**OAKID2 – Transferability and phylogenetic extension of species-diagnostic SNP markers in European white oak species**

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This EVOLTREE OPPORTUNITY project is a collaboration between the two EVOLTREE partners WSL Birmensdorf (Switzerland) and INRAE Pierroton (France). The two groups independently developed two sets of single-nucleotide polymorphism (SNP) markers (MassArray and KASP) diagnostic for the three hybridizing species *Quercus pubescens, Q. petraea*, and *Q. robur*. We aim at a) taxonomically assigning EVOLTREE ISS populations and b) perform technical comparisons between the two marker sets using a geographically and taxonomically extended sample set.

For a), we used the species-discriminatory KASP markers and high-resolution topographic and soil data to identify the environmental factors associated with taxonomic composition of individuals and populations in 15 mixed EVOLTREE ISS populations of *Q. petraea* and *Q. pubescens* in the Valais, an inner-Alpine valley in Switzerland. Our results show that a multitude of topographic and edaphic factors affect the taxonomic composition and admixture levels of these two hybridizing oak species at local scale, and that regional heterogeneity of these factors promote taxonomic diversity and admixture. This study is currently under review in a scientific journal.
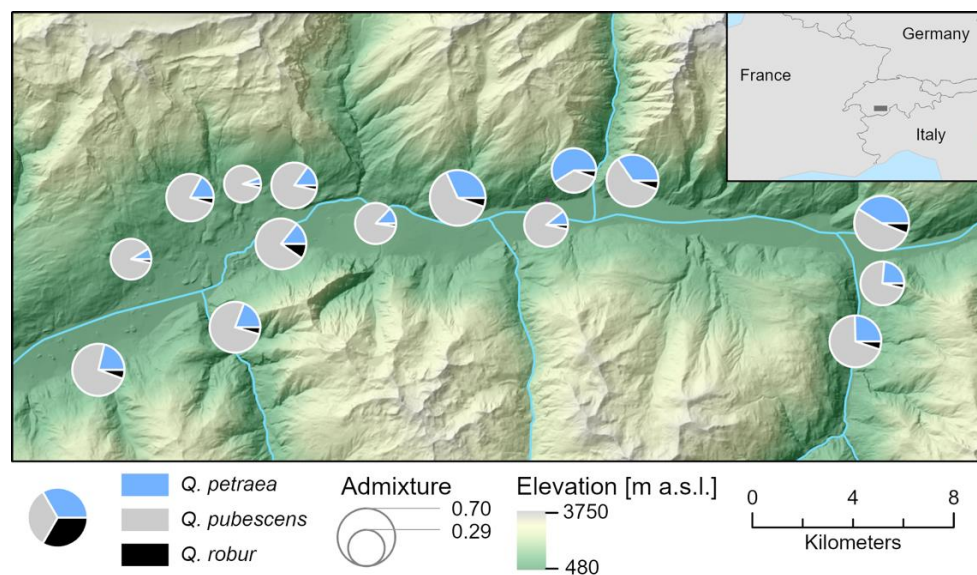
Map with sampling locations of populations represented as pie charts, which indicate mean genetically assigned taxon proportions (colors of charts) and admixture index (S, size of charts) averaged per population.

For b), we performed a cross-validation of the diagnostic marker sets in the complementary reference sample set and expanded the test dataset to additional European white oak species (*Q. frainetto/canariensis/faginea*) to assess the geographic transferability and the taxonomic universality of the markers developed for this project. This work is still ongoing. First results show that both marker sets can reliably assign the complementary reference sample set, but taxon assignment is less accurate. Furthermore, the two marker sets can distinguish between additional taxa with varying power depending on the marker set and taxa. Altogether, preliminary results suggest geographic transferability of the diagnostic marker sets developed in this project.