STUDIES ON ECOLOGY OF EDAPHIC MICROBIAL POPULATIONS AND THEIR ACTIVITIES IN MAIZE FIELDS

(**Abstract**)

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Three maize fields differing in agricultural systems were selected for the present study. They were terrace land, valley land and jhum land agricultural systems. Analyses of various physico-chemical characters of the soils of all the three agricultural fields reveal that in general the nutrients followed a trend valley land > terrace land > jhum land. Both quantitative and qualitative assessment of soil microflora and their various activities viz., dehydrogenase and urease enzyme activities and carbon dioxide evolution measurement were carried out at monthly intervals for two crop cycles of maize (*Zea mays* L.). Results demonstrate that the microbial populations and their various activities also followed the trend valley land > terrace land > jhum land. Qualitatively, the composition of mycoflora was found to be almost similar in all the three agricultural fields. *Penicillium chrysogenum*, *Trichoderma viride*, *Aspergillus niger* and *Mucor hiemalis* were found to be of frequent occurrences in all the study sites. *Pythium* sp. was rarely obtained from the soil of jhum land agriculture whereas, this species was commonly isolated from the soil of valley land and terrace land agricultures. *Zygorhynchus* sp. and *Paecilomyces* sp. could be isolated only from the soil of terrace land agriculture. *Phoma humicola* and *Endomyces* sp. were restricted to valley land soil. *Blakeslea* sp., *Cunninghamella echinulata* and *Gongronella* sp. could be isolated from the jhum land soil only.

Relationships between dehydrogenase and urease activities, carbon dioxide evolution, microbial population and physico-chemical characters of the soil were worked out. Statistically no significant correlation was obtained between dehydrogenase activity and microbial populations. However, a positive correlation was obtained between carbon dioxide evolution and fungal population. Urease activity was positively correlated with moisture content, bacterial population, organic carbon and total nitrogen.

Decomposition of maize litters in field condition was studied using litter bag method for a period of seven months. It was found that the rate of decomposition was largely influenced by the types of litter. The rate of decomposition of leaf was more than that of stem and root. The weight loss of all the litters followed Olson's (1963) negative exponental model. Both fungal and bacterial populations were minimum at the early stages of decomposition coinciding with the slow rate of decomposition at the time and attained maximum at the later stages of decomposition. Qualitatively, composition of mycoflora was almost similar in case of all the three types of litters. In decomposed litters, *Trichoderma viride*, *Penicillium chrysogenum*, *Fusarium moniliforme*, *Absidia glauca* and *Mucor hiemalis* were the most common fungal species. The pattern of change in cellulose, hemicellulose, lignin, sugar and amino acid was almost similar for all the litters. Loss in sugar and amino acid was more rapid and the lignin content of the litters degraded at the slowest rate. Increment in the total nitrogen was noted in all the litters which declined towards the end of the experiment.

Under laboratory condition, the rate of litter decomposition by *Trichoderma viride* and *Absidia glauca* was very slow as compared to that under field condition. Fastest rate of decomposition was observed in the set amended with mixed culture of *Trichoderma viride* and *Absidia glauca* and slowest rate was recorded in case of *Absidia glauca* alone.

The study of the mycoflora of gut contents and casts of earthworm did not show difference in species composition. It was found that fungal numbers was maximum in fore-gut and exhibited a decreasing trend towards the distal region of the gut canal while the number of bacteria and actinomycetes increased towards the distal end of the gut canal. *Penicillium chrysogenum*, *Fusarium moniliforme*, *Geotrichum candidum* and *Aspergillus niger* were found to be present throughout the gut canal. Casts of the earthworm contained always higher number of microorganisms (fungi, bacteria and actinomycetes) than the surrounding soil.