DNA-metabarcoding to assess the impact of cropland management on soil functions

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Introduction: Ecosystem services in Bulgaria:

- **Background:**
  - Biodiversity in agroecosystems provide critical functions that support agricultural productivity: two examples are soil nutrient circulation and pollination of pollinator-dependent crops. The level of generation of these ecosystem services is associated with the qualities of the agricultural fields and the landscape.

- **Aim:**
  - To assess how the biological and abiotic qualities of cropland soils that underpin important ecological functions supporting ecosystem services, are associated with cropland practices.
Introduction:
What is the impact of cropland management on soil functions?

Large-scale intensive production.  
Small scale extensive production.
Introduction:
What is the impact of cropland management on soil functions?

Soil management: not plowing
plowing
Introduction:
Soil functional diversity revealed by environmental DNA (eDNA) metabarcoding.

- Drummond et al. 2015
  - Ribosomal markers:
    - 18S marker
    - Eukaryotic marker
    - 16S marker
    - Procaryotic marker

- Next generation sequencing

- Comparison with reference database
Methods:
Soil sampling in 60 Bulgarian vineyards.

- Three management practices:
  - conventional large-scale agricultural (20)
  - eco-certified production (20)
  - traditional small-scale (20)
Methods:
Soil sampling in 60 Bulgarian vineyards.
Methods: Soil sampling in 60 Bulgarian vineyards.

- eDNA soil sampling:
  - within a 20 x 25 m grid: 20 subsamples
  - from the subsample mix: 15 g soil for DNA analysis per vineyard
Methods: Soil sampling in 60 Bulgarian vineyards.

- Samples taken for assessment of:
  - nematode communities using traditional methods
  - soil characteristics (texture, pH, N, C, P, K)
Methods:
Analysis – status as of February 1.

- Analysis done by SpyGen
  - DNA extraction, amplification
  - Next generation sequencing
  - Comparison with reference database
- 18S marker
  - Analysis completed
- 16S marker
  - Analysis not completed
- Chemical analysis
  - Partly completed
- Traditional taxonomy
  - Analysis not completed
Preliminary results: eDNA, 18s eukaryotic marker.

- All vineyards combined:
  - Total number of MOTUs (molecular taxonomic units): 1331

- Average number of MOTUs/sample: 210

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<tbody>
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<td>Ascomycota</td>
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<td>Phaeophyceae</td>
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Preliminary results:
eDNA, 18s eukaryotic marker.
Management type (intensive/organic/private)
Preliminary results: eDNA, 18s eukaryotic marker. Management type (intensive/organic/private)

- Non-metric multidimensional scaling
Preliminary results:
eDNA, 18s eukaryotic marker.
Soil management (plowing, grass)
Preliminary results: eDNA, 18s eukaryotic marker. Soil management (plowing, grass)

- Non-metric multidimensional scaling
Next steps

- Add bacterial diversity to the dataset (16s marker)
- Add data on soil properties to the analysis
- Compare the results from the traditional taxonomic analysis of nematodes to the eDNA dataset.
- Identify functional groups and relate their presence to the management type.
Thank you

- On behalf of the fieldteam:
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- And:
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