

## SCOUTING CANNABIS SATIVA ASSOCIATED MICROORGANISMS IN OPEN FIELD, MAY WE GET SOMETHING MORE THAN YIELD?

CALASTRI E.\*, CREMONESI P.\*, BIFFANI S.\*, MATTANA M.\*, GENGA A.\*, PIZZI F.\*

\*) CNR-IBBA Istituto di Biologia e Biotecnologia Agraria, Consiglio Nazionale delle Ricerche

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Soil metagenomics is nowadays demonstrating to be a promising approach to unravel the effect of different cropping system on the community structure and diversity of the entire soil microbiome. The characterization of the soil microbial diversity associated with the cultivation of a minor crop could get an insight into its agroecological value. *Cannabis sativa* associated microorganisms have been largely investigated under controlled conditions, instead, there is still little data on the biodiversity of soil microbial communities associated with this crop in open field conditions. In this study we aimed to investigate the fungal, bacterial and metazoan communities of two agricultural experimental sites cultivated with four varieties of *Cannabis sativa* and to rank the relative impact of two different treatments: a bio-stimulant (AMF inoculum) and an elicitor (MeJa). We set two experimental fields, located into well-established agricultural areas, maximizing differences between sites in chemical-physical pedologic parameters, in order to study the influence of the varieties on the resident soil microbiota. Within each field study area three replicate blocks, consisting in twelve experimental plots each, have been designed following a split-plot randomized block design (four cultivars by three treatments). Soil sampling have been performed at two time-points: T0 before sowing, and T1 after harvesting. Within each plot, six soil cores were sampled and total genomic DNA was extracted after pooling and homogenizing the soil cores. PCRs with primers targeting 18S rRNA for metazoans, ITS1-ITS2 for fungi and V3-V4 region of the ribosomal 16S rRNA for bacteria were used for library preparation and sequenced in three MiSeq (Illumina) runs with 2×250-base paired-end reads. Microbial

diversity responses due to the different combinations of factors was assessed within- (alpha diversity) and across- (beta diversity) samples. Taxonomic classification of all the microbial communities under study, down to the genus-level, was performed on counts of relative abundance. Further analysis on the microbial communities' structure dynamics could let us pinpoint the role of this recently re-introduced crop in soil diversity augmentation.

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