



ABSTRACT

Title: From Ancient Fermentations to Modern Mycology: Detecting Yeasts Across Millennia

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Abstract content:

The sequencing of the *Saccharomyces cerevisiae* genome transformed our understanding of yeast biology. Archaeological biomaterials now offer an unprecedented opportunity to explore the long-term evolution, ecology, and domestication of yeasts through time.

Our studies apply molecular and cultivation-based approaches to detect and characterize yeasts in both ancient and modern samples, aiming to evaluate their significance for understanding yeast diversity, adaptation, and human–microbe interactions.

We analysed archaeological and historical specimens from the Hallstatt salt mines (Austria) and the 5,300-year-old Tyrolean Iceman using metagenomics, ancient DNA authentication, genome reconstruction, phylogenetic analyses, and cultivation-based isolation. Whole-genome sequencing and comparative genomics were employed to characterize recovered fungal taxa.

In Iron Age Hallstatt paleofeces, authenticated ancient DNA revealed domesticated *Saccharomyces cerevisiae* and *Penicillium roqueforti*, providing the earliest molecular evidence for beer brewing and blue-cheese production in Europe. In the Iceman, cultivation and genomic analyses recovered viable psychrophilic yeasts including species of *Glaciozyma*, *Mrakia*, *Phenoliferia*, and *Goffeauzyma*, demonstrating long-term microbial persistence in frozen environments.

Combining ancient DNA, cultivation, and genomics enables the detection of both domesticated and environmental yeasts across millennia. These findings illuminate the evolutionary history of yeast domestication, adaptation to extreme environments, and the broader diversity of fungi, extending the legacy of the *S. cerevisiae* genome into paleogenomics and microbial ecology.