



# LAGO GRANDE DI MONTICCHIO DNA ANALYSIS

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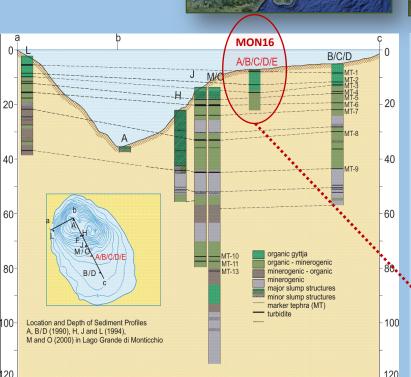














### STUDY SITE

THE HIGH RESOLUTION MONTICCHIO (MON) SEDIMENT RECORD

- ❖ A key archive for reconstructing climate and environmental changes in the Mediterranean for the last glacial—interglacial cycle. Several cores extracted in the past decades (left).
  - Mainly annually laminated
  - Key marker tephra layers
  - Macrorefugia for modern European biota
- MON16: five new cores (A-E) extracted in 2016.
  - Micro-facies analyses, XRF
  - DNA analyses





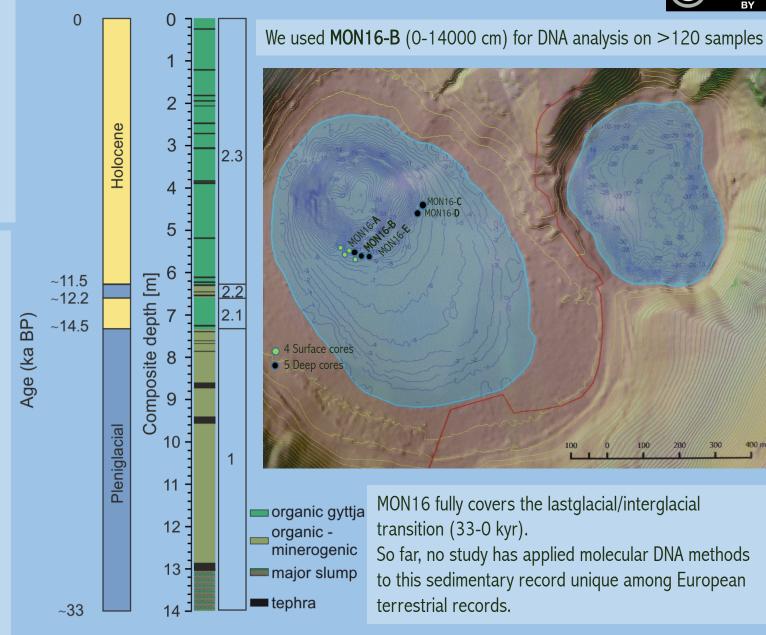
- Maar lake, located within 100-140 km of the Campanian volcanoes documenting major explosive events.
- Lies far enough south to have escaped direct effect of the Weichselian glaciation.
- One of the major glacial microrefugia for European biota.
- Mediterranean climate with distinguished seasonal changes.

#### MACRO-LITHOLOGY

- Unit 1: olive grey organic-minerogenic mud, non-slightly laminations, bottom disturbed.
- Unit 2.1: reddish brown organic material, clear lamination.
- Unit 2.2: ca. 5 cm thick pale greyish sandy homogenous intervals, slightly lamination.
- Unit 2.3: brownish organic mud, good lamination.
- Tephra layers.

## DATING (0-33 kyr BP)\*

- Varve chronology, anchored at tephra Agnano Pomici Principali (11999 $\pm$ 52 a BP).
- Tephrochronology.
- Radiocarbon dating, on terrestrial fragments.



\*See: EGU2020-715 | Displays: <u>CL5.1/GM2.10/SSS3.6</u>





#### **AIMS**

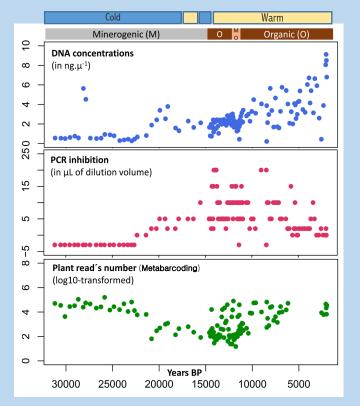
- Reconstruct late Pleniglacial-Holocene vegetation at high taxonomic resolution in southern Europe.
- Link plant community to climate change.
- Compare metabarcoding and shotgun DNA sequencing approaches for vegetation reconstruction.

#### **METHODS**

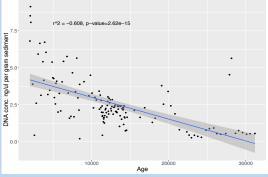
- Metabarcoding of plants (trnL g/h).\*
  - Curated plant database containing *trn*L sequences.
- Shotgun sequencing & capture enrichment (on-going).
  - DNA enrichment to target rbdL & matK genes of major orders of plants (3684 species).
  - Bait set designed using ancestral plant sequence reconstruction.
  - We are currently testing probes designed on the four major orders: Fagales, Pinales, Asterals and Poales.

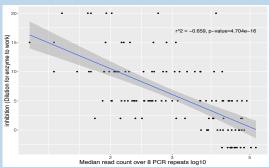
- Sønstebø et al. (2010) Mol Ecol Res 10:1009-1018
- \*\* Co-extracted plant secondary metabolites

# **DNA QUALITY & QUANTITY** (120 samples)









- Nr DNA sequences amplified/sequenced strongly negatively correlated to PCR inhibition.\*\*
- DNA concentration negatively correlated to age.
- No correlation between DNA concentration and PCR inhibition.





#### **RESULTS**

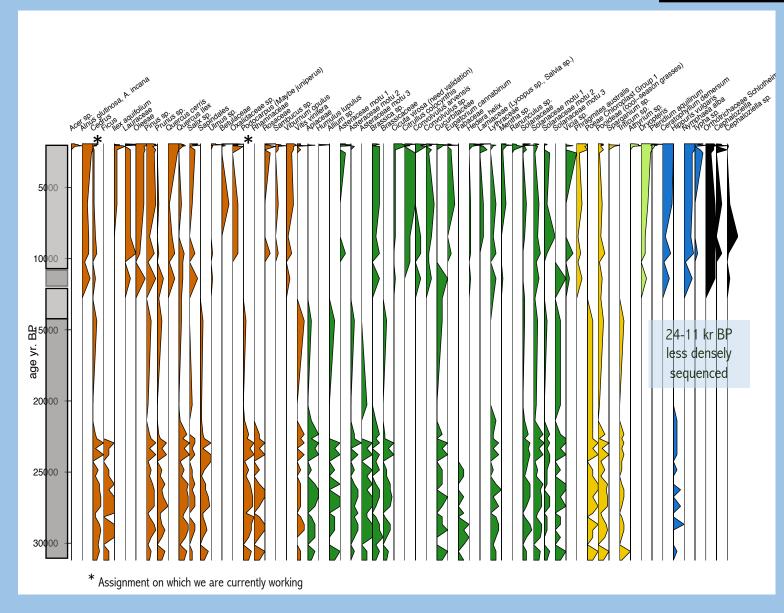
METABARCODING (37/120 SAMPLES)\*

- **0-33 KYR BP: 62 TAXA** (27 extended to the Pleniglacial; 10 only Pleniglacial):
  - 22 trees/shrubs \_\_\_\_
  - 25 herbs
  - 5 grasses  $\blacksquare$
  - 3 ferns
  - 4 aquatics
  - 3 liverworts

Very restrictive assignment: 100% match, only abundant taxa shown and present in > 2 samples. Less densely sequenced in the middle part of the core due to inhibition.

- 0-15 KYR BP: 58 TAXA \*\*
- More taxa can be found: PCR inhibition negative effect removed 2/3 of our samples!

**SHOTGUN SEQUENCING & CAPTURE ENRICHMENT:** ONGOING STUDY Preliminary results not shown.



<sup>\*</sup> Due to PCR inhibition and low read count

<sup>\*\* 40</sup> taxa detected with pollen in Allen et al. 2002 (0-15 KYR BP)





#### **NEXT:**

**METABARCODING:** Increase the number of samples, increase resolution, map climatic transitions better and include low-abundant and rare taxa.

SHOTGUN SEQUENCING & CAPTURE ENRICHMENT: We are currently testing the new bait set designed based on ancestral plant sequences from Fagales, Pinales, Asterals and Poales.

Want to know more?
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<a href="https://laurap.it/index.html">https://laurap.it/index.html</a>

SEE ALSO OUR RESEARCH ON GLACIAL SURVIVAL OF SPRUCE IN SCANDINAVIA

https://presentations.copernicus.org/EGU2020/EGU 2020-21385\_presentation.pdf THIS SESSION 16:38-16:41; D633 | EGU2020-21385

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