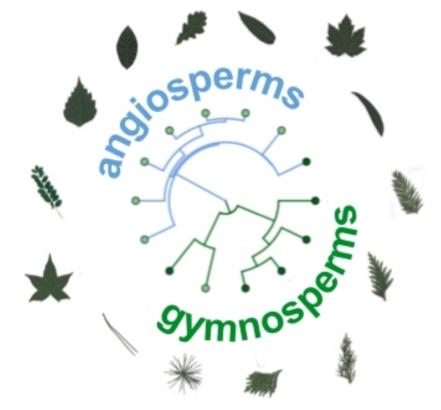


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EGU22 - 10463

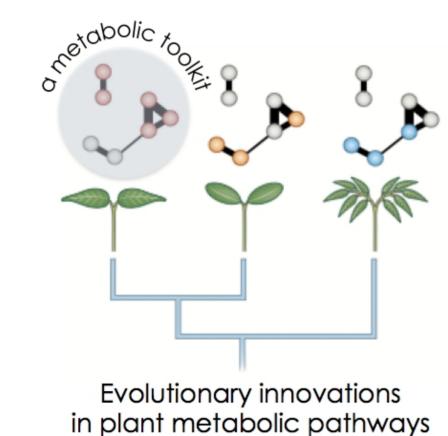


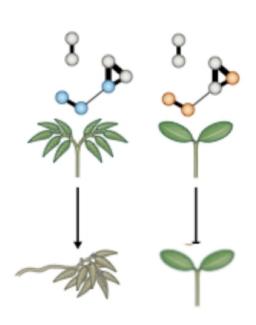






#### Different factors shape plant metabolic 'toolkits'

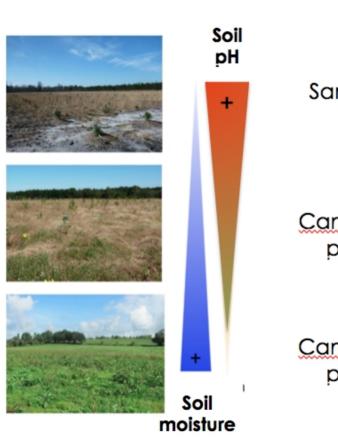




Resistance to environmental stress

Sedio, New Phytologist, 2017

### Study site characteristics



Sandy podzol pH: 3,9

Cambisol eutric pH: 4,4-4,7

Cambisol dystic pH: 4,7-5,7



#### Different plant functional types and species sampled





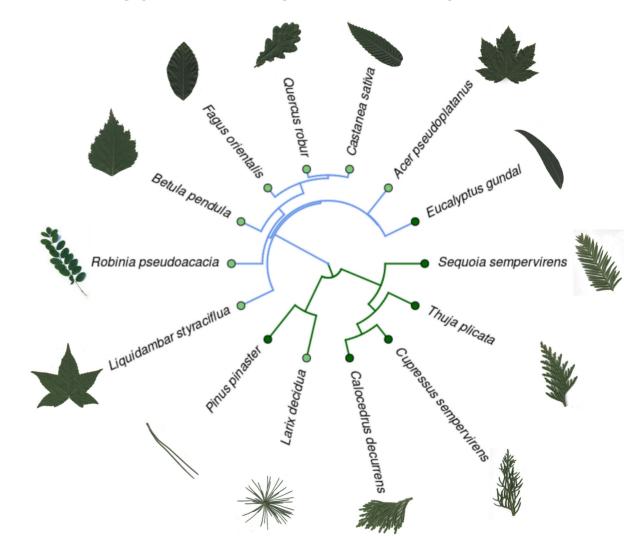


#### Plant material

#### 14 species

angio-/gymnosperms, deciduous/evergreen, 8 families

197 trees sampled in total

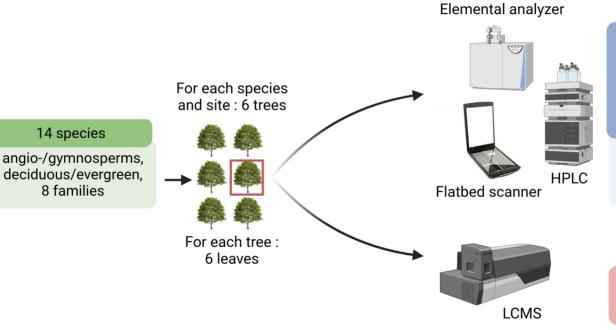


#### Leaf traits and metabolomes sampled on each species and site









#### **Chemical composition**

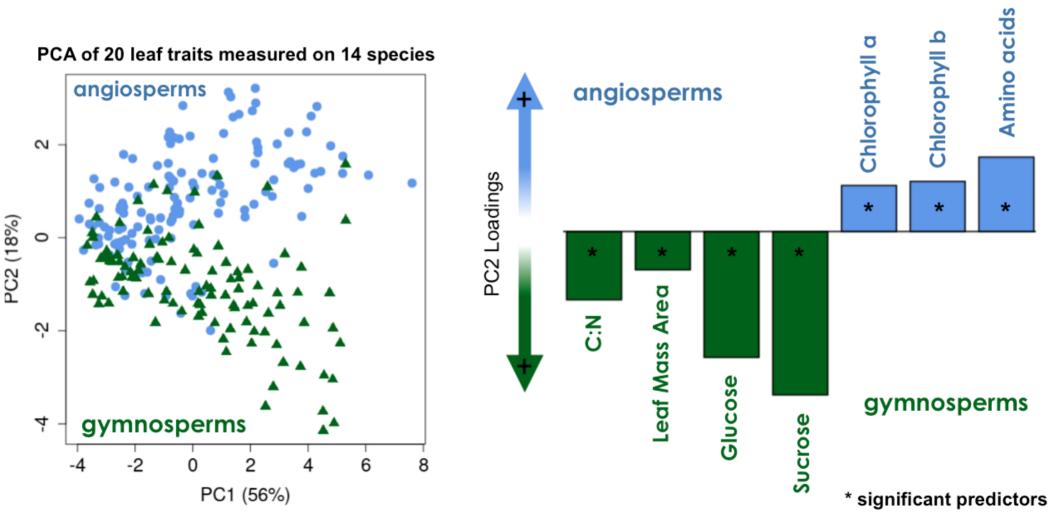
Elemental contents: C, N, P, Si Majors compounds: chlorophylls, sugars, amino acids Phenolic composition: total polyphenols

> Colors & Area RGB chromatic coordinate, LMA

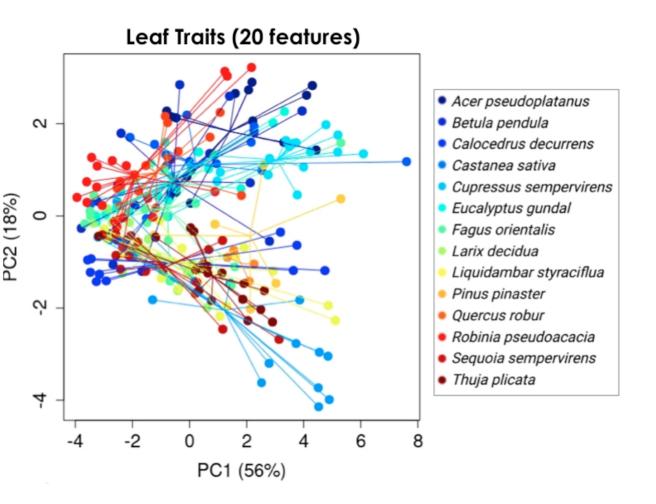
#### Metabolome

Metabolomics: 7607 RT-m/z pairs

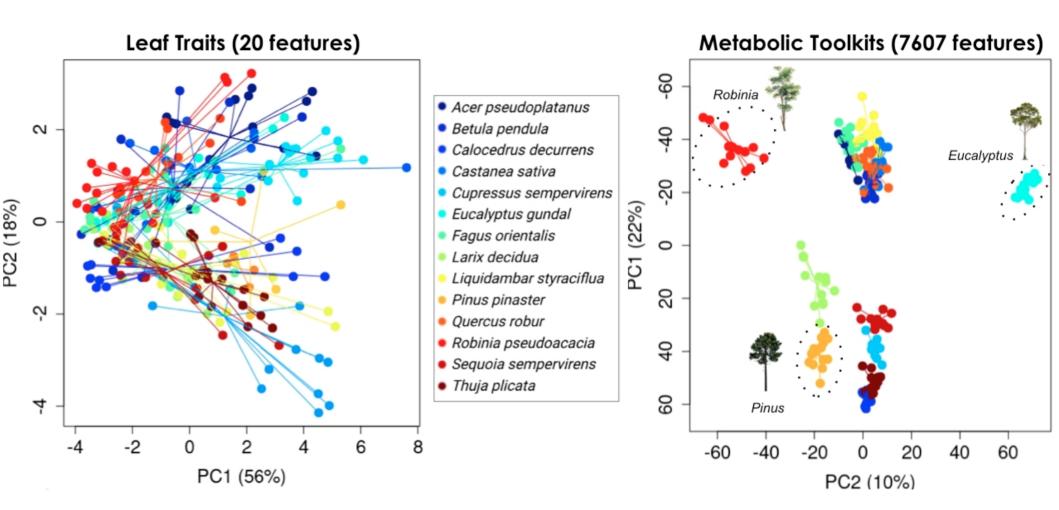
#### General leaf traits resolve differences between plant functional types



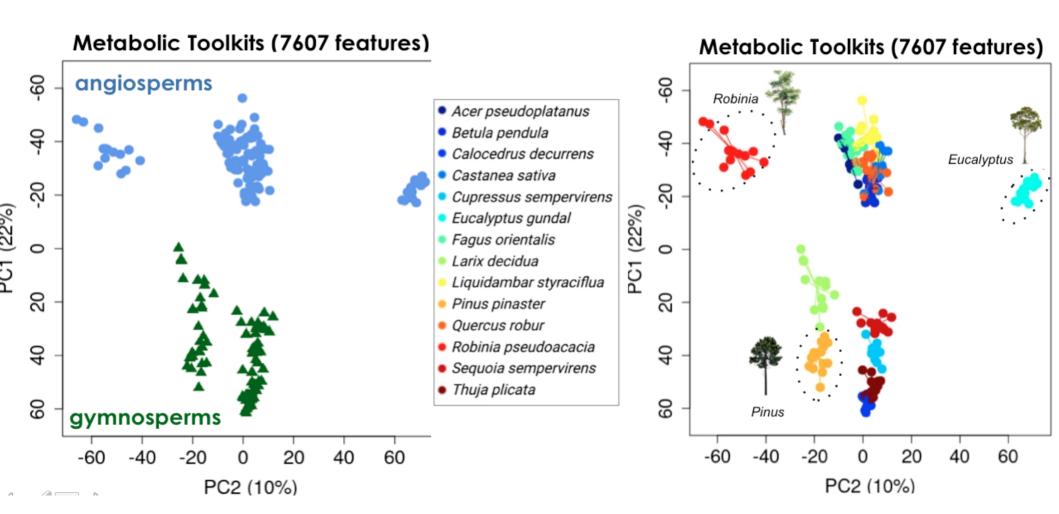
#### General leaf traits cannot resolve differences between plant families



#### Different plant families have distinct metabolic 'fingerprints'

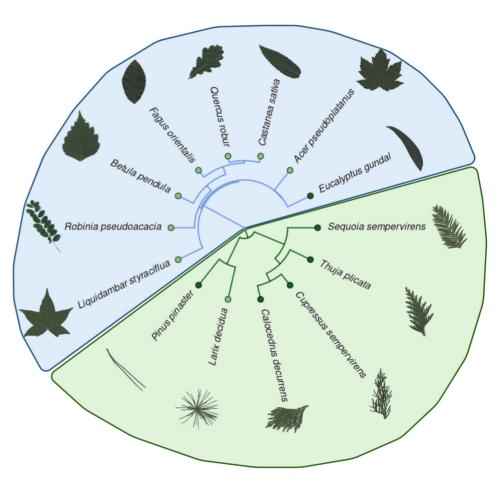


#### Different plant families have distinct metabolic 'fingerprints'



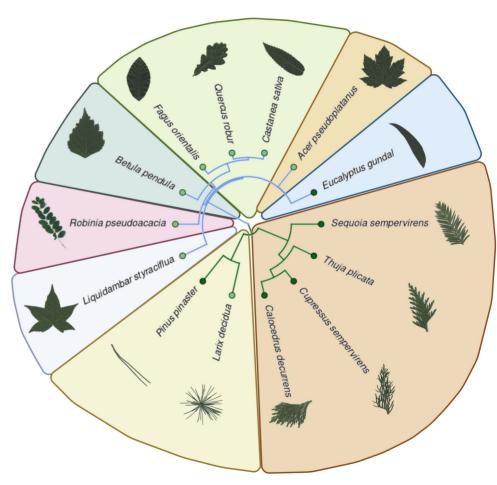
## Broad PFT groupings can be predicted from leaf traits

|                   |                                     | PLS-DA prediction accuracy      |  |
|-------------------|-------------------------------------|---------------------------------|--|
|                   | Dataset                             | Leaf<br>traits<br>(20 features) |  |
|                   | Cross-validation site <b>pH 4.4</b> | 84%                             |  |
| angiosperms<br>vs | validation site <b>pH 3.9</b>       | 83%                             |  |
| gymnosperms       | validation site <b>pH 4.7</b>       | 78%                             |  |



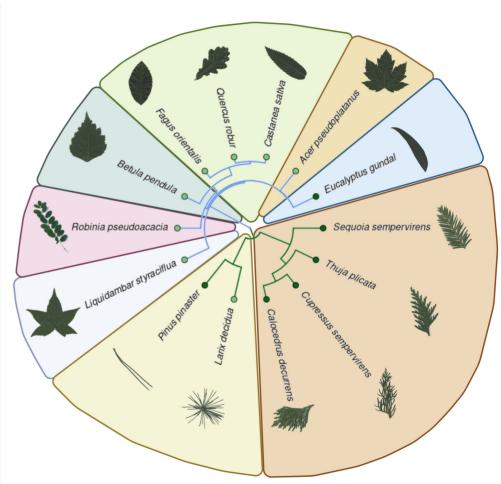
## Predicting plant family groupings from leaf traits is less reliable

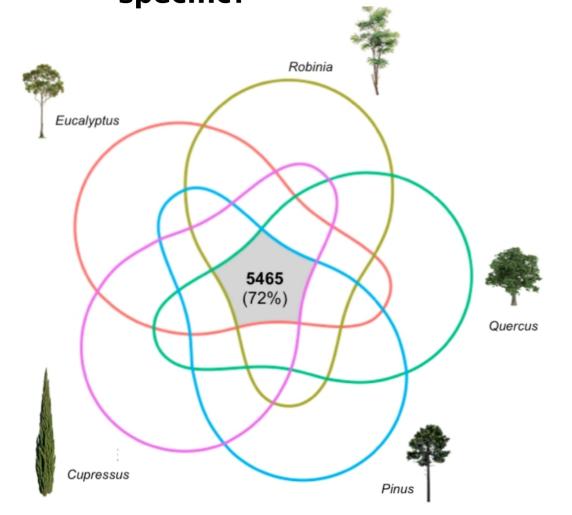
|                            |                                     | PLS-DA prediction accuracy      |  |
|----------------------------|-------------------------------------|---------------------------------|--|
|                            | Dataset                             | Leaf<br>traits<br>(20 features) |  |
|                            | Cross-validation site <b>pH 4.4</b> | 84%                             |  |
| angiosperms vs gymnosperms | validation site <b>pH 3.9</b>       | 83%                             |  |
|                            | validation site <b>pH 4.7</b>       | 78%                             |  |
| plant<br>families          | Cross-validation site <b>pH 4.4</b> | 70%                             |  |
|                            | validation site <b>pH 3.9</b>       | 46%                             |  |
|                            | validation site <b>pH 4.7</b>       | 54%                             |  |



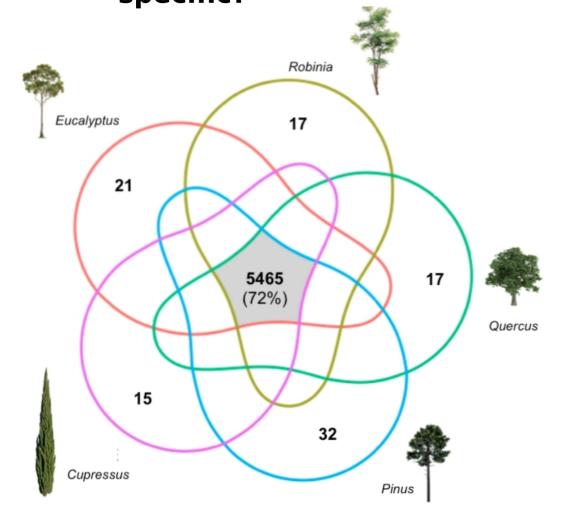
# Possible to predict PFT and family groupings from metabolic fingerprints

|                                  | Dataset                             | PLS-DA prediction accuracy      |  |
|----------------------------------|-------------------------------------|---------------------------------|--|
|                                  |                                     | Leaf<br>traits<br>(20 features) | Metabolic<br>toolkits<br>(7607 features) |
| angiosperms<br>vs<br>gymnosperms | Cross-validation site <b>pH 4.4</b> | 84%                             | 100%                                     |
|                                  | validation site <b>pH 3.9</b>       | 83%                             | 100%                                     |
|                                  | validation site <b>pH 4.7</b>       | 78%                             | 100%                                     |
| plant<br>families                | Cross-validation site <b>pH 4.4</b> | 70%                             | 100%                                     |
|                                  | validation site <b>pH 3.9</b>       | 46%                             | 100%                                     |
|                                  | validation site <b>pH 4.7</b>       | 54%                             | 100%                                     |



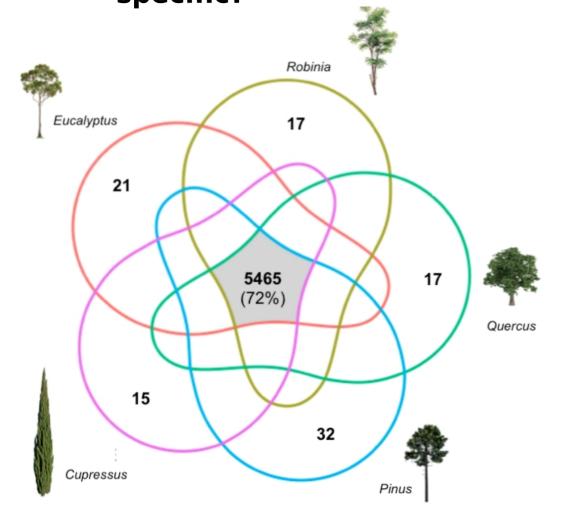


European temperate tree species share a core set of metabolites



European temperate tree species share a core set of metabolites

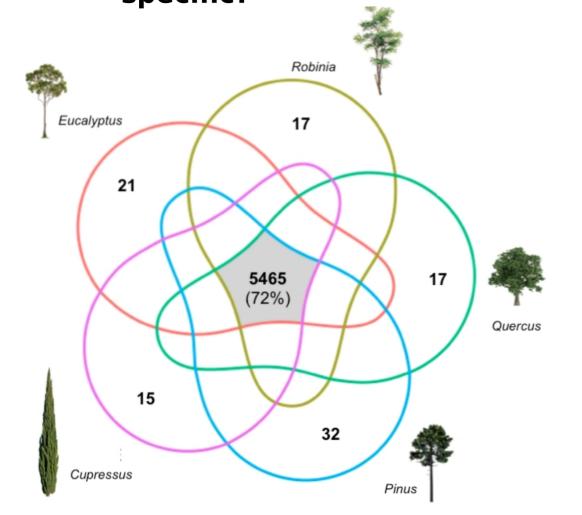
Each tree species had a **distinct** metabolic fingerprint



European temperate tree species share a core set of metabolites

Each tree species had a **distinct metabolic fingerprint** 

The unique metabolic toolkits were conserved across sites



European temperate tree species share a core set of metabolites

Each tree species had a **distinct metabolic fingerprint** 

The unique metabolic toolkits were conserved across sites

Thank you for your attention

# Robinia Eucalyptus 5465 (72%)Quercus Cupressus Pinus

## Acknowledgements

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