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Exploring archaeobotanical collections: from plant remains to past foodways

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Abstract text

This presentation explores the formation and research potential of archaeobotanical collections, focusing on the preservation, variability, and interpretation of plant-related material in archaeological contexts. Special attention is given to the different categories of archaeobotanical evidence, including plant macroremains, microremains, and biomolecular data, as well as the specific preservation conditions that shape their survival and analytical value.

The presentation introduces several case studies that demonstrate how botanical remains can be used in archaeological research. Macrobotanical remains from medieval cesspits, and charred cereal assemblages provide highly informative evidence for past foodways and agricultural practices. Plant microremains, such as phytoliths and starch grains, from dental calculus and pottery food crust, have been studied in combination with biomolecular data from potsherds and human skeletal remains. These multiproxy studies have proven particularly useful in detecting the nuances of consumption practices of selected archaeological communities and illustrate the broad interpretative potential of archaeobotanical collections in archaeological research.

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2

Collections without walls: from fungaria and herbaria to global digital biodiversity infrastructures.

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Abstract text

Natural history collections have shaped my scientific trajectory, from working with fungal specimens in fungaria and plants in herbaria to developing global digital infrastructures. These collections remain the backbone of taxonomy and biodiversity science, preserving physical evidence of life across centuries. Yet today, they are being transformed into interconnected, dynamic systems that extend far beyond institutional walls.

Through my work on the UNITE database, I have seen how DNA sequences can function as collection objects in their own right. By organising fungal sequences into species hypotheses, UNITE links molecular data—including eDNA signals—to taxonomy. At the same time, new collection types are emerging: purified DNA, sequence libraries and eDNA samples from soil, air and water. These capture otherwise hidden biodiversity and complement traditional specimens, bridging past and present observations.

With PlutoF, we aim to integrate specimens, sequences, eDNA data and metadata into a FAIR-by-design environment, maintaining essential links to voucher material. Globally, infrastructures such as INSDC, GBIF and the Catalogue of Life provide the backbone for integration, while DiSSCo ERIC offers a vision of unified digital collections across Europe.

Together, these developments are creating collections without walls—living, connected systems for understanding biodiversity change.

3

Herbarium collections reveal the adaptive significance of leaf form in Solanum

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Abstract text

Understanding the adaptive significance of variation in leaf form is a central goal of plant ecophysiology and evolutionary biology. Herbarium collections provide an unparalleled resource for addressing this question because they contain phenotypic data spanning broad geographic, environmental, and phylogenetic scales. Using herbarium specimens from 100 species of Solanum, I quantified variation in leaf form and combined these measurements with climatic and phylogenetic data to test hypotheses about adaptation using Bayesian phylogenetic comparative methods. The resulting analyses reveal how patterns of leaf variation are associated with environmental gradients. More broadly, this study highlights the scientific value of herbarium collections as a foundation for ecological and evolutionary research. The ability to analyze trait evolution across diverse lineages depends on generations of field collecting, specimen preservation, curation, and, increasingly, digitization. By transforming historical specimens into accessible datasets, ongoing digitization efforts are expanding the scope of questions that can be addressed and enabling new syntheses. Herbarium collections are therefore not only archives of biodiversity, but also essential infrastructure for understanding plant adaptation.

4

Bringing new tools to historical collections: insights into the fossil record of early microorganisms

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Abstract text

Extensive palaeobotanical collections were amassed throughout the nineteenth and early twentieth centuries with the primary aim of documenting and describing fossil plants. Housed in museums and universities across the globe, these collections now represent an invaluable scientific legacy. Beyond their original purpose, they provide exceptional opportunities to investigate fossil microorganisms and their associations with plants, shedding new light on the structure, function, and evolution of ancient terrestrial ecosystems.
Collections comprise a wide range of materials, including thin sections — paper-thin slices of rock glued to microscope slides — and larger rock blocks. Thin sections have traditionally been investigated using brightfield microscopy, which provides detailed anatomical information and reveals the spatial relationships among distinct fossil organisms. Because many fossils are preserved in three dimensions, emerging non-destructive imaging approaches, such as scanning laser confocal microscopy (CSLM), offer opportunities for enhancing their characterization. Rock blocks, also represent valuable resources for the preparation of new thin sections. Recent advances in *in situ* molecular and geochemistry applied to these samples provide high spatial-resolution biogeochemical complements to morphological research.
Drawing on specimens preserved in these historical collections I will present results obtained on cherts formed around hot springs and in volcanogenic settings to describe fungi and other microorganisms. In particular, the Devonian Rhynie cherts (Scotland, UK) preserve a uniquely informative record of early terrestrial ecosystems. Also, the Carboniferous Esnost and Grand'Croix cherts (Massif Central, France), of volcanic origin, provide insights into early forests. These deposits all offer a record of early interactions between plants and microorganisms and how these organisms adapted to the changing face of terrestrial habitats.

5

From overlooked agrobacterial diversity to breakthrough plant transformation

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Abstract text

Agrobacteria-mediated transformation is a foundational technology in plant biology and biotechnology, enabling transgene delivery, genome engineering, and functional genomics across diverse plant species. Despite the extensive natural diversity within the agrobacteria species complex, modern transformation systems rely predominantly on a small number of laboratory-adapted strains. The potential of naturally occurring agrobacterial diversity to improve plant transformation efficiency remains largely unexplored. We investigated a diverse collection of agrobacterial strains representing distinct evolutionary lineages to assess their transient transformation capabilities in *Nicotiana benthamiana*. Comparative analyses revealed substantial variation in transient transformation efficiency among strains, with *Rhizobium rhizogenes* A4 as being one of the most effective strains. Leveraging this, we developed AS109, a disarmed derivative of A4, which displayed markedly enhanced transient expression in solanaceous species, including tomato, eggplant, and pepper, compared with commonly used laboratory strains. Furthermore, AS109 enabled efficient transient gene expression in several non-solanaceous crops, including sweetpotato, faba bean, and lettuce, indicating a broader host range than existing transformation strains. These findings demonstrate that natural agrobacterial diversity represents an underexploited resource for plant biotechnology and provide a framework for expanding the plant transformation toolbox through the exploration and deployment of diverse agrobacterial lineages.