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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.
  - Mainly annually laminated
  - Key marker tephra layers
  - Macrorefugia for modern European biota

- MON16 new core:
  - 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 ± 52 a BP).
- Tephrochronology.
- Radiocarbon dating, on terrestrial fragments.

MON16 fully covers the lastglacial/interglacial transition (33-0 kyr).
So far, no study has applied molecular DNA methods to this sedimentary record unique among European terrestrial records.

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

- 120 samples
- Metabarcoding of plants (*trnL* g/h).*
  - Curated plant database containing *trnL* sequences.
- Shotgun sequencing & capture enrichment (on-going).
  - DNA enrichment to target *rbcL* & *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.

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**DNA QUALITY & QUANTITY**

- **Co-extracted plant secondary metabolites**

**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
  - 3 ferns
  - 4 aquatics
  - 3 liverworts
  
  Very restrictive: only included the more abundant species

- **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.

* Due to PCR inhibition and low read count
** 40 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:** Test the new bait set designed based on ancestral plant sequences from Fagales, Pinales, Asterals and Poales.

**Want to know more?**

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**See also our research on glacial survival of spruce in Scandinavia**
This session 16:38-16:41; D633 | EGU2020-21385

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