theta = 4N\mu$$

# Experimental evolution

Foll *et al.* (2014) Influenza Virus Drug Resistance

doi:10.1371/journal.pgen.1004185

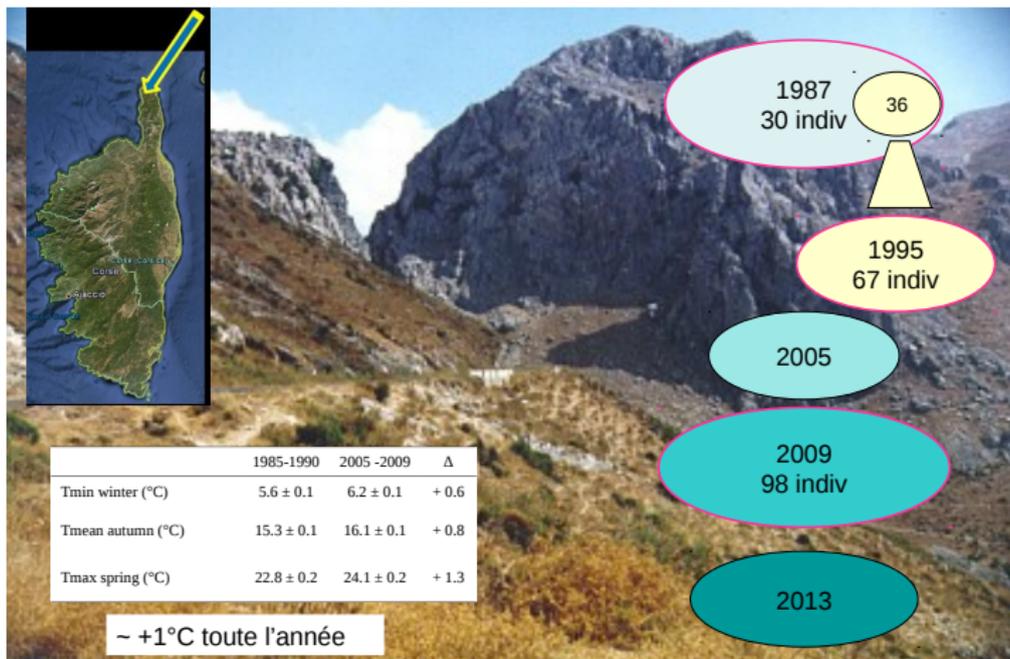


# Temporal samples in natural populations



# Medicago truncatula, Corsica

## Pop Corse F20089



# Medicago truncatula, Corsica

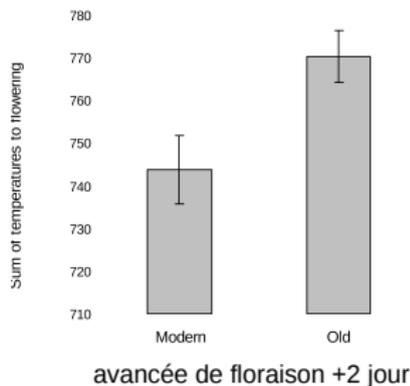
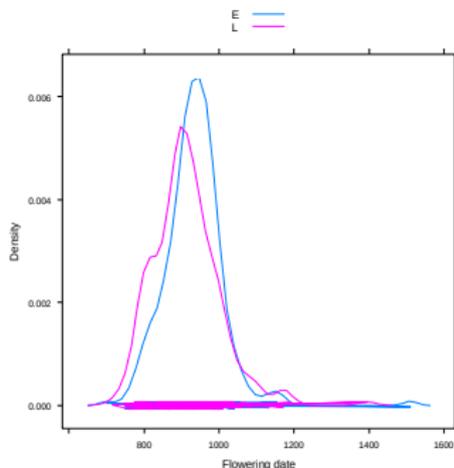
## Changement phénotypique

Mesure de la date de floraison en serre

55 individus / année ( $\sim 100$ )

5 blocs

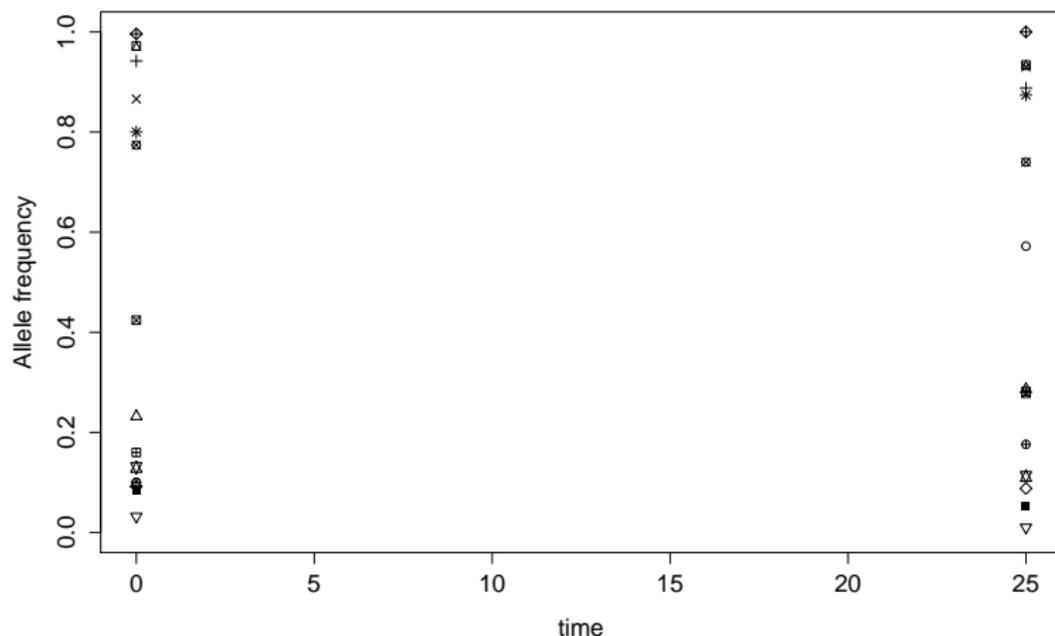
2 traitements vernalisation



# Temporal $F_{ST}$ outliers

A modified version of method proposed by Goldringer & Bataillon (2004) [doi:10.1534/genetics.103.025908](https://doi.org/10.1534/genetics.103.025908)

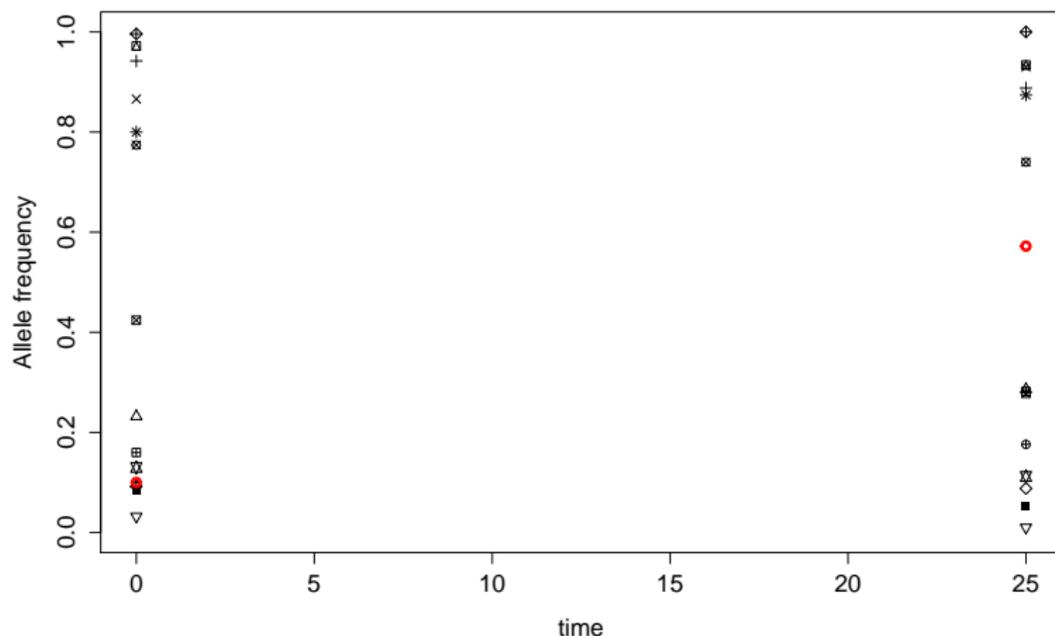
Variance in allele frequencies ( $F_C$ ) from all loci:  $\hat{N}_e$



# Temporal $F_{ST}$ outliers

A modified version of method proposed by Goldringer & Bataillon (2004) [doi:10.1534/genetics.103.025908](https://doi.org/10.1534/genetics.103.025908)

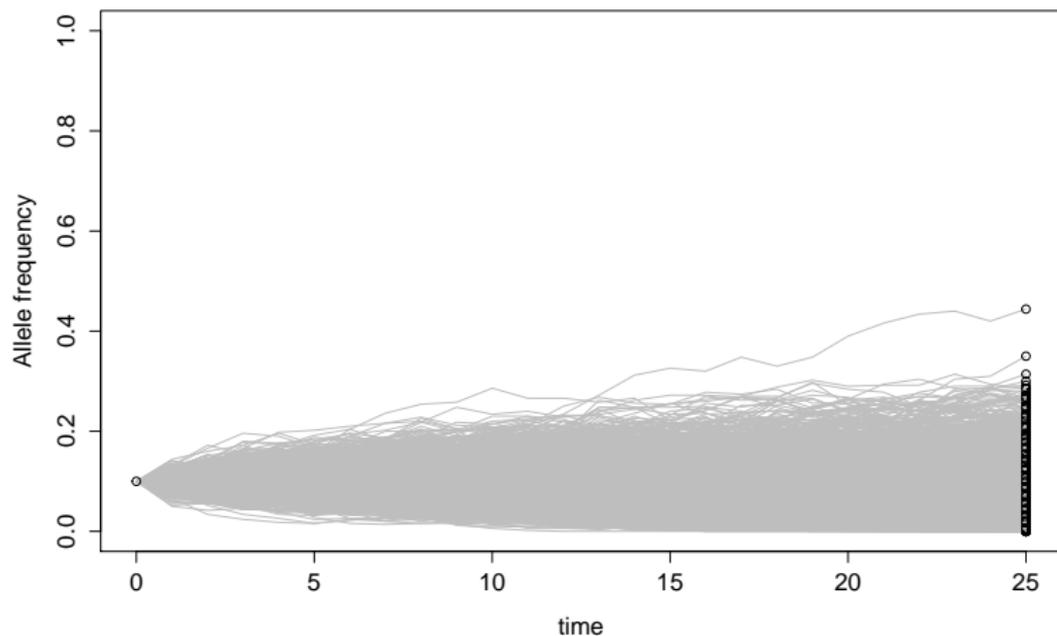
Is variance in allele frequencies ( $F_C$ ) in a focal locus compatible with  $\hat{N}_e$ ?



# Temporal $F_{ST}$ outliers

A modified version of method proposed by Goldringer & Bataillon (2004) [doi:10.1534/genetics.103.025908](https://doi.org/10.1534/genetics.103.025908)

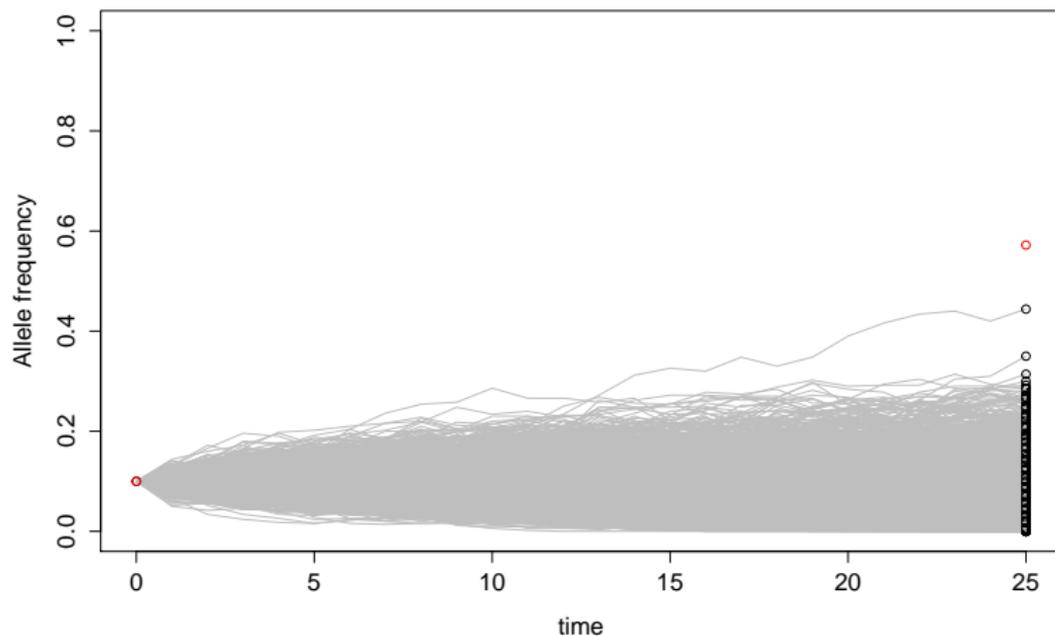
Simulation of drift from focal locus initial frequency and  $\hat{N}_e$



# Temporal $F_{ST}$ outliers

A modified version of method proposed by Goldringer & Bataillon (2004) [doi:10.1534/genetics.103.025908](https://doi.org/10.1534/genetics.103.025908)

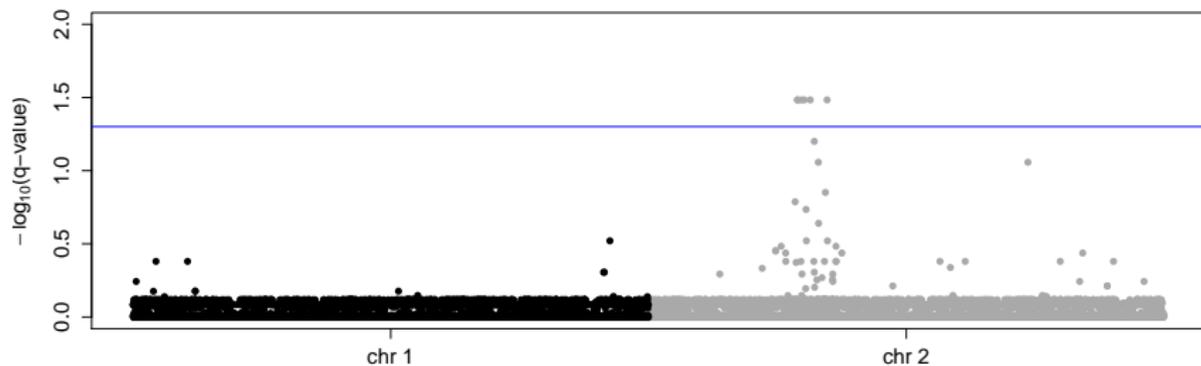
Significance of observed  $F_C$  in focal locus is evaluated from distribution



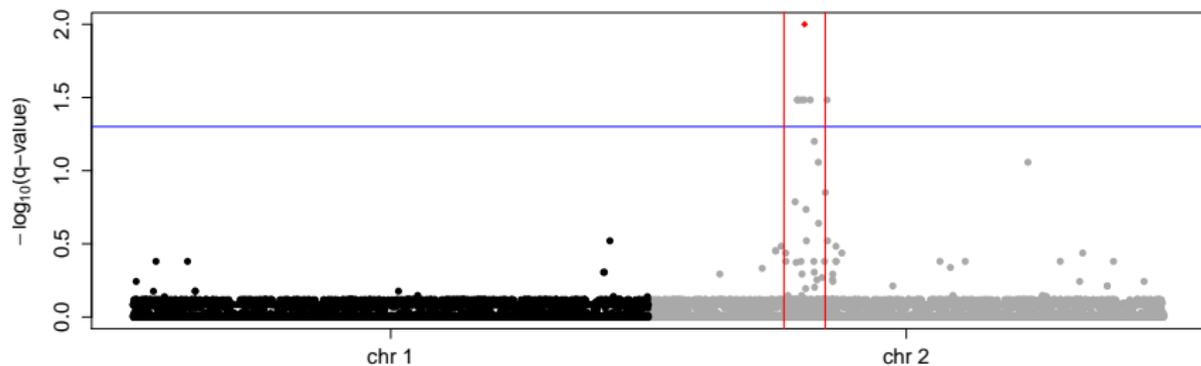
# Simulations

- Software: SLiM (Messer 2013, [doi:10.1534/genetics.113.152181](https://doi.org/10.1534/genetics.113.152181) [messerlab.org](http://messerlab.org))
- N=500 diploid individuals
- 2 chromosomes (500Mb),  $\mu=1e-8$ ,  $r=1e-8$
- Neutral period (till mutation-drift equilibrium)
- New advantageous mutation/existing allele becomes advantageous ( $s=0.5$ )
- First sample: 50 diploid individuals
- Selection period (25 generations)
- Second sample: 50 diploid individuals
- 10000 polymorphic SNP loci are studied

# Manhattan plot: results from a single simulation replicate

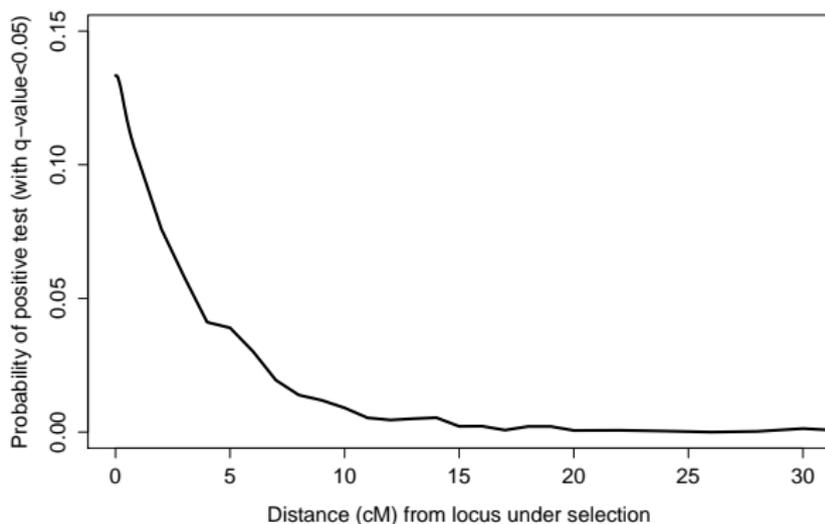


# Manhattan plot: results from a single simulation replicate



# Power and False Positive Rate

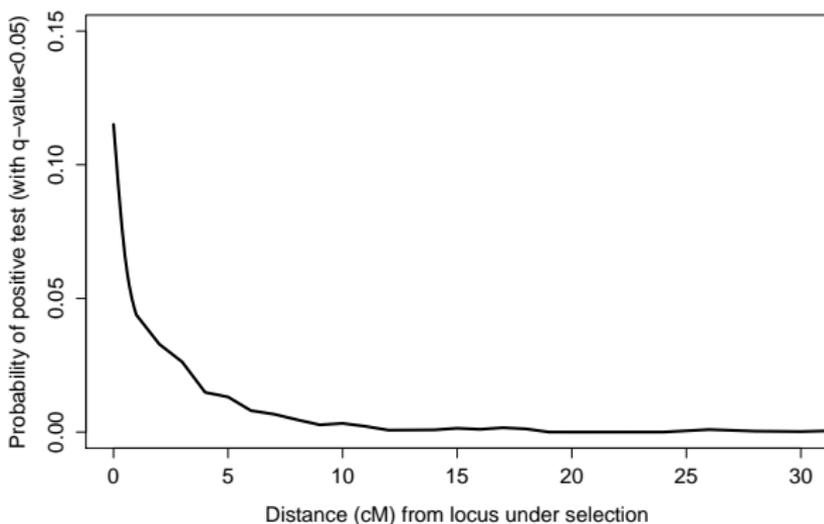
Selection on new mutation  
 $W = 1.00, FPR = 1.46 \times 10^{-4}$



# Power and False Positive Rate

Selection on standing variation

$$W = 0.61, FPR = 2.92 \times 10^{-4}$$

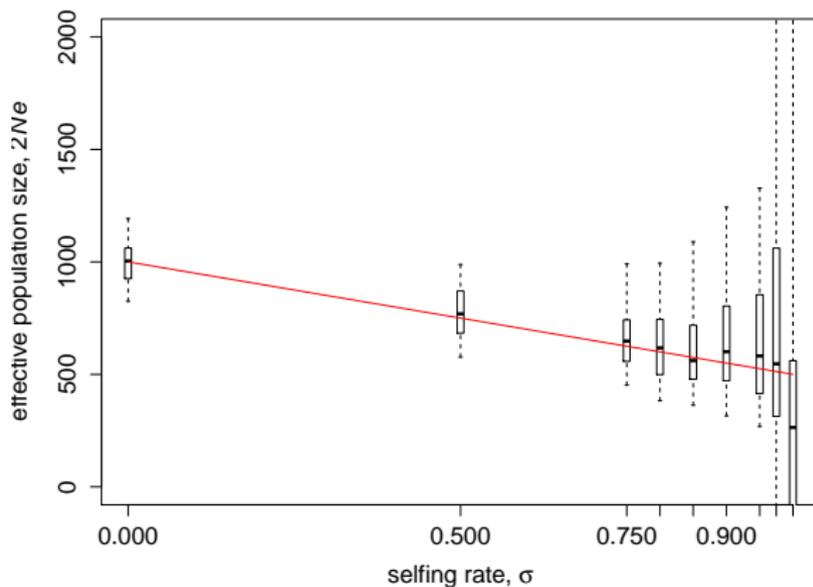


# Consequences of selfing

- Reduction of effective population size
- Increase of homozygosity
  - ▶ reduction of effective recombination
  - ▶ increased LD
  - ▶ hitchhiking

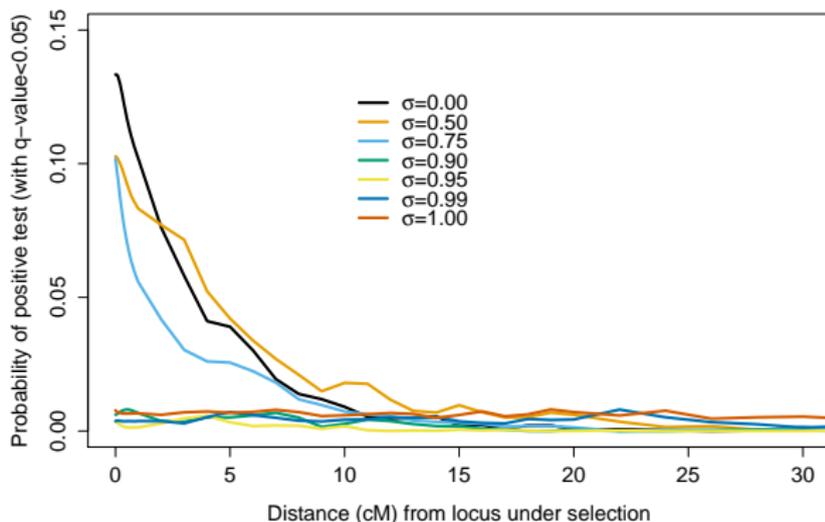
# Effective population size

## Neutral scenario



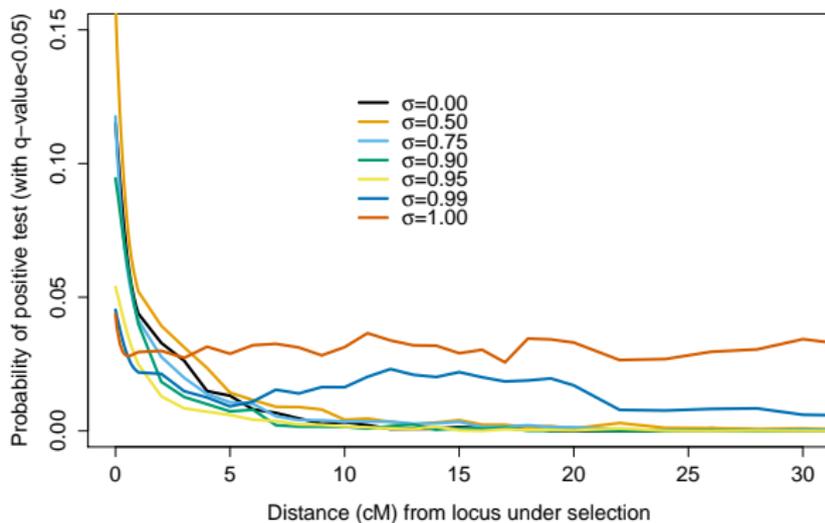
# Power and False Positive Rate

## Selection on new mutation



# Power and False Positive Rate

## Selection on standing variation



# Conclusions

- Temporal  $F_{ST}$  outlier approach can detect regions under selection (parameter combination studied)
- Footprint of selection in a  $\sim 20\text{cM}$  region (parameter combination studied)
- Selfing reduces power ( $0.75 < \sigma < 0.90$ )
- Increase of false positives with selfing is not very problematic ( $FPR < 0.05$ )

# Acknowledgements

- Comité d'organisation ETEE 2015 - Empirisme et Théorie en Écologie et Évolution
- Collaborators:
  - ▶ Arnaud Becheler (currently at UMR EGCE, Gif-sur-Yvette) & Renaud Vitalis: Evaluation of temporal  $F_{ST}$  outlier method
  - ▶ Laurène Gay & Joëlle Ronfort (UMR AGAP): *Medicago truncatula*
- Project SelfAdapt funded by Métaprogramme ACCAF (INRA)

# Images

- Figures 1 and 3 from Foll *et al.* (2014). CC BY  
[doi:10.1371/journal.pgen.1004185](https://doi.org/10.1371/journal.pgen.1004185)
- Photos of Corsican sampling site and common garden experiments provided by Laurène Gay
- Signs. Public domain ([Wikimedia Commons](#))

## Abstract

In a single isolated populations, allele frequencies will change through time subject to the processes of selection (acting on specific loci) and genetic drift (acting on the whole genome). Genetic data collected at different times can be used to make inferences on the effective population size (i.e. strength of drift) and to detect outlier loci, whose changes in allele frequencies are unlikely to be only the product of the inferred demography. However, the presence of self-fertilization may pose a problem for the detection of loci under selection. Selfing reduces the effective size of populations and the effective recombination among loci (promoting hitch-hiking). We investigated the effect of the presence of partial selfing reproduction in the power and false discovery rate for the detection of selected loci. In addition, we characterized the footprint of selection along the chromosome containing the selected site.