



Molecular genetics segregate clones and provenances of stone pine, a tree rooted deep in the Alentejo

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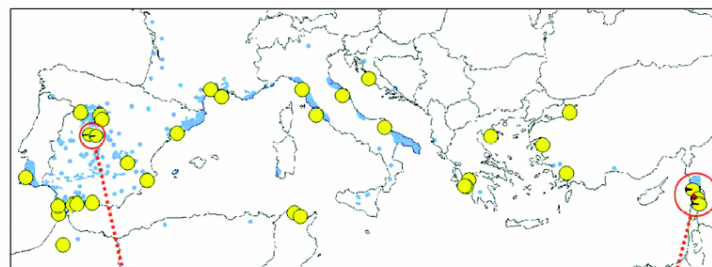
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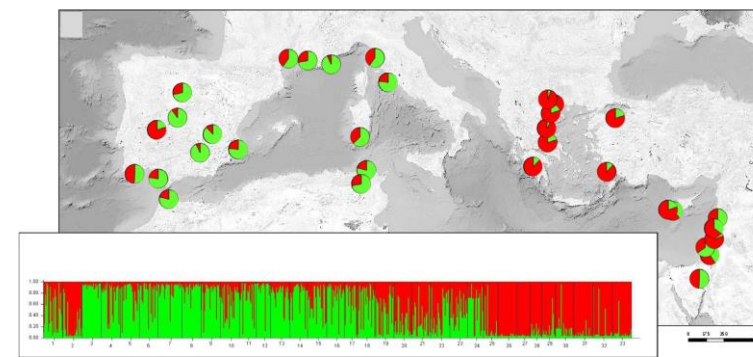
Introduction

Pinus pinea

- A native Mediterranean forest tree, associated with mixed open woodlands \supset {pines, oaks, junipers, ...}
- Since 18th c., one of the pines widely used in restoration, namely on coastal sands (doubling area from 0.3 to 0.7+ Mha)
- S. 20th c., breeding programs targeting edible pine nuts (cf. KN by F. Pérez, “Clones” by C. Guadaño afterwards)
- 20th-21st c., private planting of agroforestry and agronomic orchards (some 0.25+ Mha -> 1 Mha total area)
- Nevertheless, it is a relict species with **extremely low genetic variation**, both at quantitative and molecular traits
 → its breeding was limited by **low variation** to be captured and by a **lack of suitable genomic tools** for identification



“Genetically depauperate but widespread:
 the case of an emblematic
 mediterranean pine”
 cpDNA (Vendramin *et al.*, 2008)



nuSSRs (Jaramillo-Correa et al. 2020)

Only 15 clones as
 basic materials in 2015 (ES)

7 SSRs (Pinzauti et al. 2012):

- Low allelic polymorphism
- 16% errors in genotyping
- Inconsistent results

Introduction

Quantitative Genetics

- International common-garden provenance trial FAO *Silva Mediterranea* (since 1994)

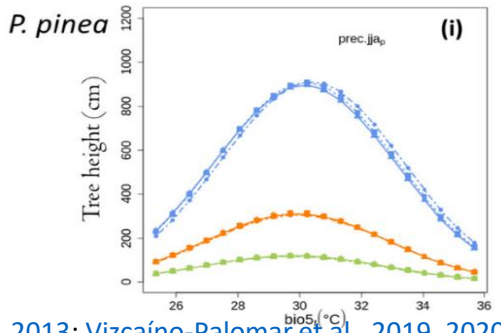
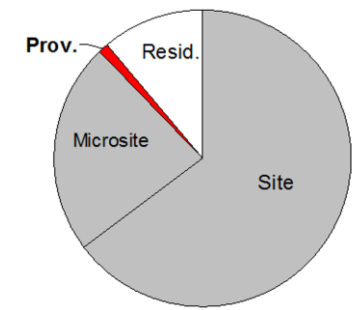
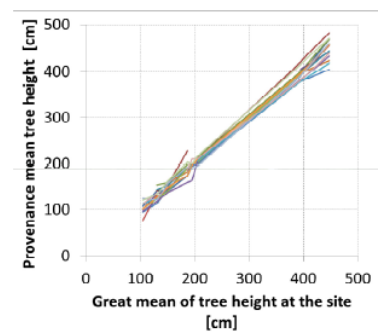
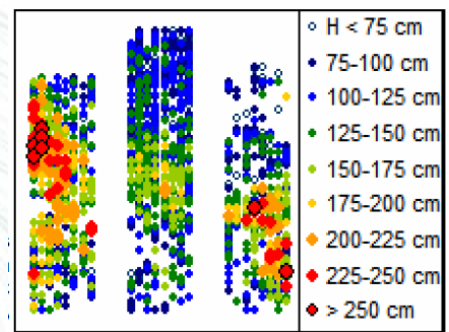
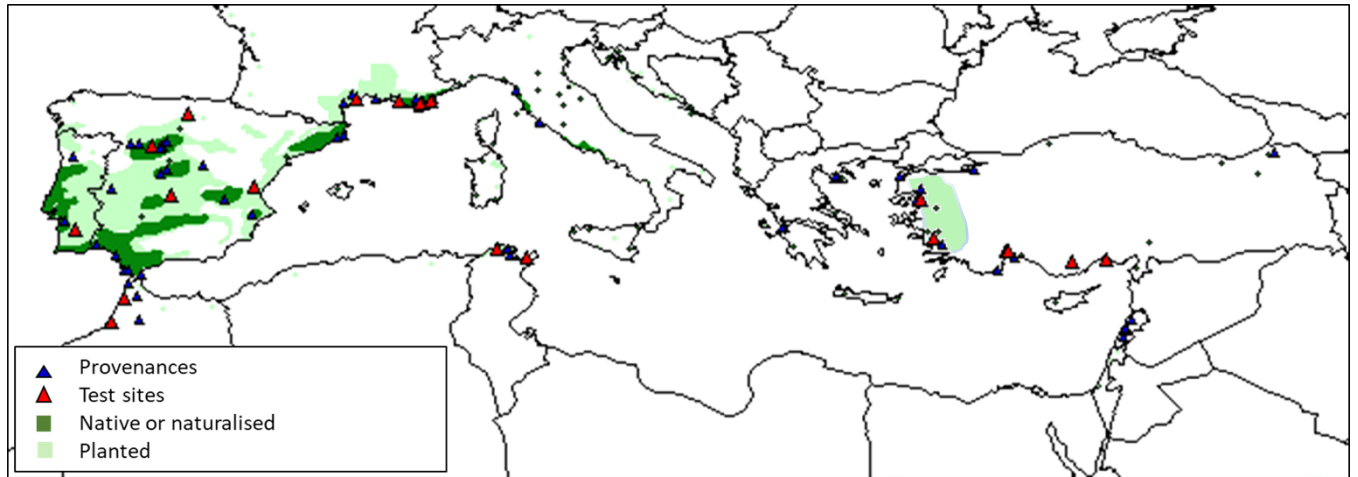
...“extremely low genetic variation”

Phenotypic plasticity >> Genetic local adaption

- Difference in cone production between clones (cf. presentation **Guadaño et al.**)

...huge microsite effects mask genetic contribution

Tree height in a range of field trials varied within test sites, but did “*nearly not*” depend on the origin of the plants.



(Mutke *et al.*, 2010, 2013; Vizcaino-Palomar *et al.*, 2019, 2020)

Material & methods

Olsson et al. (in rev.). **Managing genetic resources with genomic tools: the case of *Pinus pinea*, a multipurpose forest tree with low genome diversity.** For. Eco. Manage.

Aims: Clonal identification, Parentage analyses and genetic relationships, Population genetic structure

Materials: 1 925 individuals sampled

- 37 populations (full distribution range)
- 323 Spanish and Portuguese selected clones
- 16 progenies (half-sib families)

Methods: 2 245 markers retained in quality filtering

- from **Axiom's 4TREE** array developed by B4EST project consortium



● species distribution, red triangles: sites sampled in this study

Axiom SNP scoring *Pinus pinea* (SNP – Single-Nucleotide Polymorphism)

SNPs submitted 128 279

SNPs retained 36 784

***P.pa.* SNPs in the TF 4TREEarray:**

(PolyHRes+NoMHom) 5 671

Best



This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 773383

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Material & methods

Sampling scheme

1,925 samples

1,131 full distribution
(37 populations)

- 17 Greece (1 p.)
- 236 France (6 p.)
- 178 Italy (2 p.)
- 71 Lebanon (4 p.)
- 91 Portugal (3 p.)
- 467 Spain (17 p.)
- 71 Turkey (4 p.)

557 REINFFORCE arboreta
574 FAO *Silva Mediterranea* trial

268 clone samples ES
(252 individuals)

Provenance regions
• ES1, ES2, ES3, ES6

15 registered clones

10 - 11 ramets/ clone

91 unregistered clones

1 ramet/clone

64 clones PT

1 ramet/clone

462 Progenies
(half-sib families from 16 clones)

Best

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Results

Clonal identification

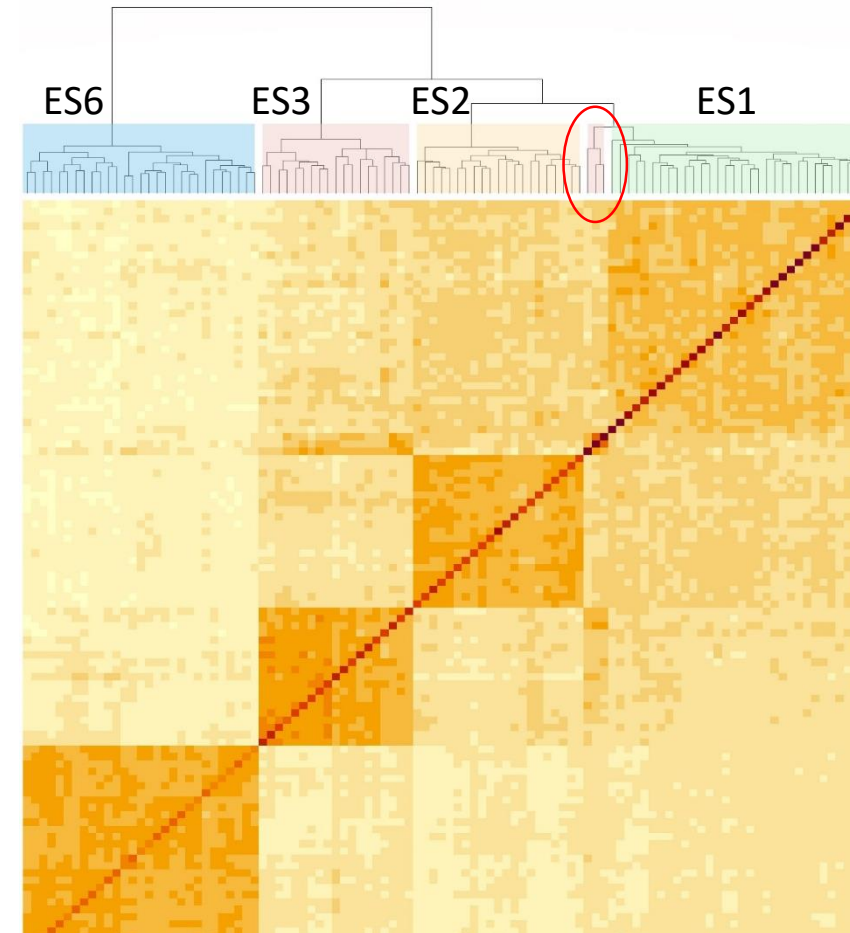
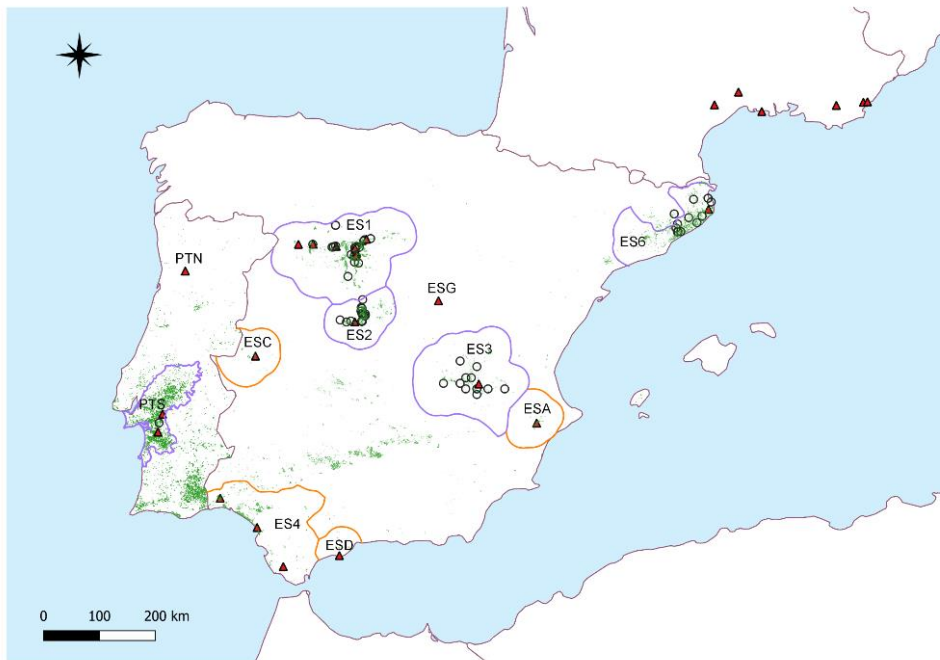
- More precise and reliable identification with 2,245 SNPs than with 7 SSRs
- Practical applications of results
 - Exclusion of 14 ramets from their corresponding genets (10%)
(possible errors during grafting, nursery handling, planting or sampling)
 - Consensus genotypes as first reference entries
in the stone pine breeding programme database
 - Registration of new elite clones (now distinguishable by SNP genotype)

upcoming ✓

Results

Parentage analysis and Genetic relationships

- Parentage analysis with *sequoia*: mother assigned for 442 out of 455 offspring (97%)
- GRM matrix of 104 clones mainly reflected expected population genetic structure (and reveals **afforestations**)

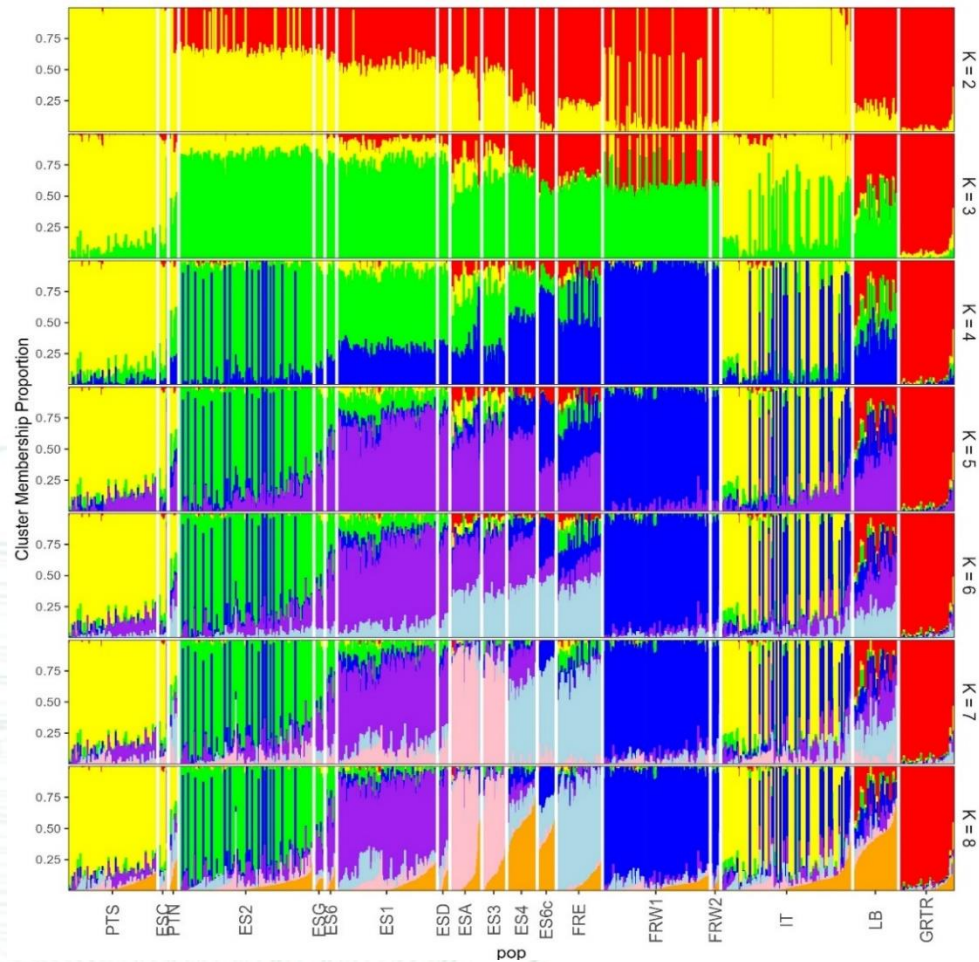


Additive GRM sommer

Results

Population genetic structure

Individual ancestry coefficients *LEA*:
sNMF, *CLUMPP*, *snpR*

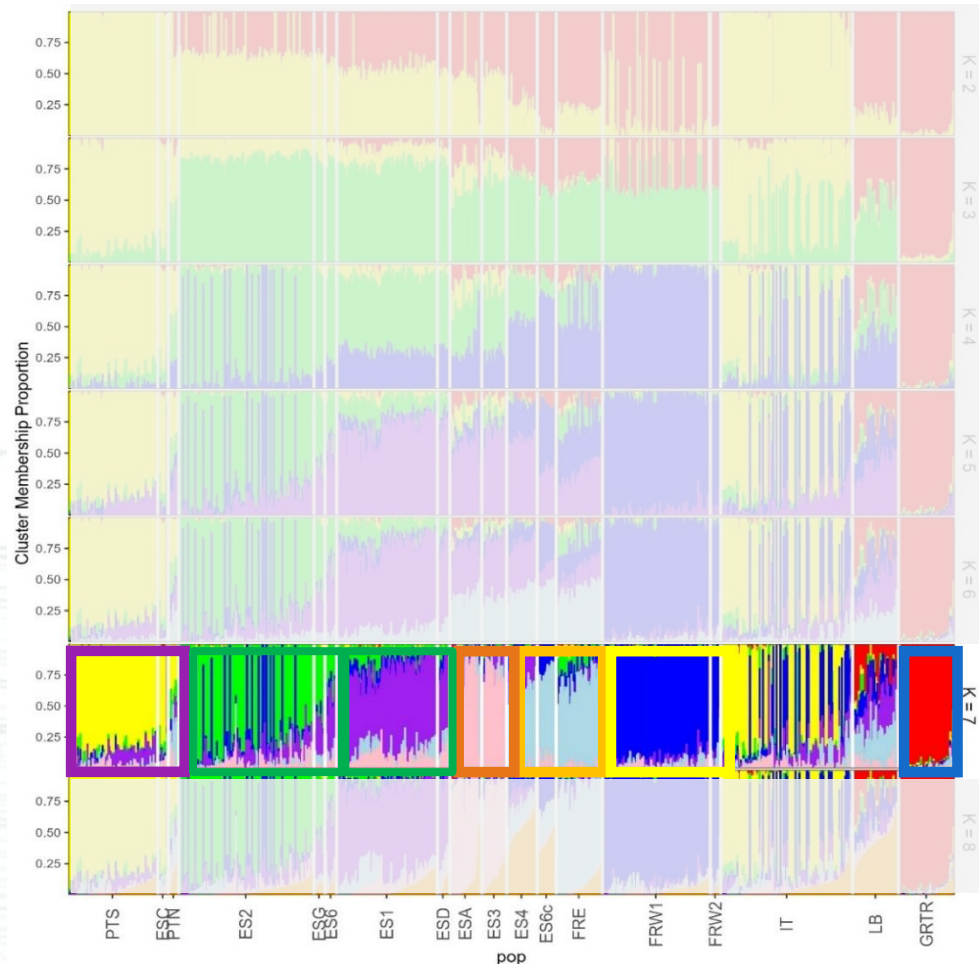


- K = 7**
- No *a priori* knowledge
 - Cross entropy
 - Well defined regions



Results

Population genetic structure



Individual ancestry coefficients *LEA*:
sNMF, *CLUMPP*, *snpR*

Portugal, Extremadura ES
¿ Tuscany ?

Inner Spain
(2 Reg of Prov.)

South eastern Spain

Andalucia, Catalonia, Provence
¿Lebanon?

Languedoc-Roussillon (planted)

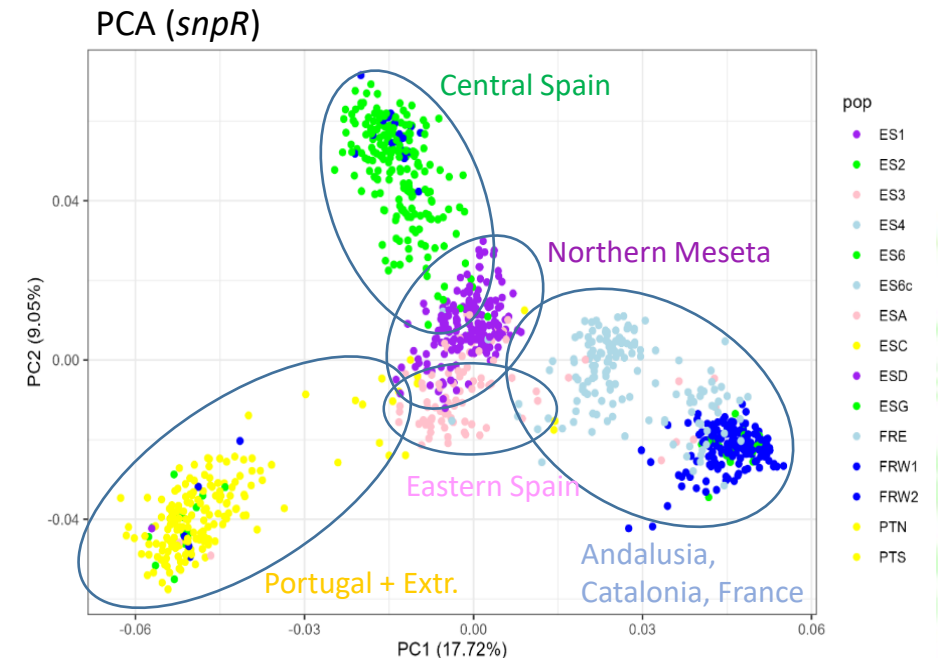
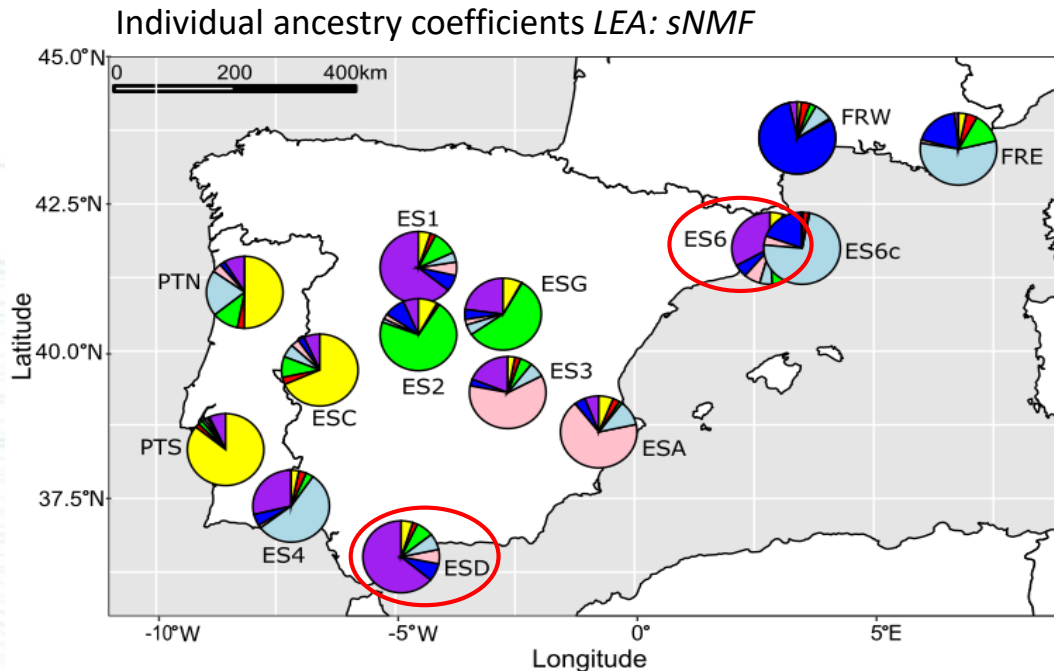
Aegean
¿minor in Lebanon?

K = 7

Results

Population genetic structure

- Global analysis with K=7
- In the Western Mediterranean, 5 gene pools
- Unexpected patterns: 2 stands sampled, **ESD** (coastal Marbella) & **ES6** (farmland edge) putative historic introductions by forestation XIXth c. (*phylloxera* aftermaths)?

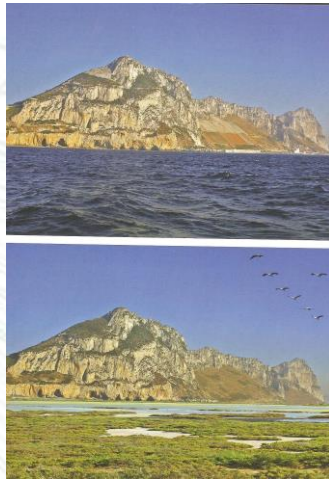


Discussion *Pinus pinea* – the “tame pine”?

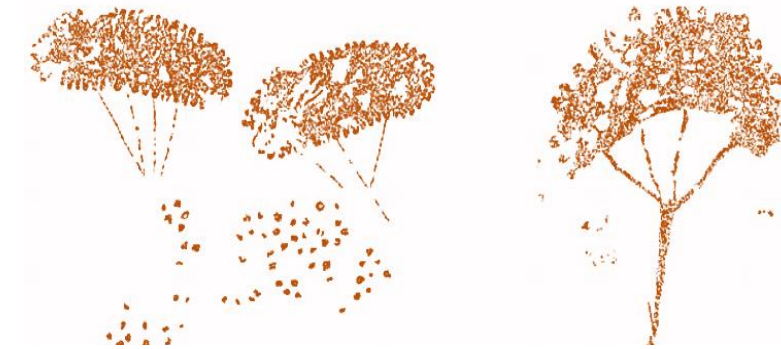
pino domestico, pino doncel, pinheiro manso,...

- Native Mediterranean tree, sparsely spread from the Portugal to the Black Sea and Lebanon
- **Where is it native, archaeophyte or naturalised alien? Are the singled-out regional clusters glacial refugia, or mere bridgeheads?**
- In Iberia, autochthony confirmed (cf. Prada et al., 1997; Blanco et al, 1997; Gil 1999; Martínez et al., 2003; Martínez & Montero 2004], especially for **open woodland landscapes** in the southwest, where its edible pine nuts have been foraged and consumed **since at least 100 000 BCE**, first by **Neanderthals**, later by **modern humans** (cf. Badal et al., Finlayson et al., Carrión et al., Cortés-Sánchez et al., Zilhão et al.,...)

The last ever Neanderthals lived “retired” in Gibraltar and at the *Costa del Sol* on seafood, snails, ...and pine nuts (<30 ka)



Broodbank, 2013

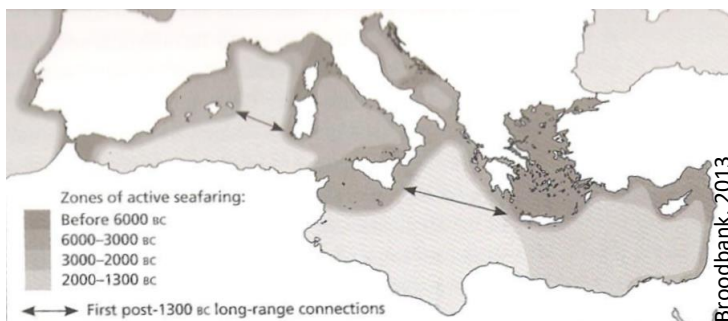


Neolithic rock art, Alcoi, Alicante, ES (Hernández et al., 2007)

Discussion *Pinus pinea* – the “tame pine”?

pino domestico, pino doncel, pinheiro manso,...

linked to the cultural landscapes of local **Megalithic, Tartessian and Phoenician sites**



~Neolithic 6 000-5 000 BCE (~cardial ware)

One sea but many routes to Sail. The early maritime dispersal of Neolithic crops from the Aegean to the western Mediterranean (de Vareilles et al., 2020; Zilhão, 2014),

...while in S-Portugal, local Mesolithic hunter-gatherers still lived on pine nuts (Soares & Tavares da Silva, 2018)

rooted deep in the Alentejo



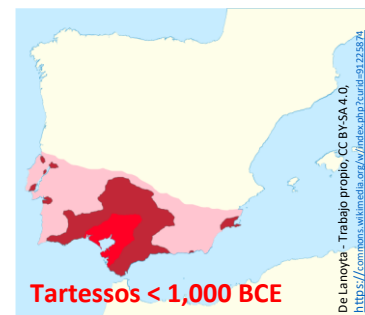
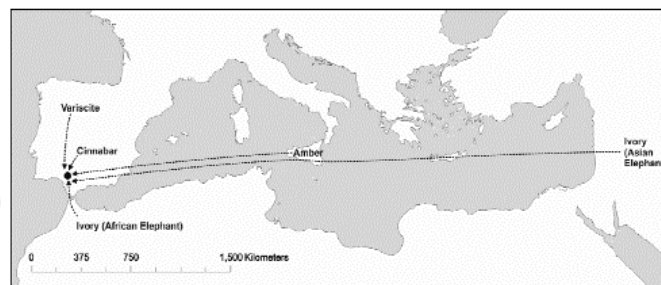
Mesolithic hunter-gatherers living on pine nuts

Soares & Tavares da Silva, 2018



Ivory vessel (Asian elephant tusk)

Copper Age ~2 500 BCE (García Sanjuan et al., 2013)



De La Noya - Trabajo propio, CC BY-SA 4.0. <https://commons.wikimedia.org/wiki/index.php?title=DeLaNoya>

Discussion *Pinus pinea* – the “tame pine”? (s. 1 000 BCE)

Linked to the **Megalithic, Tartessian and Phoenician** cultures

A. Tartessos (Andalusia, ES) [Neanderthal 50 kyr](#)

B. Alcácer do Sal (Tagus & Sado estuaries, PT)

Neanderthals 100 kyr ([Zilhão, 2020](#)), Phoenician *Bevipo/Keition*

C. Inner Spain [Bronze 3.5 ka](#)

1. Emporion (Catalonia, ES)

Greek Emporion (trade post) between →Massalia and →Tartessos

2. Nora (Sardegna, IT) Phoenician colony

[or *Tartessian*, founded by “king Nórax, grandson of Geryon”]

3. Massalia (Bouches-du-Rhône, FR)

Greek colony founded from →Phocaea

4. Phocaea (Foça, Izmir, TR) [*“Arganthonios, king of Tartessos, funded their city wall”*]

Greek city 80 km south of →Pergamon (Bergama), capital famous for its Cybele temple

5. Kozak (Izmir, TR) in 1920 “the most relevant stone pine forest in Turkey”, but in 1930 < 10.000 ha
20 km north of →Bergama

6. and, of course, the very Phoenicia itself (Lebanon)

...and we know that, and even *when*, Phoenicians did introduce stone pine first in Sicily [Stika et al., 2007; [Moricca et al. 2021](#)]

In Classic empires it was widely planted, as sacred tree of →Cybele, cones were ceremonial offers and grave good...

(and its closed cones were used as [stoppers for shipped wine amphoras!](#))



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Pergamon (by Klaus-Peter Simon - Own work, CC BY-SA 3.0,
<https://commons.wikimedia.org/w/index.php?curid=12767093>)

Conclusions

- We successfully **identified clones**, genetic relationships and **gene pools**
- Deep insight into the **natural and cultural story** of this pine
- Better **traceability** of genetic material and **knowledge-based conservation**
- Genome-wide markers will allow to develop low-input breeding strategies



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B4est



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