

# Negative selection and polygenic adaptation in maritime pine

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# Single genes vs. polygenic adaptation

## MOLECULAR ECOLOGY

Molecular Ecology (2012) 21, 1548–1566

doi: 10.1111/j.1365-294X.2012.05479.x

### INVITED REVIEWS AND META-ANALYSES

#### The genetic differentiation at quantitative trait loci under local adaptation

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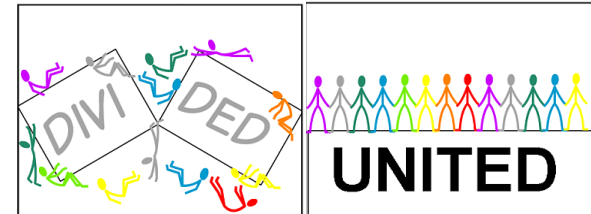
Heredity

Heredity (2012), 1–11  
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www.nature.com/hery

### ORIGINAL ARTICLE

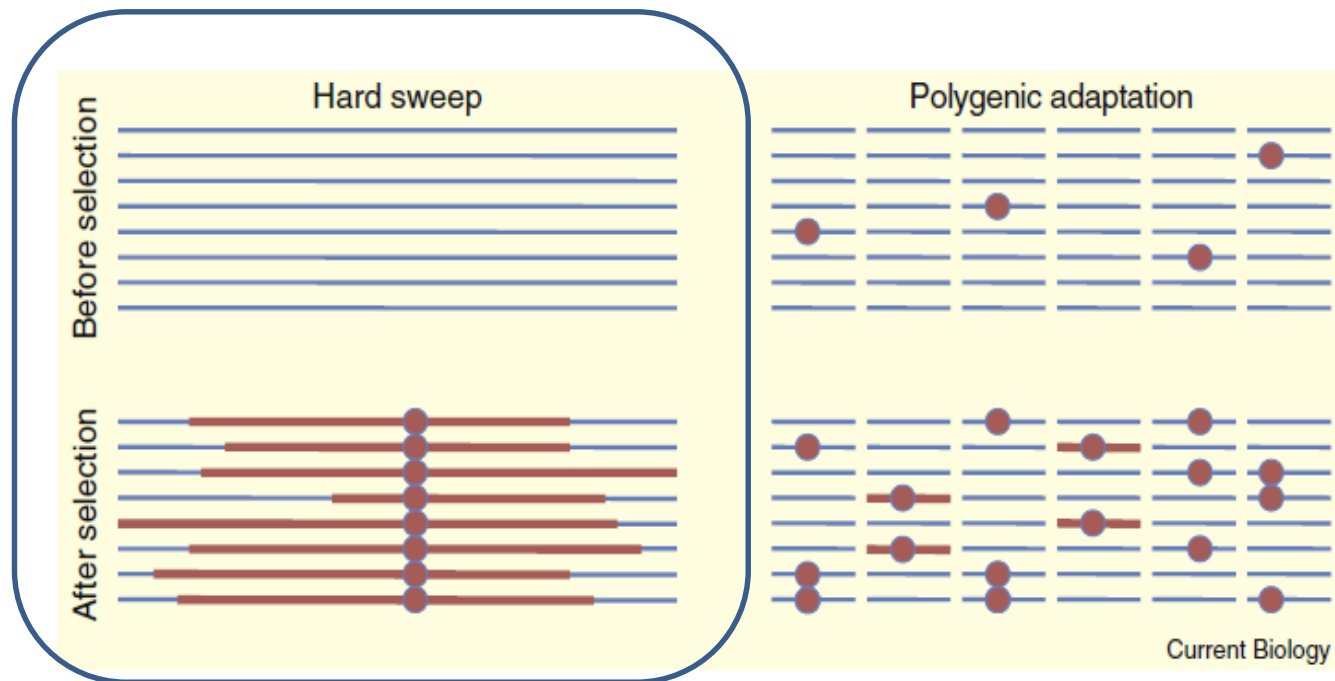
#### Decoupling of differentiation between traits and their underlying genes in response to divergent selection

A Kremer<sup>1,2</sup> and V Le Corre<sup>3</sup>



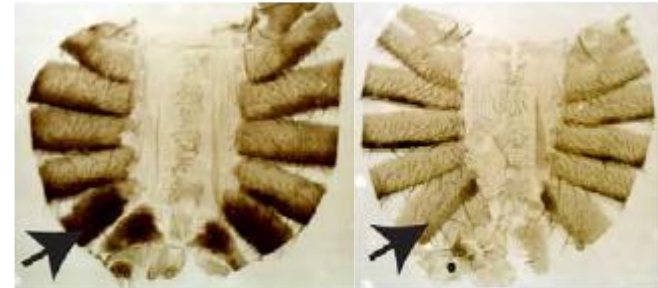
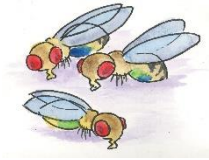
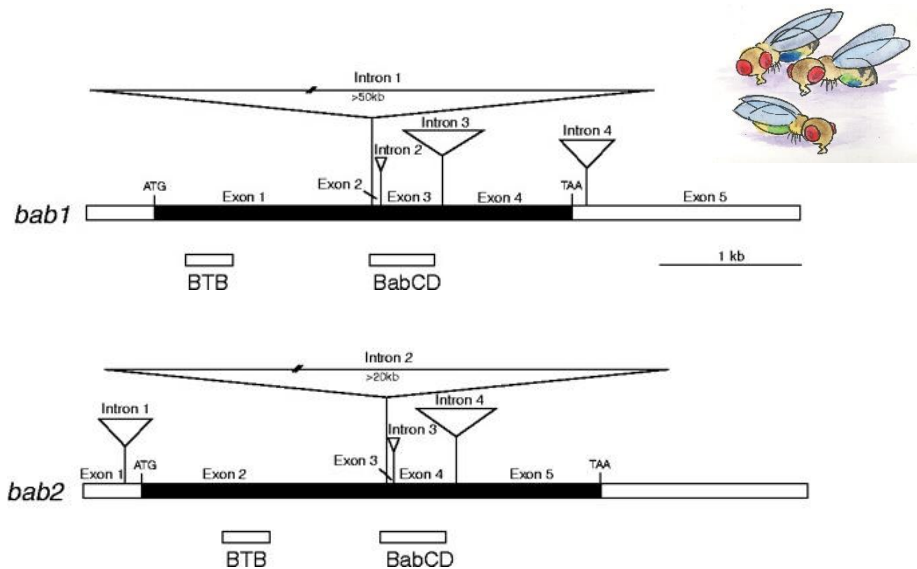
Polygenic traits controlled  
by small effect SNPs

Most methods  
are designed  
to detect hard  
sweeps



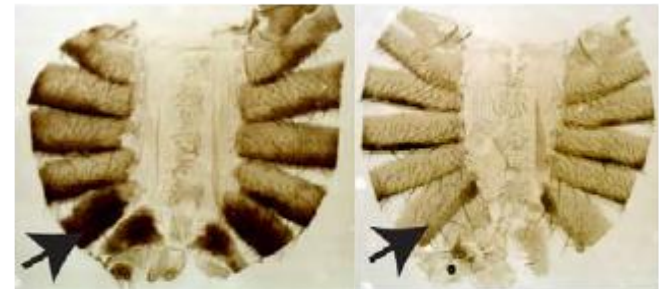
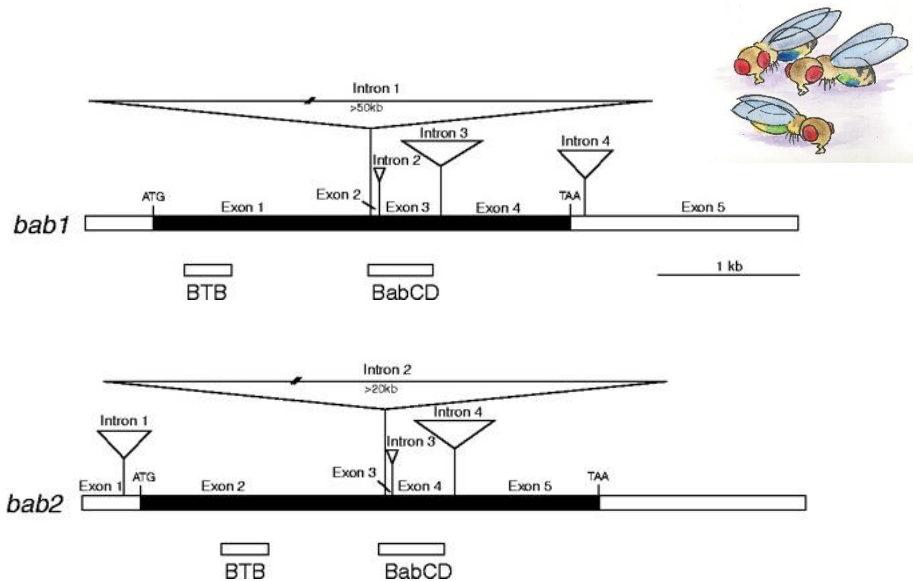
Pritchard et al. (2010) *Current Biology*

# Case study from Remington 2015 *Evolution*



The ***bab*** locus is responsible for a major effect QTL involving 60% of the variation in female abdominal pigmentation in *D. melanogaster*



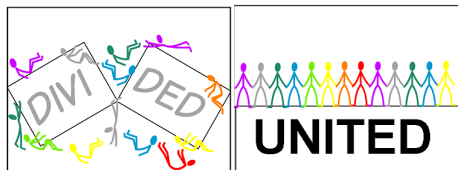


The *bab* locus is responsible for a major effect QTL involving 60% of the variation in female abdominal pigmentation in *D. melanogaster*, but single SNPs explain each <1% of variation, making them basically undetectable by standard GWAS

Bickel et al. (2011) *PLoS Genetics*

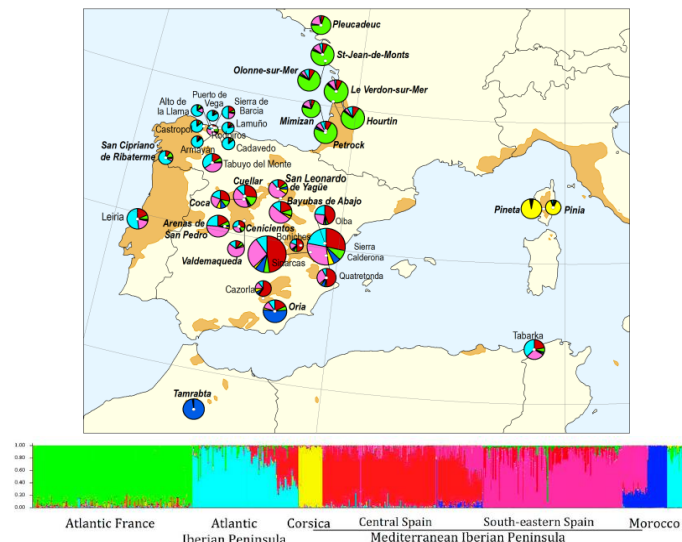
**Table 1.** Estimation of polymorphism and region effect size.

	Number of sites	Average effect size of each polymorphism	Proportion of total variation explained by average polymorphism	Total estimated effect of region	Proportion of total variation explained
Region 1	55	0.80 (.19)	0.009	44	0.512
Region 2	21	0.97 (.28)	0.011	20.37	0.237
Region 3	29	1.02 (.30)	0.012	29.58	0.344
All 3 regions	105	0.69 (.10)	0.008	72.45	0.842



# Maritime pine (*Pinus pinaster* Aiton)

Strong population genetic structure with **six large gene pools** and complex patterns of gene flow and **local adaptation**

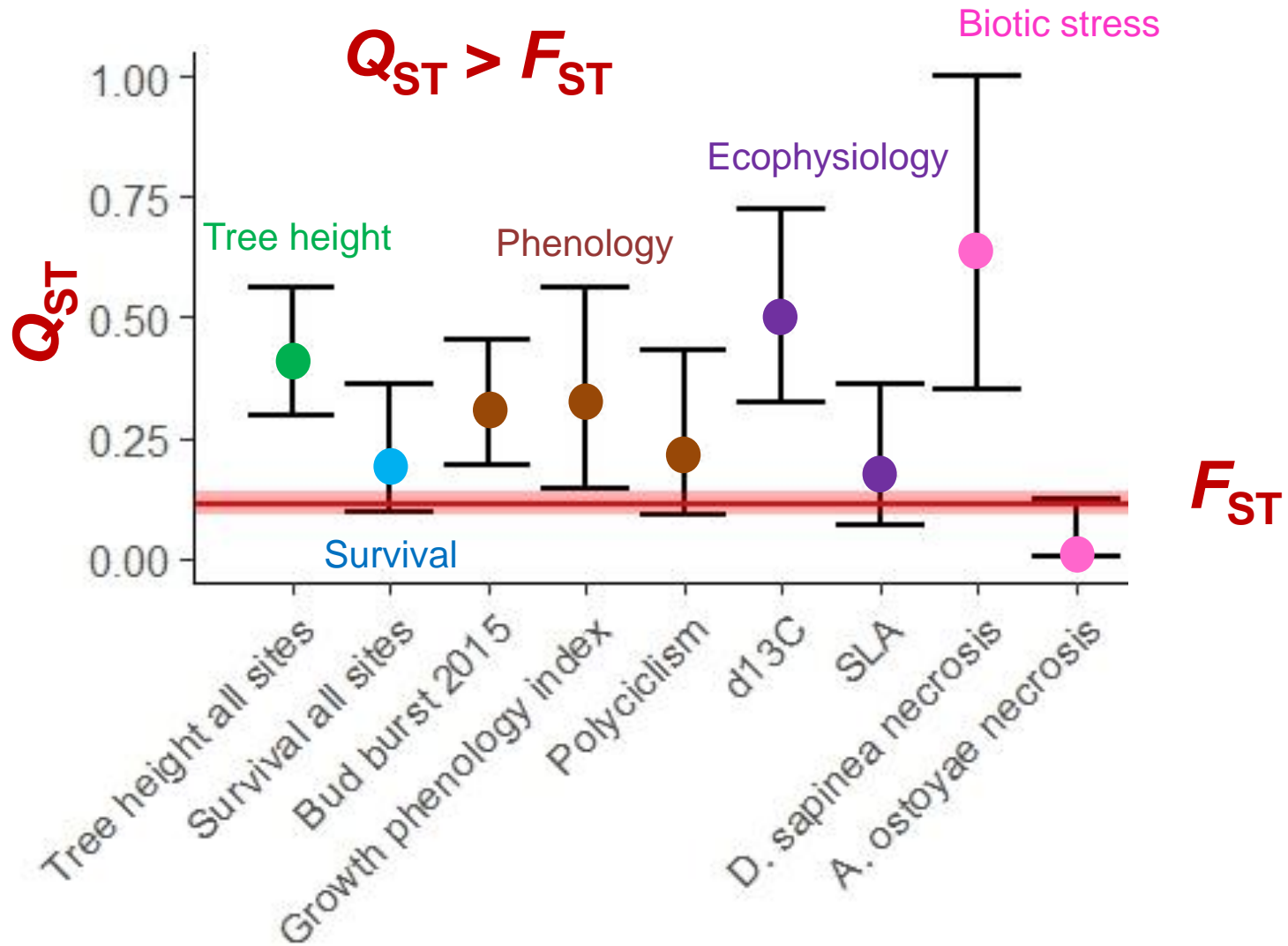


Jaramillo-Correa et al. (2015) *Genetics*

## CLONAPIN trial network

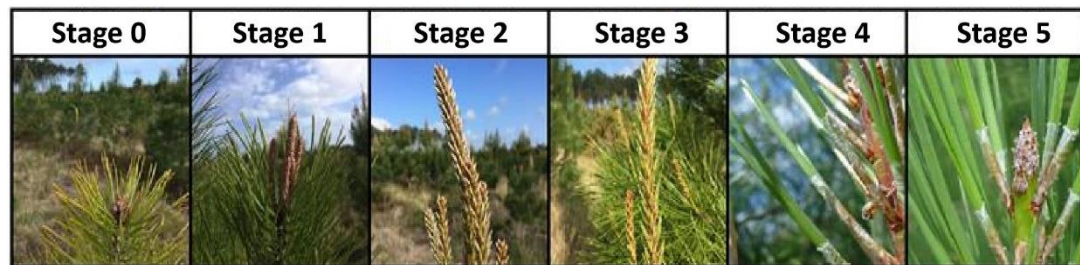
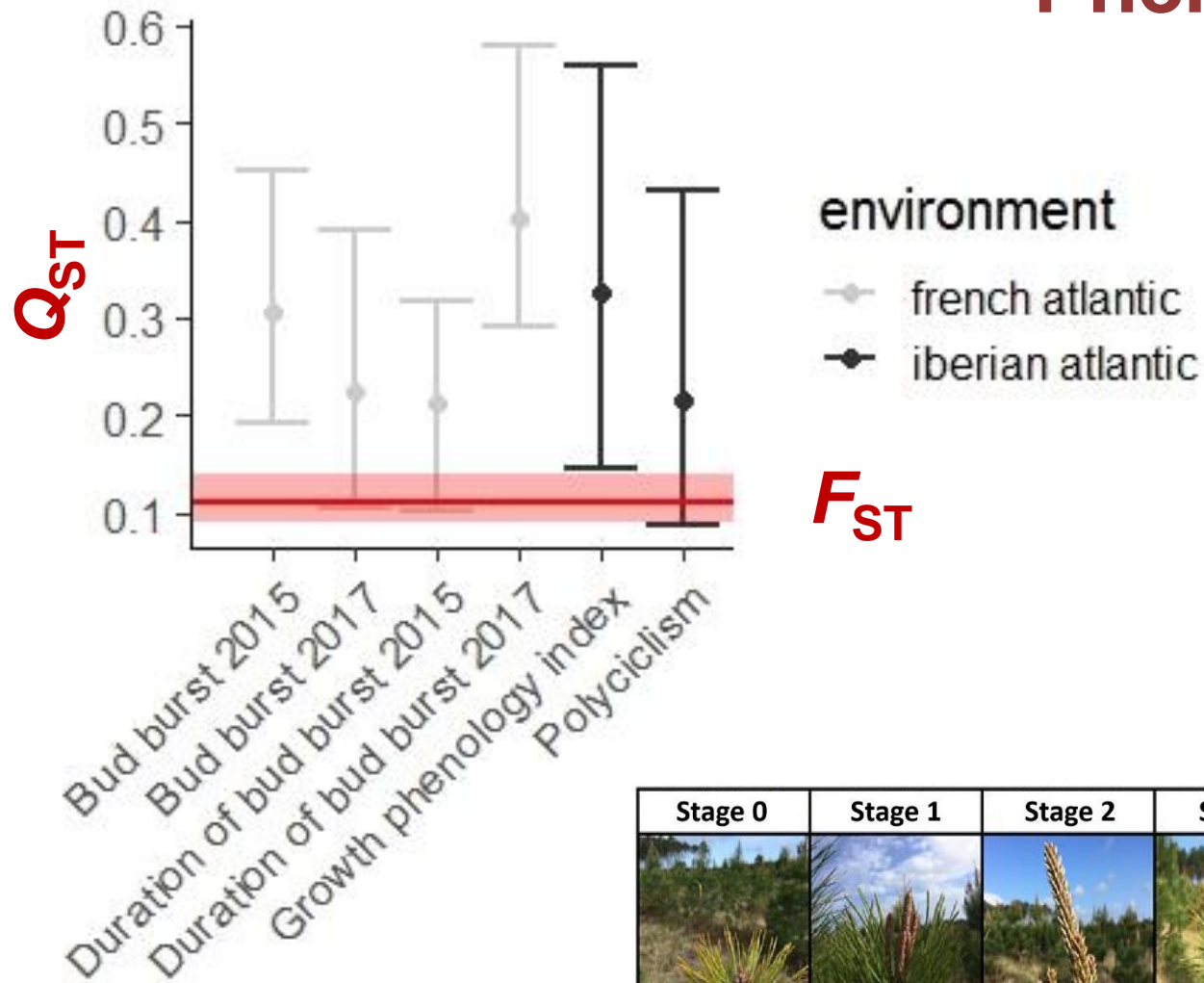
- 26,000 trees phenotyped (650 clones) in 5 common gardens in contrasted environmental conditions
- 6,100 SNPs (*Infinium* assay)
- Several phenotypic traits measured, including height, survival, phenology and response to pathogens and pests

# Evidence for local adaptation from CLONAPIN common gardens



But as always in biology, it is not simple...

## Phenology



# How to look to polygenic adaptation?

*The Annals of Applied Statistics*

2011, Vol. 5, No. 3, 1780–1815

DOI: 10.1214/11-AOAS455

© Institute of Mathematical Statistics, 2011

## Bayesian Variable Selection Regression (BVSr)

### BAYESIAN VARIABLE SELECTION REGRESSION FOR GENOME-WIDE ASSOCIATION STUDIES AND OTHER LARGE-SCALE PROBLEMS

BY YONGTAO GUAN AND MATTHEW STEPHENS<sup>1</sup>



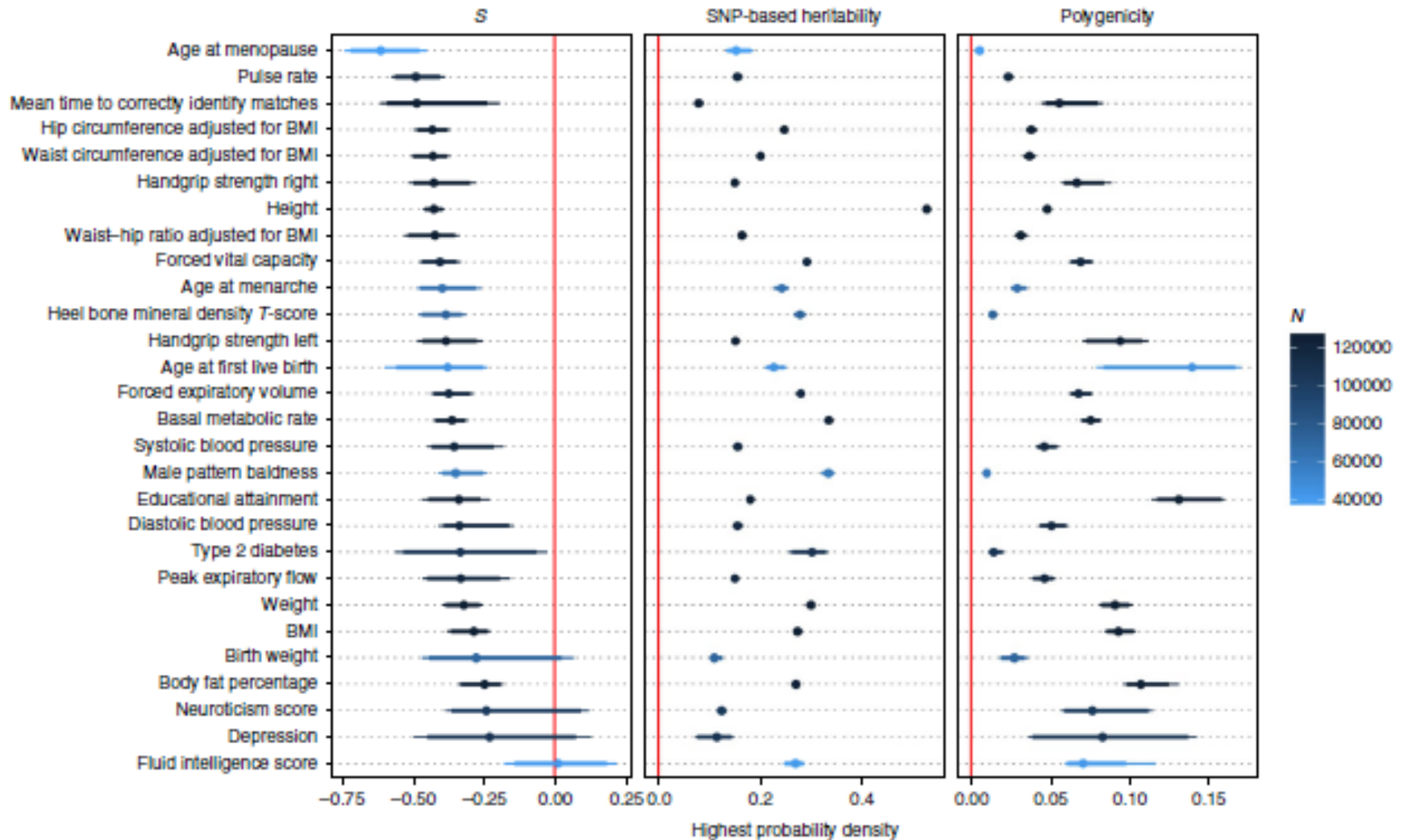
### Signatures of negative selection in the genetic architecture of human complex traits

Jian Zeng<sup>1</sup>, Ronald de Vlaming<sup>1,2,3</sup>, Yang Wu<sup>1</sup>, Matthew R. Robinson<sup>1,4</sup>, Luke R. Lloyd-Jones<sup>1</sup>,  
Loic Yengo<sup>1</sup>, Chloe X. Yap<sup>1</sup>, Angli Xue<sup>1</sup>, Julia Sidorenko<sup>1,5</sup>, Allan F. McRae<sup>1</sup>, Joseph E. Powell<sup>1</sup>,  
Grant W. Montgomery<sup>1</sup>, Andres Metspalu<sup>5</sup>, Tõnu Esko<sup>5</sup>, Greg Gibson<sup>6</sup>, Naomi R. Wray<sup>1,7</sup>,  
Peter M. Visscher<sup>1,7</sup> and Jian Yang<sup>1,7\*</sup>

Bayesian mixed linear model (BLM), including also the relationship  
between SNP effect size and minor allele frequency (S)



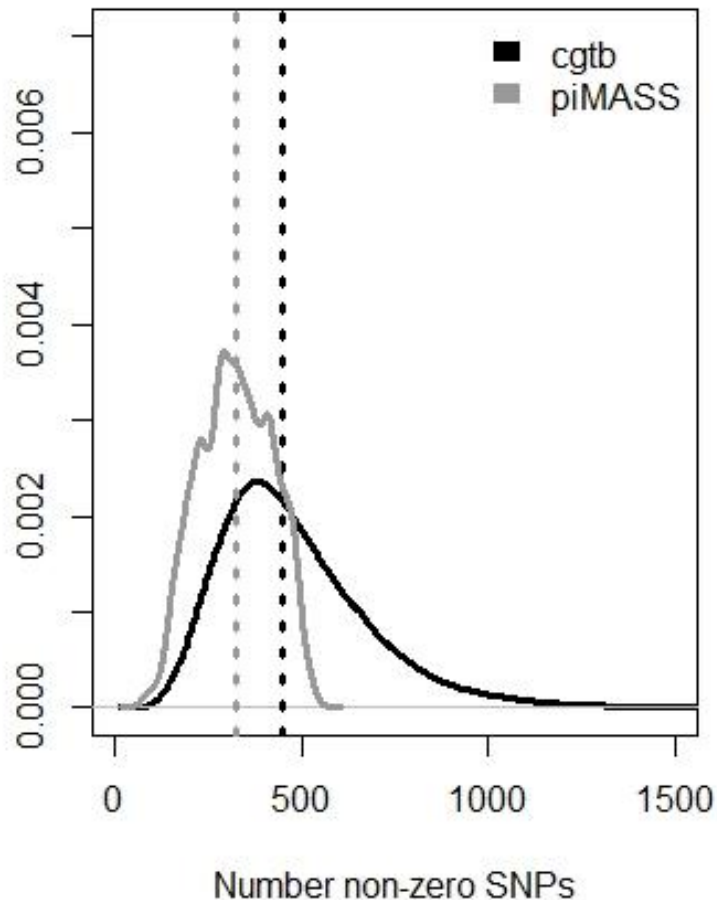
# How does it look in humans?



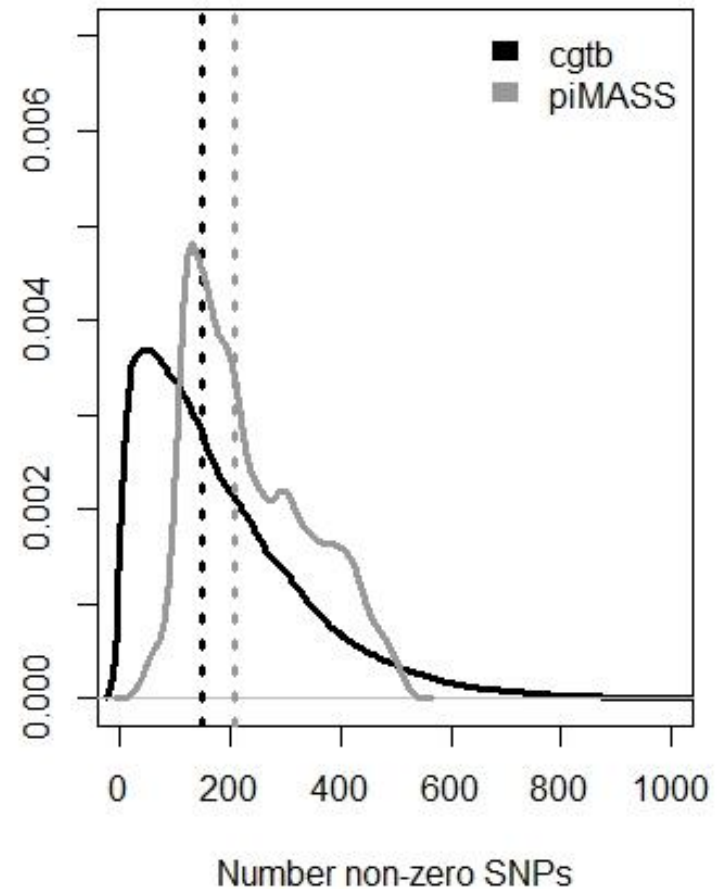
## And in maritime pine?

BVSR and BLM methods agree for most traits!

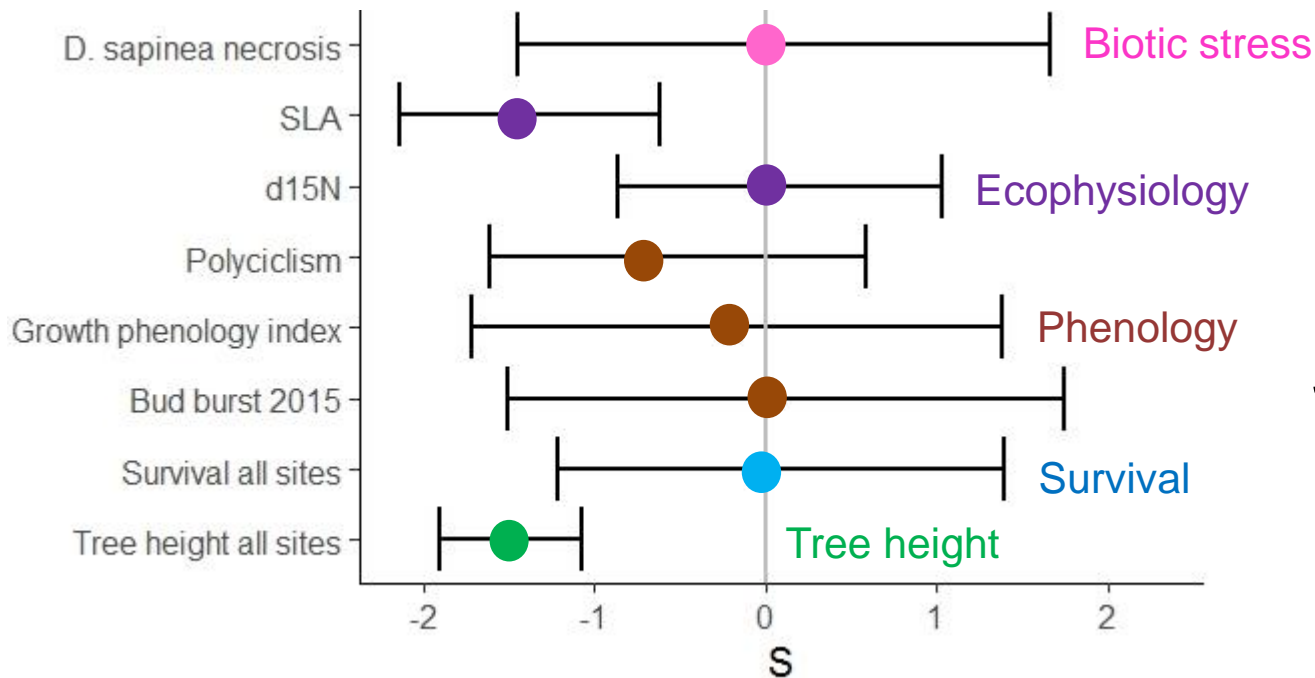
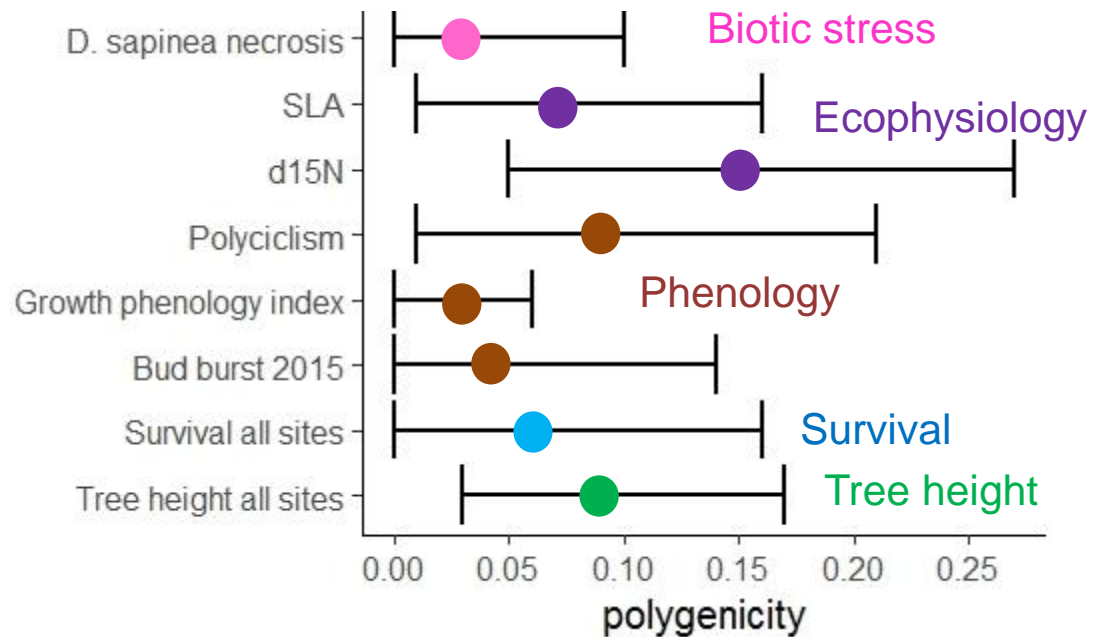
Tree height



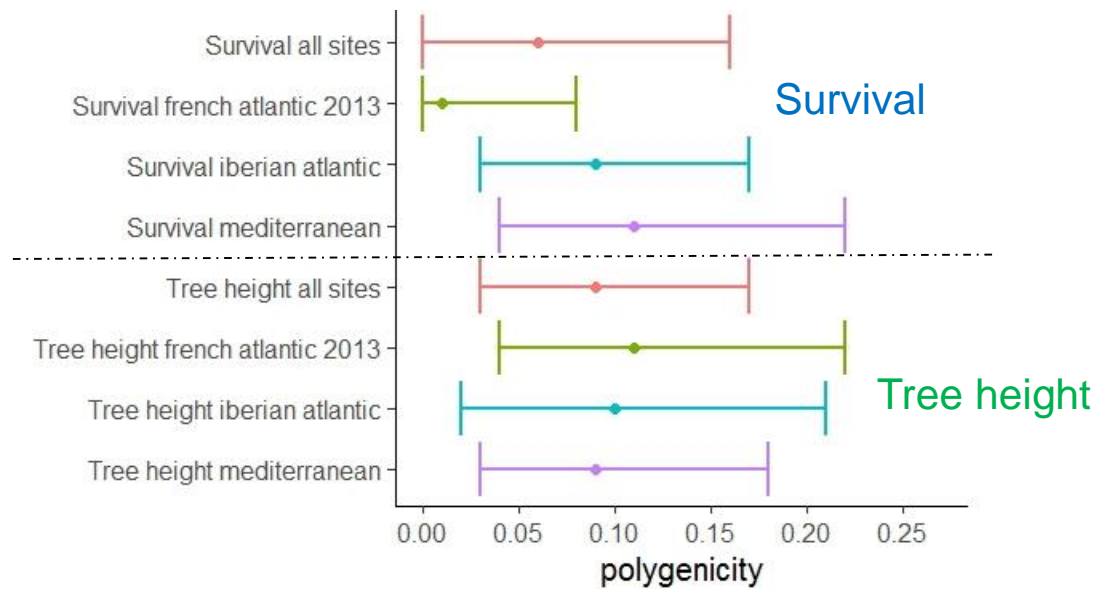
Biotic stress



Polygenicity  
values around  
5-10%

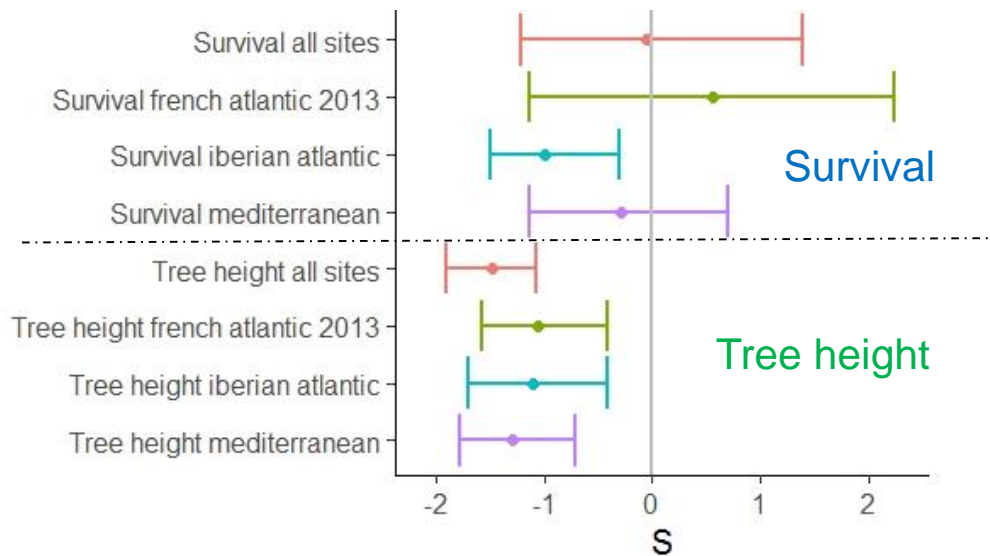


Negative  
selection is  
important for  
SLA and tree  
height



## environment

- all sites
- french atlantic
- iberian atlantic
- mediterranean



Polygenicity and negative selection are variable **across traits**, but remarkably **not across environments**



## Conclusions and perspectives

- Levels of polygenicity are high, with **over 5-10% of SNPs having non-zero effects**, and vary across traits, but not across environments (indicating similar genetic architecture)
- New methods to study **polygenic adaptation at gene and pathway level** can potentially increase our understanding on how trees adapt to a changing environment (but we need more data for GWAS!)
- Negative selection is relevant for some main adaptive traits

## What's next?

*Large common garden for Corsican populations of maritime pine (900 families from 30 populations) that has been genotyped for over 100k SNPs using sequence capture methods*

*Tree height, survival, phenology and carbon discrimination data already available*





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# Thanks so much for your attention!

*And special thanks to EVOLTRE NoE/ERG  
where all this work started*



[www.evoltree.org](http://www.evoltree.org)

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