

EGU2020-19272

<https://doi.org/10.5194/egusphere-egu2020-19272>

EGU General Assembly 2020

© Author(s) 2022. This work is distributed under the Creative Commons Attribution 4.0 License.



Shotgun DNA, pollen and biological multi-proxy analysis of Lateglacial lake sediments from Monticchio, Italy

Laura Parducci¹, Kevin Nota¹, Willy Tinner³, Jacqueline van Leeuwen³, Pim van der Knaap³, Dirk Sachse⁴, Zuobing Liang⁴, Achim Brauer⁵, Markus J. Schwab⁵, Xuery Zhao⁵, Aldo Marchetto⁶, Andrea Lami⁶, and Sabine Wulf⁷

¹Uppsala University, Ecology and Genetics, Plant Ecology and Evolution, Uppsala, Sweden (laura.parducci@ebc.uu.se)

³Institute of Plant Sciences, University of Bern, Switzerland

⁴Section Geomorphology, GFZ German Research Centre for Geosciences, Potsdam, Germany

⁵Section Climate Dynamics and Landscape Evolution, GFZ German Research Centre for Geosciences, Potsdam, Germany

⁶National Research Council of Italy, Water Research Institute (CNR-IRSA) Verbania Pallanza, Italy

⁷School of the Environment, Geography and Geosciences, University of Portsmouth, United Kingdom

We used shotgun DNA sequencing of the full metagenome preserved in varved lake sediments from southern Italy (Lago Grande di Monticchio) to investigate the whole diversity of taxonomic groups present. We combine sedimentary aDNA and pollen data as well as other biological multi-proxy data and tested if it was possible to correlate the relative abundances of plants and other biological communities to distinct climatic shifts that occurred between the Late Glacial and Holocene. In addition, we used the metabarcoding technique to compare the two sequencing approaches specifically for plants.

Our studies showed that the inhibition of DNA replication was almost absent in older (full glacial) sediment samples while it increased substantially in more recent samples. DNA provides a strong signal of plant community changes and a large number of new plant taxa were recorded. A comparison between sequencing approaches and proxies highlights differences and similarities and supports earlier findings that plants growing close to or within a lake are often recorded by DNA and that DNA provides important complementary information to that collected from palaeoecological analyses. Nevertheless, increasing DNA reference libraries and enrichment strategies prior to sequencing are necessary to improve the potential and accuracy of plant identification using the metagenomic approach.