

Dissecting the role of demography and selection in Mediterranean forest trees: an overview

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I. Spanu, S.C. González-Martínez



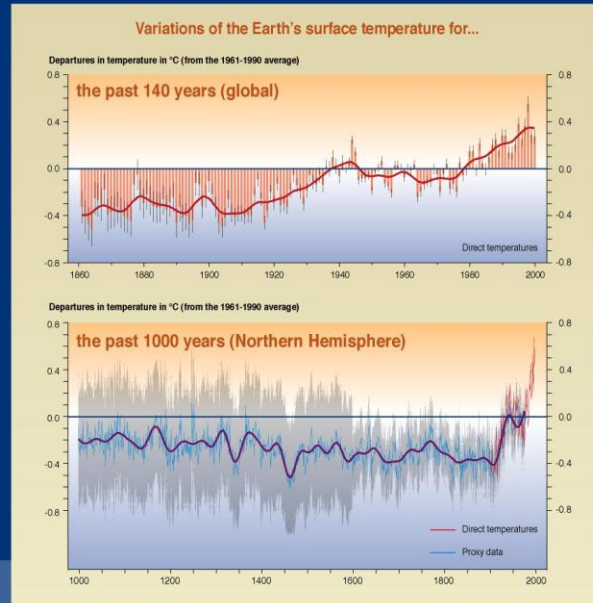
**Institute of Biosciences and
Bioresources, CNR, Florence**



**INIA, Forest Research
Centre, Madrid**

TEMPERATURES

What has already happened



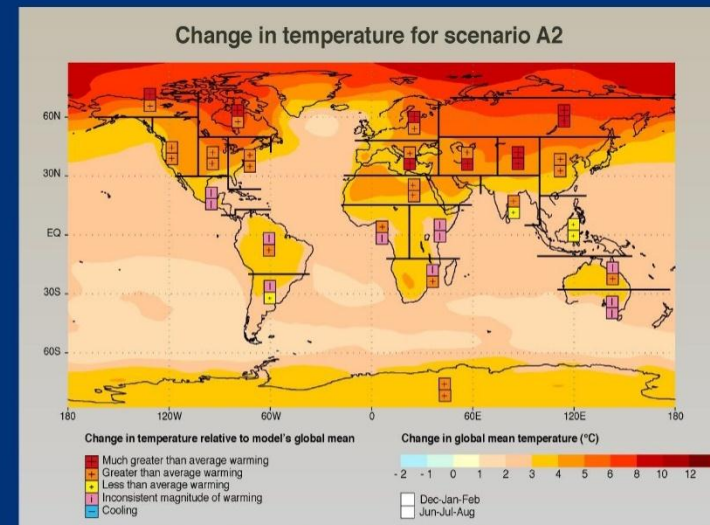
SYR - FIGURE 2-3



IPCC

INTERGOVERNMENTAL PANEL ON CLIMATE CHANGE

What is predicted



SYR - FIGURE 3-2 a

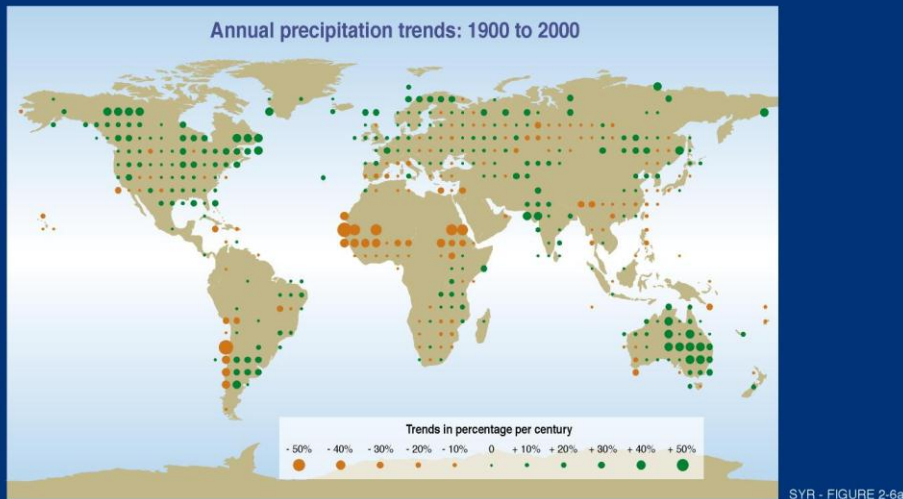
IPCC

INTERGOVERNMENTAL PANEL ON CLIMATE CHANGE



PRECIPITATIONS

What has already happened

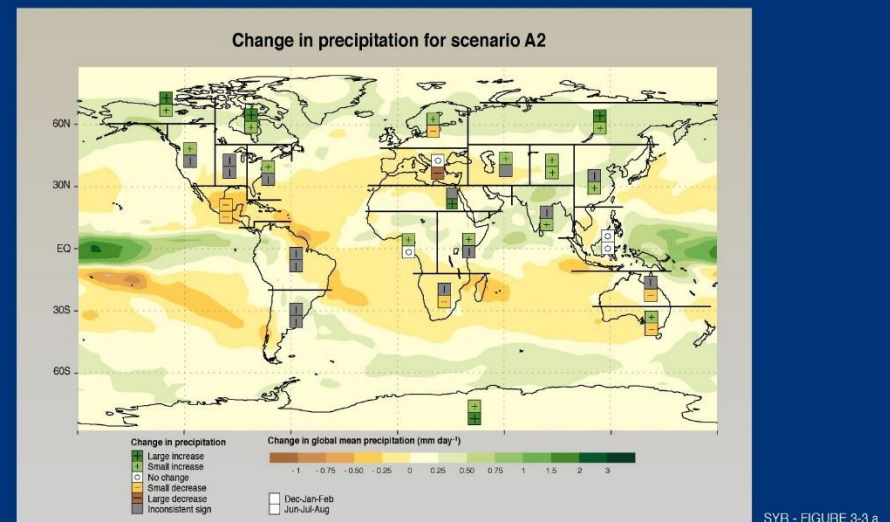


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What is predicted



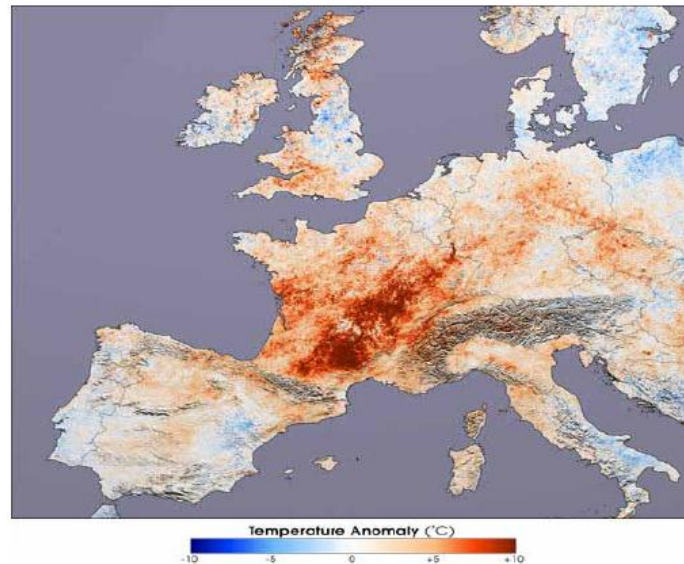
IPCC

INTERGOVERNMENTAL PANEL ON CLIMATE CHANGE



Increase in the risk of extreme events. It has already happened in Europe

Heatwave 2003



Increase in the risk of extreme events. What is predicted ? An example with France

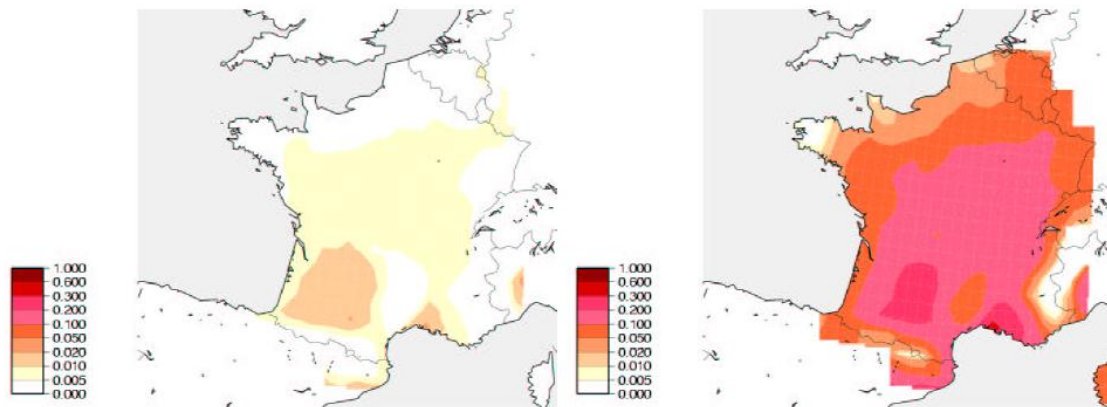
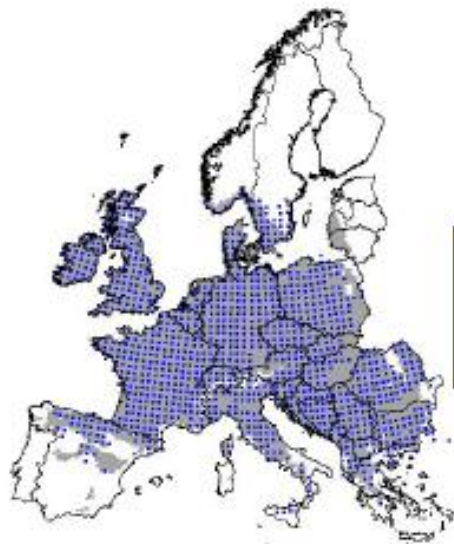


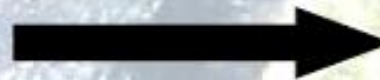
Figure 4: Probabilité d'avoir une température maximale supérieure à 35°C en été pour la période 1961-1990 (à gauche) et la période 2071-2100 (à droite).

Predicted effect of climate change on tree distributions

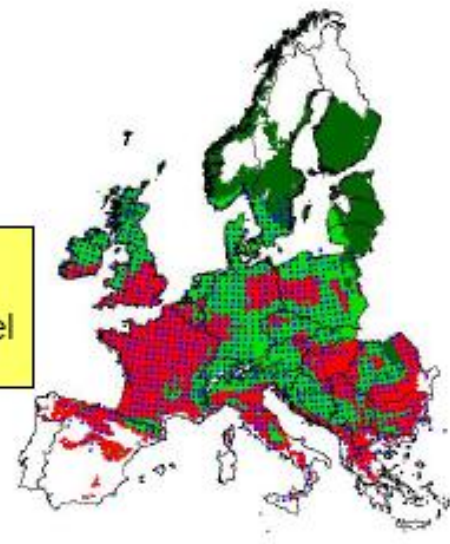


Current Distribution
simulated using BIOMOD

- Observation
- Simulation



Project future climate
Climate model - HadCM3
Greenhouse gas emissions model
- A1FI



Future Distribution: 2080
simulated using BIOMOD

- Loss of habitat
- Stable habitat
- Gain of habitat

What can trees do to cope with climate change ?

Trees have 3 possibilities to face any ecological change:

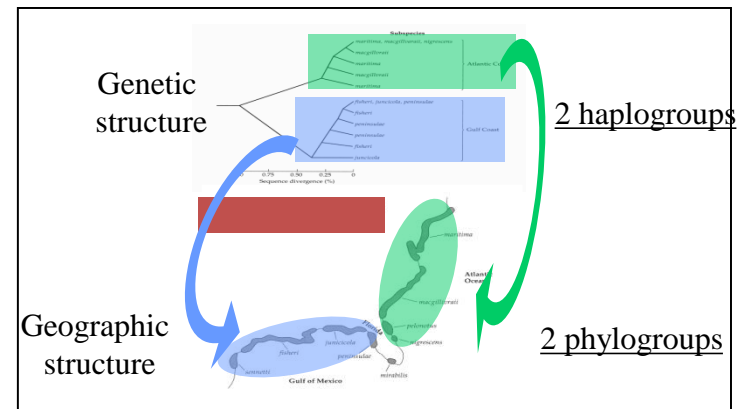
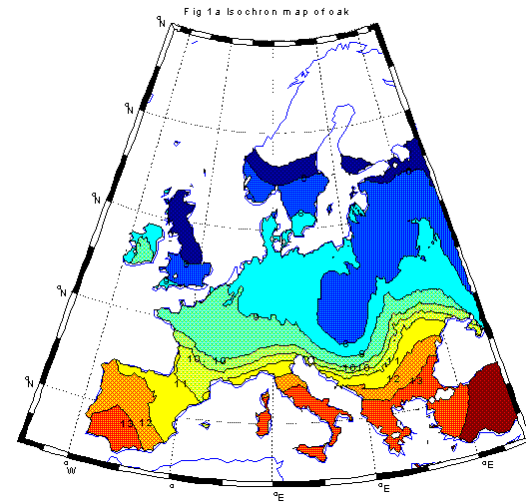
- **plasticity** / acclimatization (trees will continue to survive, grow and reproduce locally because their biological requirements are flexible)
- **adaptation** (selection of progeny with highest fitness)
- movement through **dispersal** (regeneration under friendlier environments after long distance dispersal or hybridization)

Migration potential

Postglacial history of forest trees provides additional information on the dispersal capacity of trees.

Since trees were major components of past European landscapes, they produced large quantities of pollen that survive in fossil remains.

Migration rates were inferred from historical species ranges reconstructed using pollen fossil data and genetic data..... and by performing phylogeographic studies



Why *Taxus baccata*?

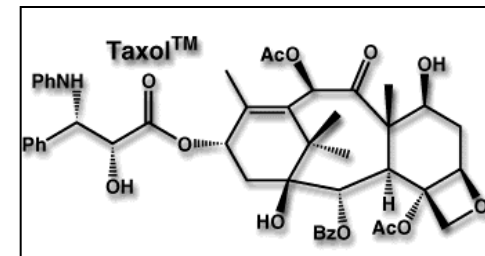


Widespread conifer, but with highly fragmented range → small effective population size, huge environmental variation

Protected by environmental laws in most European Countries

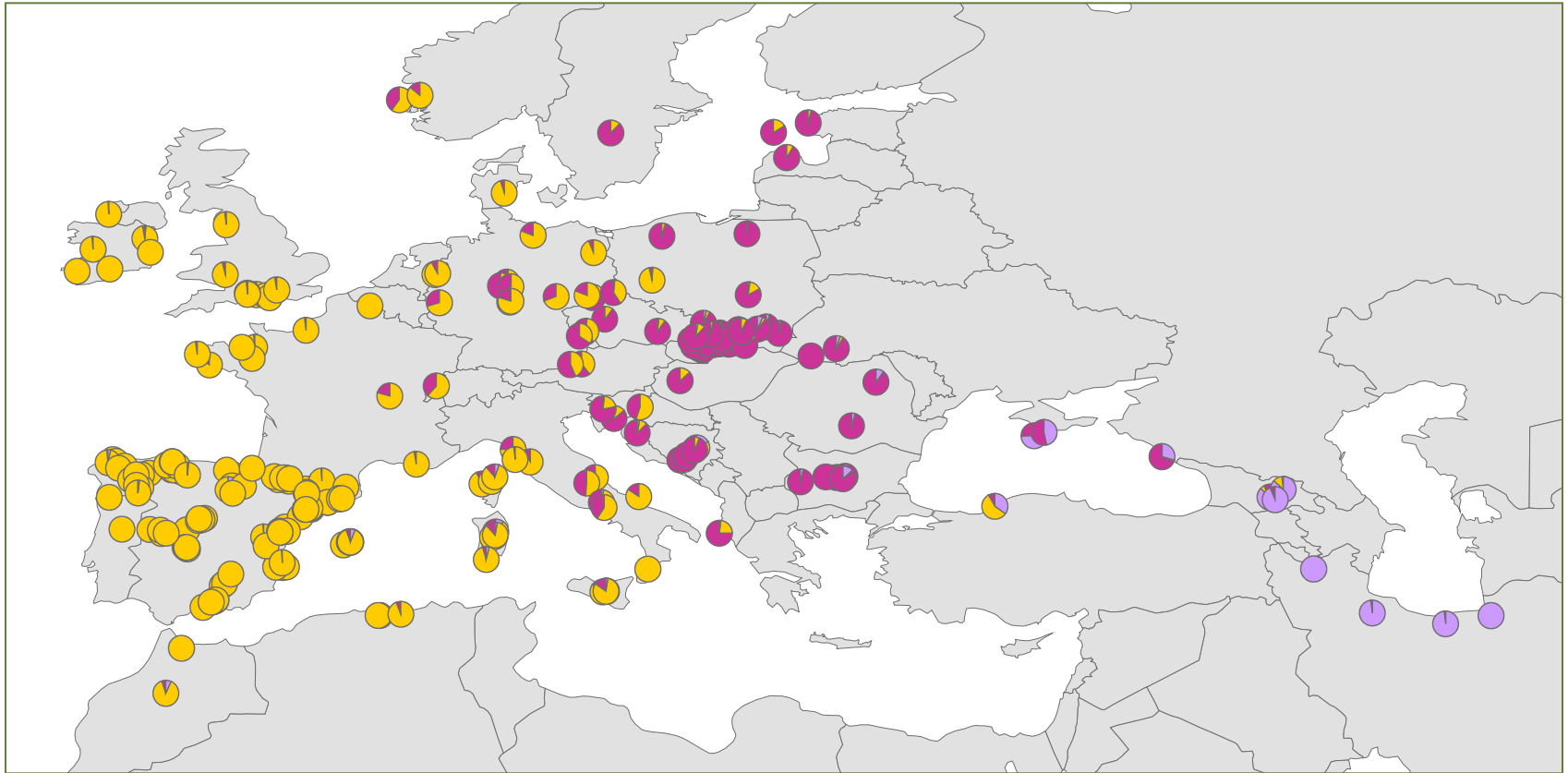


Production of taxanes, a family of diterpenes with antitumoral effect



(Thomas & Polwart 2003; Hilfinger *et al.* 2004; Jennewein & Croteau 2001)

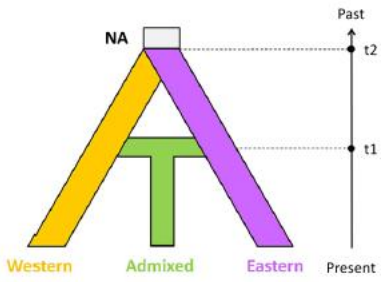
c. 5000 individuals from 243 populations screened with 7 nuSSRs



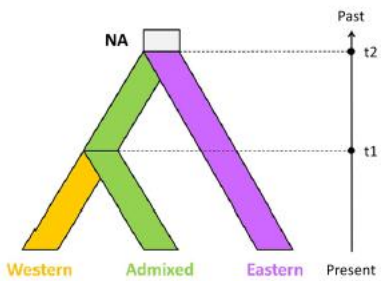
- Three gene pools with admixed populations in central Europe and Italy
- Older populations in the East (Iran)

DIYABC software was applied to infer the demographic history of *Taxus baccata*

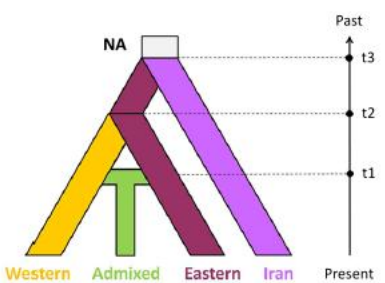
Pops in central Europe, Italy, and the Mediterranean islands (*Admixed*) were originated from “secondary contact” between two separated gene pools (*Western, Eastern*)



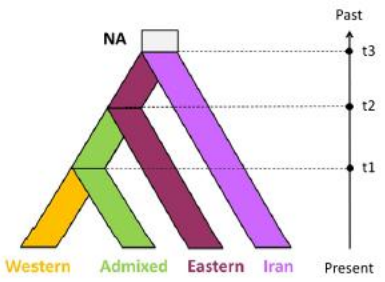
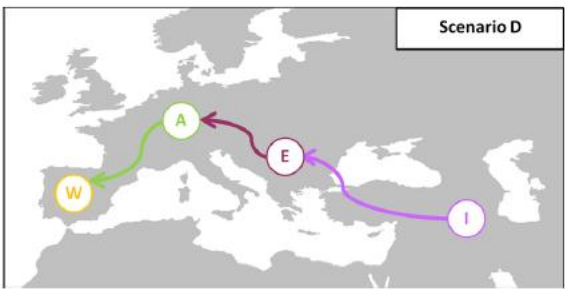
“Colonization ” from the Eastern territories to the Mediterranean area, considering two genetic pools (*Western, Eastern*)



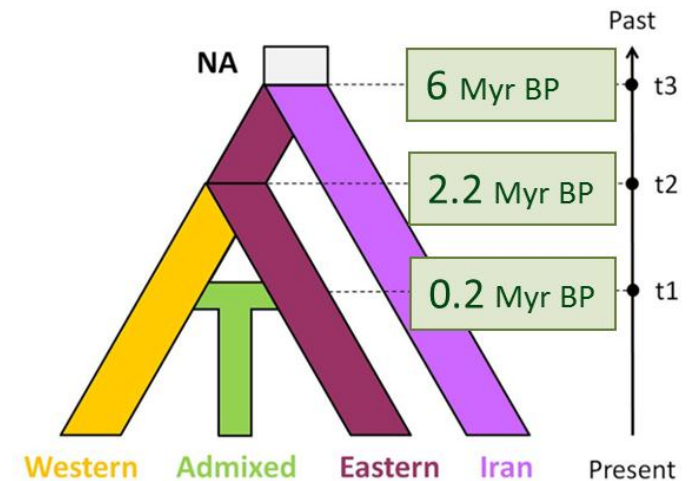
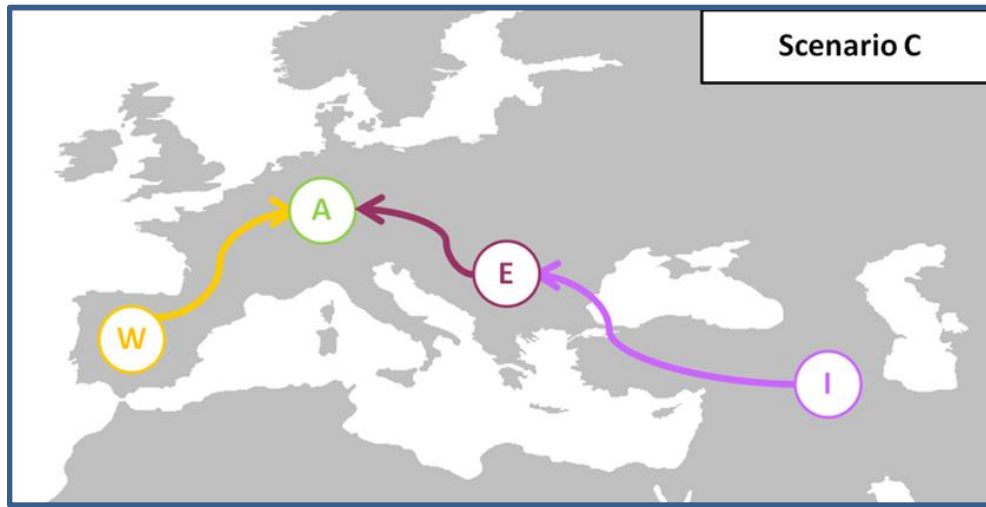
“Colonization” of Eastern Europe from Iran, separation of European samples into two genetic pools (Western, Eastern), and “secondary contact” of both pools in central Europe, Italy and the Mediterranean islands



“Colonization ” from the Eastern territories to the Mediterranean area, considering three genetic pools (*Western, Eastern, Iran*)



1 Ancient disjunction that predated the glaciations followed by secondary contact



2 Evidence of isolation by adaptation driven by climate during interglacials

Table 3 Partial Mantel (PM) correlation (r) and multiple matrix regression (MMRR) coefficients (b) between genetic distance (F_{ST}) and climate variables for the last glacial maximum (LGM, c. 21 000 yr before present, BP) and the last interglacial (LIG, c. 120 000–140 000 yr BP)

	LGM-MIROC (102)			LGM-CCSM (123)			LIG (94)		
	MMRR		PM	MMRR		PM	MMRR		PM
	$b_{Geo-MIROC}$	$b_{Env-MIROC}$	$r_{Env-MIROC}$	$b_{Geo-CCSM}$	$b_{Env-CCSM}$	$r_{Env-CCSM}$	$b_{Geo-LIG}$	$b_{Env-LIG}$	$r_{Env-LIG}$
$F_{ST} - PC1/Geo$	0.166**	-0.088*	-0.086 ns	0.317***	-0.128**	-0.132 ns	0.343***	0.056*	0.058 ns
$F_{ST} - PC2/Geo$	0.130**	0.077 ns	0.077 ns	0.285***	0.069 ns	0.072 ns	0.358***	0.015 ns	0.016 ns
$F_{ST} - BIO1/Geo$	0.164**	-0.062 ns	-0.057 ns	0.315***	-0.096*	-0.098 ns	0.357***	0.115*	0.104*
$F_{ST} - BIO2/Geo$	0.137**	0.031 ns	0.031 ns	0.306***	-0.068 ns	-0.070 ns	0.318***	0.170***	0.177**
$F_{ST} - BIO4/Geo$	0.219**	-0.199***	-0.185 ns	0.314***	-0.120***	-0.123 ns	0.490***	-0.235***	-0.209 ns
$F_{ST} - BIO6/Geo$	0.142**	-0.005 ns	-0.004 ns	0.312***	-0.065 ns	-0.065 ns	0.303***	0.106**	0.096*

*Last Interglacial (LIG)
~140,000 yr BP*

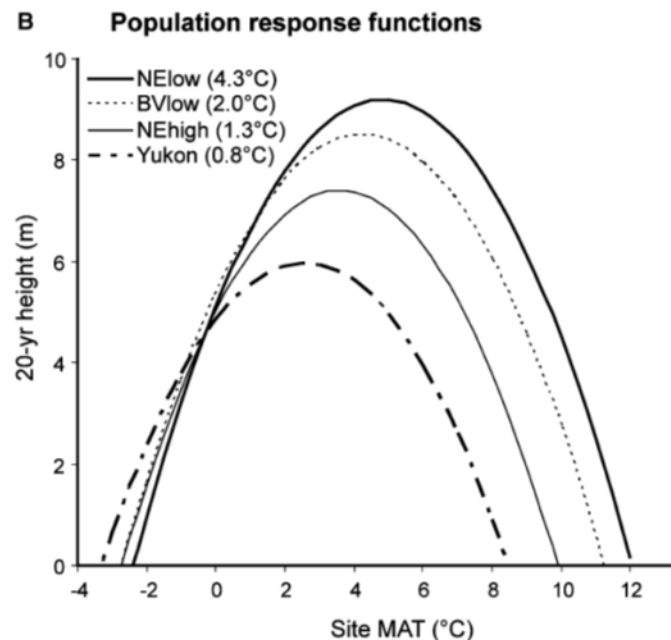
Last Glacial Maximum (LGM) ~21,000 yr BP

Confronted with global change trees will have either to migrate or to adapt in situ

Rates of spread of forest trees (<100 m/year) are **far below** what would be necessary (3,000 to 5,000 m/year) for species migration to track future climatic warming (Petit et al. 2008 Science; Nathan et al. 2011 Ecology Letters).

Thus, forest trees will probably have to adapt in situ to survive

To adapt in situ, plant species rely mostly on **standing genetic variation**, so that the level of genetic variation present in natural populations is important.

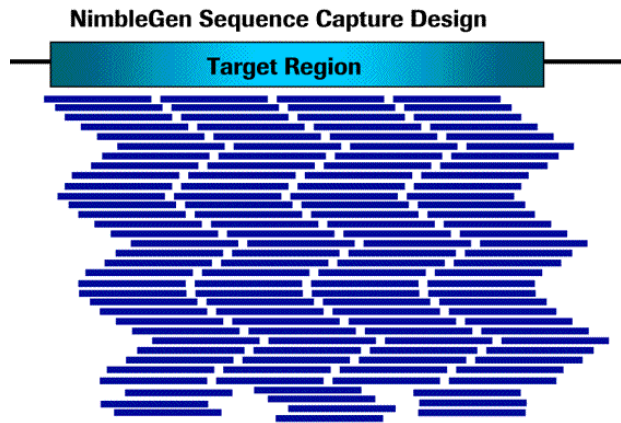


(Wang et al. 2006 Global Change Biology, for *Pinus contorta*)

Some advantages of trees are:

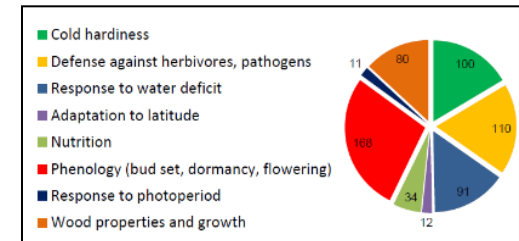
- They are undomesticated and still contain large amounts of genetic variation.
- Reaction norms from forest trees show high level of plasticity.
- Normally, tree populations have big effective sizes (i.e. better response to selection).

Gene capture experiment



1,210 genes selected for exome capture experiment considering annotation and d_N/d_S from available transcriptomes

- 618 candidate genes
- 149 conserved genes
- 443 control genes



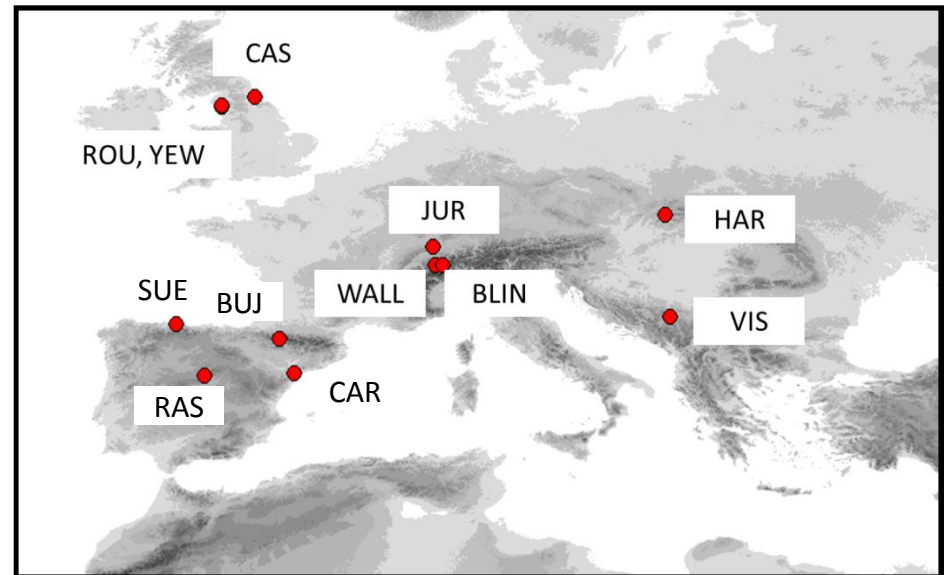
12 populations sampled in Europe along a continentality gradient



Cardó
Alt.: 610 m
T: 10.02°C

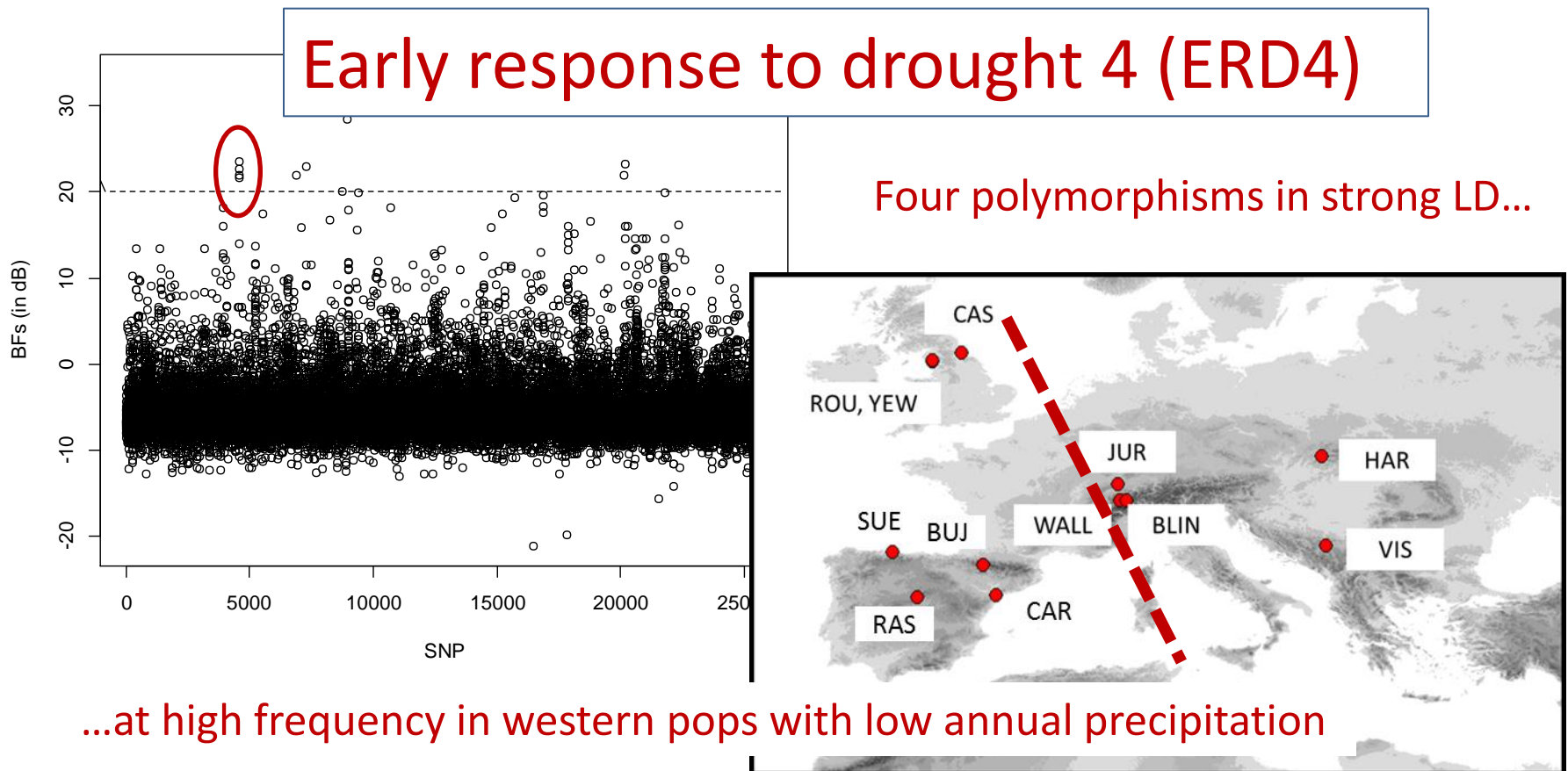


Bujaruelo
Alt.: 1300 m
T: 6°C

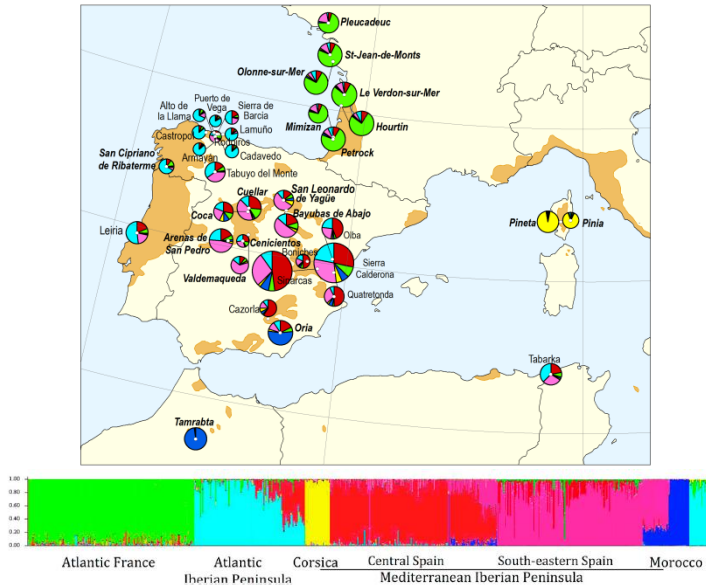


25,726 SNPs (after quality filtering)

- Stringent use of BayeScEnv & BayPass identified similar numbers of SNPs associated with temperature and precipitation.
- No shared outliers for temperature but 6 SNPs (from 3 genes) that were associated with annual precipitation using both methods.



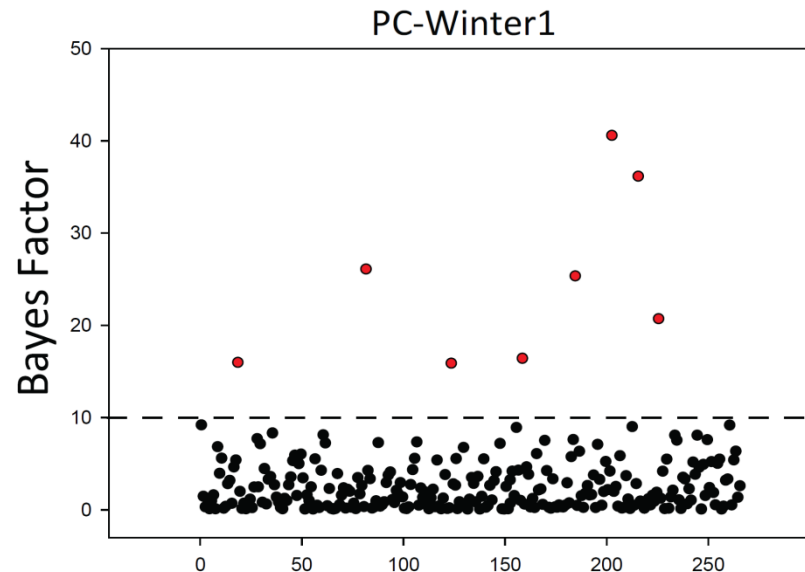
Rangewide climate adaptation in *Pinus pinaster*



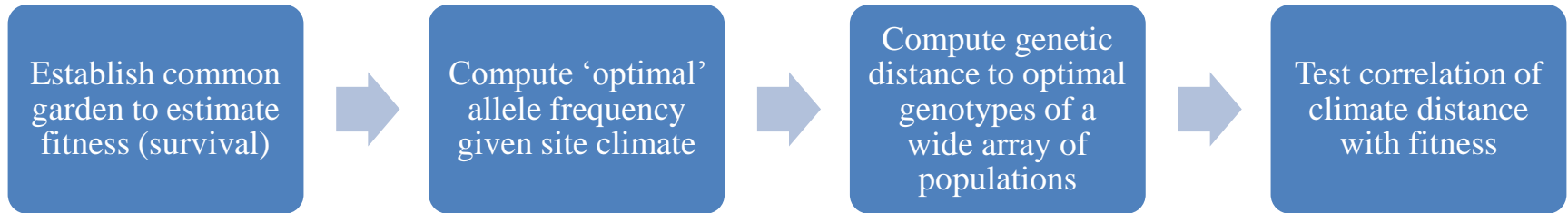
Jaramillo-Correa et al. (2015) *Genetics*

Allele frequency of **18 SNPs** from candidate genes are strongly correlated with climate, in particular winter temperatures

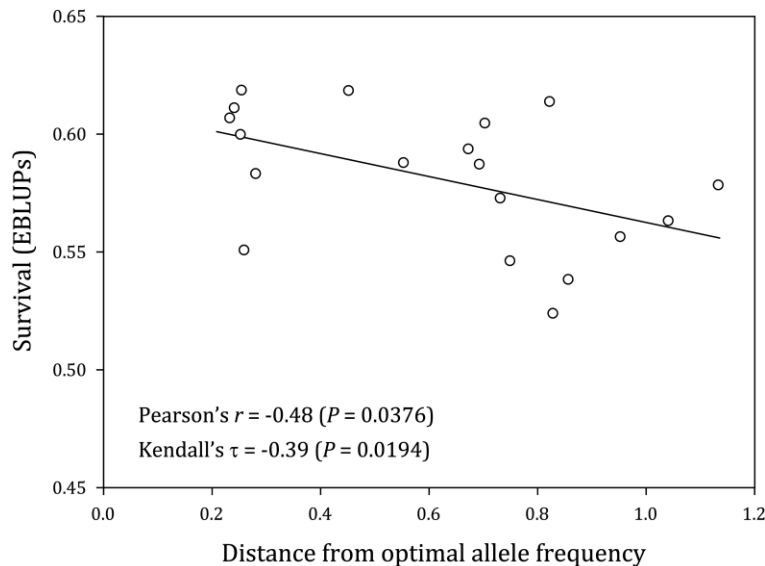
- Strong population genetic structure in maritime pine (12 nuSSRs, 2,912 SNPs)
- Association with climate PCAs using logistic regression, bayenv and LFMM
- Only significant SNP-climate associations with all 3 methods are retained



Potential to use SNPs to predict maladaptation to climate in pine?



Similar approach (but at the population level) to Hancock et al. (2011, Science) for Arabidopsis



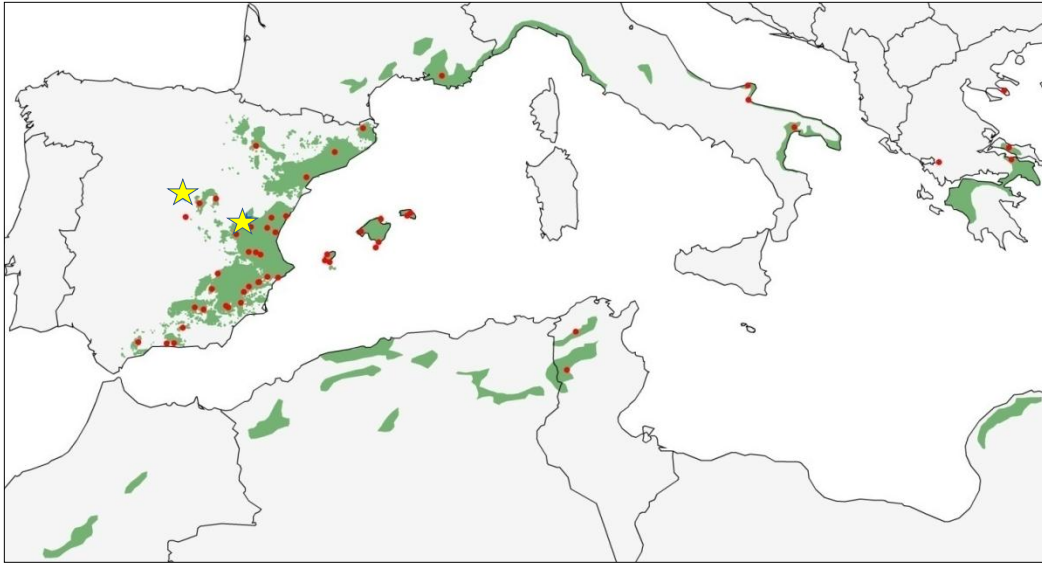
- Significant (and negative) correlations, indicating that genotypes from other environments are maladapted
- Improve niche modeling? Define conservation priorities under climate change?



Intra-specific variability and plasticity influence potential tree species distributions under climate change

Marta Benito Garzón^{1,2*}, Ricardo Alfà¹, T. Matthew Robson^{1,3} and Miguel A. Zavala^{1,4}

Association studies in Aleppo pine



- Two provenance trials
- Contrasting environments
- 717 trees from 28 populations sampled across the species natural range
- 18 years-old trees
- Unknown pedigree



Madrid



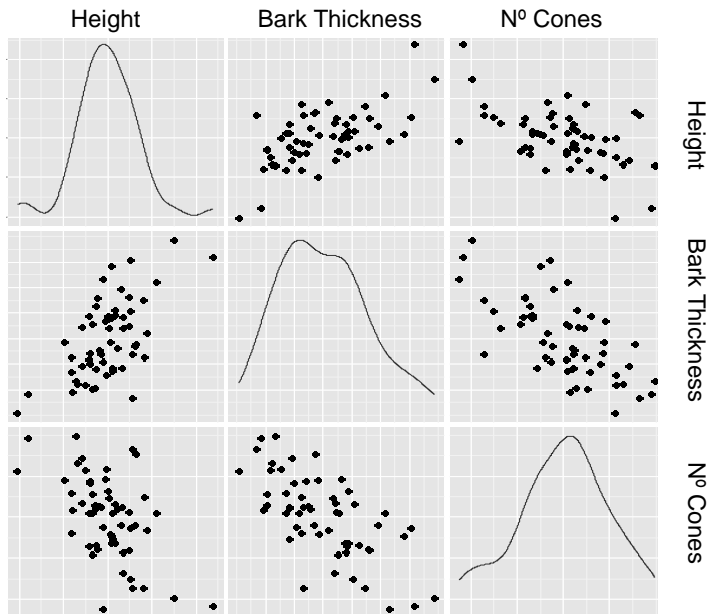
Valencia

Association studies in Aleppo pine

Phenotypes

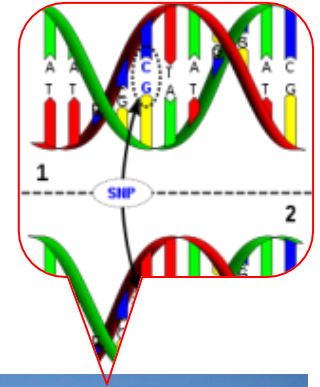
Traits measured 1997-2015:

- Survival
- Growth: Height, Stem Diameter
- Reproduction
- Wood quality: Extractives, Lignin, H/G ratio, Density
- iWUE: Cδ13

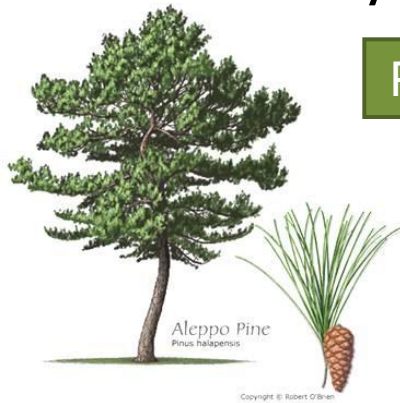


Genotypes

294 SNPs
in candidate genes



Association studies in Aleppo pine

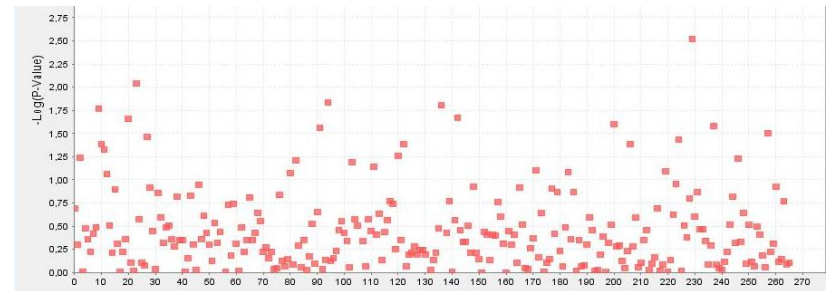


Phenotypes

717 trees

Genotypes

Single Locus Association Tests



- No significant associations found so far for growth traits
- *Ongoing studies...*

Multi-trait methods



Efficient Multiple-Trait Association and Estimation of Genetic Correlation Using the Matrix-Variate Linear Mixed Model

Nicholas A. Furlotte* and Eleazar Eskin^{†,1}

TECHNICAL REPORTS

nature
genetics

A mixed-model approach for genome-wide association studies of correlated traits in structured populations

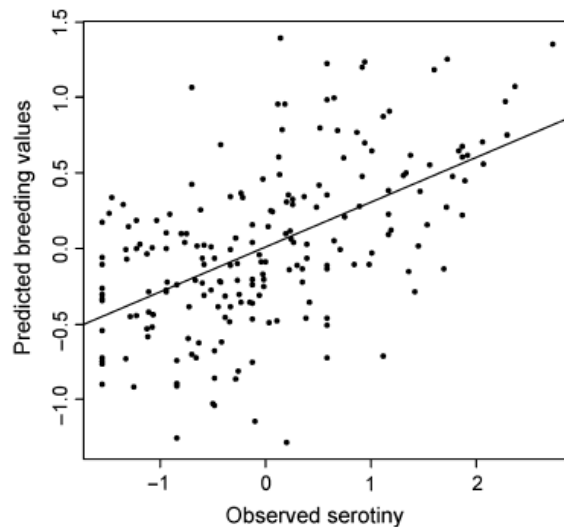
Arthur Korte^{1,4}, Bjarni J Vilhjálmsson^{1,2,4}, Vincent Segura^{1,3,4}, Alexander Platt^{1,2}, Quan Long¹ & Magnus Nordborg^{1,2}

Association genetics and phenotypic prediction *in situ* for fire-related traits in Aleppo and maritime pines



Katharina Budde

- 17 SNPs explained ~29% of phenotypic variation in serotiny.
- Similar prediction power was found for nearby regions.



(Budde et al. 2014 *New Phytol*)

Combining population genomics with association genetics for adaptive traits



Isabel Rodríguez-Quilón

- 646 clones from 37 pops planted in five sites and genotyped for 9k SNPs.
- Traits: survival and height, growth phenology, SLA and iWUE.

Two-step approach:

- Use association genetics to find SNPs associated to particular traits.
- Use these SNPs to study polygenic adaptation following landmark studies in humans (e.g. Turchin et al. 2012 *Nature*; Berg & Coop 2014 *PLoS Genet*)

The geographical scale of local adaptation

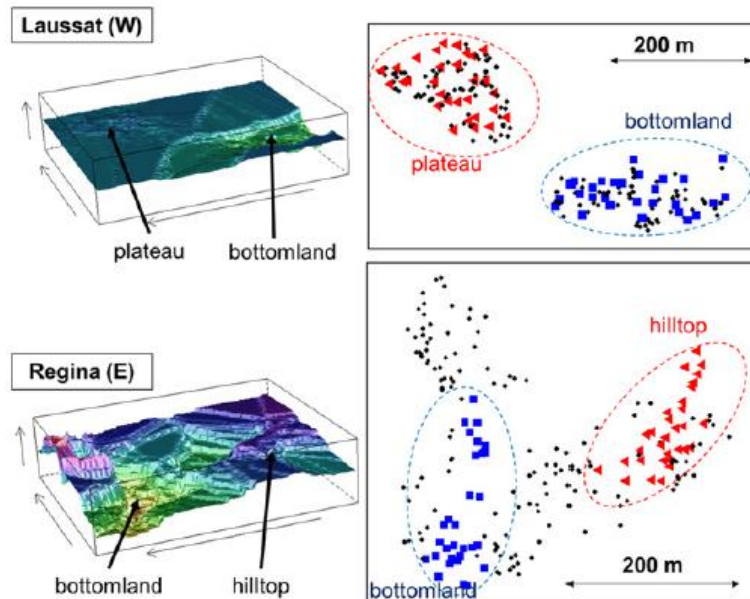
Increased evidence of selection at small spatial scales, including for forest trees

Annals of Forest Science
DOI 10.1007/s13595-015-0471-z

OPINION PAPER

Fifty years of genetic studies: what to make of the large amounts of variation found within populations?

Ivan Scotti · Santiago C. González-Martínez ·
Katharina B. Budde · Hadrien Lalagüe

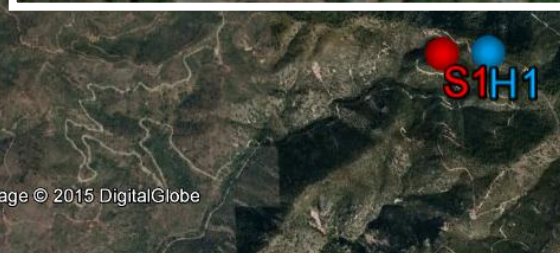
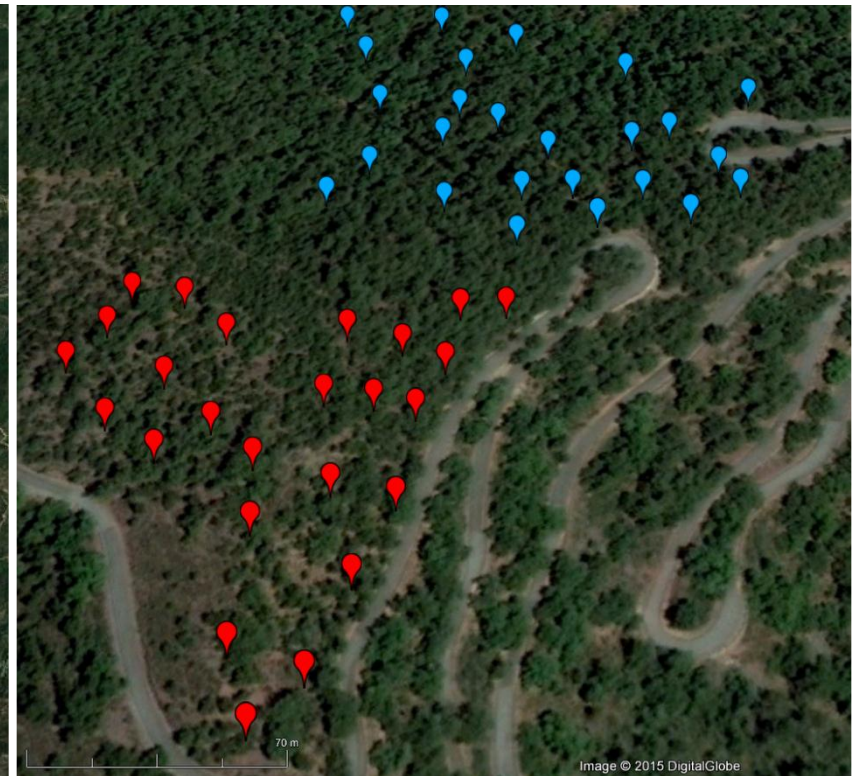
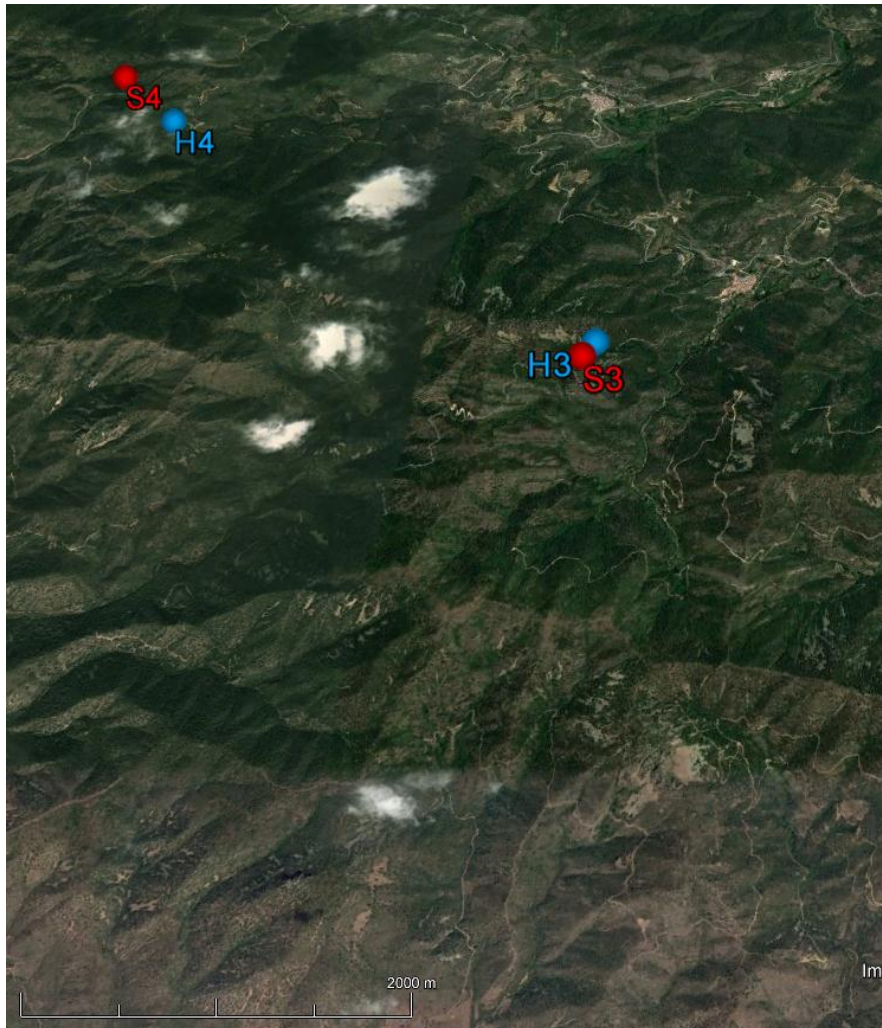


To date, the best example in forest trees is found in the neotropical tree *Eperua falcata* (Ivan Scotti & co-workers)

- Significant effect of waterlogging status to explain pairwise genetic distance
- Identification of significant outlier loci using multiple methods

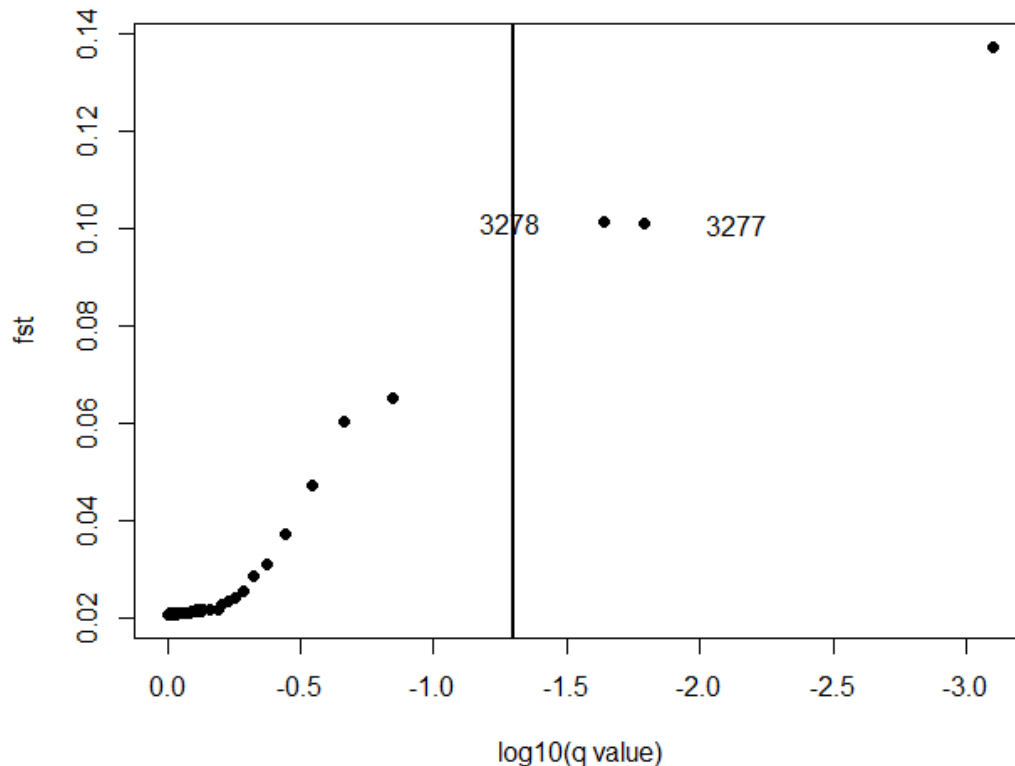
Case study in maritime pine: very local adaptation within populations

6,100 SNPs (same Infinium assay as the rangewide study)




km

Some preliminary results



- Only a handful of outlier SNPs detected using BayeScan (3 SNPs)
- SNP outliers were not related to humidity differences

Compare with Jaramillo-Correa et al. (2015) *Genetics*, where 18 SNPs associated with climate at the rangewide scale were identified using a smaller SNP subset

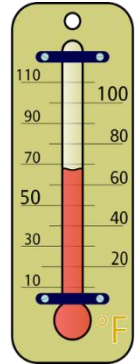
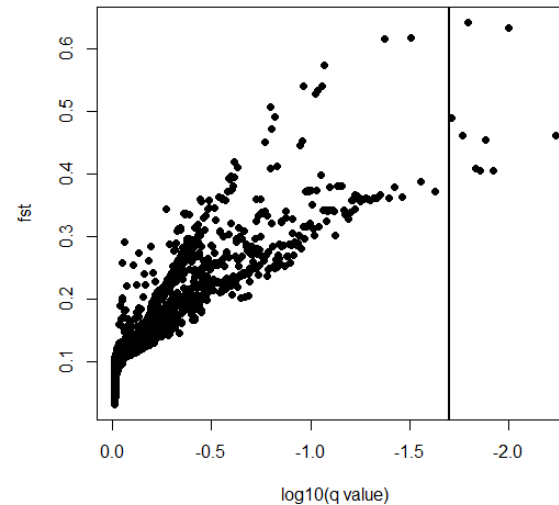
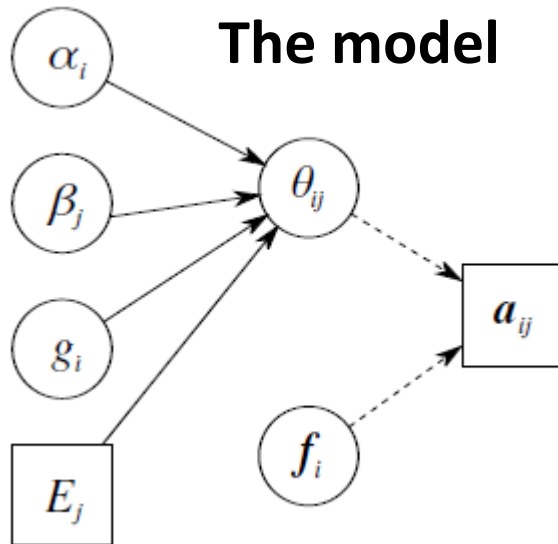


Thank you for your attention!

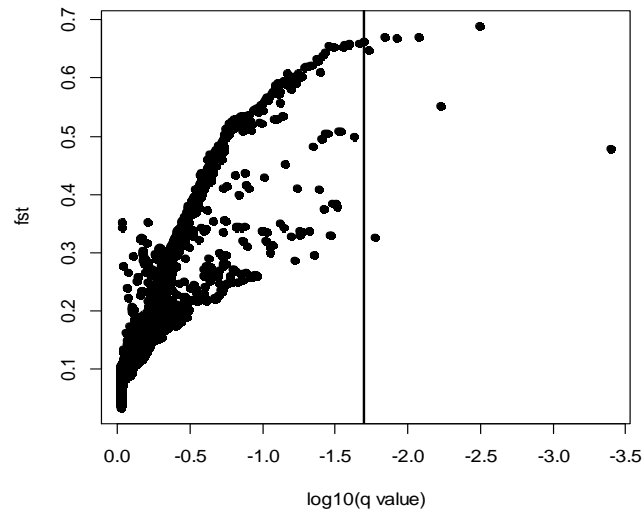
Picos de Europa (northern Spain)

Outlier detection and environmental associations

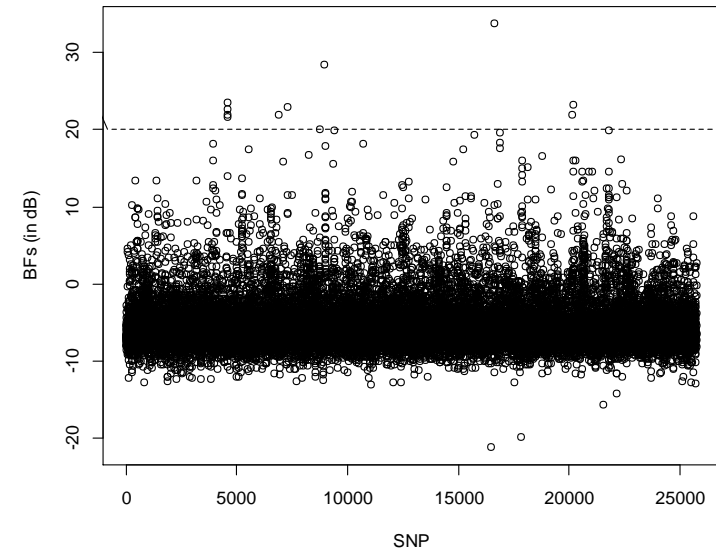
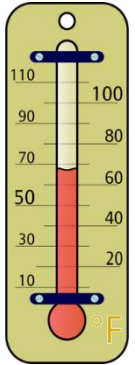
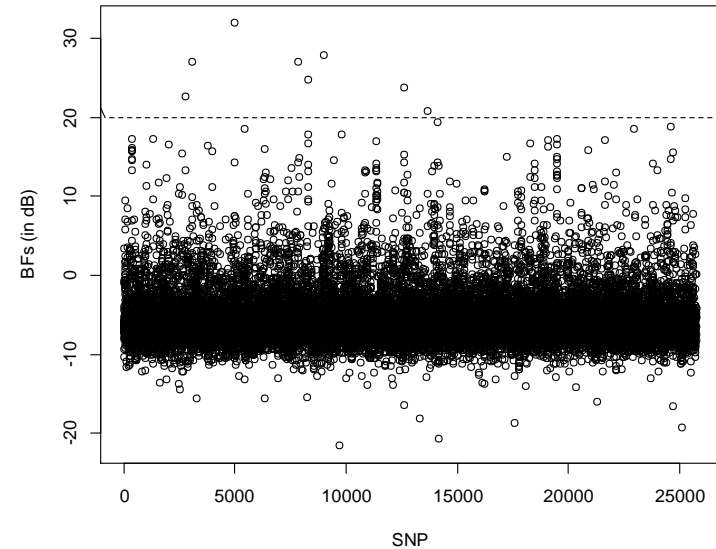
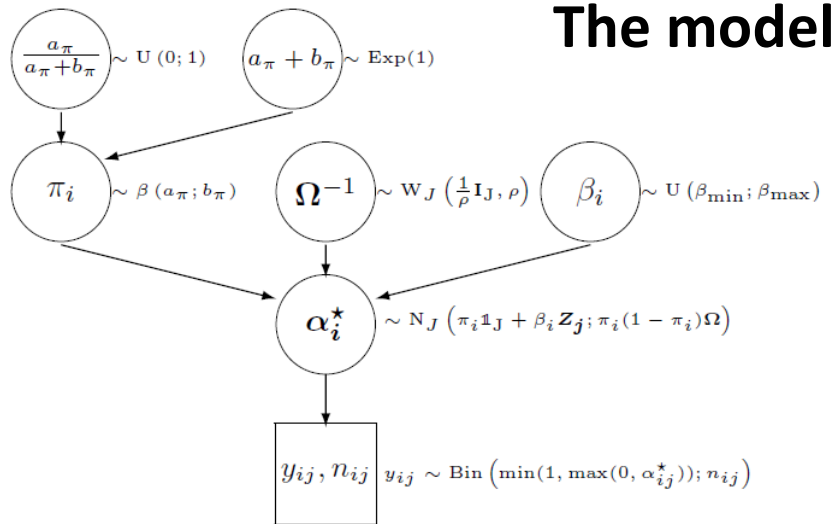
BayeScEnv (de Villemereuil & Gaggiotti 2015)



- 9 outliers associated with mean temperature ($q < 0.02$)
- 8 outliers associated with annual precipitation ($q < 0.02$)



BayPass (Gautier 2015)



- 8 SNPs strongly associated with mean temperature (BF>100)
- 11 SNPs strongly associated with annual precipitation (BF>100)