

Land use effects on soil microalgae and cyanobacteria communities

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In the current global context, with the increase of food demand due to the growing population, there is an urgent need to search for agricultural nature-based solutions as alternative to the conventional practices generating several environmental negative effects, exacerbated also by the pressing climate changes. Soil microalgal and cyanobacterial (SM&C) communities show biofertilizer, biostimulant and biopesticide properties, providing several beneficial ecological functions potentially exploitable in agrosystems. Being photosynthetic primary producers, they can enrich the soil in organic carbon and biomass; they can produce bioactive compounds making more hospitable the microenvironment for plants development; they can improve the physical properties of the soil, such as promoting the soil particles aggregation; the cyanobacteria, in particular, can fix the atmospheric nitrogen, crucial for plant growth (Ramakrishnan et al., 2023; Kalyanasundaram et al. 2020).

The aim of this work was to characterize SM&C communities in a Mediterranean olive orchard, located in Ferrandina (Basilicata, southern Italy), managed with sustainable (S_{mng} ; drip-irrigated with treated urban wastewater, light pruning, soil permanently covered by spontaneously vegetation, mowing and pruning residuals left as mulch) and conventional (C_{mng} ; severe pruning and soil tillage, chemical fertilization) practices for 22 years. After soil sampling in the surface layer (0-3 cm) of the soil, SM&C were cultivated using two selective liquid media: one containing N, for isolating the entire photosynthetic consortium, and one without N, for the nitrogen-fixer cyanobacteria. By the most probable number (MPN; FAO, 1967) method, we assessed their amount: both microalgal and cyanobacterial groups had significantly higher abundance in the S_{mng} soils ($2.210 \cdot 10^4 \text{ g}^{-1}$ and $0.408 \cdot 10^2 \text{ g}^{-1}$, respectively) compared to the C_{mng} ones ($0.872 \cdot 10^4 \text{ g}^{-1}$ and $0.240 \cdot 10^2 \text{ g}^{-1}$, respectively). Biodiversity were evaluated through light microscopy and 16S/18S/ITS rDNA metagenomics. *Anabaena* cyanobacterial genus, *Oedogonium* and *Scenedesmus* green algae and the diatoms *Navicula* and *Pinnularia* were detected in the S_{mng} soils, whereas *Trebouxia*, *Euglena*, *Chaetophora* green algae genuses and the diatom *Cymbella* were dominant in the C_{mng} soils. Metabolomic analysis were performed on lysed cells and supernatant, detecting 1888 features for microalgae and

494 for cyanobacteria, and highlighting distinctive metabolic profiles based on the different land use and two matrices analyzed. Metabolic pathways related to the biosynthesis of the secondary metabolites, hormones, amine, fatty acids and lipid showed an up-modulation in the S_{mng} soils. In particular, the secondary metabolites more accumulated were the N-containing organic compounds, the phytoalexins, the phenylpropanoids and the terpenes, that are elicitors molecules, able to activate a plant defense response, with antibiotic properties and with growth-promoting properties for plants. In light of these results, we can affirm that the sustainable agricultural practices can positively affect the soil phototrophic communities, both quantitatively in their abundance and qualitatively in their diversity and metabolic profiles, strengthening crucial ecological processes mediated by them, improving the soil health and supporting the native microbial diversity.

Keywords: phototrophic microorganisms, soil microalgae, soil cyanobacteria, soil health, sustainable land use

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