



Is local adaptation driven by polygenic selection in a Mediterranean conifer?

Marina de Miguel^{1§}, Isabel Rodríguez-Quilón^{2§}, Ricardo Alía², Andrew J. Eckert^{3*}, Santiago C. González-Martínez^{1*}

1/ BIOGECO, INRA, Univ. Bordeaux, 33610, Cestas, France; **2/** INIA-CIFOR, Ctra. de la Coruña km 7.5, 28040, Madrid, Spain; **3/** Department of Biology, Virginia Commonwealth University, Richmond, VA 23284, USA

§ These authors contributed equally; * Shared senior authors



Introduction

Under the current climate change scenario, there is growing interest to understand the genetic basis of adaptive traits in forest tree species. Identifying signatures and target genes of local adaptation in trees could help us predict the future of forests.

In forest trees, most traits related to adaptation are polygenic [1].

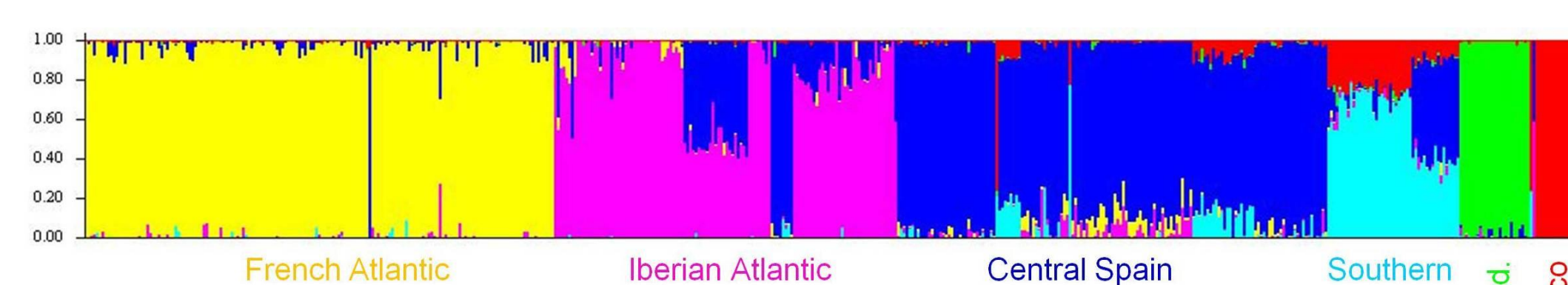
Objective

To test polygenic models in maritime pine (*Pinus pinaster* Ait.) by combining quantitative trait data from common gardens and molecular approaches.

Advantages

High genetic diversity
Big population sizes
Contrasting habitats

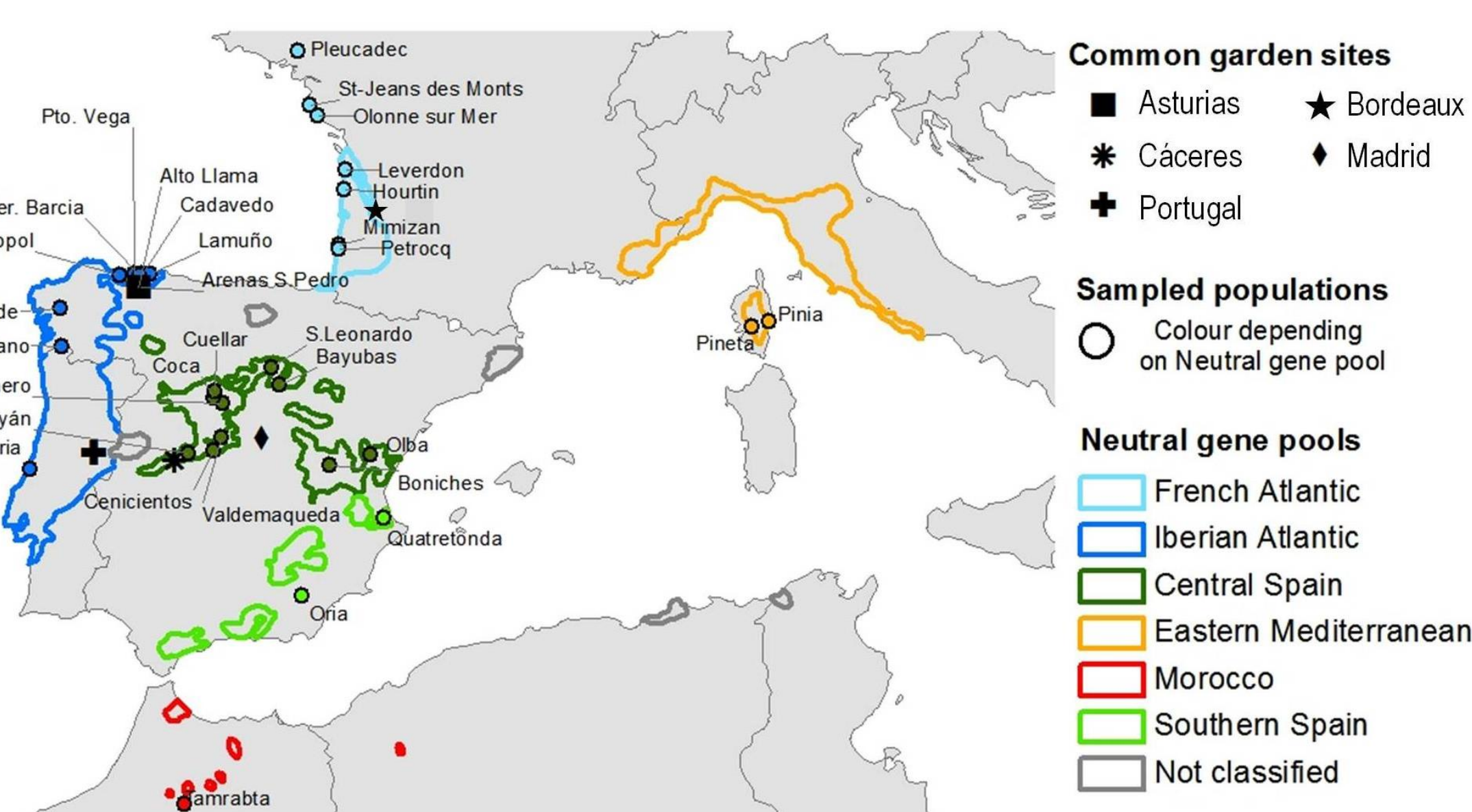
P. pinaster as study species



Challenges

Long-lived organisms
Long generation times

Strong population genetic structure



CLONAPIN trial network

- ✓ 26,000 trees phenotyped (650 clones)
- ✓ 32 populations
- ✓ 5 common gardens in contrasted environmental conditions
- ✓ 6,100 SNPs (*Infinium* assay)
- ✓ Phenotyping for fitness-related traits



A method using information from association and population genetics:

Berg & Coop 2014 [2]

Results:

height of trees / two common gardens: Asturias (Atlantic env.) and Madrid (Mediterranean env.)/3 functional groups of SNPs (cell growth & death, cytoskeleton & pathogen interaction)

Comparisons of Q_{ST} vs F_{ST} show clear adaptive differentiation for height in the different testing environments and for both main gene pools and local populations.

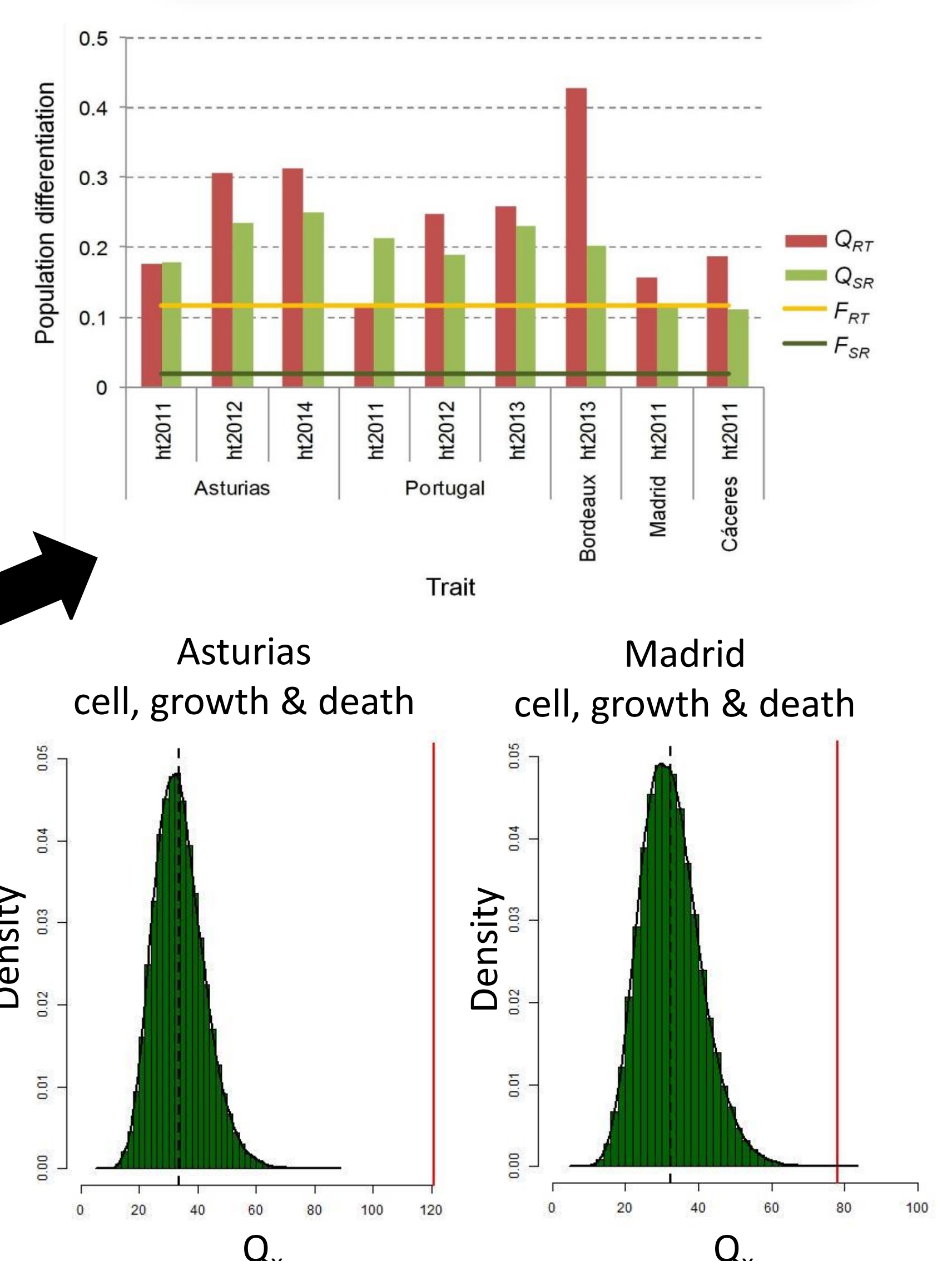
Significant Q_x (excess of variance statistics) for all tested SNP functional groups in the two analyzed common gardens. Genetic differentiation was driven by LD component.

Conclusions

Local adaptation of fitness-related traits can be explained by polygenic selection but results have to be validated by new methods correcting for significant populations genetic structure [3].

References

- [1] Savolaine et al. 2007 *Ann Rev Ecol Evol & Syst*
- [2] Berg & Coop 2014 *Plos Genetics*
- [3] Berg et al. 2018 *BioRxiv*



Null Q_x distribution
Observed Q_x value

No overlap

Acknowledgements

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