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

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

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

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01/09/2022



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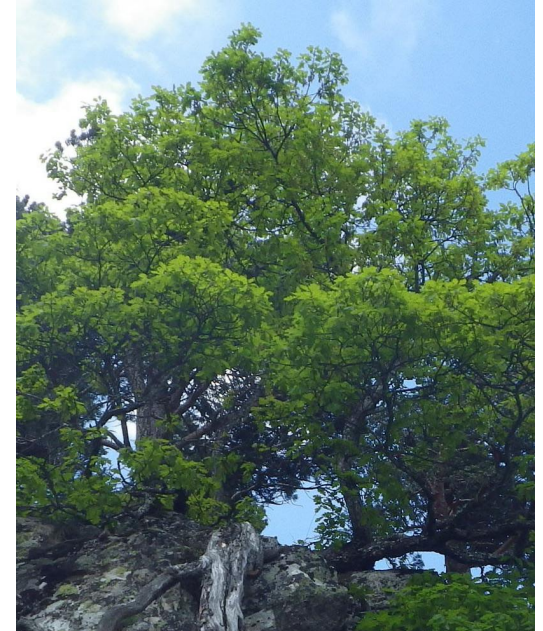


UMR
Silva

Sessile oak (*Quercus petraea*) and specialized metabolites

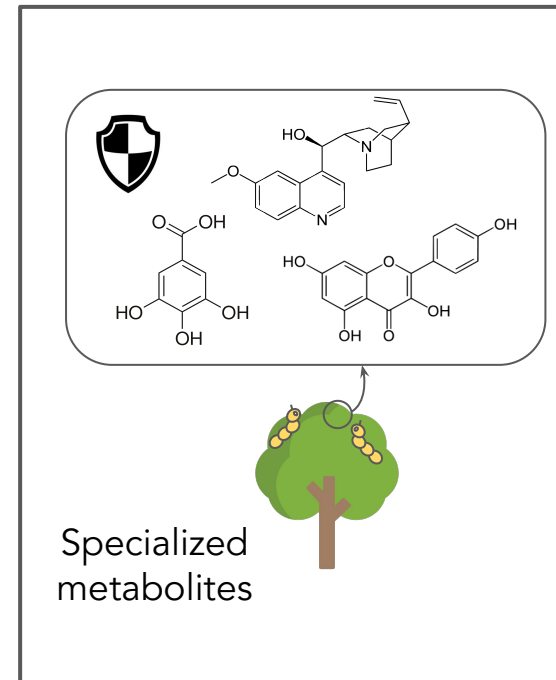
- Dominant tree species in Europe
- 15% of French forests

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



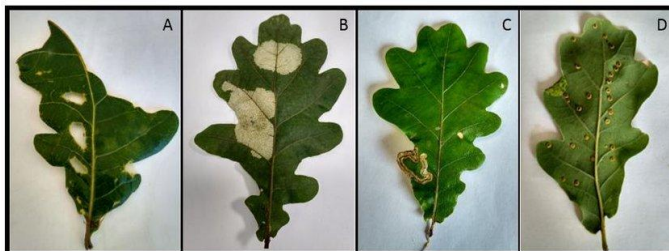
Sessile oak (*Quercus petraea*) and specialized metabolites

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Sessile oak (*Quercus petraea*) and specialized metabolites

- Dominant tree species in Europe
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 - 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?

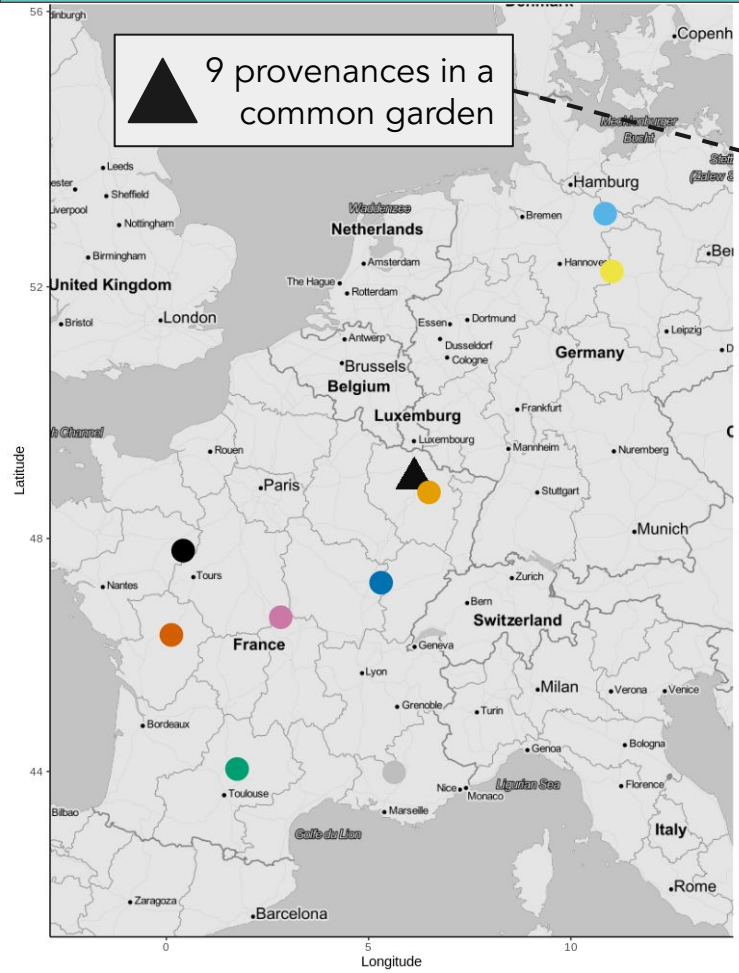
2

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

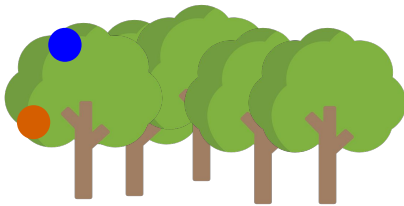
3

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

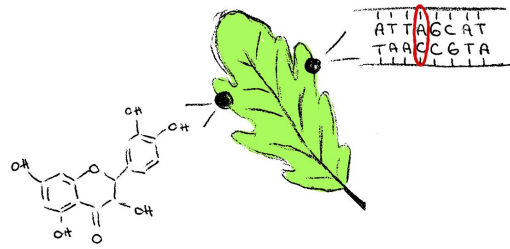
Oak leaves sampling, metabolomics & genomics dataset



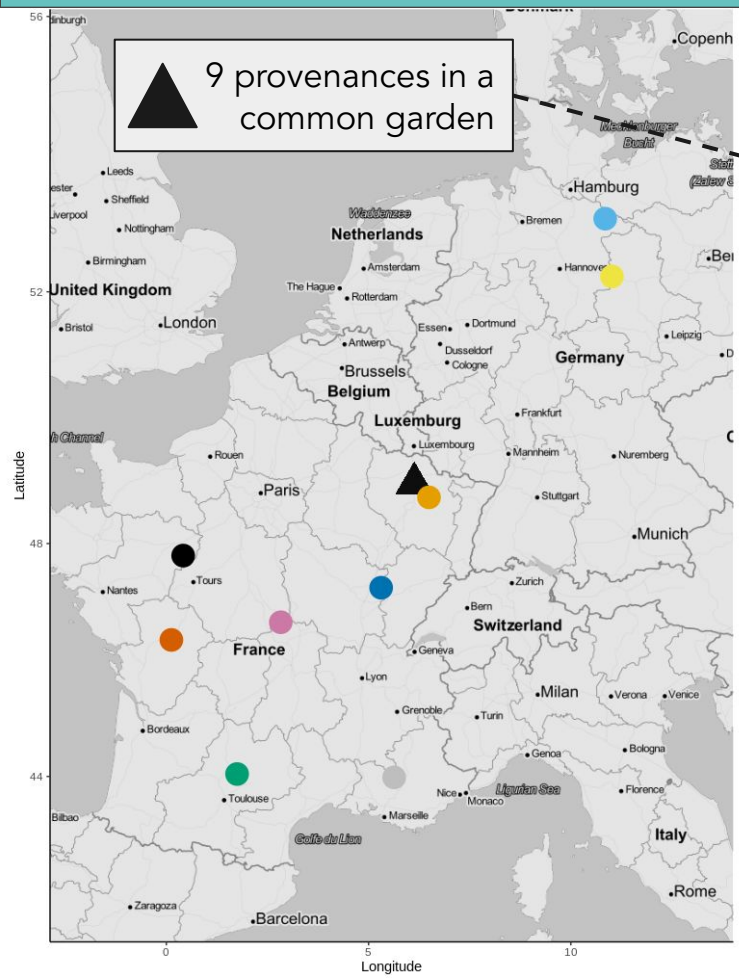
225 trees (25x9)



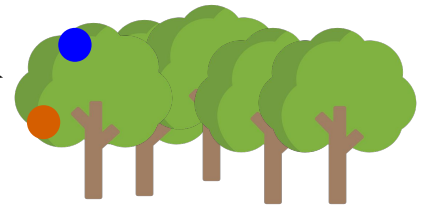
- Populations
- Berce
 - Bezange
 - Gohrde
 - Gresigne
 - Lappwald
 - Longchamp
 - St_sauvant
 - Troncals
 - Vachere



Oak leaves sampling, metabolomics & genomics dataset



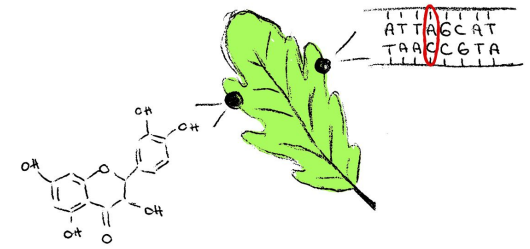
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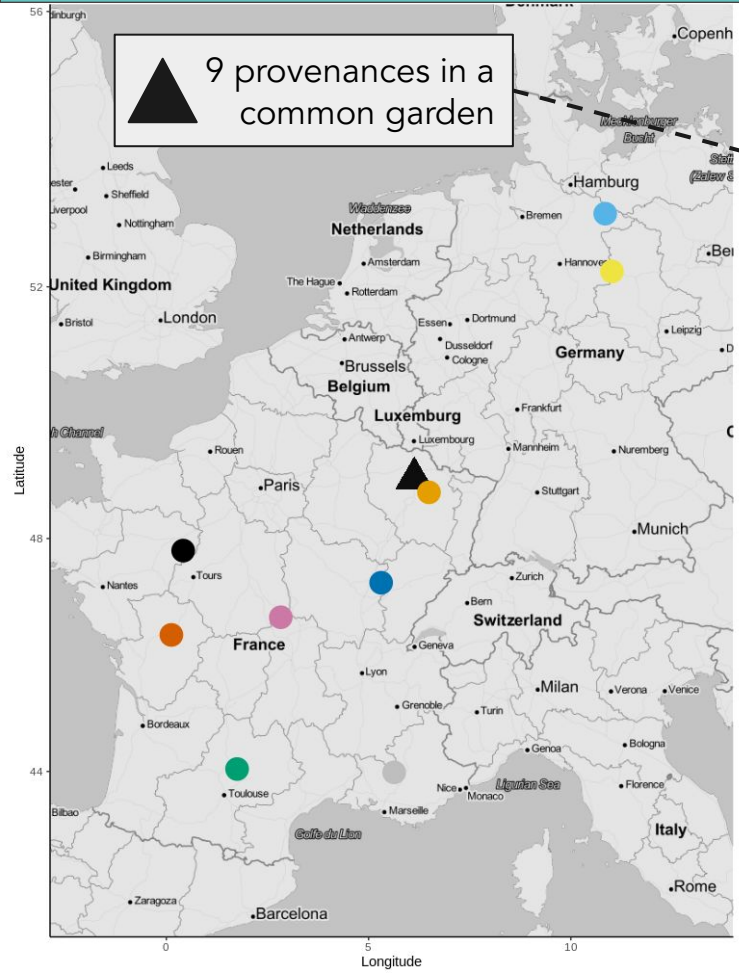
- Populations
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 - Troncals
 - Vachere

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

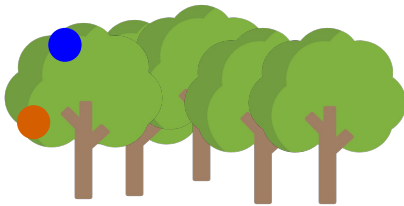
ILLUMINA Paired-end
150 bp



Oak leaves sampling, metabolomics & genomics dataset



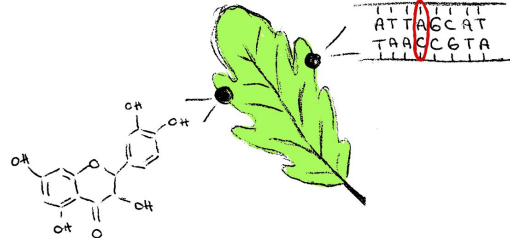
225 trees (25x9)



- Populations
- Berce
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 - Gohrde
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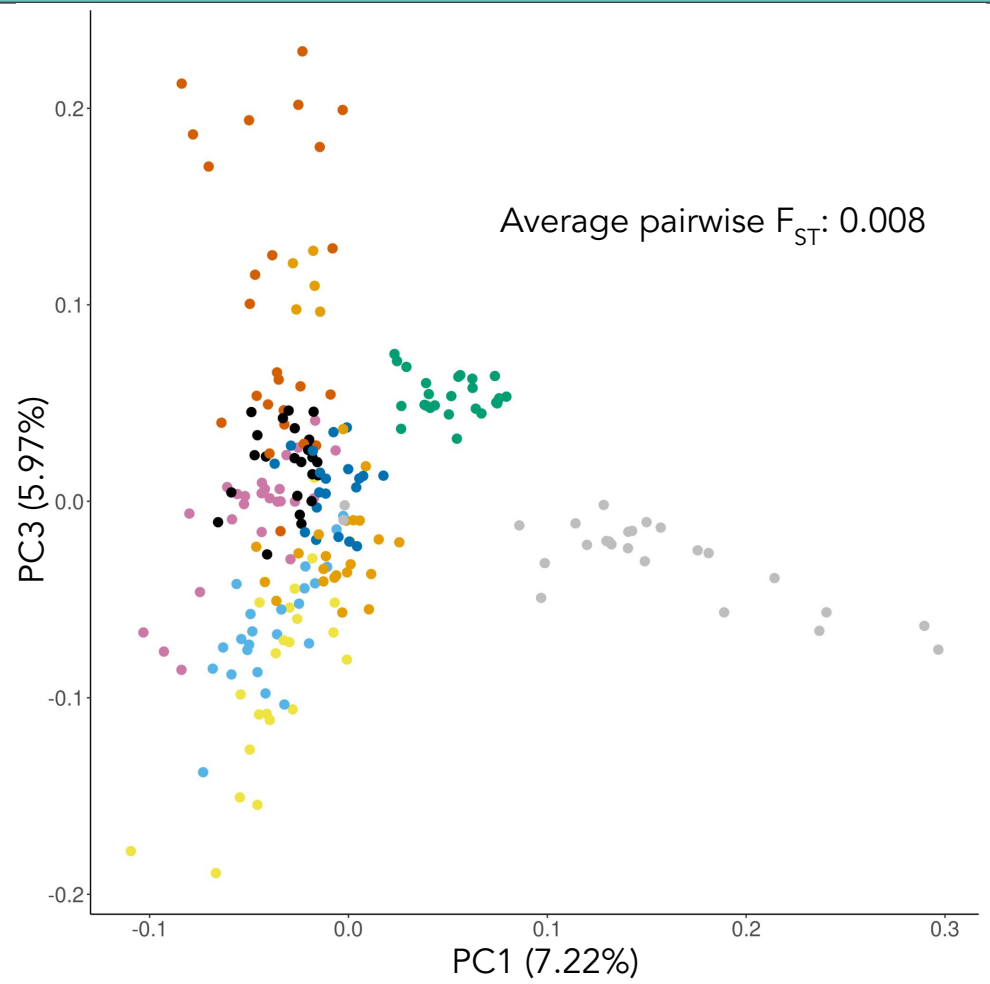
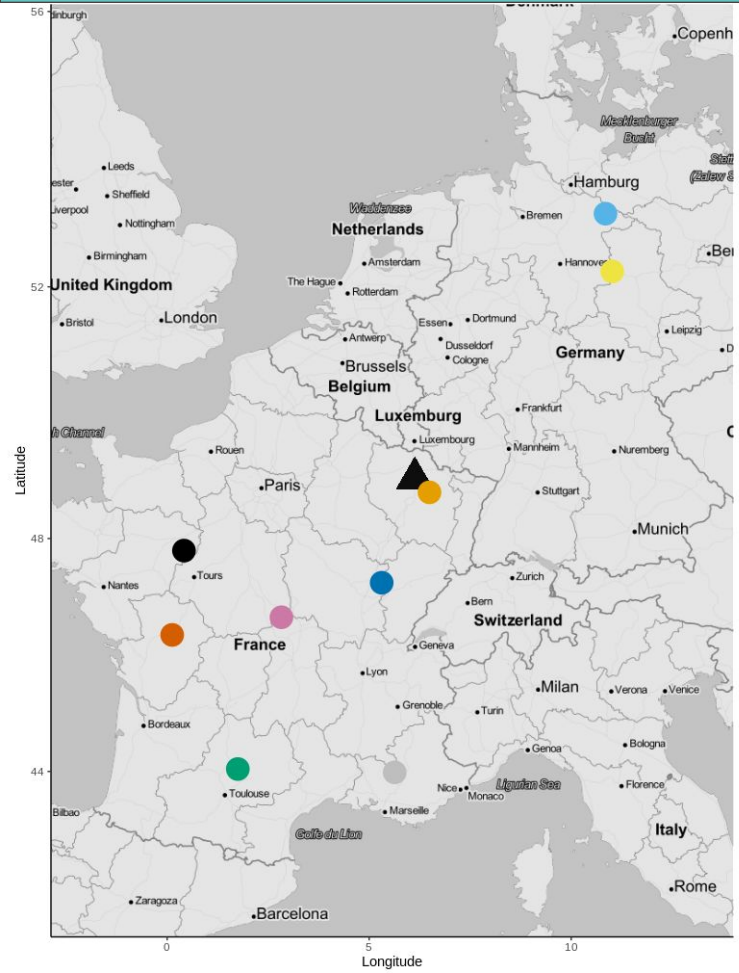
Illumina Paired-end
150 bp



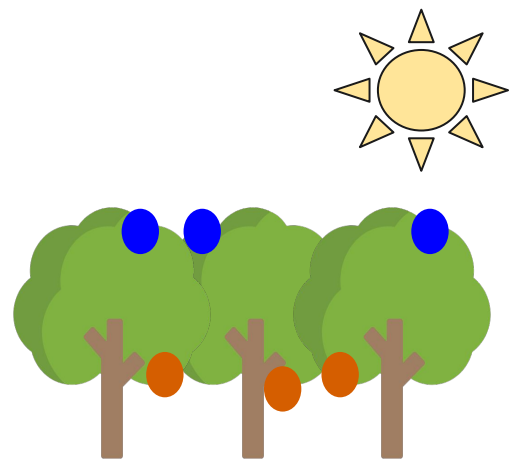
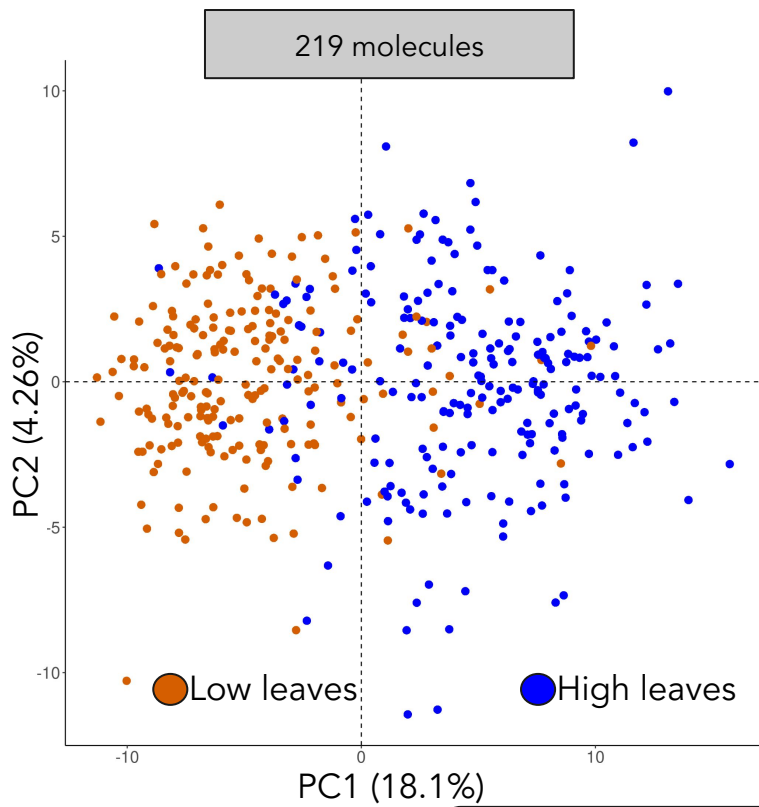
High throughput untargeted LC-MS
219 molecules

10 min gradient (QTOF)

350K SNPs capture weak population structure

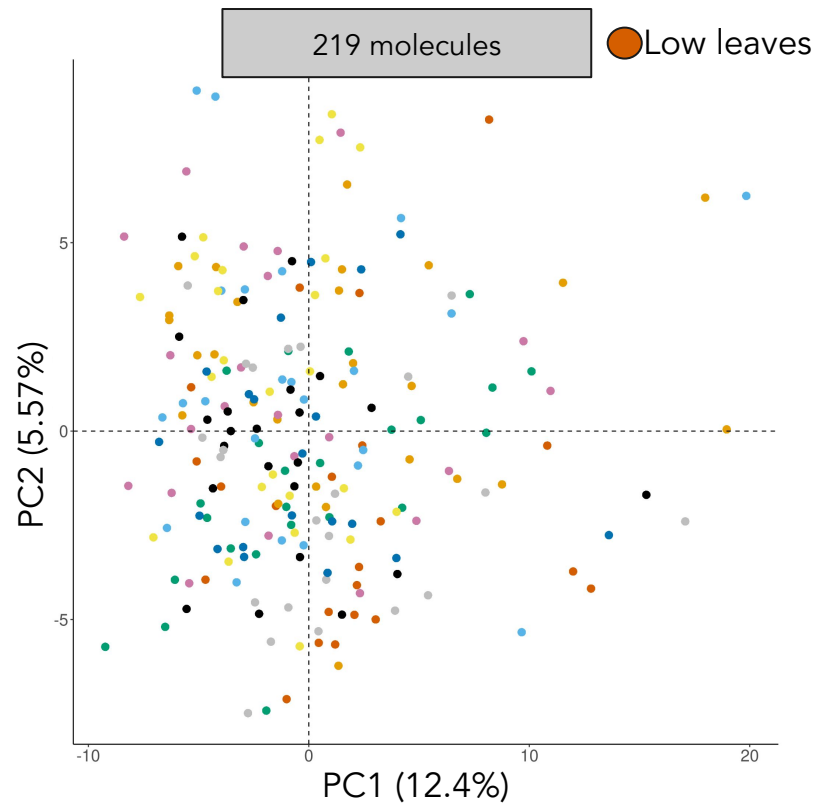


Leaf specialized metabolites profile depends on branch height



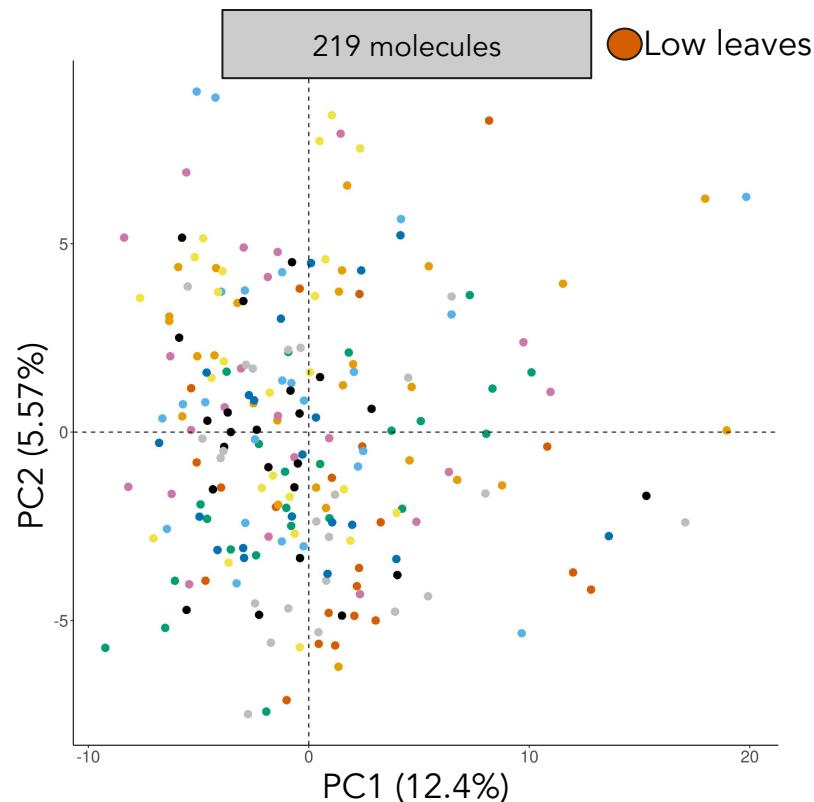
Variation within individuals, likely influenced by exposition to sunlight.

Nearly no phenotypic differentiation between provenances

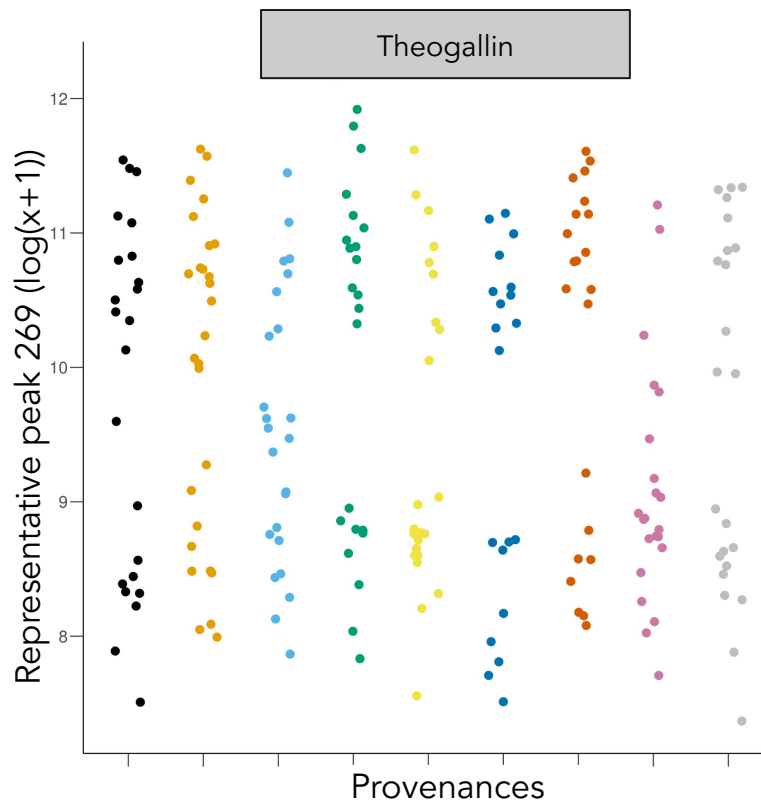


No differentiation between provenances at the leaf metabolome scale

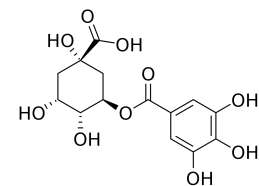
Nearly no phenotypic differentiation between provenances



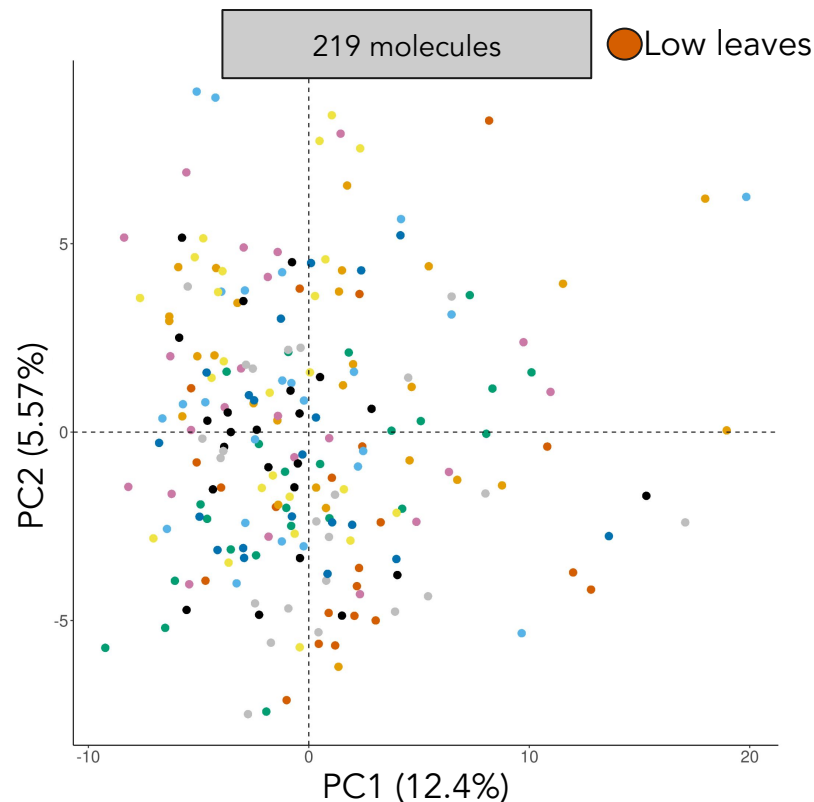
No differentiation between provenances at the leaf metabolome scale



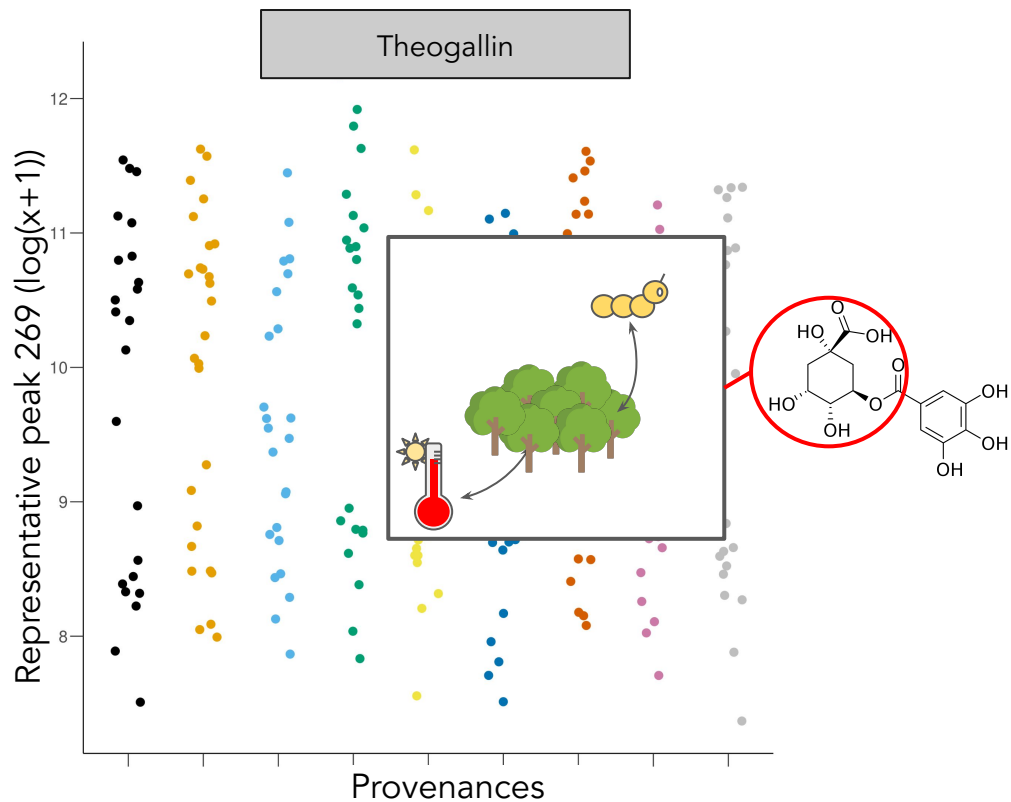
Variation within provenances at the molecule scale for the majority of molecules



Nearly no phenotypic differentiation between provenances

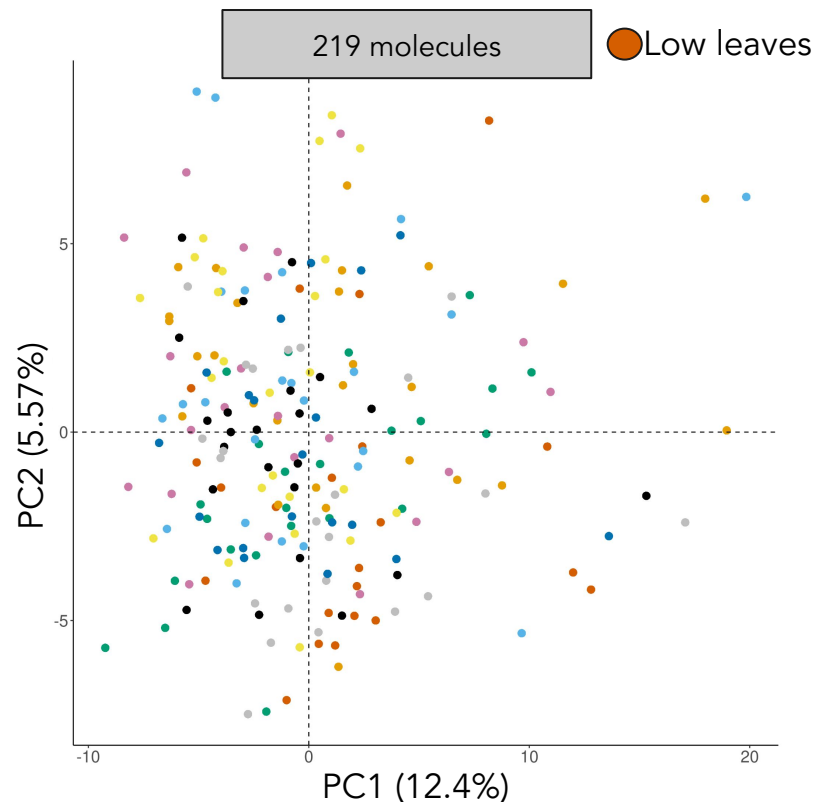


No differentiation between provenances at the leaf metabolome scale

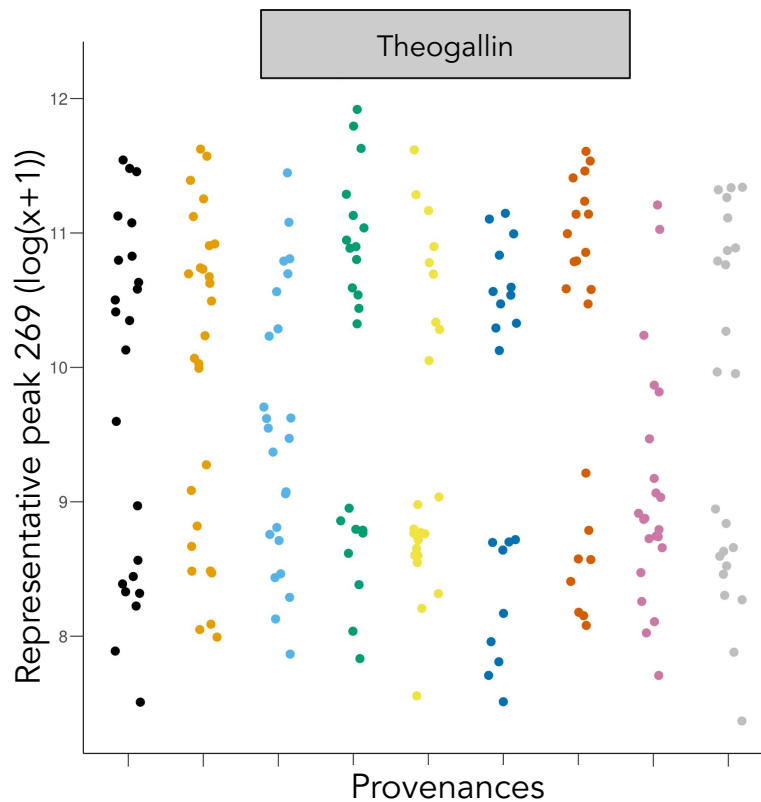


Variation within provenances at the molecule scale for the majority of molecules

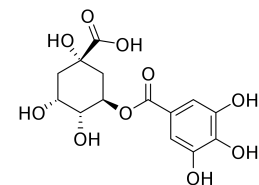
Nearly no phenotypic differentiation between provenances



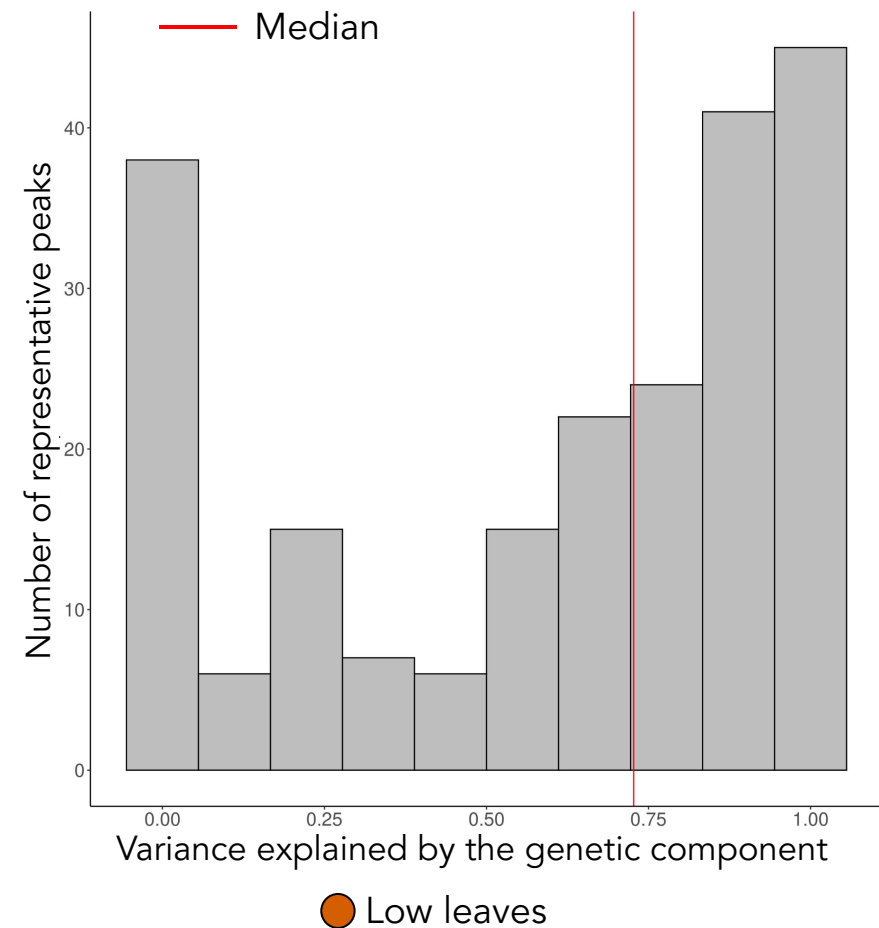
No differentiation between provenances at the leaf metabolome scale



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



Specialized metabolites variation is largely genetically determined

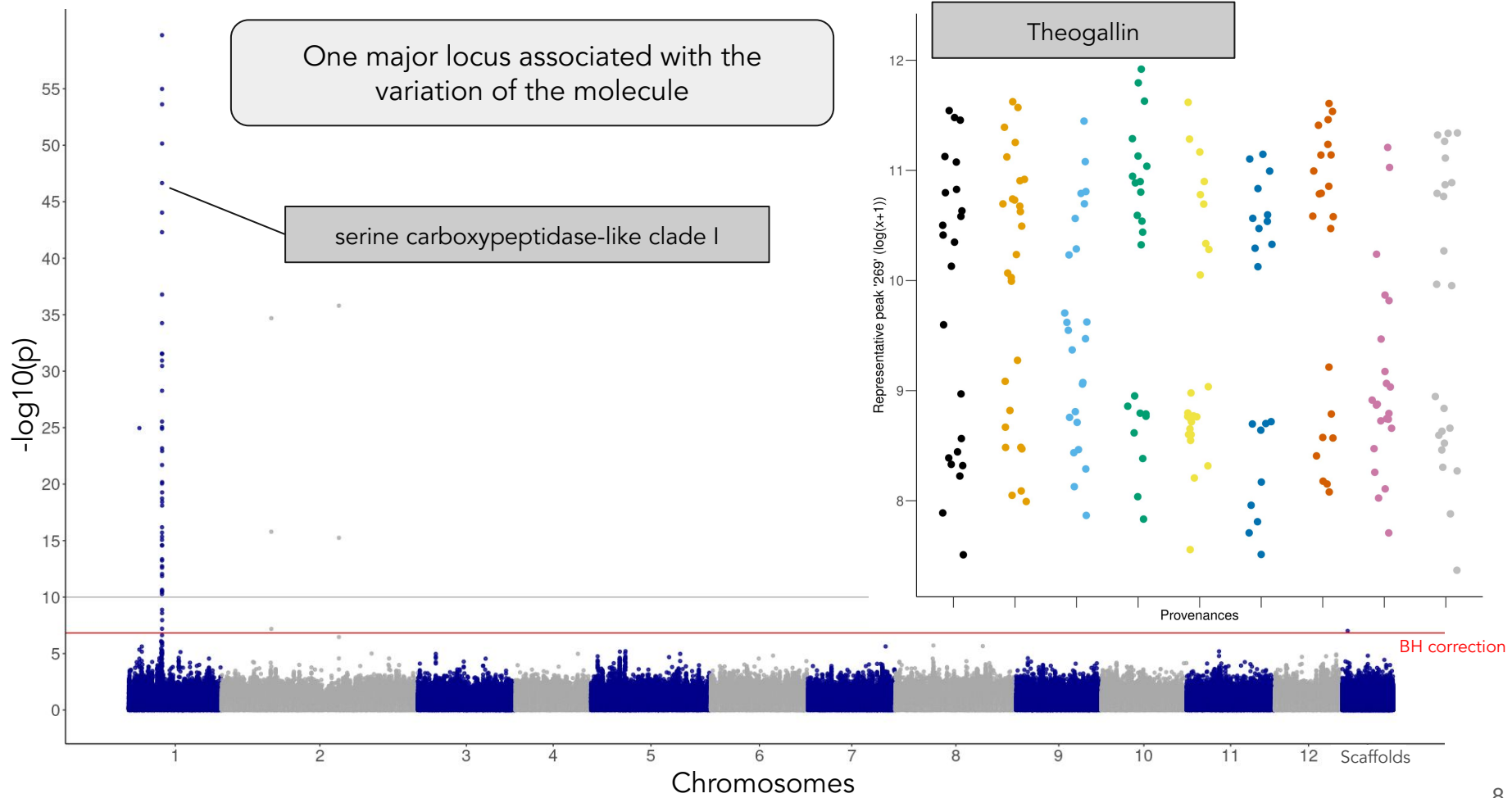


Genome-wide efficient mixed-model association
Univariate Linear Mixed Model
(GEMMA)

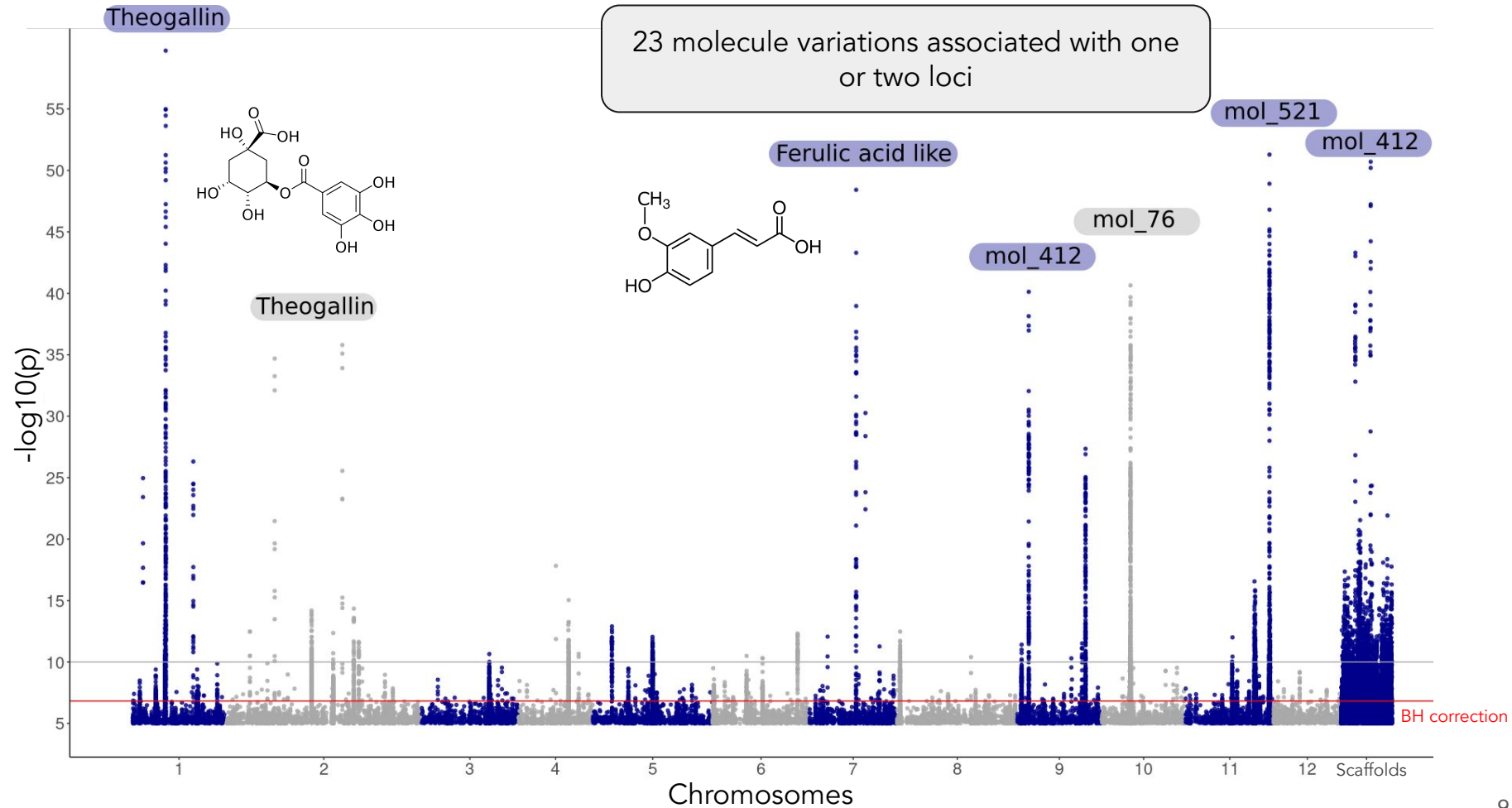
Proportion of specialized metabolites variance explained by the genetic similarity among trees (kinship matrix)

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

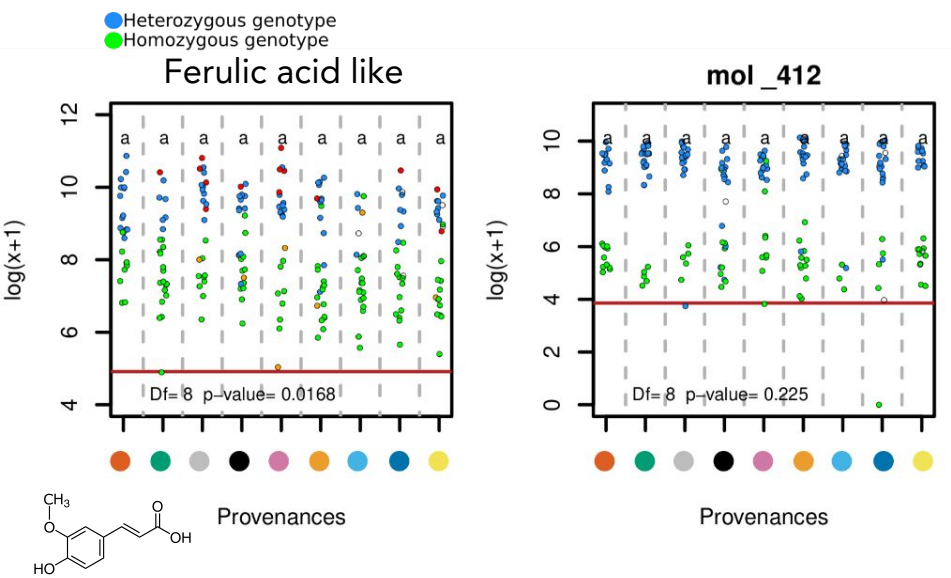
Genome wide association of specialized metabolites



Genome wide association of specialized metabolites

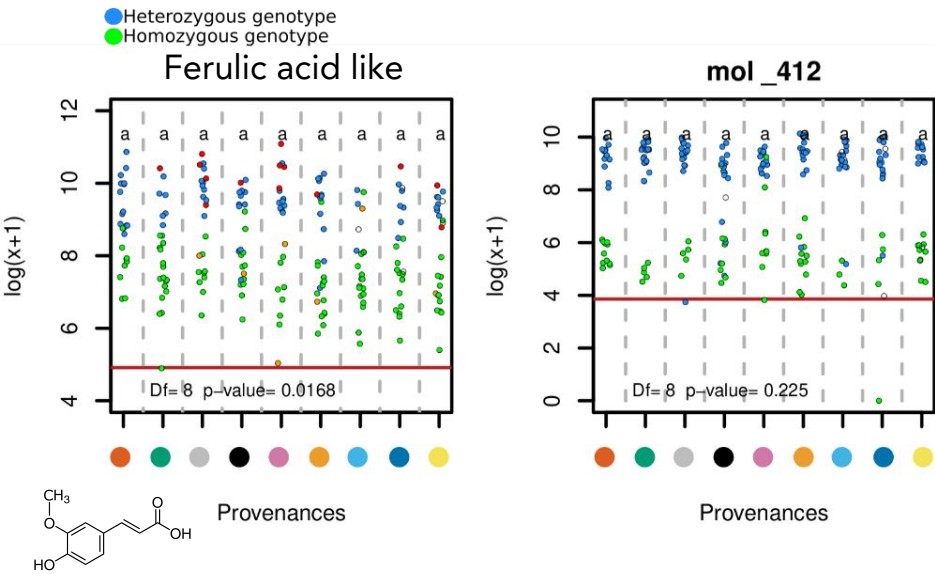


Many specialized metabolites have oligogenic architectures

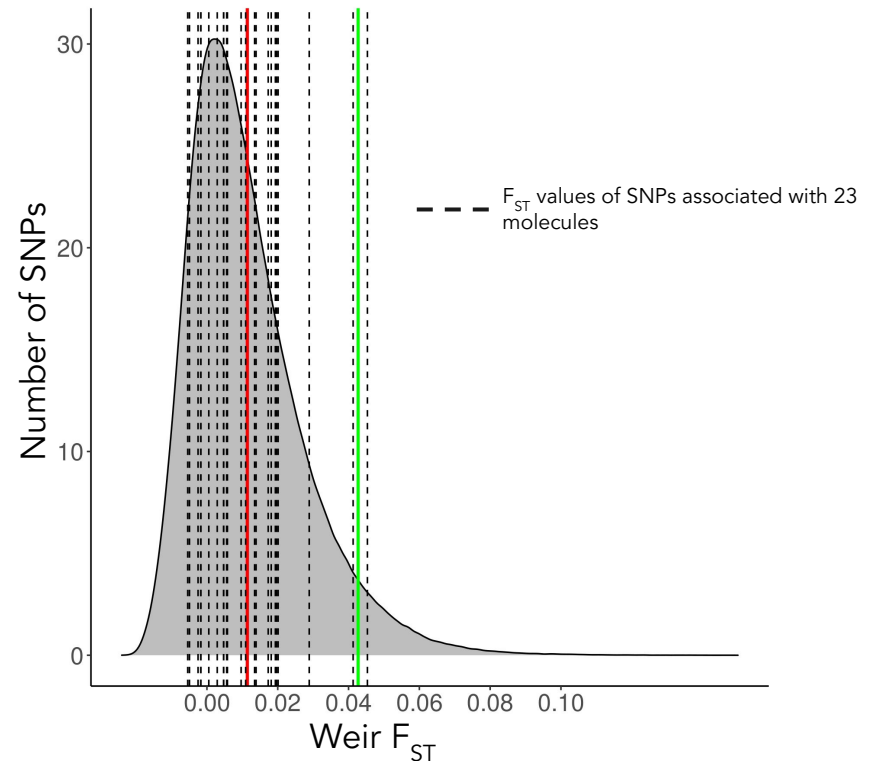


The genotypes for genetic markers associated with molecule variations are in the 9 provenances

Associated markers are not differentiated among provenances

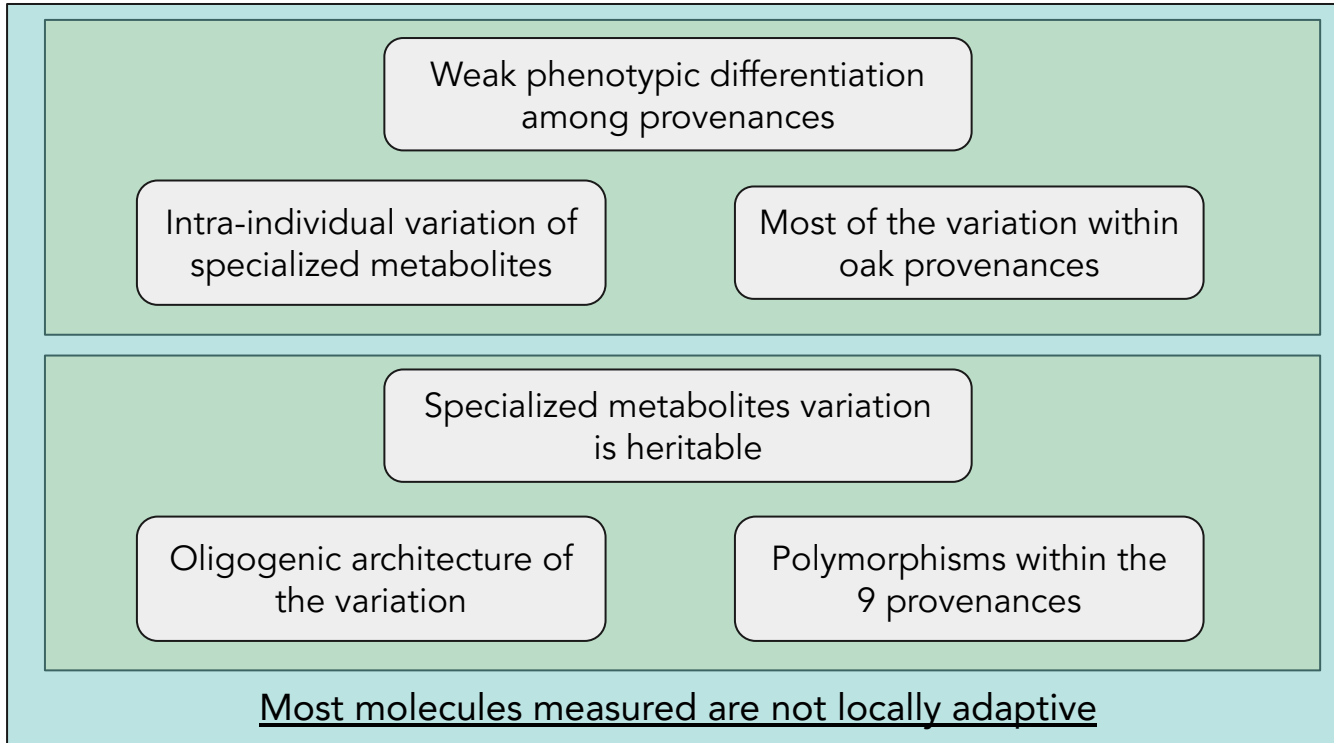


The genotypes for genetic markers associated with molecule variations are in the 9 provenances



Molecules with heritable variation have low F_{ST} values

Conclusion-No evidence of local adaptation for measured molecules

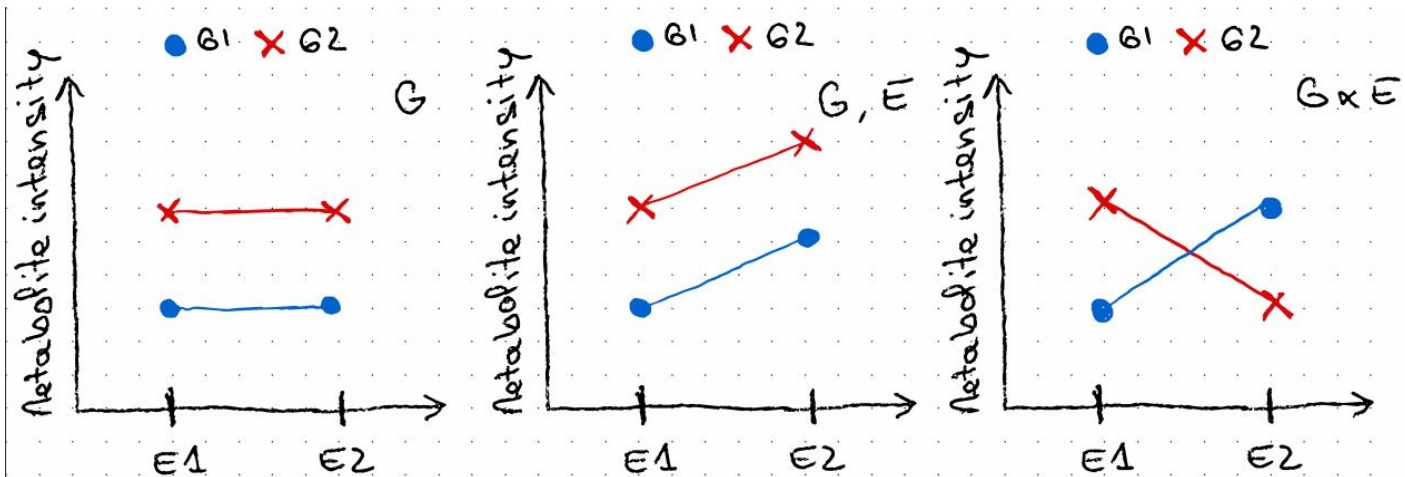


Hypothesis: Maintenance of variation within oak provenances (balanced selection)

What's next?

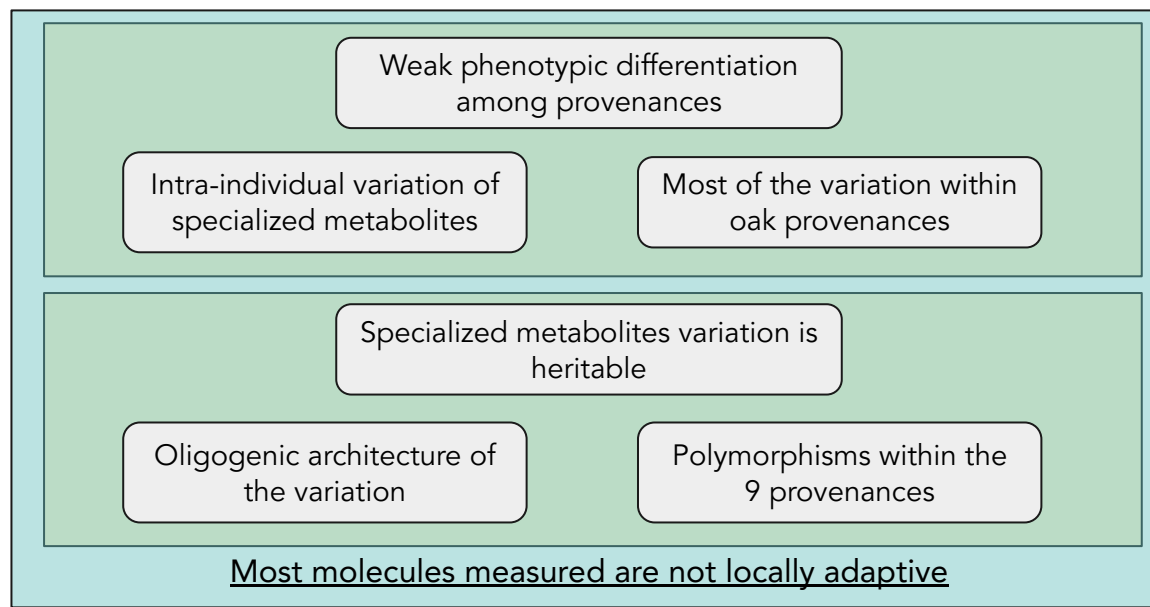
Genetic marker development at loci associated with specialized metabolites
~screening natural oak populations

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



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



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