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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*)

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

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01/09/2022



**INRAE**

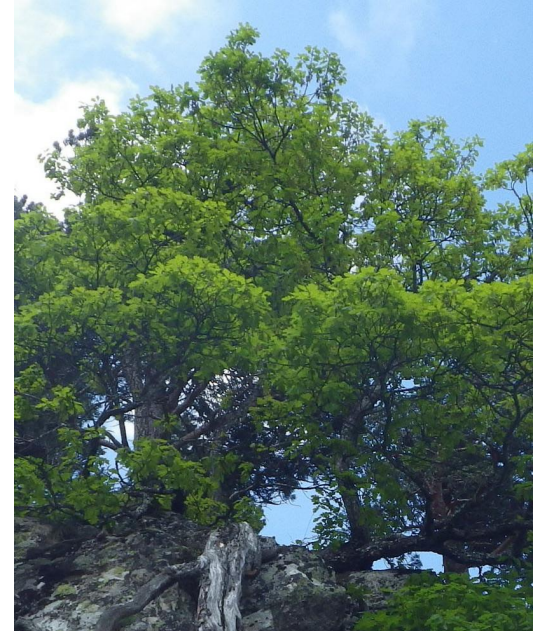
université  
de **BORDEAUX**



**UMR**  
**Silva**

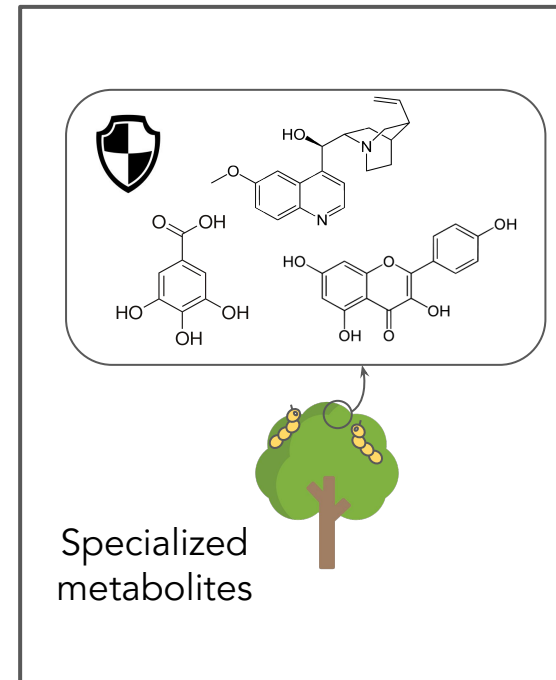
# Sessile oak (*Quercus petraea*) and specialized metabolites

- Dominant tree species in Europe
- 15% of French forests
  
- Foundation species & associated with a rich insect community
  - Influenced by specialized metabolites produced by oaks?



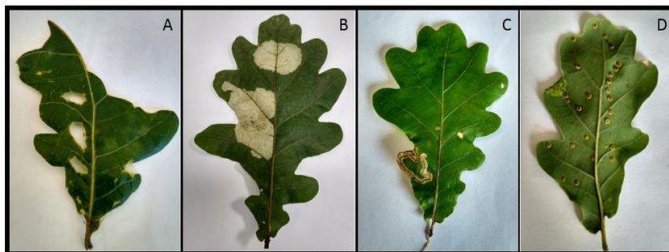
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# Sessile oak (*Quercus petraea*) and specialized metabolites

- 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?

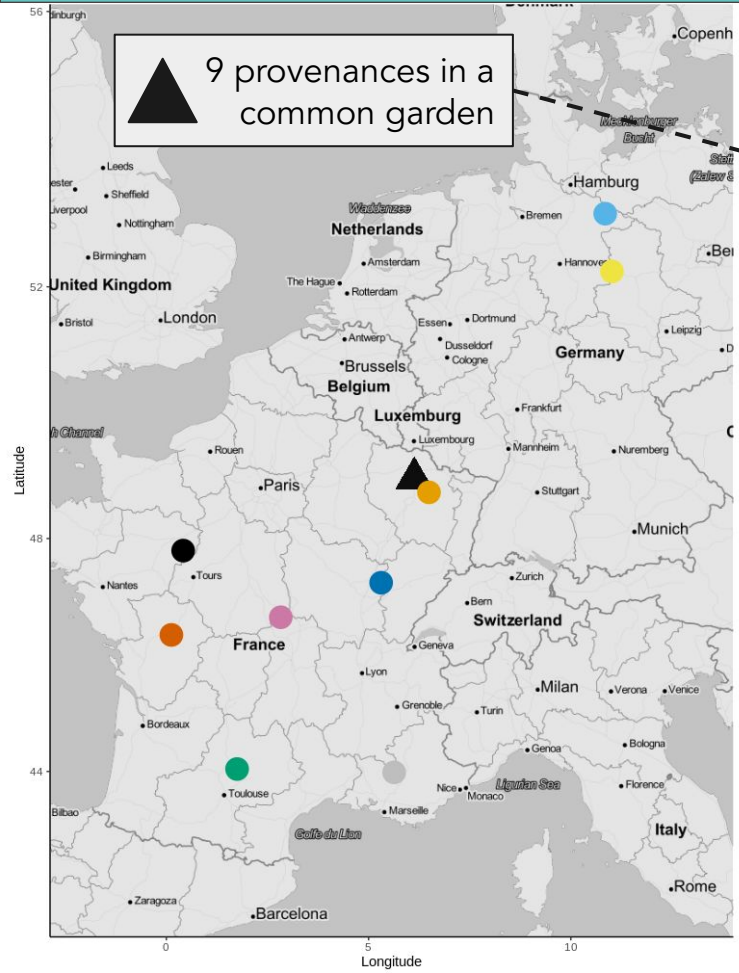
2

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

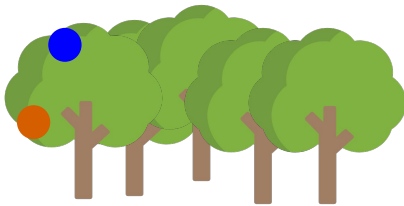
3

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

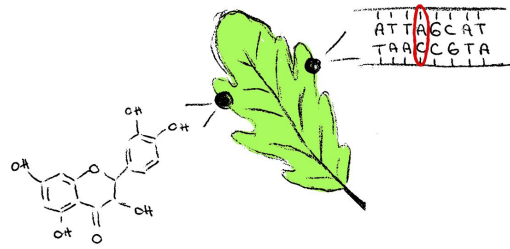
# Oak leaves sampling, metabolomics & genomics dataset



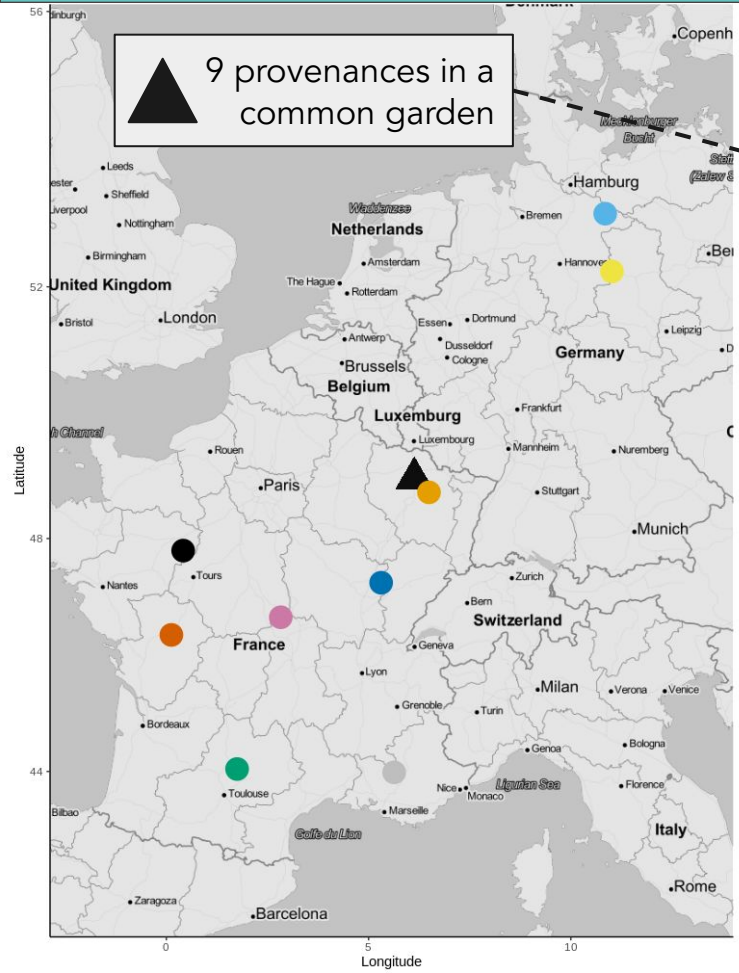
225 trees (25x9)



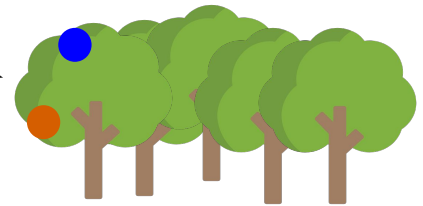
- Populations
- Berce
  - Bezange
  - Gohrde
  - Gresigne
  - Lappwald
  - Longchamp
  - St\_sauvant
  - Troncals
  - Vachere



# Oak leaves sampling, metabolomics & genomics dataset



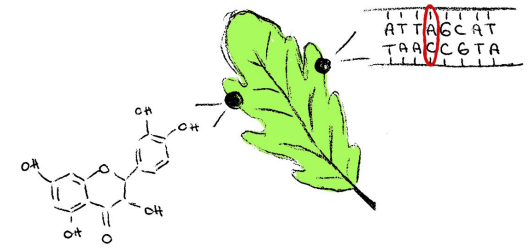
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- Populations
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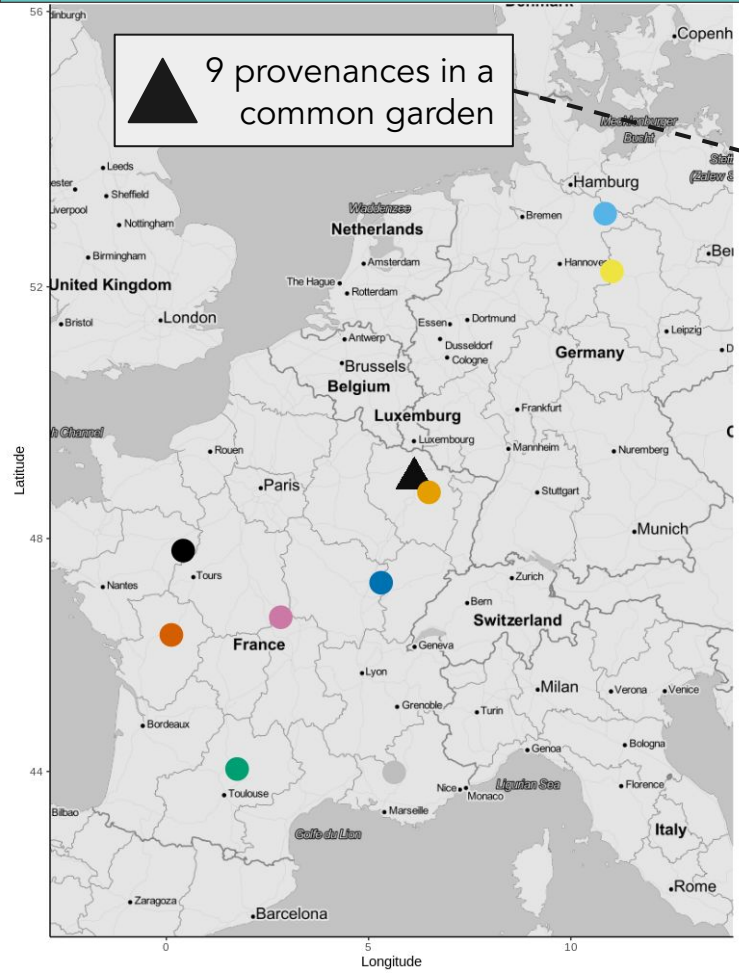
Whole genome low depth sequencing (~10X)  
~1,400,000 SNPs

ILLUMINA Paired-end  
150 bp

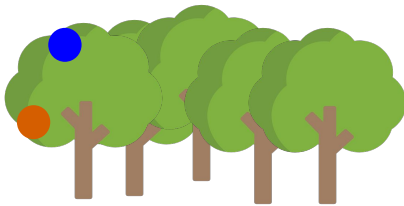




# Oak leaves sampling, metabolomics & genomics dataset

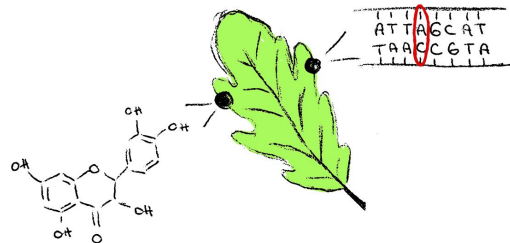


225 trees (25x9)



Whole genome low depth sequencing (~10X)  
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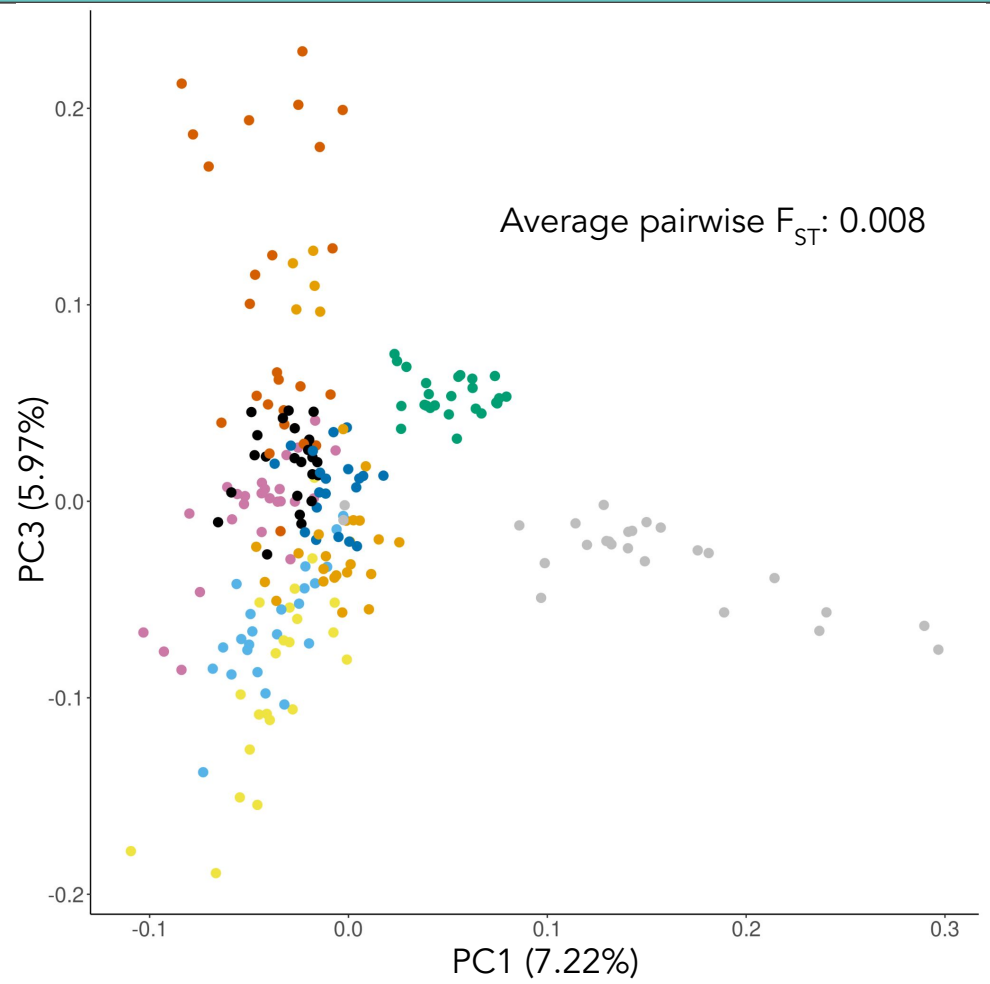
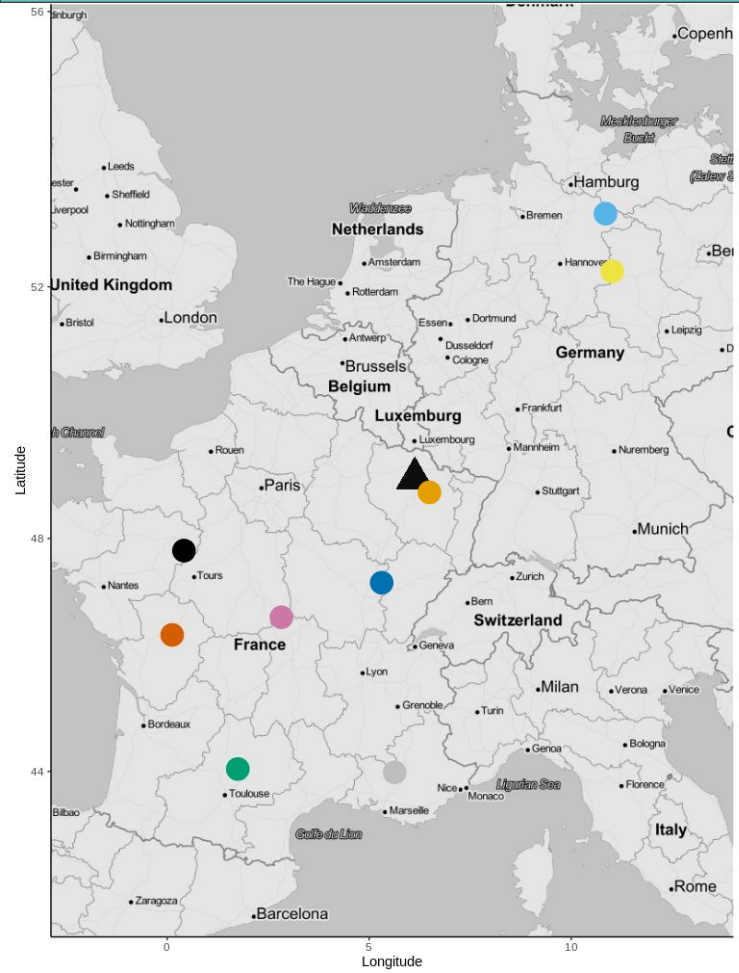
Illumina Paired-end  
150 bp



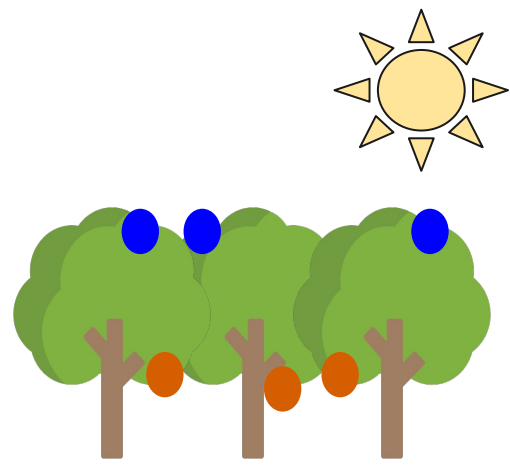
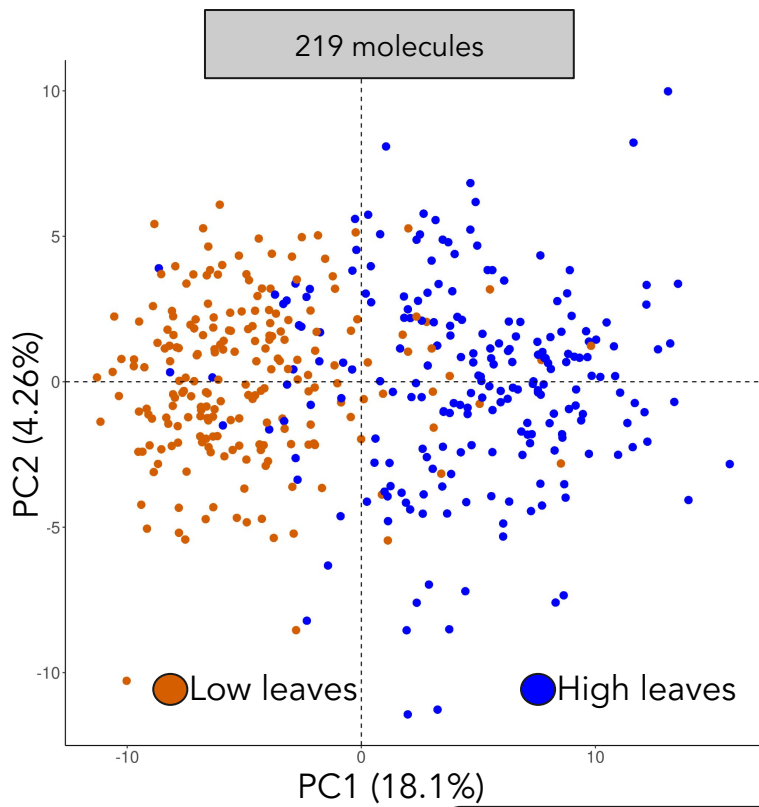
High throughput untargeted LC-MS  
219 molecules

10 min gradient  
(QTOF)

# 350K SNPs capture weak population structure

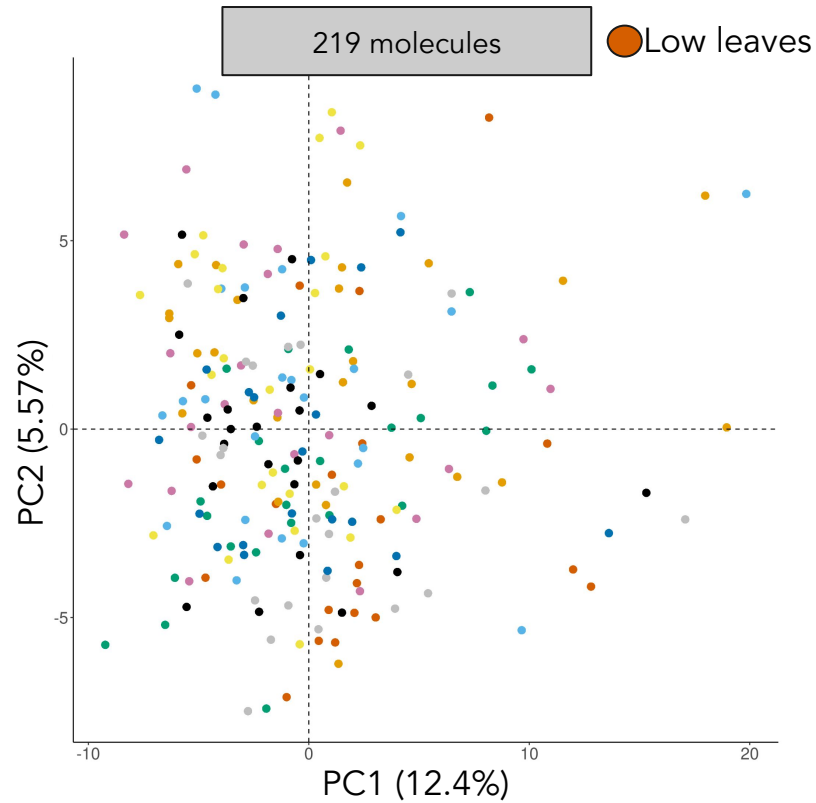


# Leaf specialized metabolites profile depends on branch height



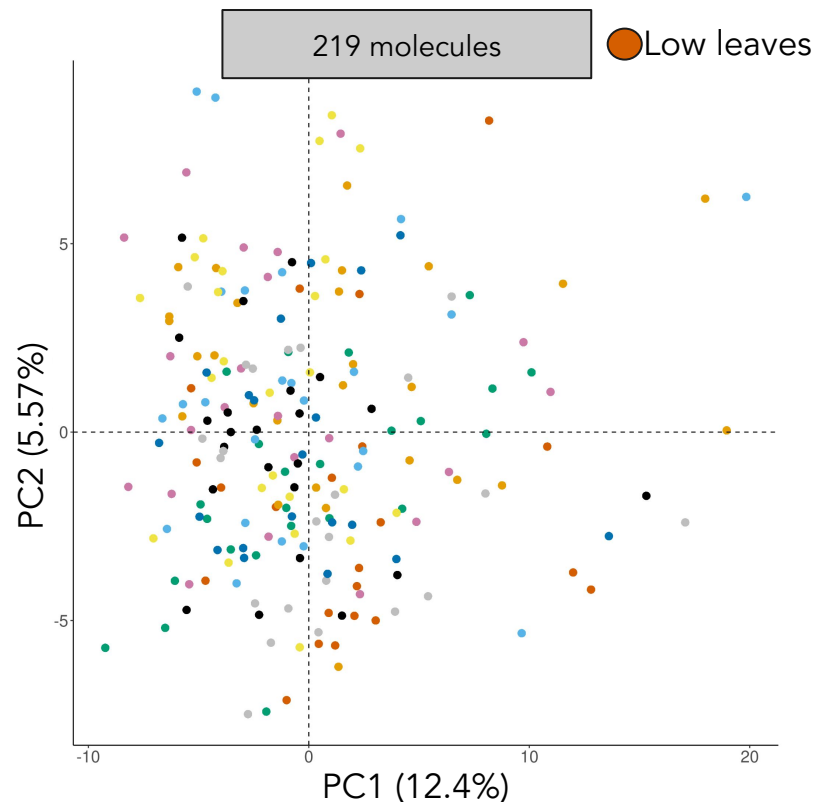
Variation within individuals, likely influenced by exposition to sunlight.

# Nearly no phenotypic differentiation between provenances

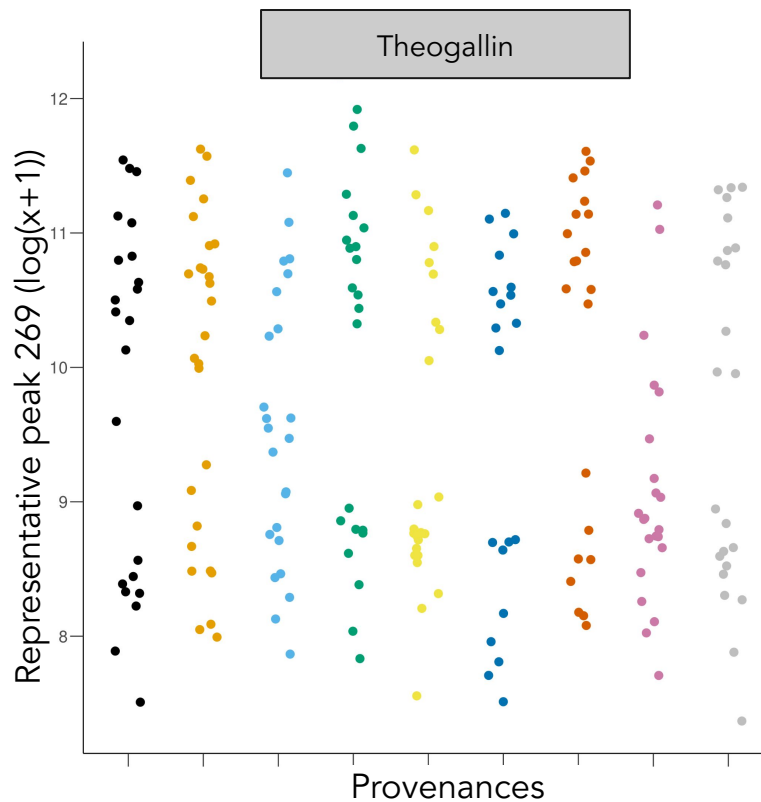


No differentiation between provenances at the leaf metabolome scale

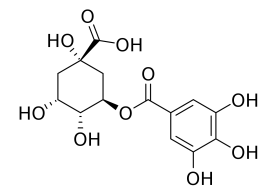
# Nearly no phenotypic differentiation between provenances



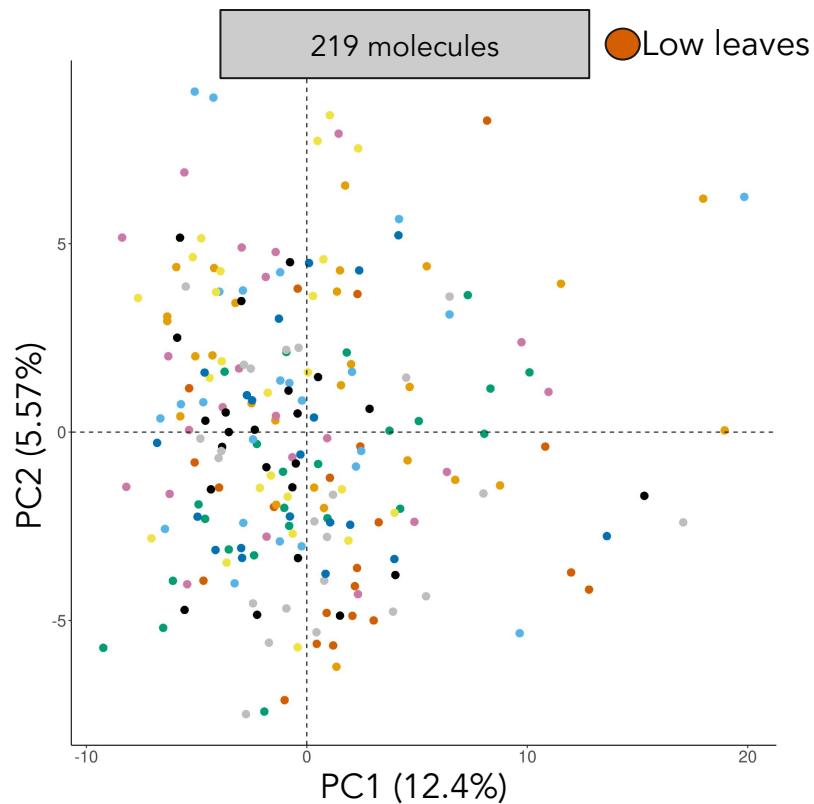
No differentiation between provenances at the leaf metabolome scale



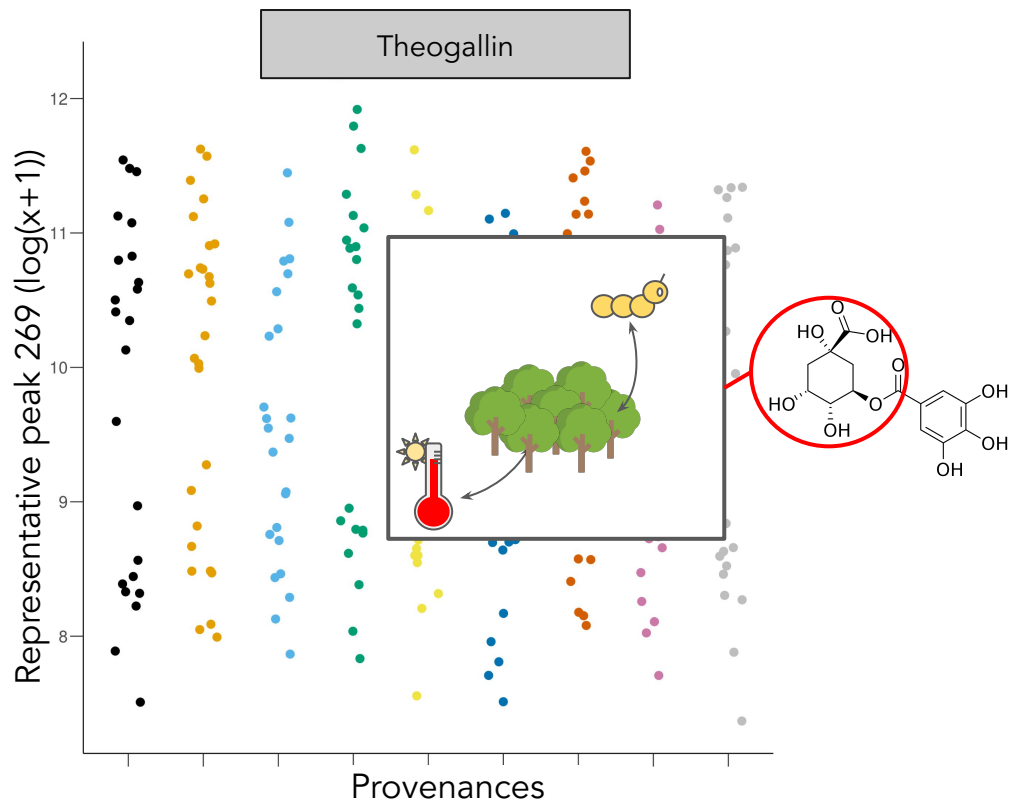
Variation within provenances at the molecule scale for the majority of molecules



# Nearly no phenotypic differentiation between provenances

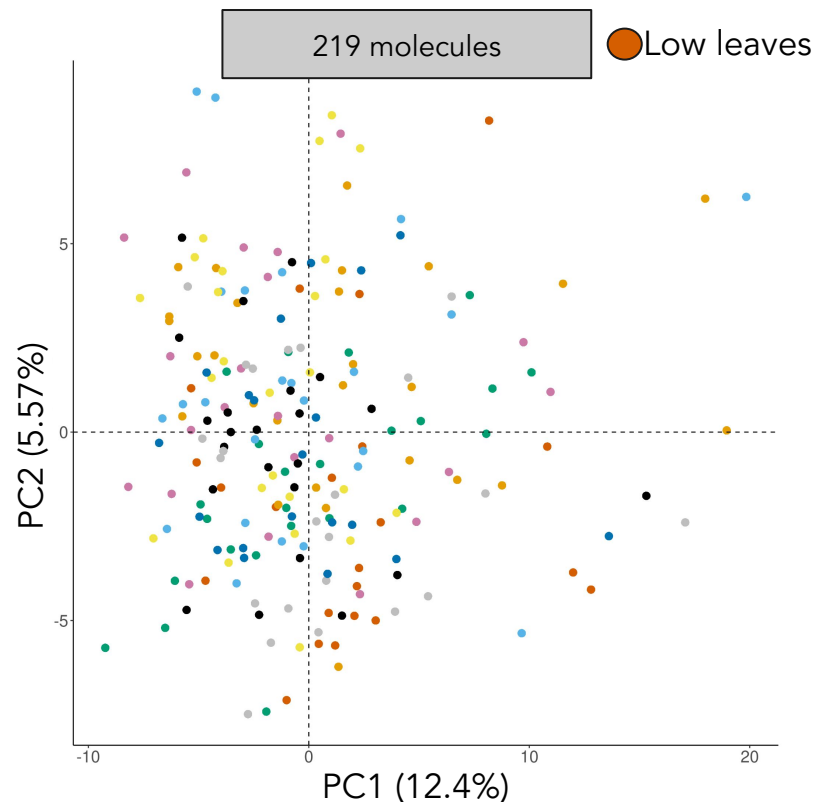


No differentiation between provenances at the leaf metabolome scale

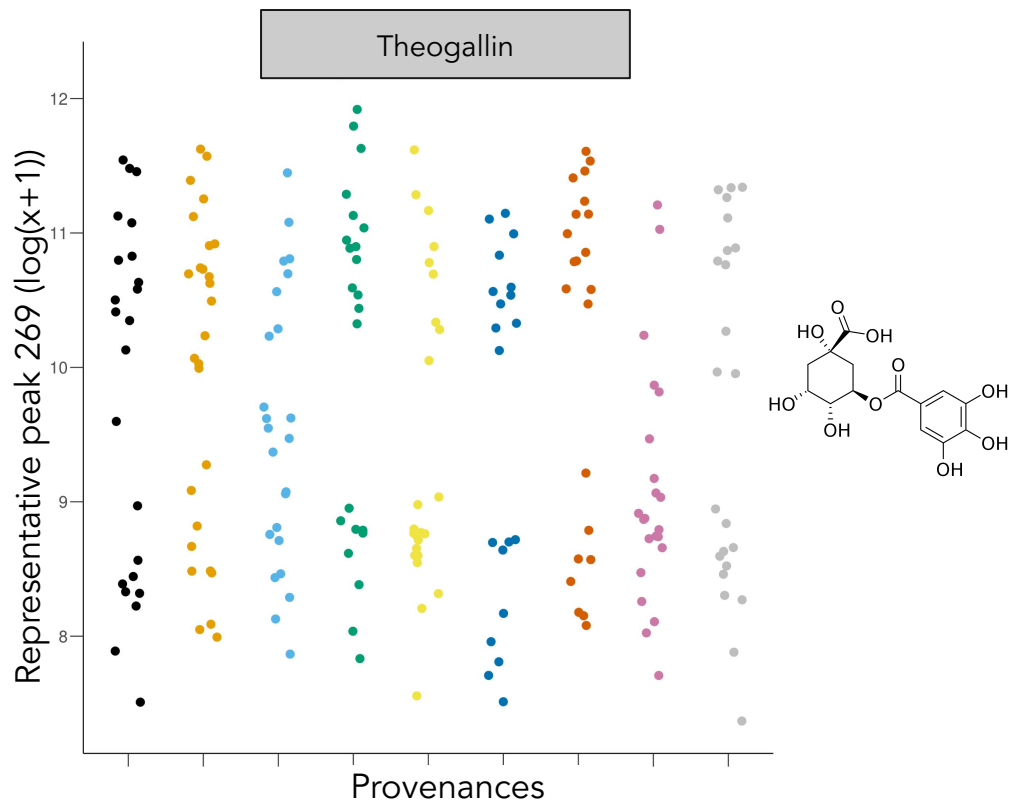


Variation within provenances at the molecule scale for the majority of molecules

# Nearly no phenotypic differentiation between provenances

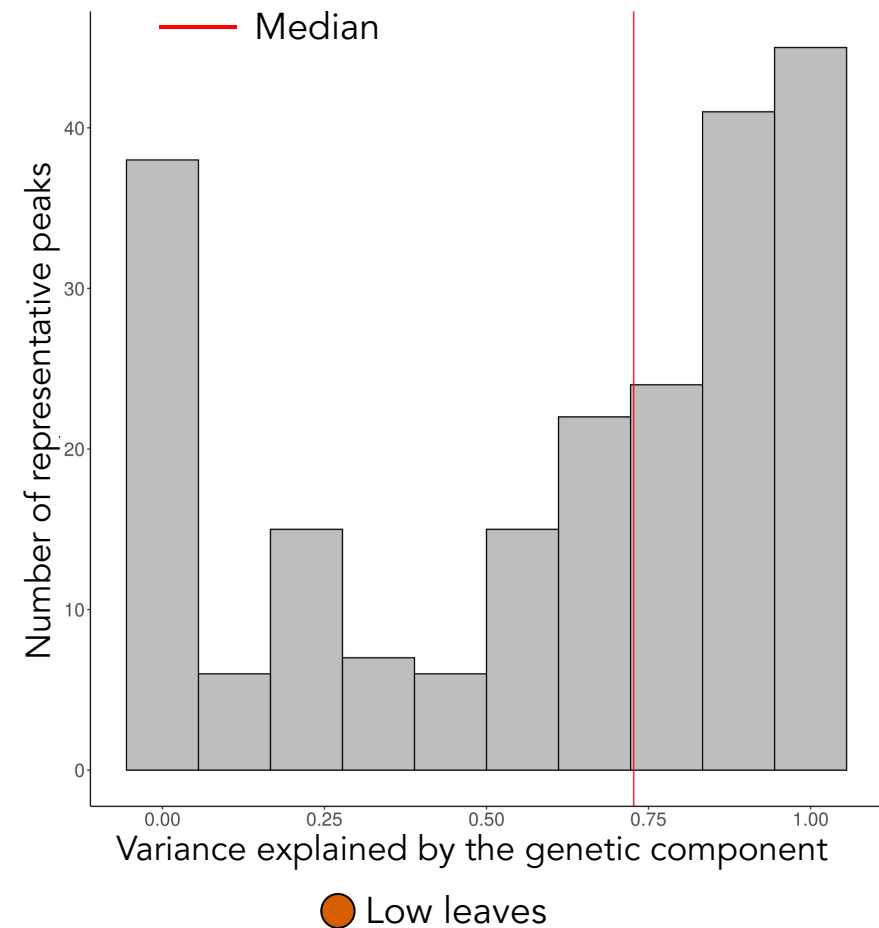


No differentiation between provenances at the leaf metabolome scale



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

# Specialized metabolites variation is largely genetically determined



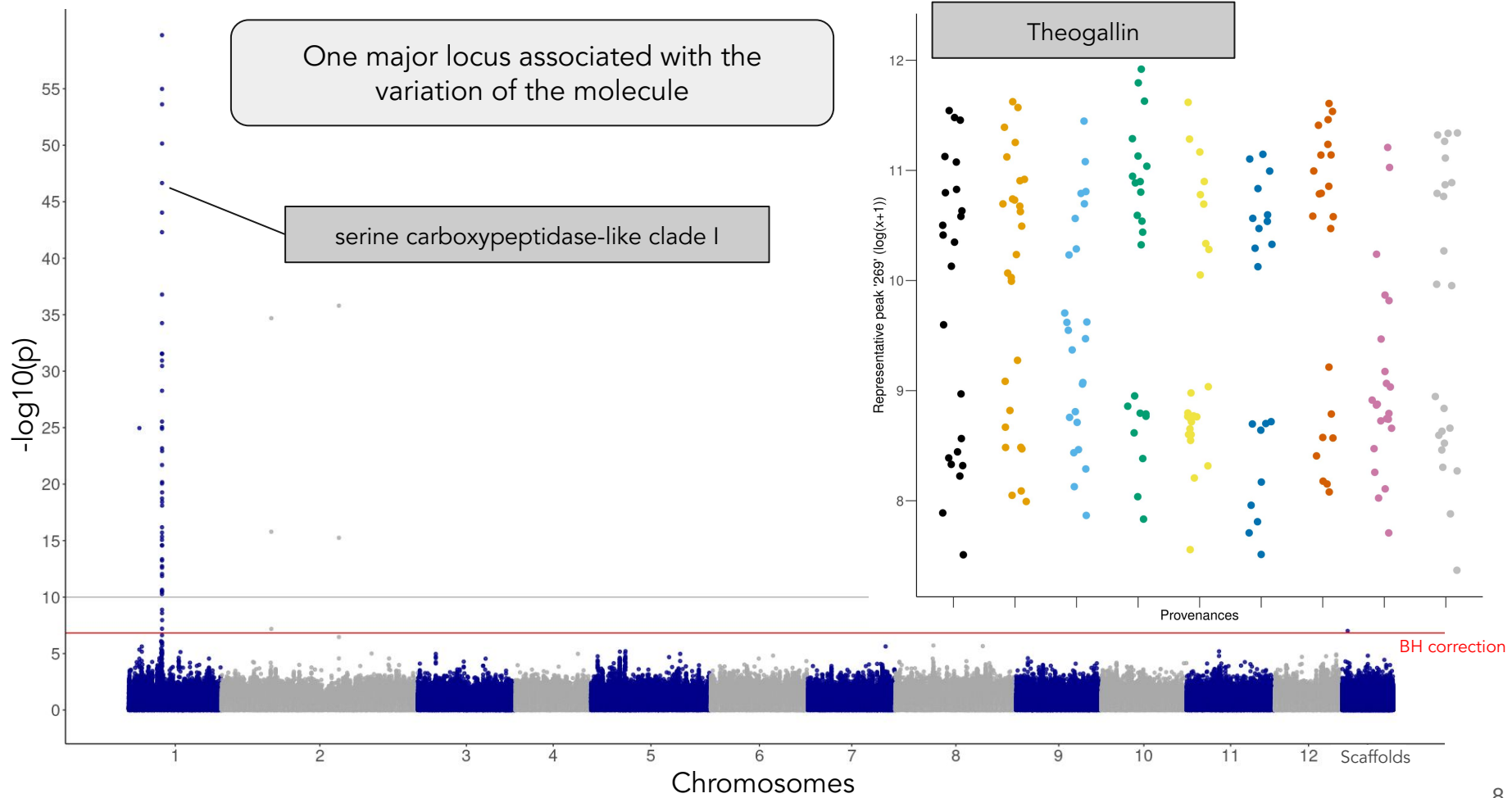
Genome-wide efficient mixed-model association  
Univariate Linear Mixed Model  
(GEMMA)

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

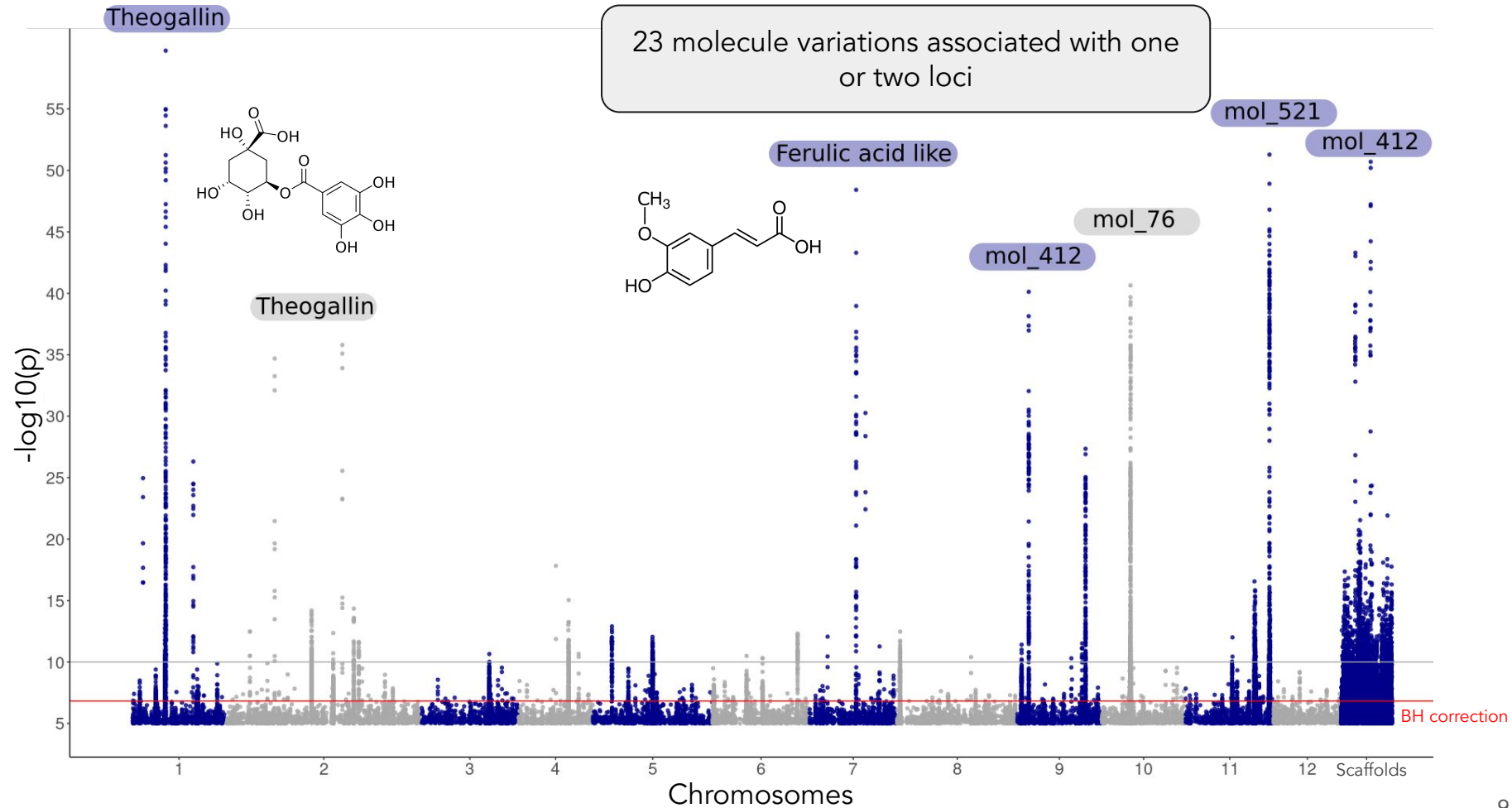
50% of molecules have more than 70% of their variation explained by the genetic variation



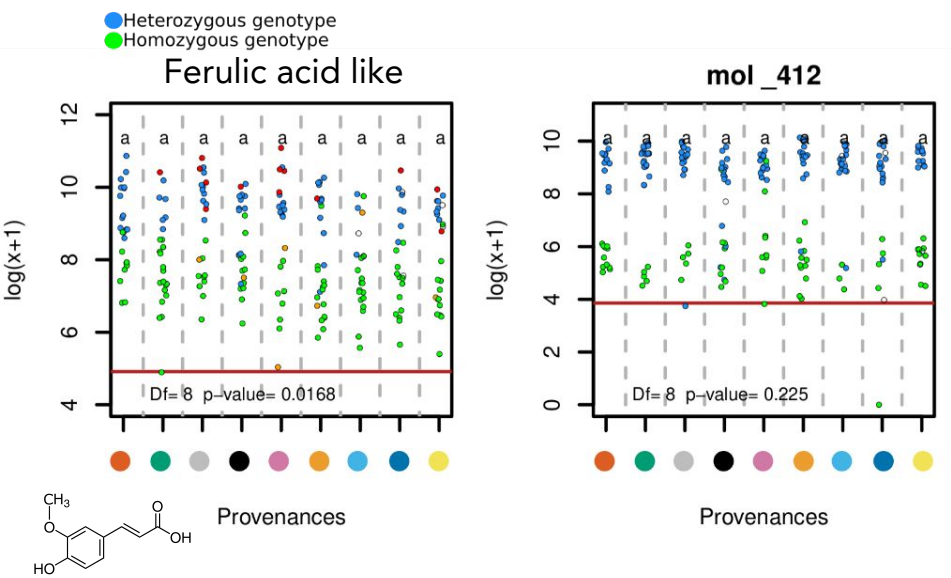
# Genome wide association of specialized metabolites



# Genome wide association of specialized metabolites

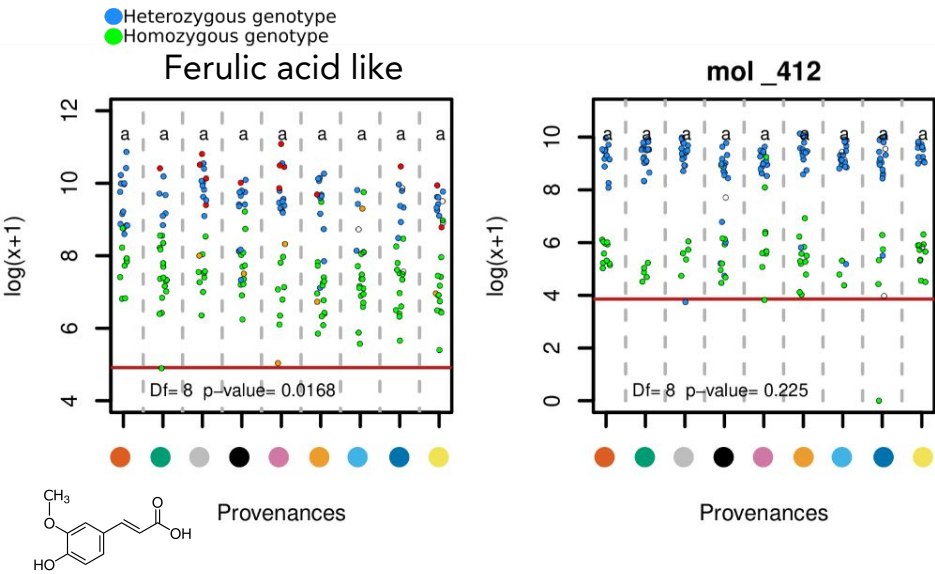


# Many specialized metabolites have oligogenic architectures

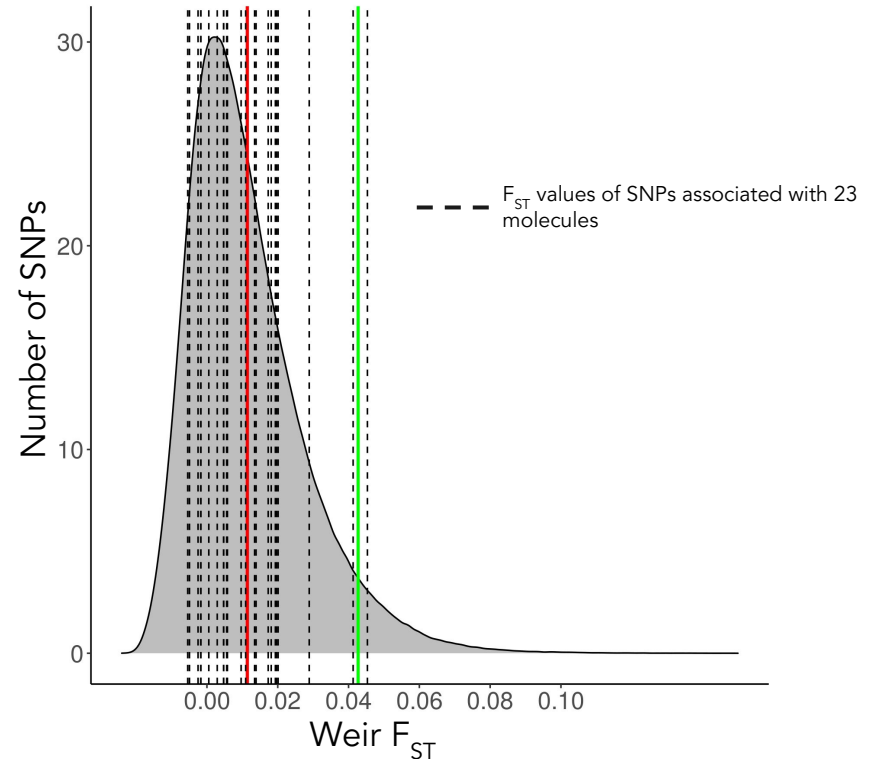


The genotypes for genetic markers associated with molecule variations are in the 9 provenances

# Associated markers are not differentiated among provenances

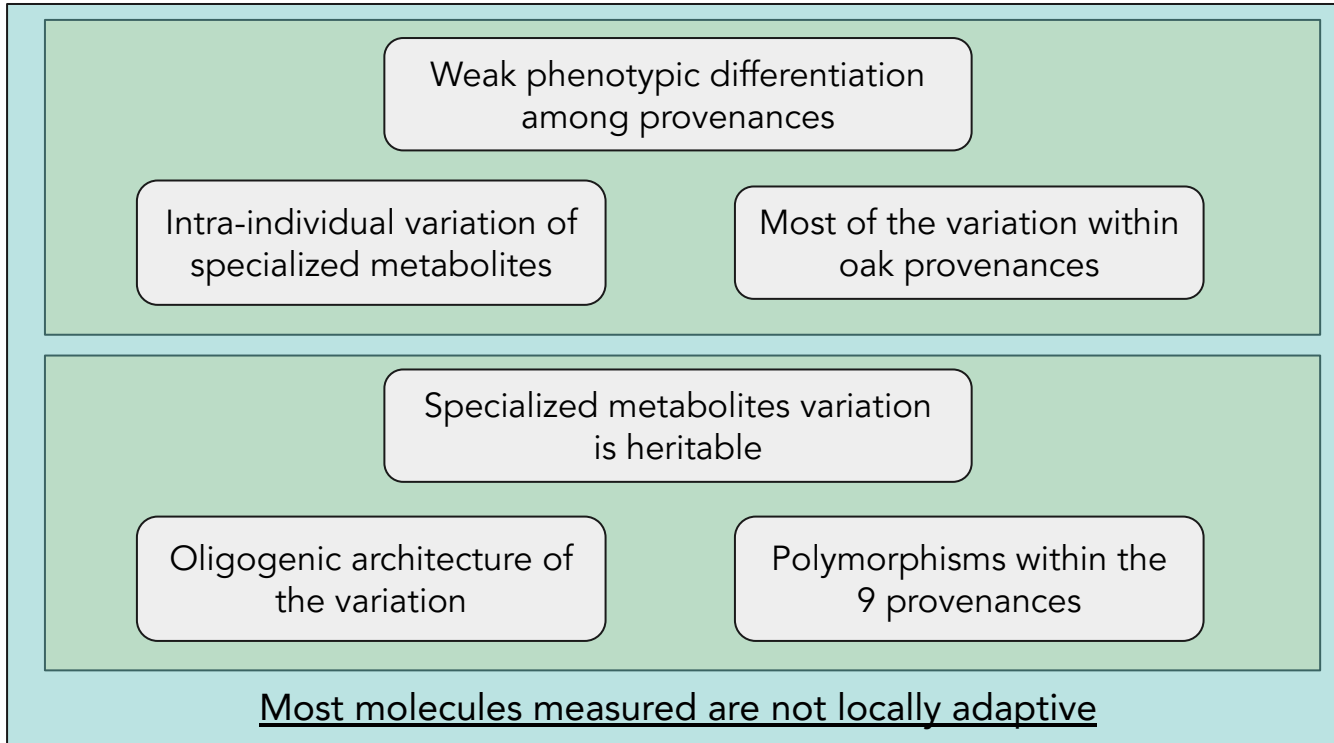


The genotypes for genetic markers associated with molecule variations are in the 9 provenances



Molecules with heritable variation have low  $F_{ST}$  values

# Conclusion-No evidence of local adaptation for measured molecules

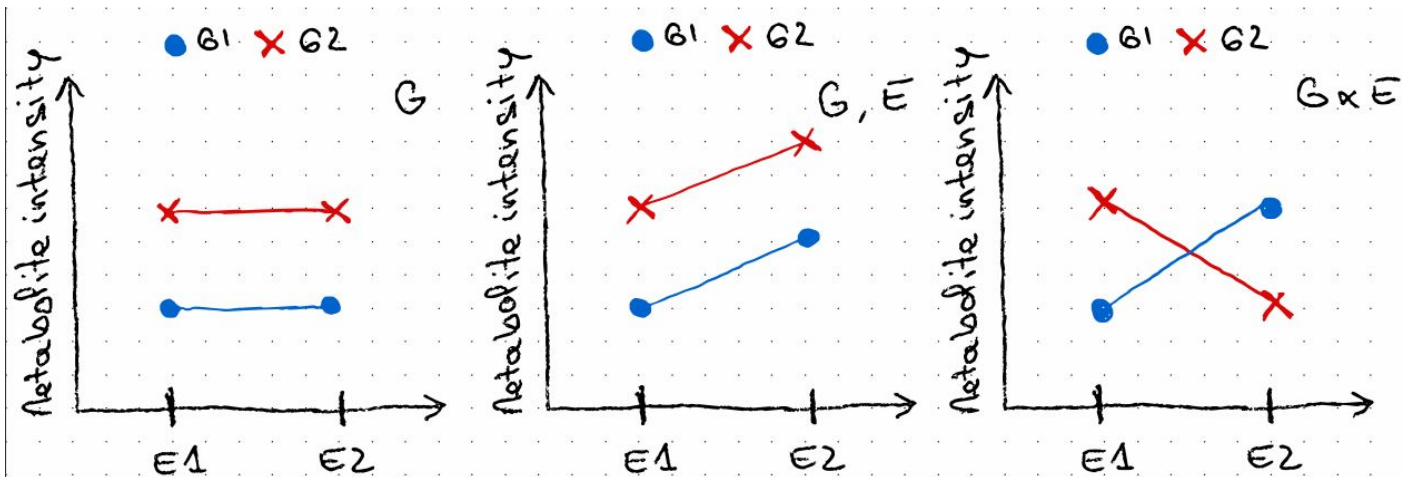


**Hypothesis:** Maintenance of variation within oak provenances (balanced selection)

# What's next?

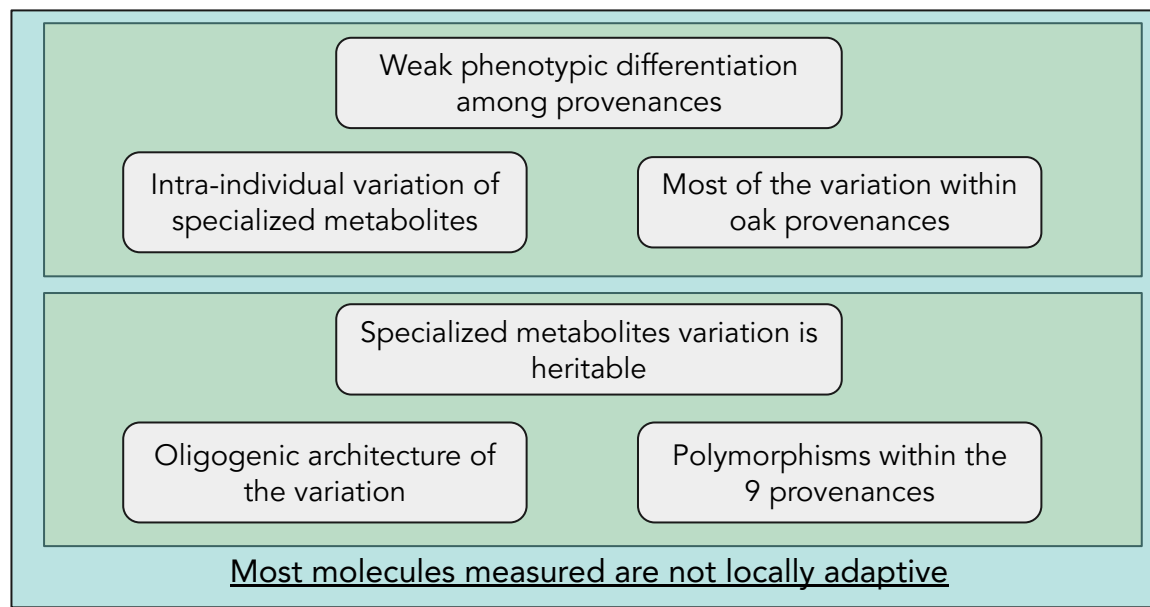
Genetic marker development at loci associated with specialized metabolites  
~screening natural oak populations

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



## Supervisors

Benjamin Brachi  
Christophe Plomion



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Antoine Kremer,  
Alexis Ducouso,  
Céline Lalanne,  
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**Hypothesis:** Maintenance of variation within oak provenances  
(balanced selection)



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Pathways for inventive researchers



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