Between and within species diversity of water use efficiency for Q. petraea and Q. robur : At the crossroad of ecology, ecophysiology and genetics

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Between and within species diversity of water use efficiency for Q. petraea and Q. robur : At the crossroad of ecology, ecophysiology and genetics.

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Climate change predictions tend towards drier summers, challenging forest management to maintain biomass production and survival while reducing water use. Sustainable forest management practices need to take into account these future environmental conditions. In this respect, genetic variation for water use efficiency (WUE), the ratio between biomass production and water use, could be mobilized for adapting forests to these future climates. A strong within species adaptive diversity of WUE related to soil water conditions would support an assisted migration forest management strategy. Here, the case of the two predominant European species *Quercus robur* and *Q. petraea* will be explored.

A strong genetic control of WUE had already been shown for one *Q. robur* family. Here, the study of the genetic architecture of WUE was enlarged to *Q. petraea* and hybrid families, to establish the across species the genetic basis of WUE.

To further clarify the functional basis of the difference in WUE and underlying traits, within and between both species, detailed ecophysiological measurements were carried out. These ecophysiological studies were complemented by gene expression studies in leaves and in guard cells. These indicated a within species variation of the molecular response to drought stress[1].

Finally, an existing common garden of *Q. petraea* allowed to characterise within and among population diversity in WUE[2] Significant differences in WUE were found among populations but a much larger variability was observed within than among populations. The population plasticity of WUE to severe drought could be related to the soil type of the provenance sites, suggesting a local adaptation in terms of drought response strategies. The genotyping of these populations allowed to detect strong associations between WUE and its plasticity and sequenced genes.

An overview will be given on this research strategy, ranging from detailed ecophysiology and gene expression to functional ecology and genomics.

References

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