
Ancient DNA from waterlogged wood as a new proxy for evolutionary studies on trees

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Résumé

Long-lived tree species build up global forest ecosystems and have been exploited by humans for thousands of years. They are presently of particular concern as their long generation times may limit their adaptability to fast-changing environments. Temporal-series from ancient tree populations can provide a unique perspective on tree evolutionary and forest use history, that may not be detected by studies relying exclusively on extant populations. This information, and a better knowledge of the interplay between forest tree species, humans and climate will likely be paramount for anticipating the potential consequences of ongoing environmental changes. In this study, we took European white oaks (*Quercus robur* and *Q. petraea*) as a tree model species group with the aim to use ancient DNA to track past population dynamics and selective trajectories in the face of major environmental changes. Since ancient DNA studies on trees, in particular in temperate regions, are still in their infancy, we first investigated subfossil and archeological wooden remains from different taphonomical and temporal contexts to define conditions that optimize access to authentic ancient DNA. Following optimized aDNA extraction methods and shotgun sequencing, we succeeded in authenticating genetic data retrieved from 167 ancient oak DNA samples aged between 550 and 9,500 years. We will present the first analyses on this extensive dataset, focusing on key drivers of endogenous DNA preservation, temporal insights on degradation, and postglacial patterns of haplotype distribution.

Mots-Clés: *Quercus petraea/robur*, oak, ancient DNA, degradation, temperate trees, chloroplast DNA

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