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Title: METABOLIC DIVERSITY OF MICROBIAL COMMUNITIES INHABITING CHICKPEA RHIZOSPHERE

Publisher: DIVISION OF MICROBIOLOGY ICAR - INDIAN AGRICULTURAL RESEARCH INSTITUTE NEW DELHI-

Language: en_US

Type: Thesis

Agrotags: null

Keywords: Chickpea, Metabolic diversity, Rhizosphere, Enzymes, BIOLOG, PLFA, nifH

Abstract: Chickpea (*Cicer arietinum* L.) is an annual cold season legume, mostly grown under rainfed conditions in arid and semi-arid parts of the world on a wide range of soils from sandy to sandy loam entisols to deep black vertisols. Chickpea forms symbiotic association with effective strains of *Mesorhizobium* sp and able to fix atmospheric nitrogen (N). Several root-associated microbial communities derived from the chickpea rhizosphere soil show spatio-temporal variation and are known to improve plant growth and health by assisting in nutrient uptake, plant hormone production, imparting disease resistance and stress tolerance. Hence the measurement of microbial activities in such soils is central to understand the microbial functions in the soil ecosystem. Soil microorganisms produce extracellular enzymes which in turn produce readily usable dissolved compounds to plants. These metabolic activities of soil microorganisms in rhizosphere differs both quantitatively as well as qualitatively with the soil types. As they may exist in a viable but non-culturable (VBNC) state in addition to their viable and cultural state, the approaches like PLFA (Phospho Lipid Fatty Acids) extraction is used to analyze the structure and function of non-culturable communities giving a real time snap shot of soil microbial community on the basis of fatty acid composition. CLPP (Community Level Physiological Profiling) is another approach provides information about metabolic potential of microbial communities based on carbon substrate utilization. In the present investigation, nine soil samples from different chickpea growing regions were collected. A pot experiment was set up with these soils with two chickpea cultivars (BG 372 and BG 256) without any fertilizer application. Sampling of plants was done at 55 DAS and soil chemical and biological properties were analyzed. The soil nutrient studies revealed that both soil type and genotype influenced the available N, P, K and organic carbon content. The pH measured was among various locations and soil types (bulk and rhizosphere) was found to be neutral to alkaline. The activity of soil enzymes like dehydrogenase and alkaline phosphatase were influenced by both the genotypes in all locations and highest dehydrogenase activity was observed in Dharwad soil (87.88 μ g TPF/g soil/h) with BG 256 genotype. In contrast urease was comparable in bulk and BG 372 rhizosphere soils of New Delhi site 2, Pune site 1 and Pune site 2. Genotype BG 372 enhanced β -Glucosidase activity in rhizosphere soils of Dharwad, New Delhi site 1, New Delhi site 2, Pune site 1 and Pune site 2. The biomass content analyzed by PLFA technique varied significantly and BG 372 variety had a pronounced effect on biomass content in soils of Dharwad, Jharkhand, New Delhi site 2, Pune site 1 and Pune site 2. The ratio of Gram positive to Gram negative bacteria was influenced both by soil types and genotypes with most rhizosphere soils corresponding to higher ratios. Through BIOLOG studies, average substrate utilization pattern was found to be higher for rhizosphere soils than bulk soils. The total bacterial and diazotrophic community as estimated through 16S rDNA and nifH gene copy numbers using qPCR was higher in rhizospheres. The plant dry weight recorded for both genotypes performed equally in all locations, except for Haryana soil with BG 256 and Pune site 1, Kanpur with BG 372 being higher. The plant N and P content were higher BG 256 grown in Haryana soil and BG 372 grown in Pune site 1 soil. Principal component analysis and K-means non-hierarchical cluster mapping grouped soils into three, each having different edaphic or enzyme drivers. However, the study signifies that the interaction between soil type and genotype jointly has more influence on soil microbial activities (metabolic diversity) rather than the soil type and genotype alone. Keywords: Chickpea, Metabolic diversity, Rhizosphere, Enzymes, BIOLOG, PLFA, nifH

Description: T-10162

Subject: Microbiology

Theme: METABOLIC DIVERSITY OF MICROBIAL COMMUNITIES INHABITING CHICKPEA RHIZOSPHERE

These Type: M.Sc

Issue Date: 2019

Appears in Theses (/handle/1/30364)

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