Leaf specialized metabolome of Quercus pubescens exposed to amplified drought

Amélie Saunier, Stephane Greff, Elena Ormeño, Catherine Fernandez

Leaf specialized metabolome of *Quercus pubescens* exposed to amplified drought

Amélie Saunier[1,2], Stéphane Greff[1], Catherine Fernandez[1], Elena Ormeno[1]

[1]Aix Marseille Univ, Avignon Université, CNRS, IRD, IMBE, Marseille, France. [2] Department of Environmental and Biological Sciences, University of Eastern Finland, P.O. Box 1627, 70211 Kuopio, Finland

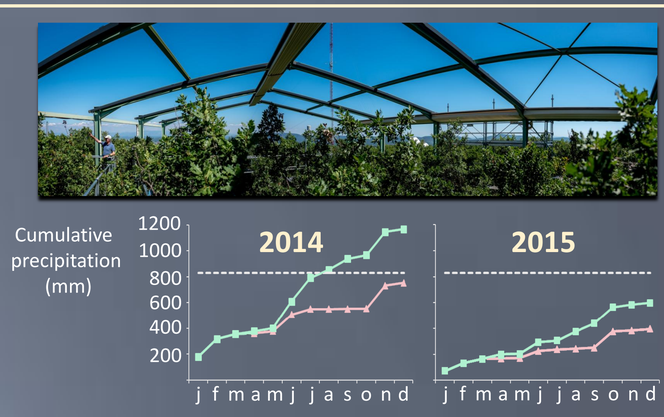
Context of the study

The intensification of summer drought expected with climate change in the Mediterranean region can induce metabolism modifications in plants to help them cope with such conditions. In the long term, these modification may impact diversity and global ecosystem functioning.

In this experiment, we studied the specialized metabolome of *Quercus pubescens* leaves under natural (ND) and amplified drought (AD).
The objectives of this study are to understand:
1/ how recurrent drought impact *Quercus pubescens* metabolome
2/ evaluate *Quercus pubescens* sensitivity to recurrent drought stress

Materiel and Methods

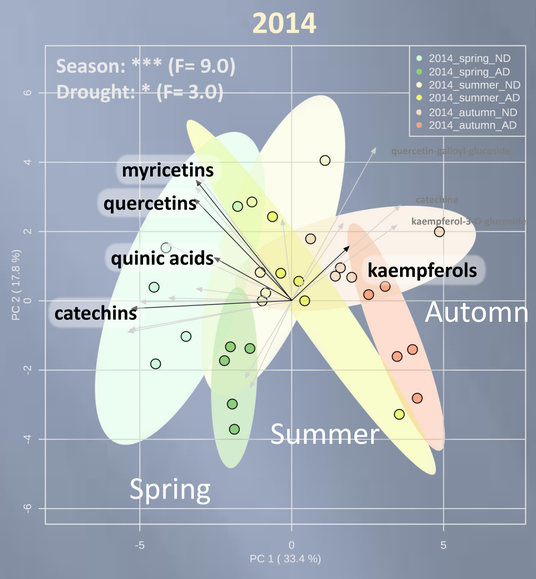
- an *in situ* experimental site, equipped with a rainfall exclusion device, allowed reduction of natural rainfall by 30% over the tree canopy.
- leaves of ND and AD plots were collected in spring, summer and fall during 3 years (2nd, 3rd and 4th years of drought application).
- a **targeted approach** was used to focus on phenolic metabolites.
- an **untargeted approach** permitted to study a broader metabolome variation according to drought.



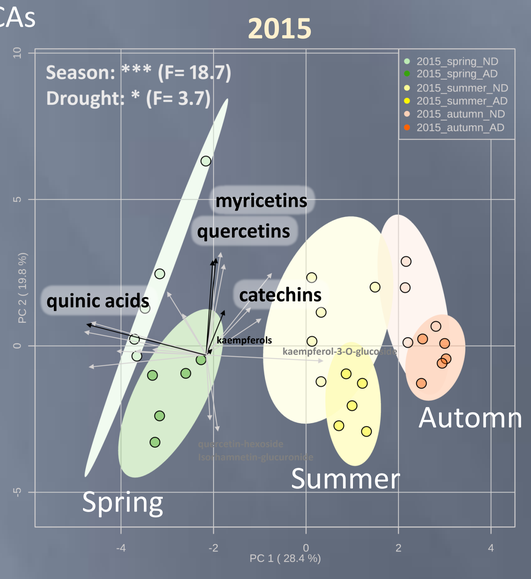
Drought were particularly strong in 2015 compared to the annual mean of cumulated precipitations calculated on the period 1967-2000 (dash lines).
In consequence, ND endured by oaks in 2015 was higher than AD in 2014.

Results

Targeted approach: a drought effect was observed for both years ($p < 0.05$), while the metabolomic profiles were mainly influenced by phenology ($p < 0.001$, two-ways permanova).



PCAs

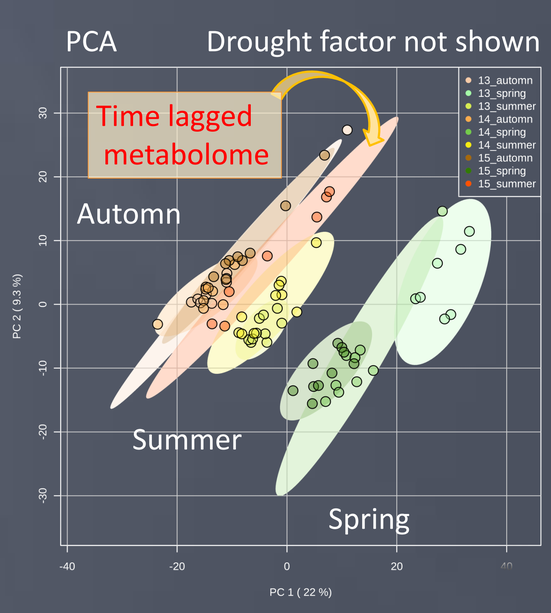


We observed:
- a decrease of global myricetins and quercetins concentrations with drought application at each season.
- an increase of kaempferols concentrations in summer.

The harsher conditions of 2015 stressed the effects of season on oak metabol (wic profiles (F= 9.0 in 2014, F=18.7 in 2015). Kaempferol-3-O-glucoside, specific to automn, was enhanced in summer 2015, whatever drought treatment.

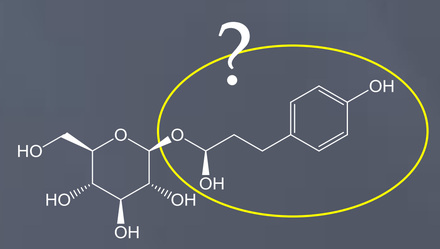
Untargeted approach: The effect of drought on *Quercus* metabolome was weak (ns in 2013 ; $p < 0.05$ for 2014 and 2015) whereas metabolome is mainly driven by seasons ($p < 0.001$ for all years, two-ways permanova).

In 2015, the particular dry year, we observed that the global metabolome of ND and AD leaves sampled in summer presented an early "automnal" pattern, suggesting a seasonal time lag of the chemical content.

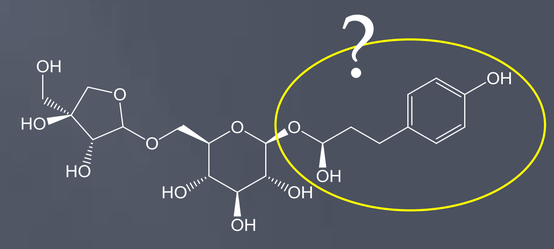


Seven metabolites were highlighted as drought biomarkers using an univariate analysis (Venn diagrams). These biomarkers, still under study, likely belong to the phenylpropanoid pathway with one corresponding to kaempferol pentoside.

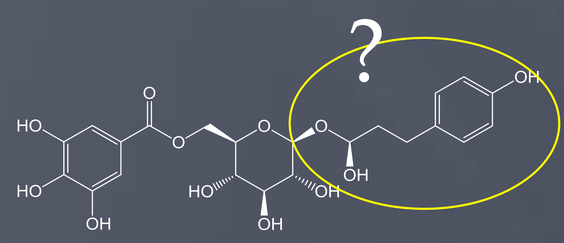
Three of them might be linked to rhododendrin (with apiosyl rhododendrin and galloyl rhododendrin / waiting for co-injection of standard to be confirmed).



Rhododendrin



Apiosyl-rhododendrin



Galloyl-rhododendrin

Conclusions

Targeted and untargeted approaches permitted to demonstrate a time lag of the phenylpropanoid pathway over leaf phenology when trees were exposed to drought. Quercetins, catechins and myricetins, specific to summer leaves were down-regulated to favor the biosynthesis of kaempferols, specific to automnal leaves. Further studies would be necessary to understand how this time lag phenology may impact ecosystem functioning.

Acknowledgments

This work was supported by the French National Research Agency (ANR) through the SecPriMe² project (ANR-12-BSV7-0016-01); Europe (FEDER) and ADEME/PACA for PhD funding. We are grateful to FR3098 ECCOREV for the O_3HP facilities (https://o3hp.obs-hp.fr/index.php/fr/). We are very grateful to J.-P. Orts and I. Reiter. We thank all members of the DFME team from IMBE and particularly S. Dupouyet and A. Bousquet-Mélou for their help during measurements and analyses. We also thank the MALLABAR platform for metabolic fingerprinting analyses (funded by CNRS, Provence Alpes Côte d'Azur Region, Total foundation and ANR SecPriMe² project) and P2M2 from Rennes University for metabolic profiling. Finally, we thank Jean-Charles Martin for providing the "in house" filtering scripts for R.