

# Integrating Leaf Morphology and Whole-Genome Sequencing to Resolve Species Boundaries in the White Oak Species Complex

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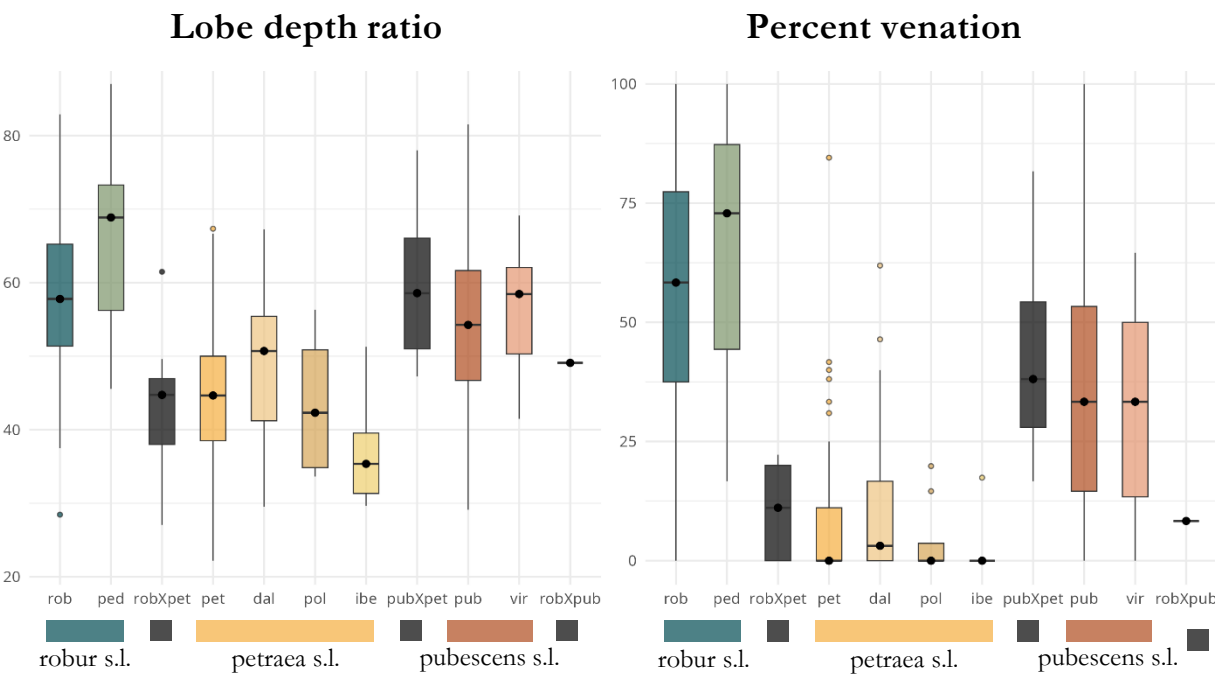
## Background & Aims

Leaf morphology is frequently used to distinguish major species of the white oak species complex (*Quercus* sect. *Quercus*), but its reliability diminishes in sympatric zones with frequent hybridization and for local (sub-)species. Importantly, **the relationship between leaf morphology and genomic patterns remains poorly understood.**

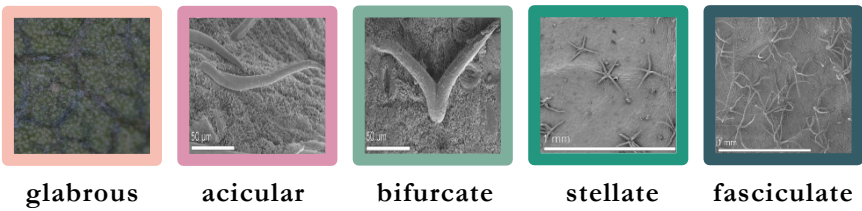
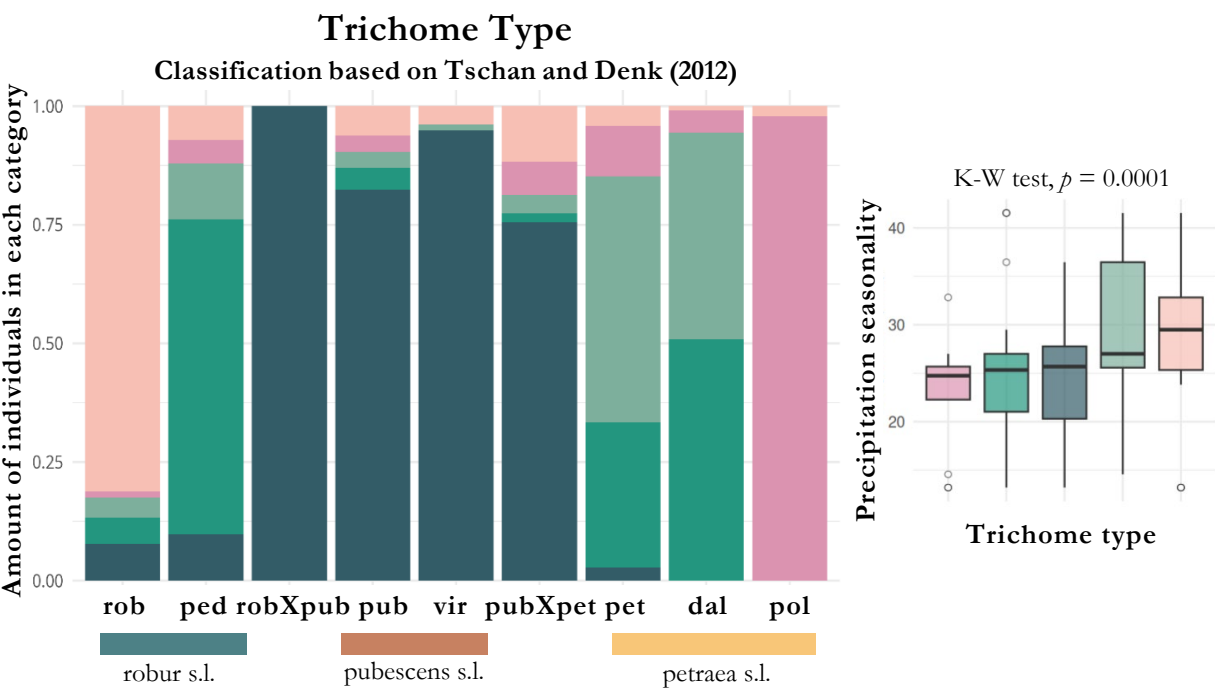
The project HybOakAdapt combines genomic and morphological data from a broad geographic range to better understand to what extent **morphological divergence reflects genomic differentiation.** The findings provide the basis for studying adaptive introgression (check also poster **S2 P25!**).

## Traits of Interest

Multinomial logistic regression and type II ANOVA identify five morphometric traits as good predictors of species *sensu lato*: lobe depth ratio, percent venation, lamina shape, petiole length ratio, and basal lamina shape. Hybrids generally fall within the range of one parental species, though in some cases they exceed the variation observed in either parent.



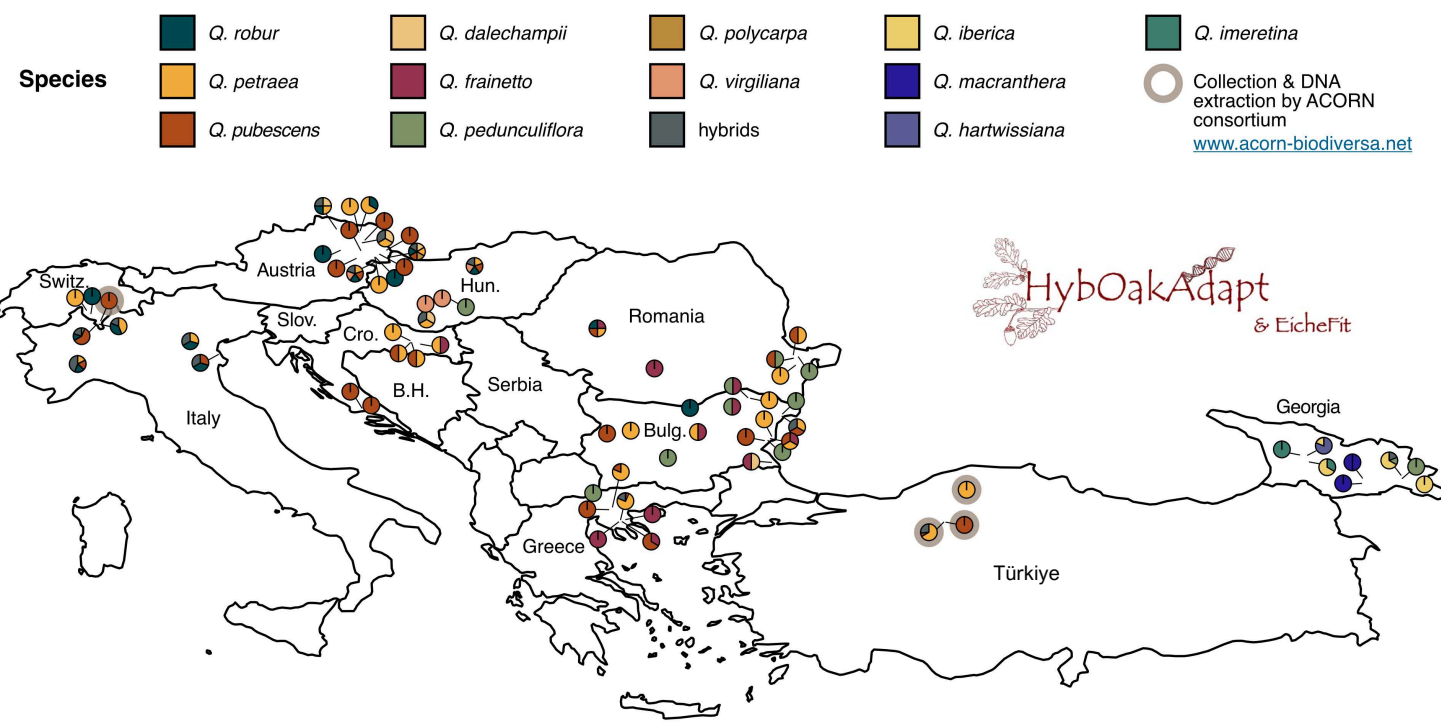
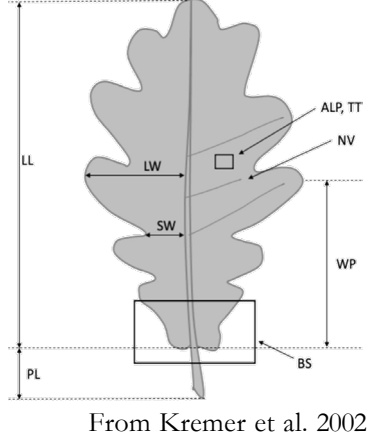
The predominant trichome type appears to be a useful trait for distinguishing some of the subspecies. The trait shows a significant association with precipitation seasonality suggesting a role in climate adaptation.



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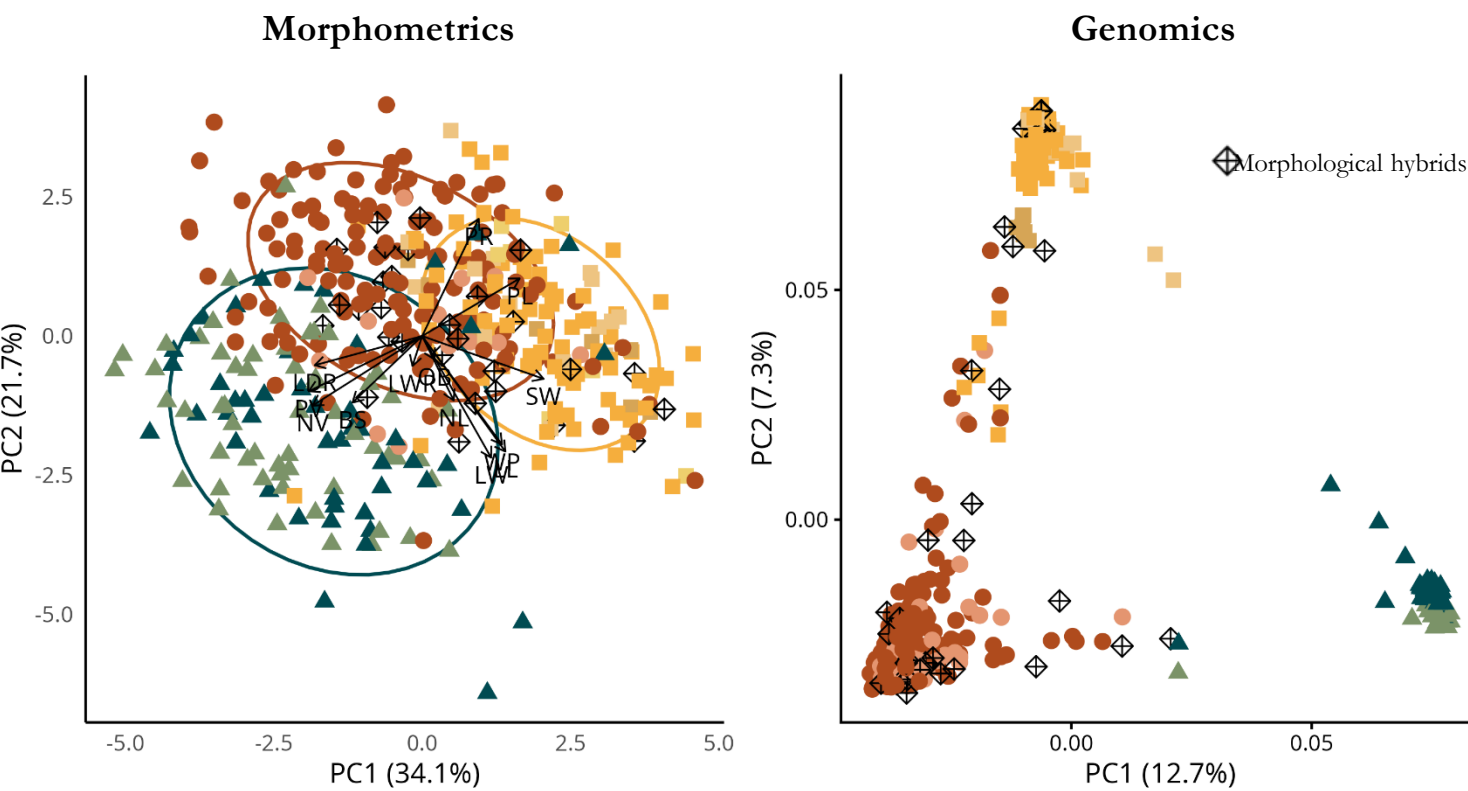
## Study Design

- A subset of the sampling shown on the map, including **38** populations for a total of **416** trees collected across Central and Southeastern Europe, Türkiye & the Caucasus
- **12** (sub-)species in both **pure & mixed stands**
- Leaf **morphometrics** and **analysis of trichome type and density** using six leaves per tree



## Morphometrics vs. Genomics

**Leaf morphometrics** (left PCA) show **greater overlap of the three main clusters** corresponding to *Q. petraea* s.l., *Q. robur* s.l. and *Q. pubescens* s.l. **compared with whole-genome data** (right PCA, ~ 2,000,000 SNPs). Subspecies and regional varieties are closely related to their corresponding main lineages in both analyses. **Trees described as hybrids based on phenotype do not always exhibit intermediate genotypes.**



## Outlook

- Currently testing the **PHENOPlant** phenotyping platform (Vienna BioCenter) for **high-throughput analysis of leaf morphometrics**
- Identification of genomic regions associated with morphological trait variation and potential local adaptation

