Genetic architecture of leaf specialized metabolites in sessile oak (Quercus petraea)

Domitille Coq–Etchegaray, Stéphane Bernillon, Grégoire Le Provost, Antoine Kremer, Alexis Ducousso, Benjamin Brachi, Céline Lalanne, Fabrice Bonne, Annick Moing, Christophe Plomion

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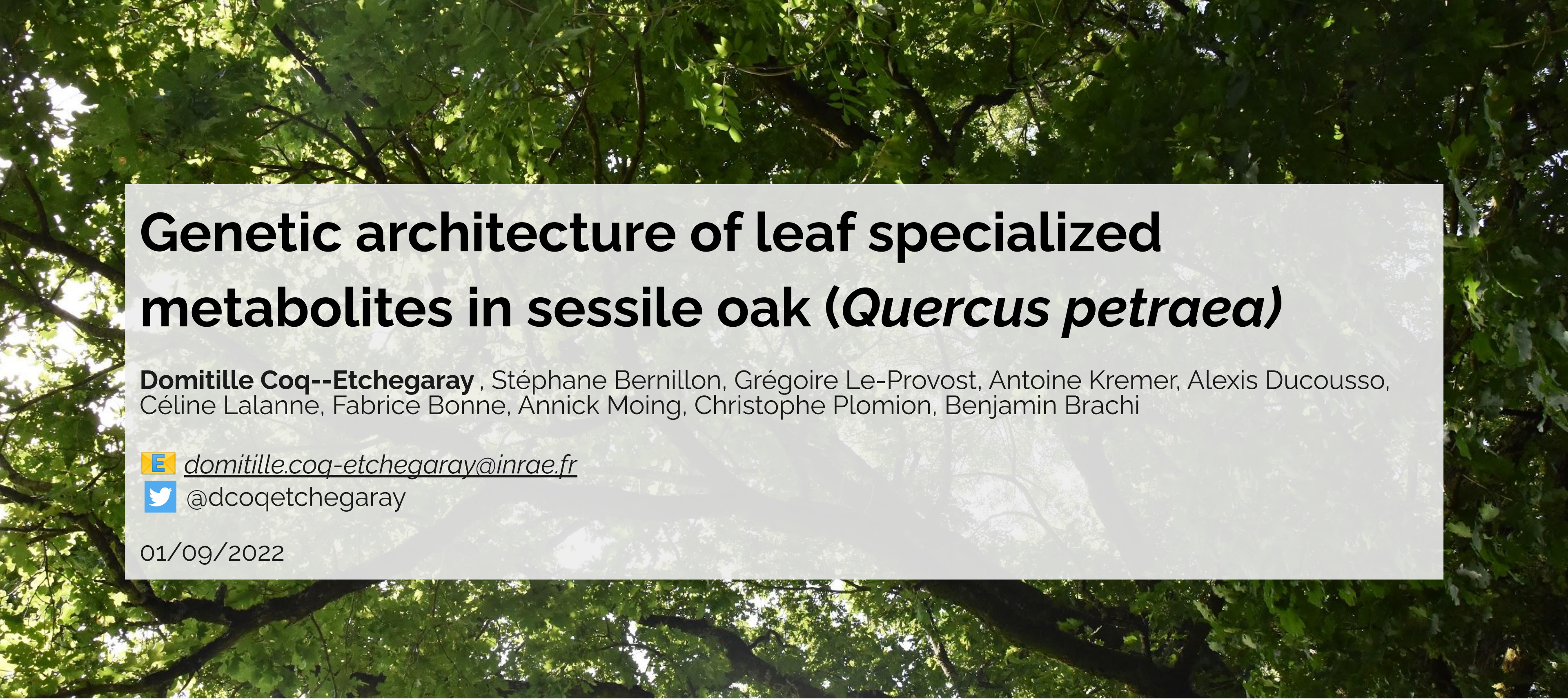

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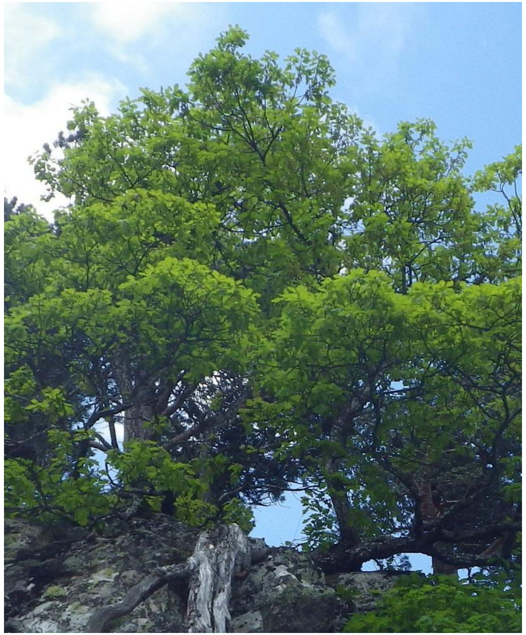
01/09/2022

Sessile oak (*Quercus petraea*) and specialized metabolites

- Dominant tree species in Europe
- 15% of French forests

- Foundation species & associated with a rich insect community
  - Influenced by specialized metabolites produced by oaks?



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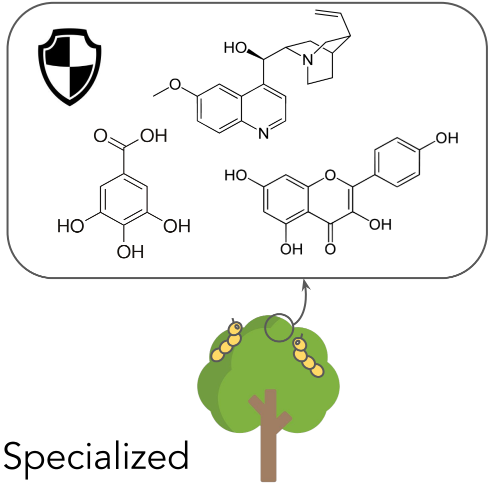


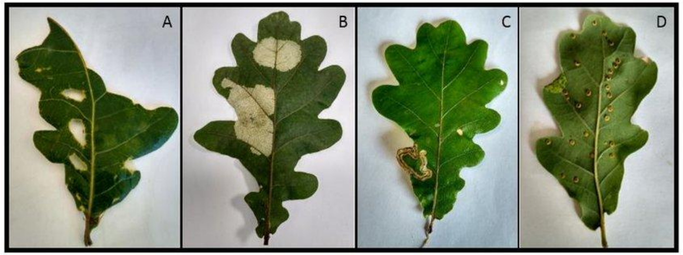
Specialized metabolites

Sessile oak (*Quercus petraea*) and specialized metabolites

- Dominant tree species in Europe
- 15% of French forests

- Foundation species & associated with a rich insect community
    - Influenced by specialized metabolites produced by oaks?

- Leaf metabolites in oaks:
    - Impact leaf herbivory (ex: Bertić *et al.* 2021)
    - Resistance to abiotic stresses (ex: Aranda *et al.* 2020)



Source: Valdés Correcher, E. (2020). *Drivers of insect herbivory in Pedunculate oak (Quercus robur) from tree to biogeographical scale.* 201.

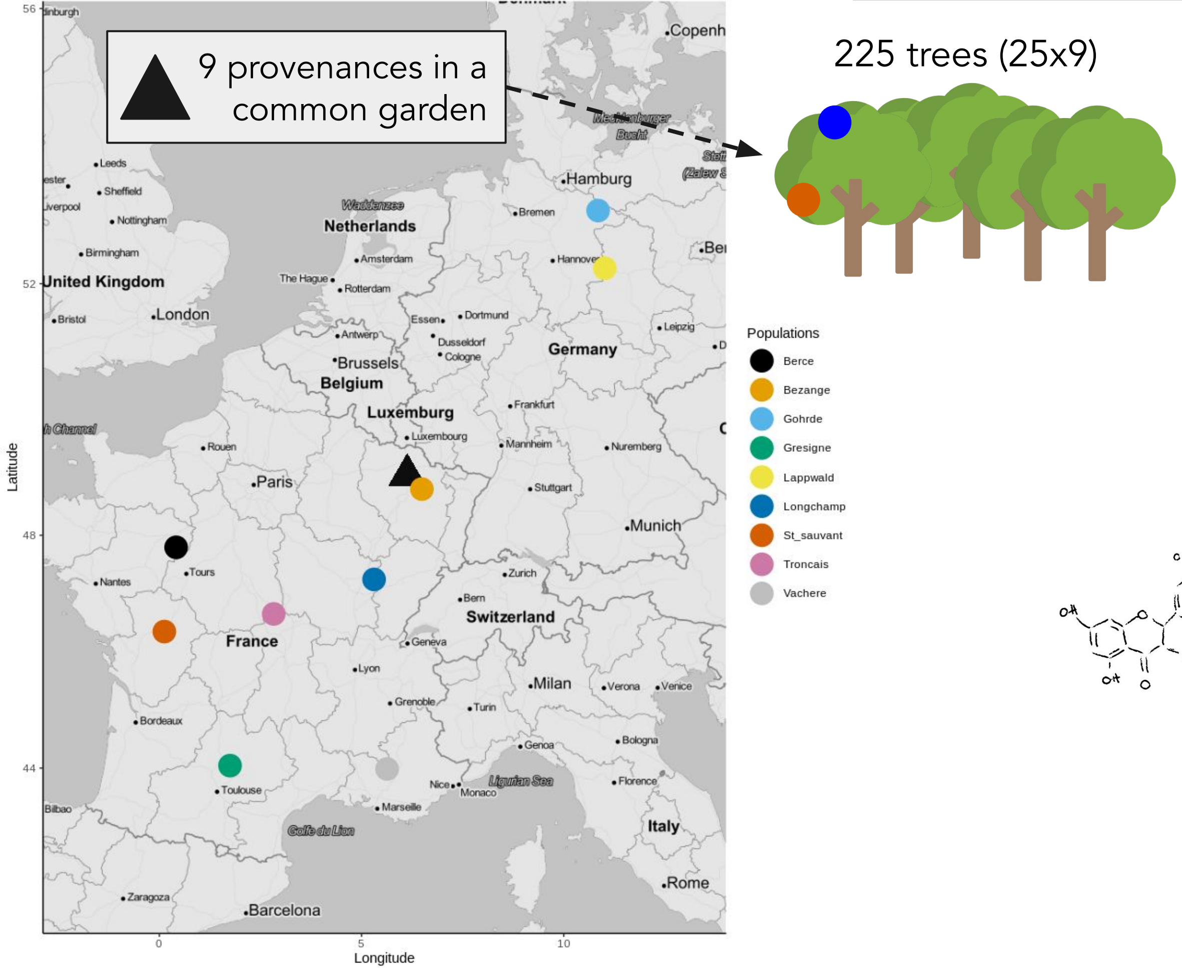
Genetic basis of leaf specialized metabolites within sessile oaks

1. Is there variation for specialized metabolites among and/or within oak populations?

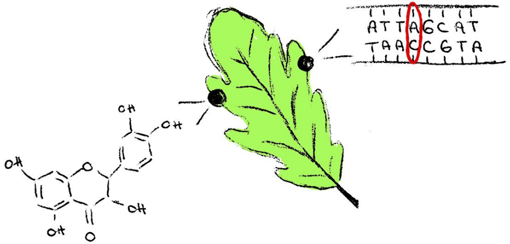
2. What proportion of the variation in leaf specialized metabolites is explained by genetic variation?

3. Is the variation of specialized metabolites locally adaptive? In what proportion?

Oak leaves sampling, metabolomics & genomics dataset


9 provenances in a common garden

225 trees (25x9)



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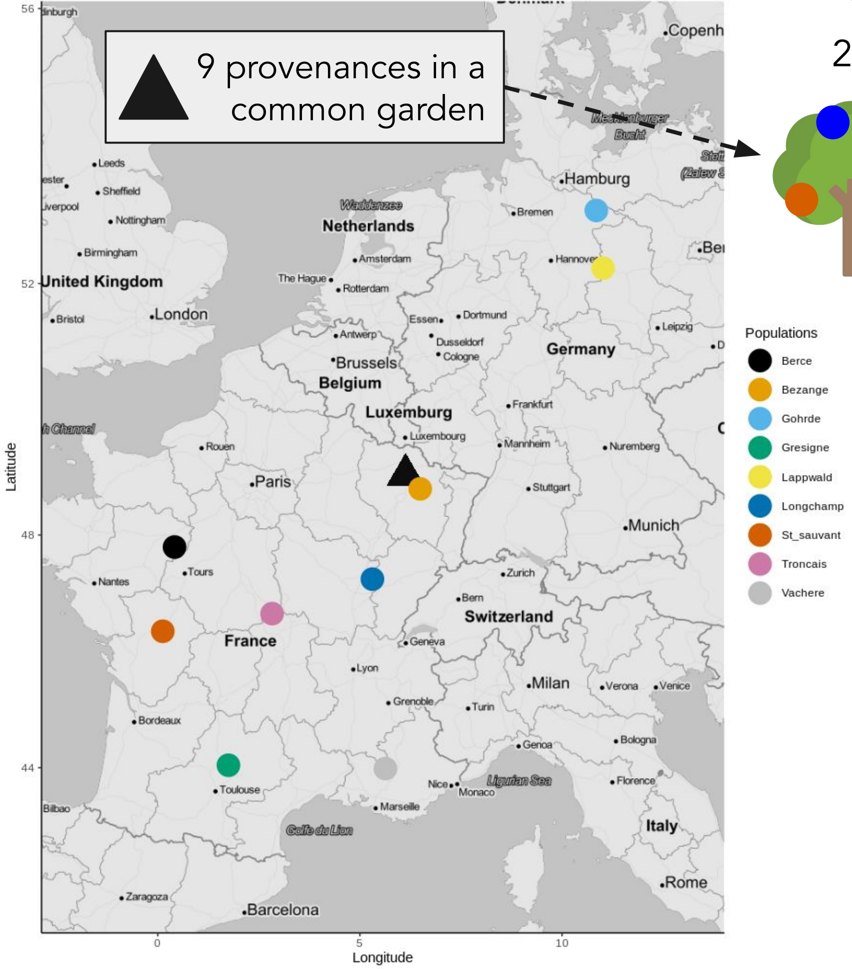

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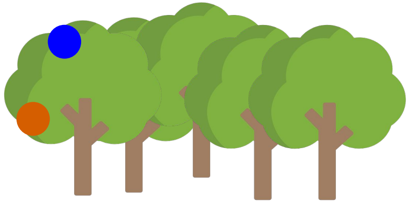
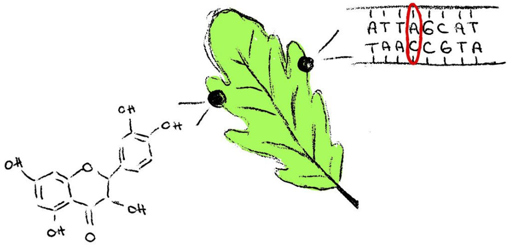


Whole genome low depth sequencing (~10X)

~1,400,000 SNPs

Illumina Paired-end
150 bp



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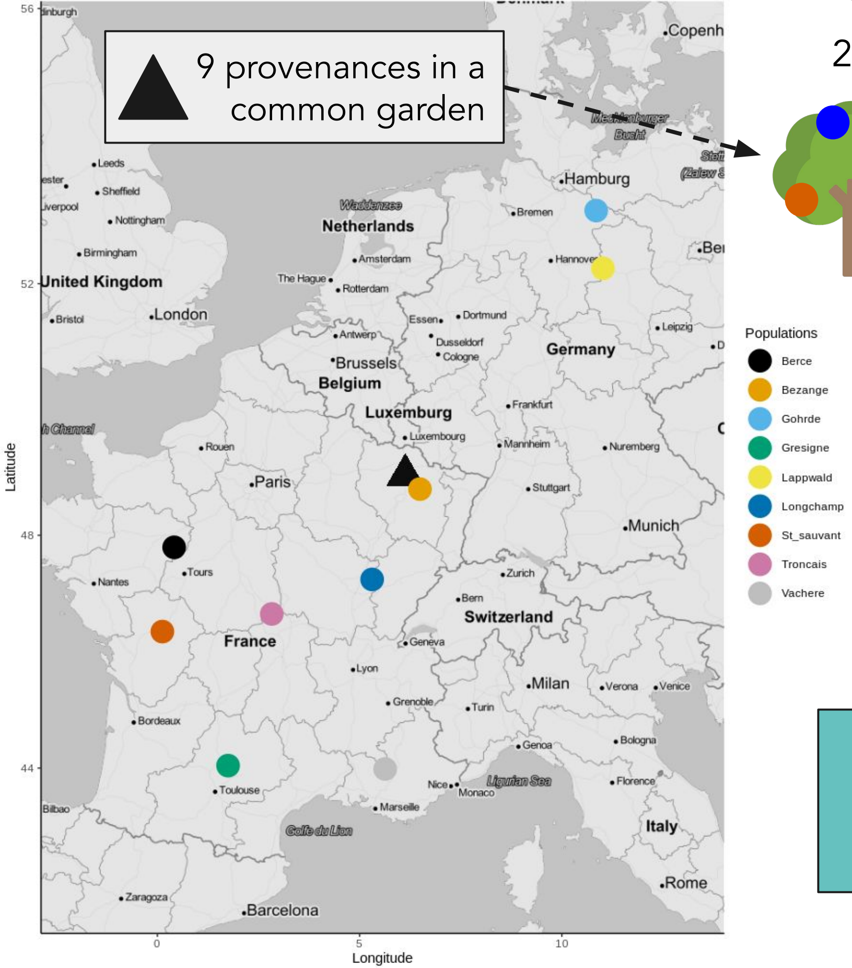

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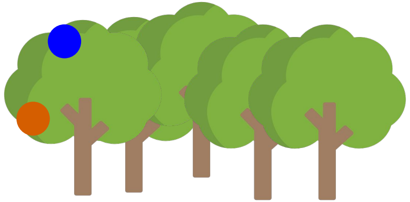
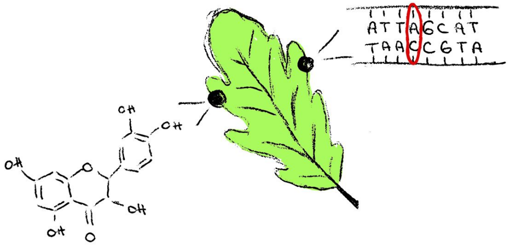




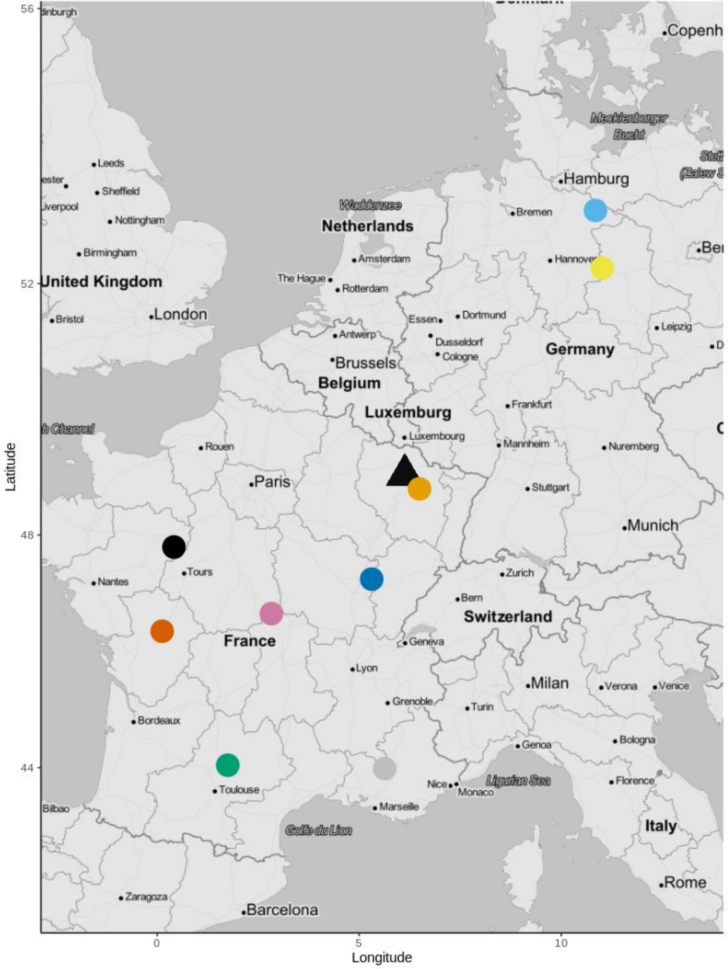
Whole genome low depth sequencing (~10X)
~1,400,000 SNPs

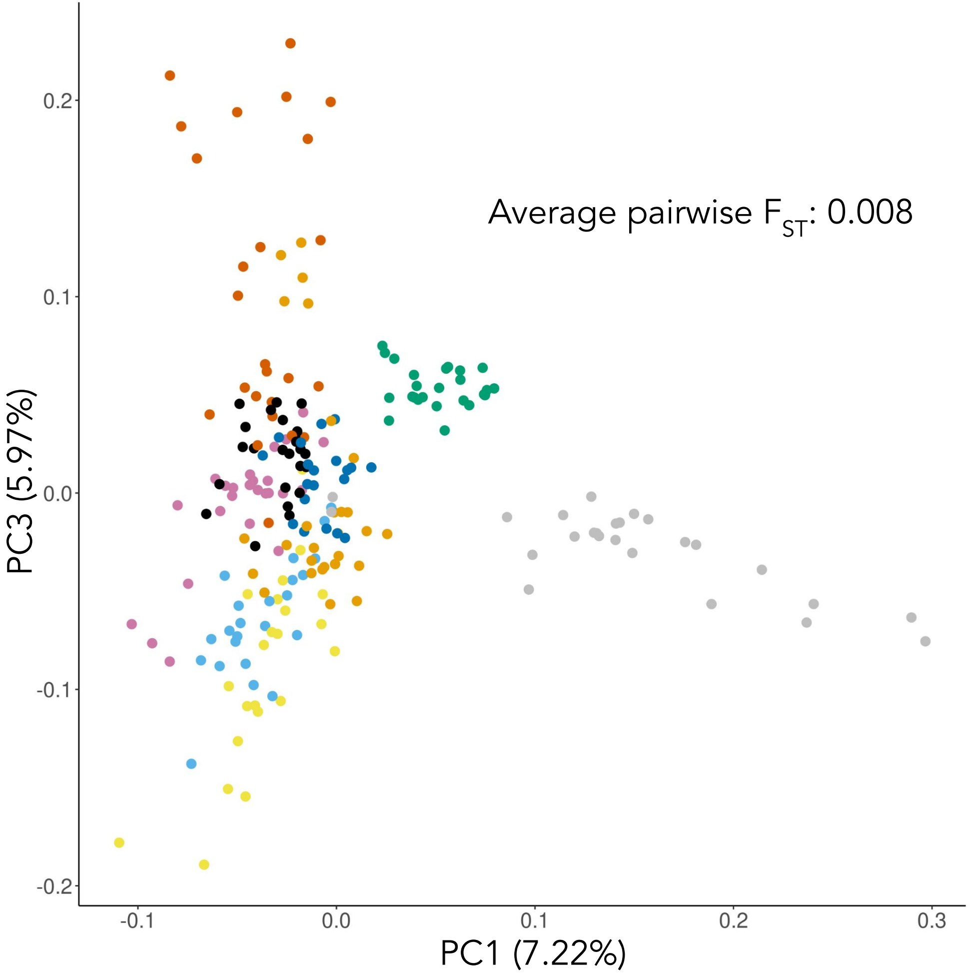
Illumina Paired-end
150 bp

High throughput untargeted LC-MS
219 molecules

10 min gradient
(QTOF)

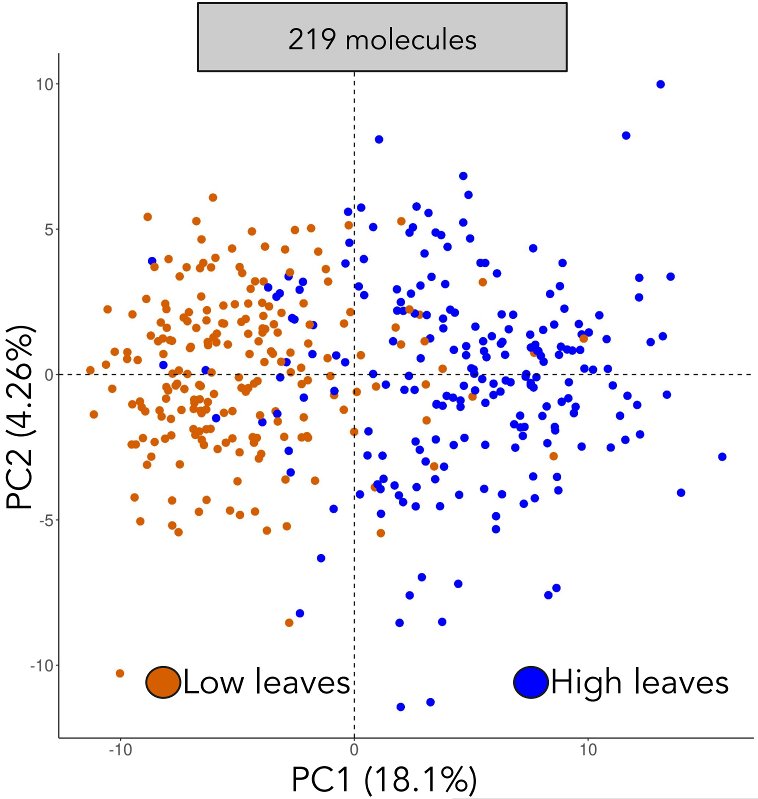
350K SNPs capture weak population structure

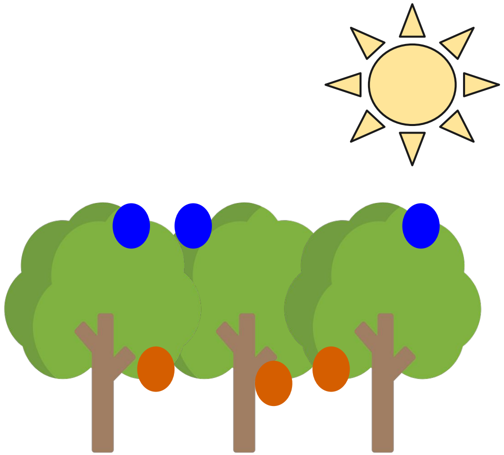




Average pairwise F_{ST}: 0.008

Leaf specialized metabolites profile depends on branch height



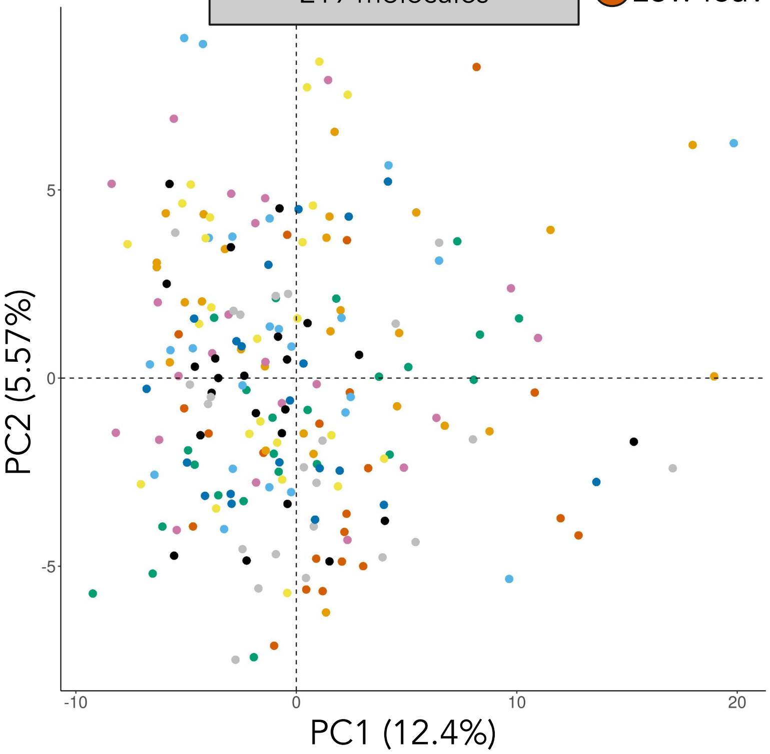


Variation within individuals, likely influenced by exposition to sunlight.

Nearly no phenotypic differentiation between provenances

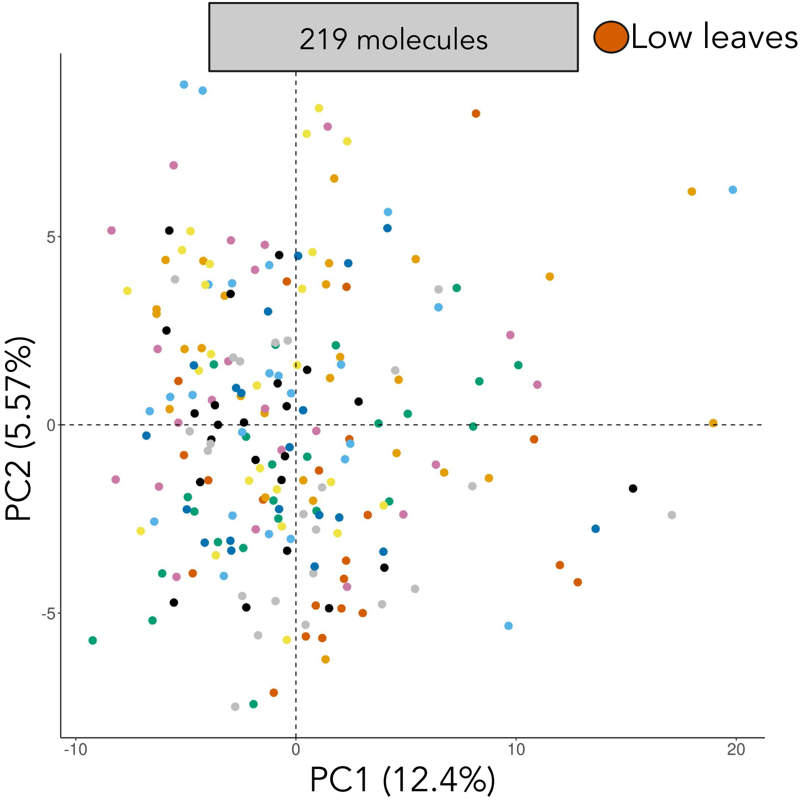
219 molecules

● Low leaves



No differentiation between provenances at the leaf metabolome scale

Nearly no phenotypic differentiation between provenances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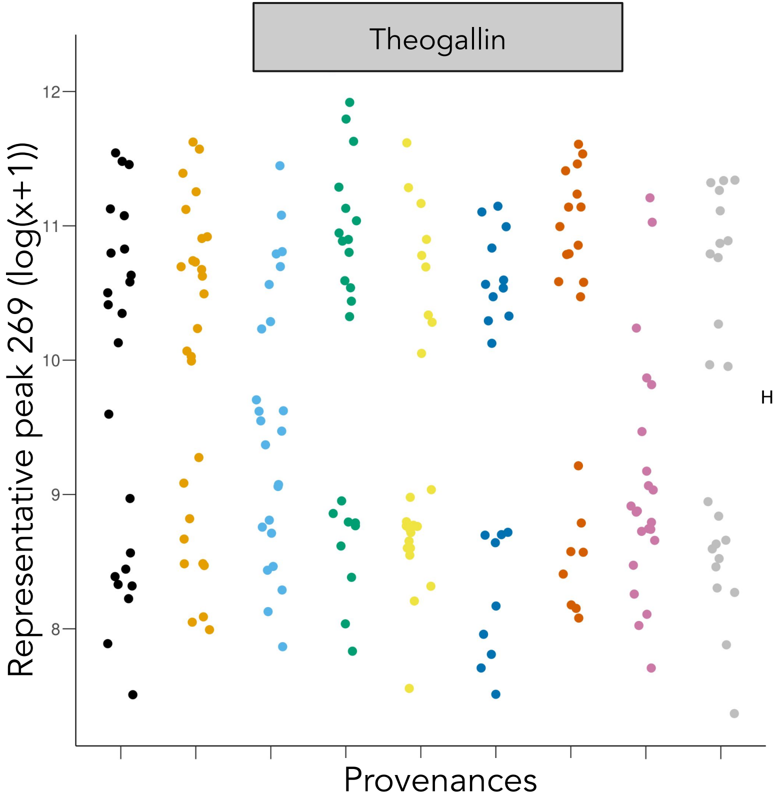
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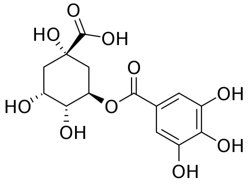
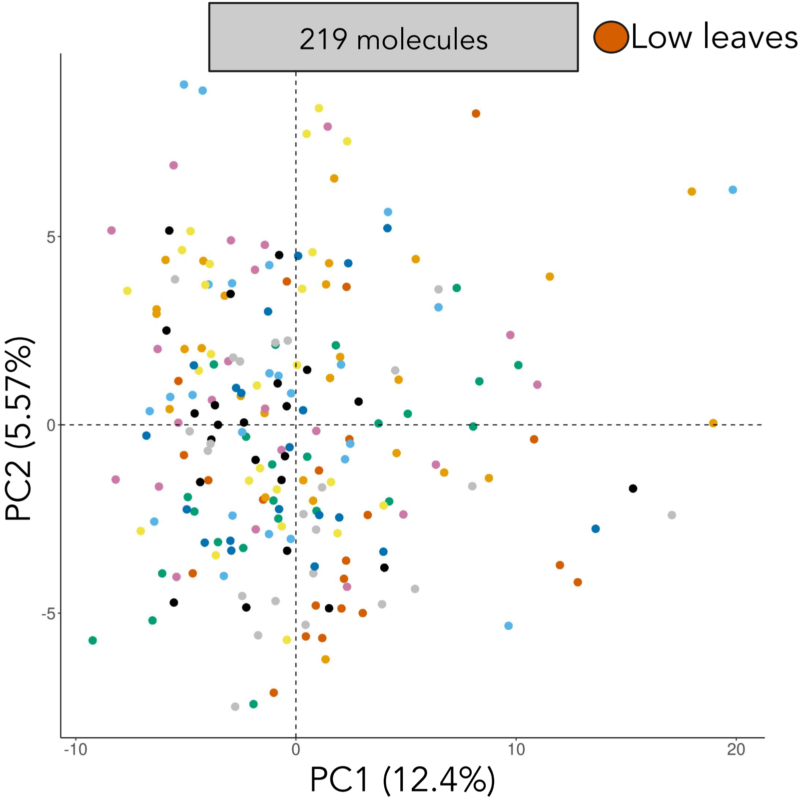


No differentiation between provenances at the leaf metabolome scale

Variation within provenances at the molecule scale for the majority of molecules

Nearly no phenotypic differentiation between provenances



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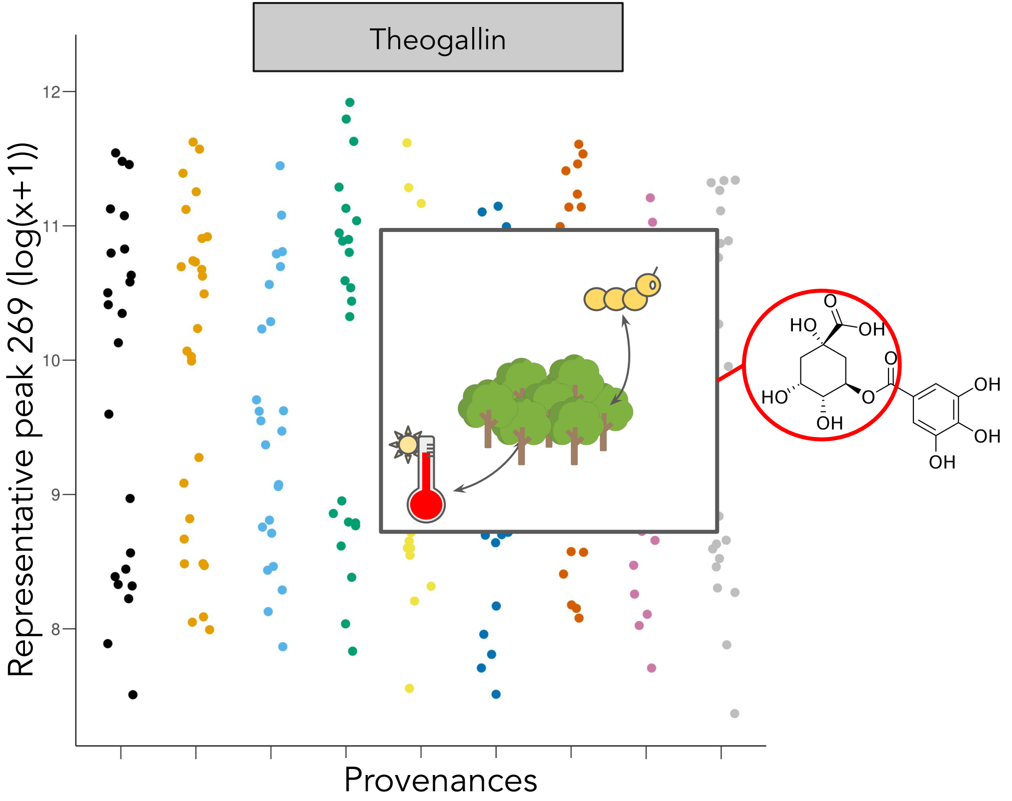

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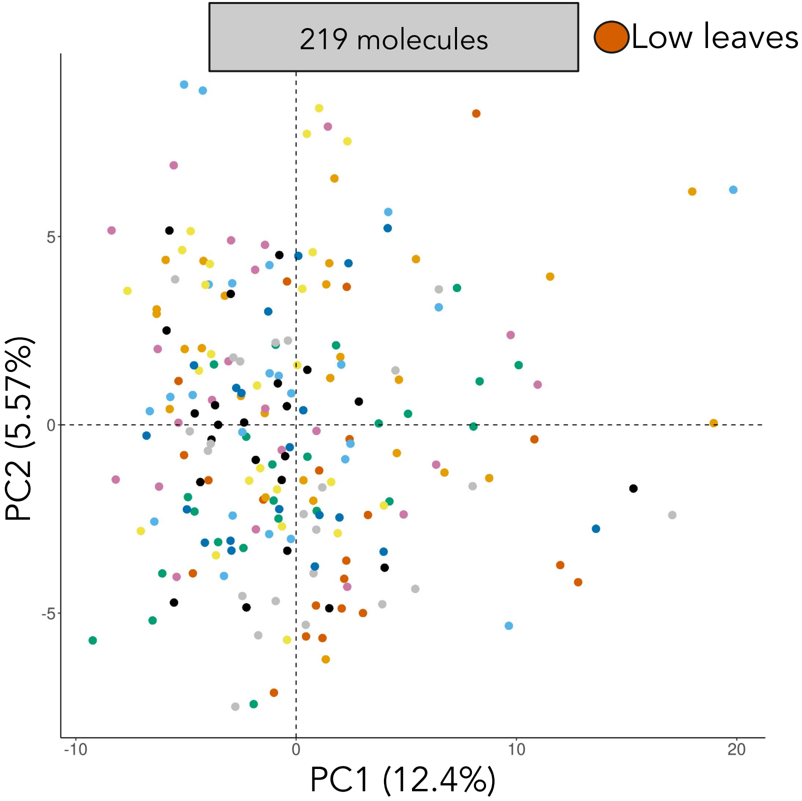

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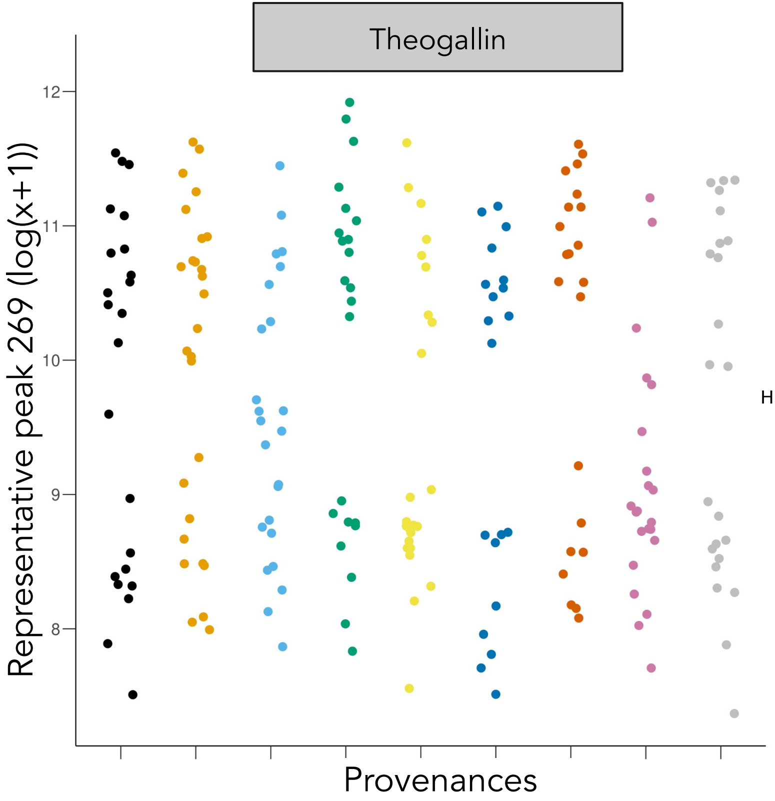
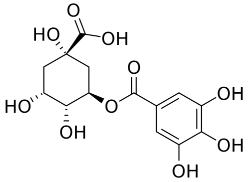
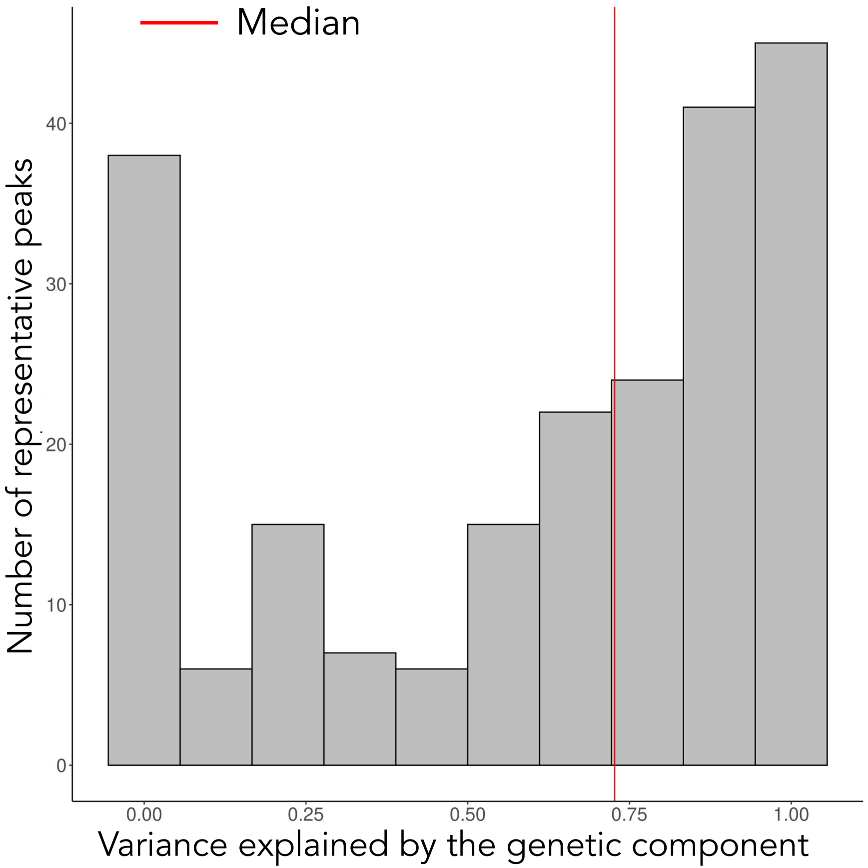




Variation within provenances at the molecule scale for the majority of molecules

Specialized metabolites variation is largely genetically determined



● Low leaves

Genome-wide efficient mixed-model association

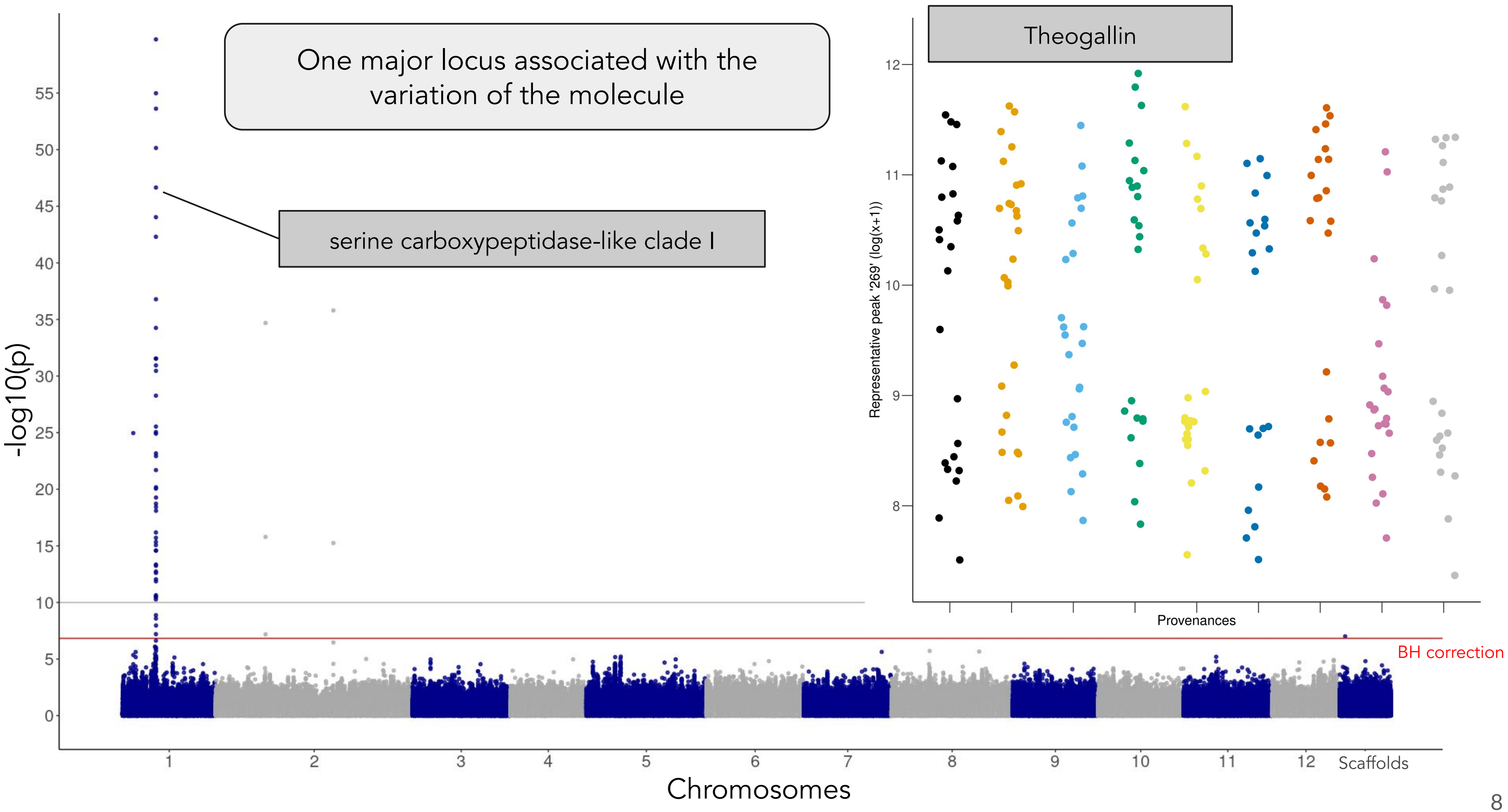
Univariate Linear Mixed Model

(GEMMA)

Proportion of specialized metabolites variance explained by the genetic similarity among trees (kinship matrix)

50% of molecules have more than 70% of their variation explained by the genetic variation

Genome wide association of specialized metabolites

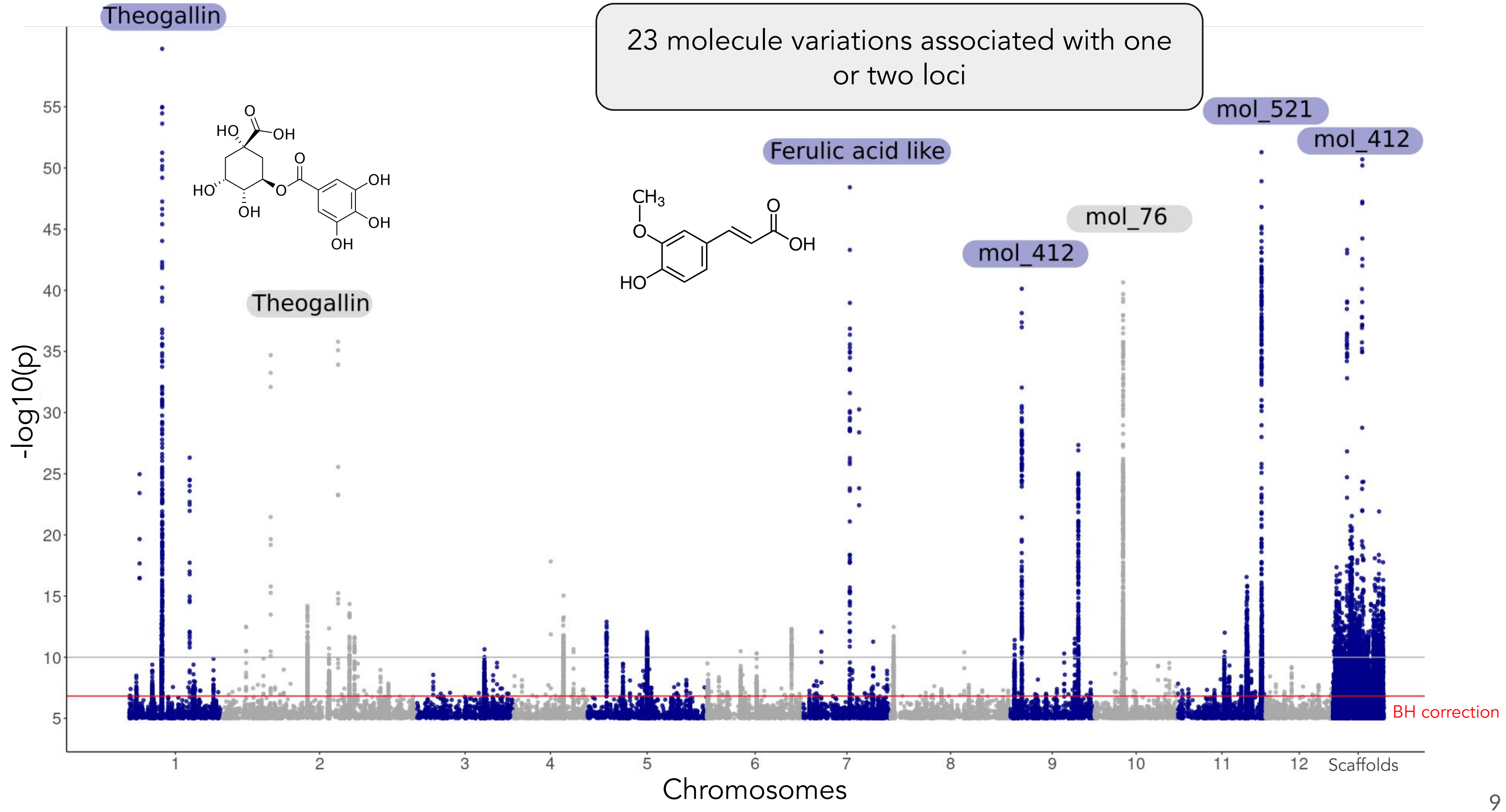


One major locus associated with the variation of the molecule

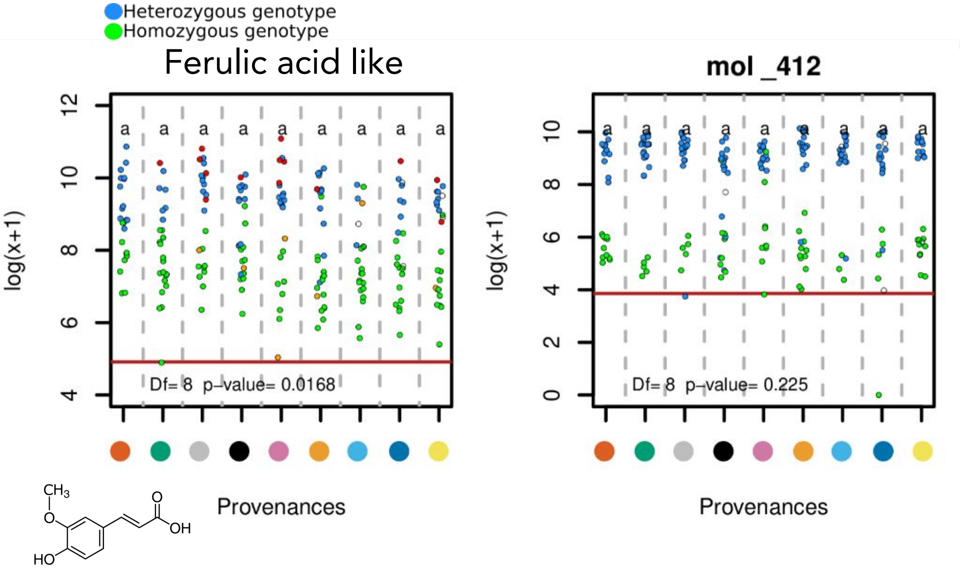
serine carboxypeptidase-like clade I

Genome wide association of specialized metabolites

23 molecule variations associated with one or two loci

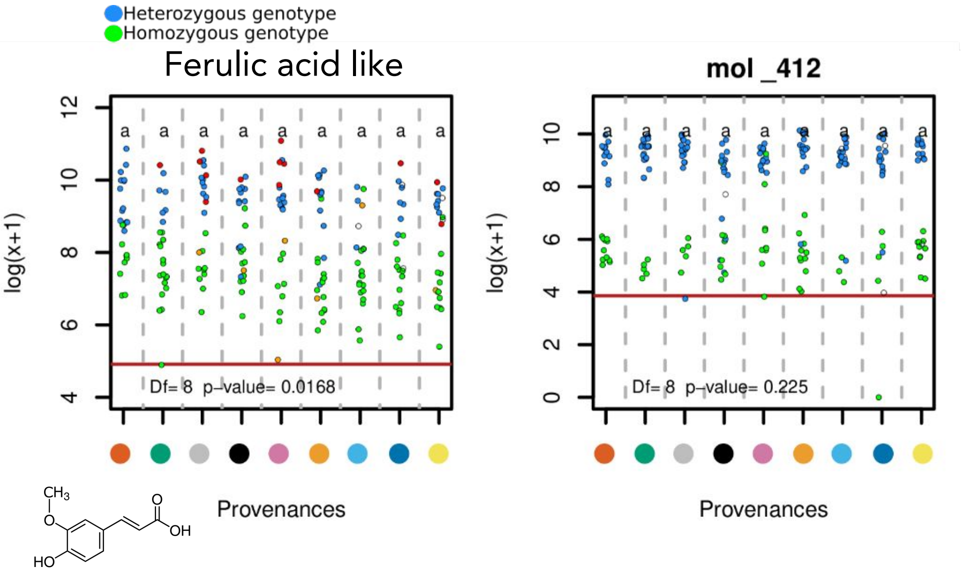


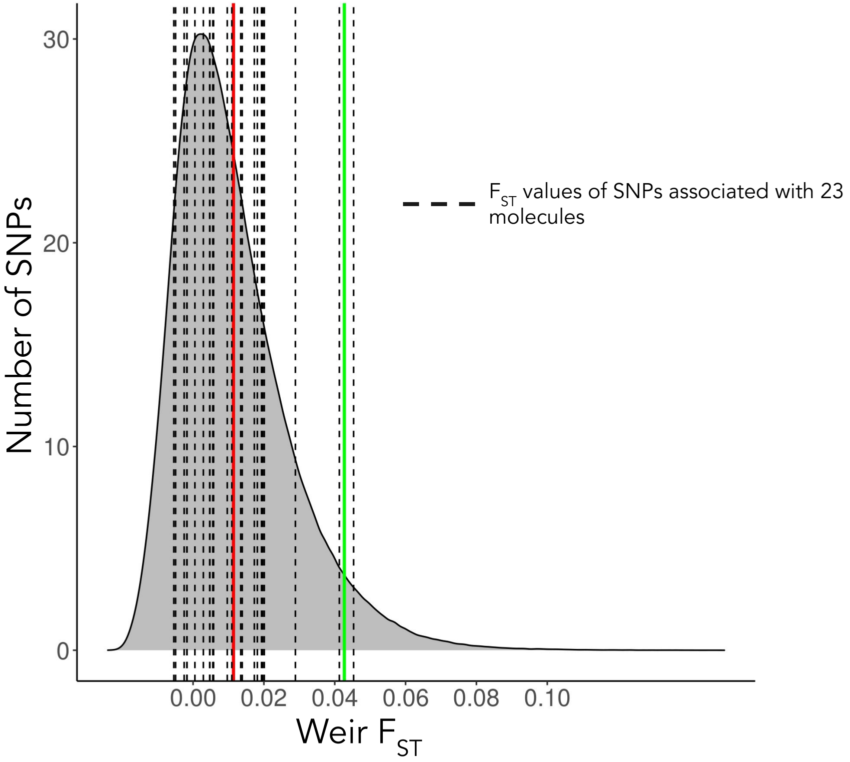
Many specialized metabolites have oligogenic architectures



The genotypes for genetic markers associated with molecule variations are in the 9 provenances

Associated markers are not differentiated among provenances





The genotypes for genetic markers associated with molecule variations are in the 9 provenances

Molecules with heritable variation have low F_{ST} values

Conclusion-No evidence of local adaptation for measured molecules

Weak phenotypic differentiation among provenances

Intra-individual variation of specialized metabolites

Most of the variation within oak provenances

Specialized metabolites variation is heritable

Oligogenic architecture of the variation

Polymorphisms within the 9 provenances

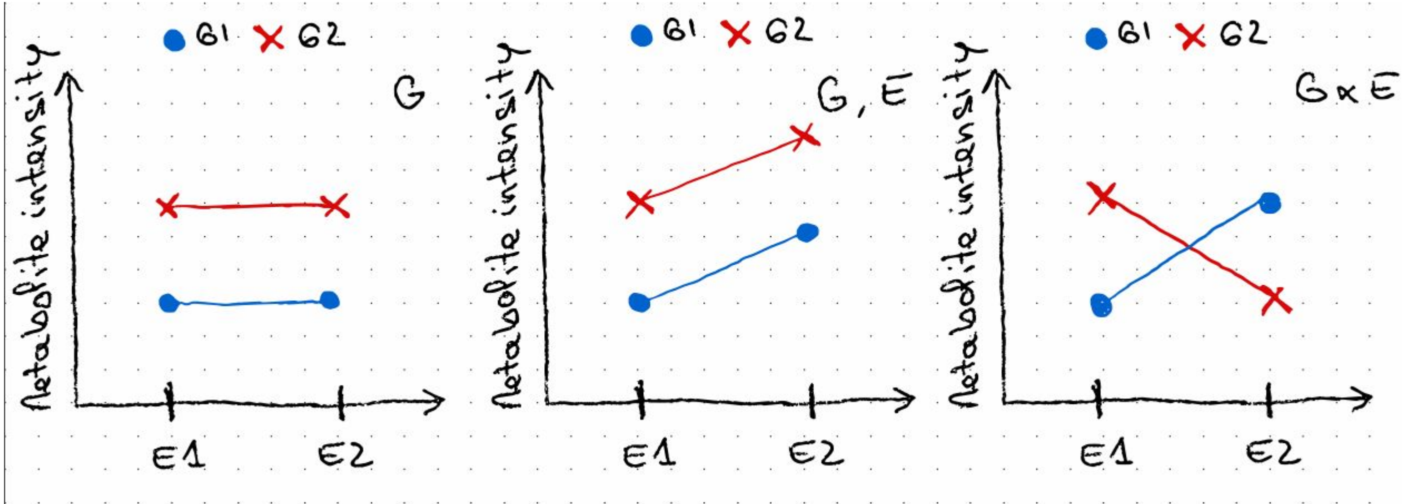
<u>Most molecules measured are not locally adaptive</u>

Hypothesis: Maintenance of variation within oak provenances (balanced selection)

What's next?

Genetic marker development at loci associated with specialized metabolites
~screening natural oak populations

Is the variation of specialized metabolites correlated with tree growth ?
(fitness)



Supervisors
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