Studies on soil bacterial diversity of Himachal Pradesh using 16S rDNA and nif H gene and soil enzyme activities

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ABSTRACT

Soil is a complex, living and dynamic natural resource and is one of the most diverse habitats on earth. Soil micro-organisms represent a considerable fraction of the living biomass on earth. Understanding the structure and function of soil microbial communities is thus central to predicting how ecosystems will respond to future environmental conditions. Our aim was to find out any significant change in the microbial community structure (in terms of 16S rDNA community structure and nif/H community structure) and function (in terms of enzyme activities i.e. urease, dehydrogenase, arginine deaminase and nitrate reductase) of Chamba valley soil in Himachal Pradesh in cultivated and uncultivated field. In the cultivated field organic manure was used by the farmer in maize plantation whereas uncultivated field was barren with natural vegetation. Soil physio-chemical parameters like soil organic carbon, pH, particle size, bulk density and cation exchange capacity were also studied. Also microcosm experiment was conducted to see the effect of nitrogen mineral fertilizer and organic amendments (i.e. cow dung and corn cob) on soil health. It was observed that Chamba soil is sandy loam in nature with slightly alkaline pH. Microbial activity was higher in the month of May as compared to January based on enzyme assay, bacterial count, microbial biomass and cloning experiments. nif/H diversity of May month cultivated soil sample was observed. It was seen that nif/H is present in phylogenetically diverse bacterial groups and thus can be used as potential bio-indicator of soil health. From the microcosm experiments it was observed that the use of nitrogen mineral fertilizers makes the soil acidic. C/N ratio is an important factor in determining plant health. Lastly corn cob is a good amendment which enhances plant length and also maintains soil pH and microbial diversity.

Key Words: Micro-organisms, 16S rDNA, nif/H, urease, dehydrogenase, arginine deaminase and nitrate reductase