Tree decline of Italian pedunculate oak populations: a multidisciplinary approach for selecting and producing resistant forest genetic resources

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evoltree

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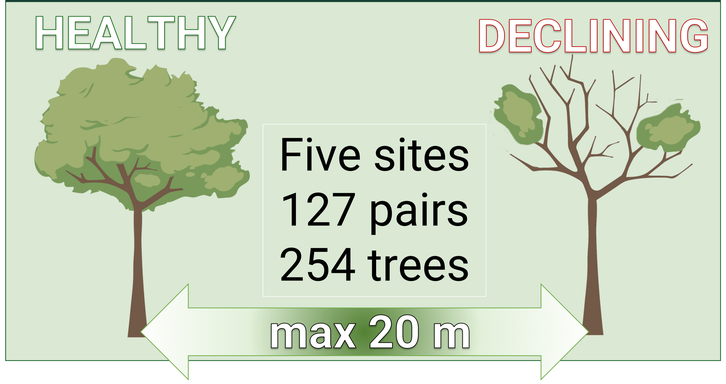
OBJECTIVE

Widespread phenomena of decline have been observed since the late 1990s in pedunculate oak (*Quercus robur* L.) populations of northern Italy. The causes of this decline are still unknown.

Are there genetic variants that provide some resistance to decline?

METHODS

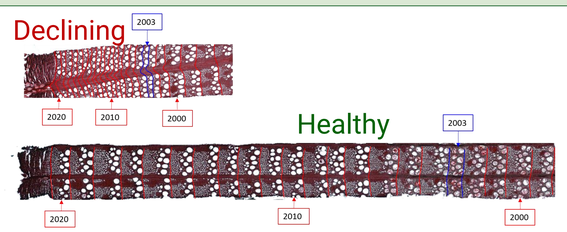


GENOTYPE-PHENOTYPE ASSOCIATION

GENOMIC

SPET design of 90k probes:
- at least one probe per gene
- covering genomic regions involved in responses to biotic and abiotic stresses
- covering genome as homogeneously as possible

PHENOMIC

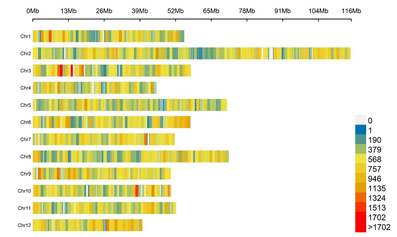


$$mean\ tree\text{-}ring\ widths\ of\ the\ last\ 20\ years_i = \beta_0 + \beta_1 \times Site_i + \beta_2 \times Age_i + \beta_3 \times Microsite_i + \varepsilon_i$$

ε = ***index of dendrochronological decline*** *(DD)*

FIRST RESULTS

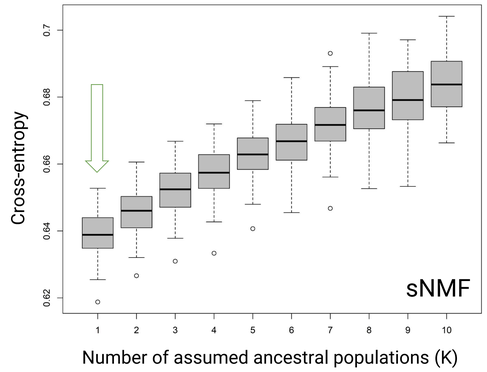
Distribution of SNP number in the 12 chromosomes over 1Mb windows

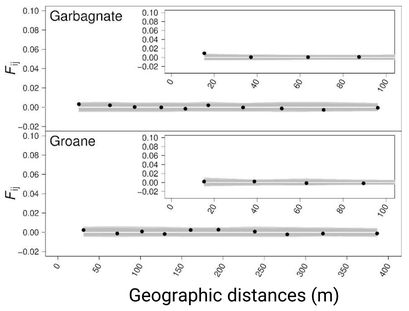


408.219 SNPs

~27 Mb coverage
(3.3% of the 815 Mb genome)

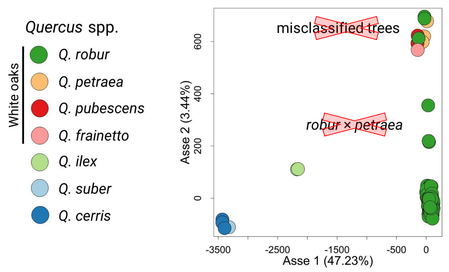
Genetic structure among and within populations





NO GENETIC STRUCTURE AMONG AND WITHIN POPULATIONS

Detection of hybrid and related trees



Pop_1	Ind_1	Pop_2	Ind_2	Kinship
Fagiana	FAG013D	Fagiana	FAG012D	0.498
Geraci	GER010S	Geraci	GER010D	0.495
Groane	GRO023D	Groane	GRO022D	0.202
Geraci	GER004D	Geraci	GER001S	0.189
Geraci	GER014D	Geraci	GER010S	0.181

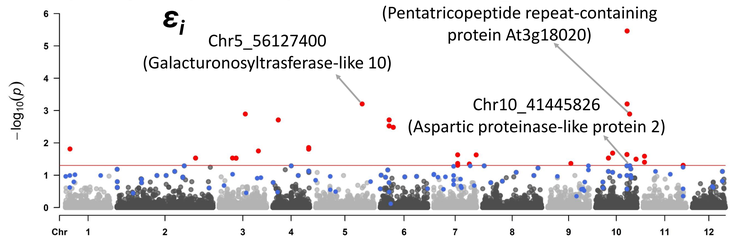
FINAL DATASET: 244 TREES

Genotype-phenotype association

«Only one gene, **a galacturonosyltransferase-like 10**, showed increasing expression during gall development» (Hearn et al. 2019)

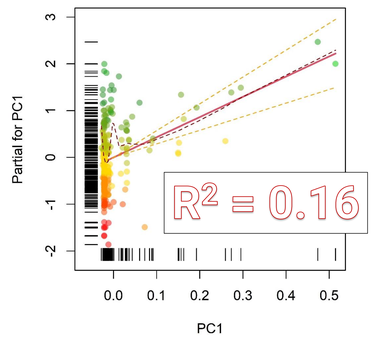
«The **genomic region on chromosome 10** was enriched in two classes of RLK genes, which encode a major family of PRRs and showed a high frequency of signatures of positive selection in oak» (Bartholomé et al. 2020)

$$DD_i = \beta_0 + \beta_1 \times SNP_i + \varepsilon_i$$



- EMMAx + PLINK software (33 SNPs, 4 non-synonymous mutations)
- PLINK software (102 SNPs)

$$DD_i = \beta_0 + \beta_1 \times PC1_i + \beta_2 \times PC2_i + \beta_3 \times PC3_i + \varepsilon_i$$



TAKE-HOME MESSAGES

- ❖ Resistance to decline is seemingly polygenic
- ❖ Preliminary but promising indications for selecting resistant forest genetic resources

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