

Adapted relict oaks (*Quercus* spp.) for climate resilient forests

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INTRODUCTION

Relict oaks (*Quercus* spp.) on extremely dry and unproductive sites in Central Europe often show poor growth characteristics, making them undesirable for practical forestry. Such oaks are most probably autochthonous, have long-term habitat continuity and might have reached the climax community in the early Holocene and stayed more or less unchanged since then. They might thus have adapted to regular water shortage over many generations and harbour valuable genetic resources for adaptation to future climates. Here, we aim to investigate adaptive genomic signatures in relict oaks in southern Germany (Figure 1) and Alsace using a multifaceted approach to assess the use of their reproductive material for establishing climate resilient oak forests.

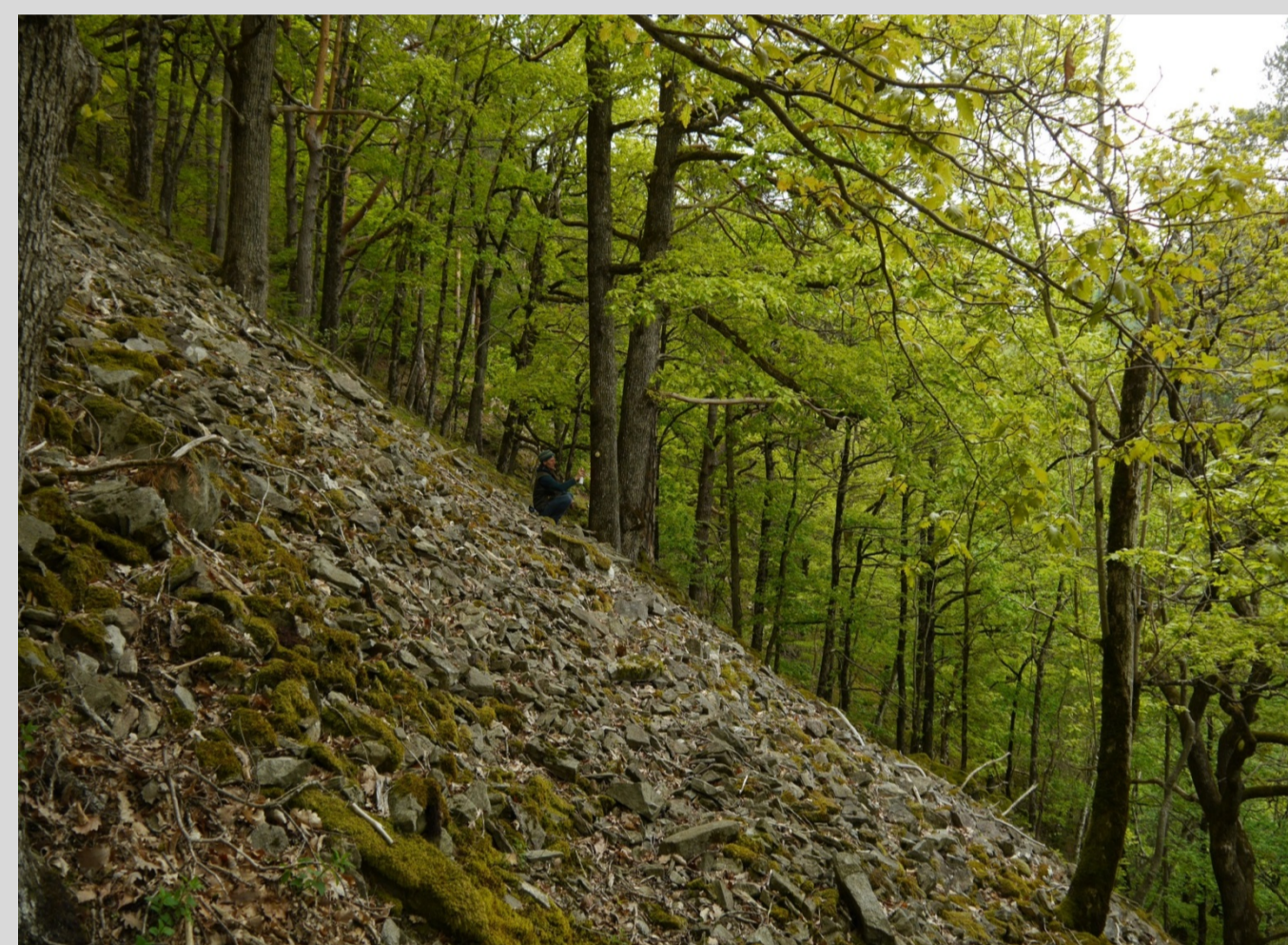


FIGURE 1: Sessile oak (*Quercus petraea*) stand on a dry and steep sites in Falkensteig in the southern Black Forest. (Photo: Charalambos Neophytou)



FIGURE 2: *Rhyncolus sculpturatus*, a primeval forest relict species found in the study sites. (Photo: Jochen Schünemann)



FIGURE 3: Mosses and lichens in Linthal, Alsace. (Photo: Charalambos Neophytou)

MATERIAL AND METHODS

- ❖ Relictness and habitat continuity: Sessile oak as a focal species, water balance, habitat type, topography (slope, exposure), geological substrate (silicate, lime stone, etc.), indicator species such as beetles (Figure 2), mosses and lichens (Figure 3).
- ❖ Refugial origin, autochthony, species identity and genetic variation: Systematic sampling of 30-48 trees per population (60 populations in total including humid sites for comparisons), genotyping with 16 nuclear (neutral and EST) and 9 chloroplast microsatellites (SSRs), comparing with the existing data on managed oak forests in the same region.
- ❖ Stress physiology: Performing reciprocal tests in three different sites, measuring responses of adult trees and their progenies in dry and humid sites to drought stress (e.g. ascorbate and tannins).
- ❖ Local adaptation: Hybridization-based genome capture method applied on DNA pools (PoolSeq), targeting of 30 Mbp genic sites in the oak genome with 200X average coverage with the target fragment size of 300-400 bp, including allele frequency experiment, performing outlier and association analyses, searching for sequence alignments in the existing databases using BLAST.

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RESULTS

The pilot project performed on beetle fauna confirms the presence of the indicator species (Figure 2) in two of our study sites, Falkensteig and Staufen, hinting the relictness and habitat continuity in the project sites.

cpSSR analysis performed with 13 populations so far pointed out low haplotype diversity within the stands ($h_T = 0.148$), which is similar to the previous findings from the same region ($h_T = 0.125$ and 0.162 respectively in the old stands (>100 y) and in the younger stands (<70y); Neophytou & Michiels 2013). Overall genetic diversity among populations was high ($G_{ST} = 0.74$). Haplotype diversities in the stands were shown in Figure 4.

First results from the stress physiology experiment indicated the differential accumulation of ascorbate and tannins (ascagaline and vescalagine) in some contrasting sites (dry vs. humid). However, physiological response to drought stress is very complex and thus needs to be further studied in order to draw any conclusions.

29 populations were scanned with nSSRs up to now for species identification (Neophytou 2014) and the stands predominated by sessile oak were selected as suitable for PoolSeq experiment. Allele frequency validation for pooling is currently in progress.

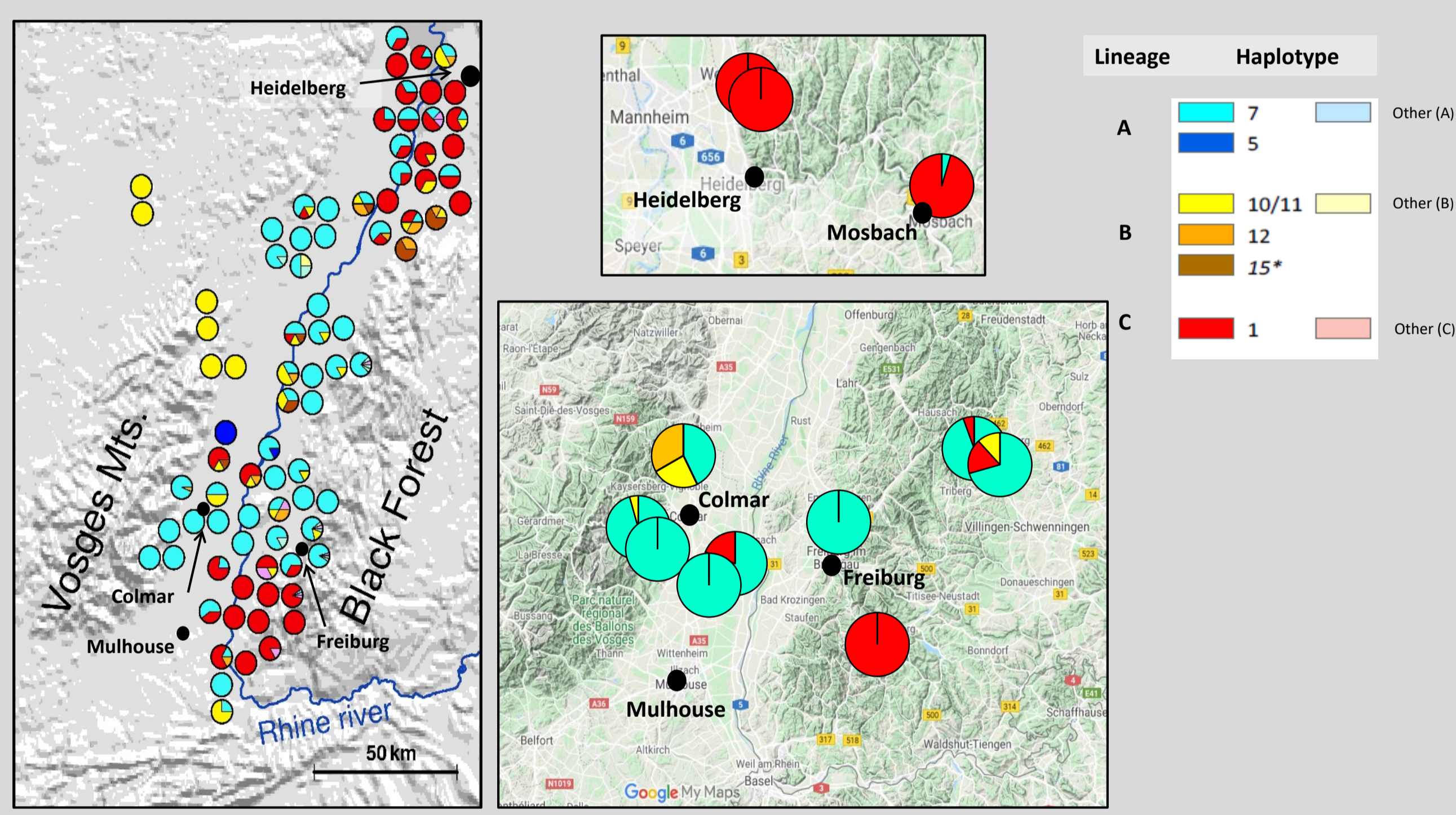


FIGURE 4: Haplotype diversity results based on cpSSRs: Left, Upper Rhine Valley by Neophytou & Michiels (2013); Center, 13 populations in the present study; Right, haplotypes and lineages by Petit et al. (2006), except for the Haplotype 15 (showed as 15*) by Neophytou & Michiels (2013).

CONCLUSIONS

The preliminary results are supporting our initial hypothesis of relictness and autochthony in the stands. Such stands could provide a basis for the establishment of a progeny trial to test genetically determined growth characteristics. The spatial pattern and haplotype diversity results are in line with the previous studies conducted in the Upper Rhine Valley (Neophytou & Michiels 2013; Neophytou et al. 2015). It is possible to reliably assign oak species using nSSRs. Further data is expected to reveal more about oaks and species' local adaptation in the near future since the study is still ongoing.

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