CHAPTER 6

SUMMARY AND CONCLUSION
Chapter 6
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The present investigation entitled “Studies on the activity of soil microorganisms associated with kharif rice (Oryza sativa l.) crop” was carried out during the years 2006-2007 and 2007-2008. The study embodies the results of the quantitative determination of soil microflora inhabiting Sali rice field, quantitative estimation of rhizosphere and non-rhizosphere microflora of rice crop and the influence of certain edaphic factors, diversity in microfungal species composition in rhizosphere and non-rhizosphere soil of rice crop, seed mycoflora and its relationship with rhizosphere mycoflora, study of root exudates, cultural filtrates and various microbial activities like degradation of rice stubbles, soil enzyme activities and soil respiration.

1) The soil of the experimental site was acidic in nature. The soil moisture percent was highest in the month of July and lowest in the month of December. The data indicated a fluctuating soil moisture content that correspond to various stages of rice growth. The soil temperature was maximum in the month of June (35.1°C) and minimum in the month of January (26.5°C). Water holding capacity was recorded maximum in the month of April and minimum in the month of January. Soil organic carbon ranged from 0.8 to 1.9% and nitrogen from 0.08 to 0.23 %. Available K ranged from 200.6 to 315 kg ha⁻¹ and available P ranged from 7 to 9.4 kg ha⁻¹.

2) Quantitative analysis of soil microflora of rice field at three different depth (0-10, 10-20 and 20-30 cm) revealed a wide variations of microbial population during the cropping season. Maximum population of bacteria (94.0 cfu/ g dry soil x10⁵) was recorded from 0-10 cm soil layer in the month of October and actinomycetes (70.6x10⁵ CFU/g) in the month of November. Similarly, highest population of fungi (75.6x10⁴ CFU/g) was recorded from 0-10 cm layer and in the month of December. The present study demonstrated that microbial population decreased with the increase in the depth in rice field soils. The depth and month wise variations of bacterial, actinomycetes and fungal
population were found to be statistically significant ($P < .05$). Correlation analysis showed significant relationship between some of the soil parameters with that of distribution of microbial population. Bacteria and actinomycetes population showed positive correlations with soil moisture, organic carbon, nitrogen and available phosphorus content. Whereas, fungi showed strong correlations with pH, available phosphorus and available potassium but do not showed any significant relationship with soil moisture, organic carbon and total nitrogen.

3) Depth-wise variation of fungal population revealed 24 fungal species belonging to 13 genera. Highest number of fungal colonies were isolated from 0-10 cm soil depth followed by 10-20 cm and 20-30 depth. In all the three soil depth maximum number of colonies were recorded in the month of December. The composition of fungal species showed marked variation within the three soil depth. The most abundant fungal species were *Penicillium digitatum* (6.2%) and *Cladosporium herbarum* (5.4%).

4) Quantitative analysis of rhizosphere and non-rhizosphere microflora of *Aijung* varieties of rice was carried out in relation to age of the plant. It was observed that the rhizosphere microflora was higher than non-rhizosphere. Moreover, the rhizosphere microflora increases with the increase in age of the plant up to the flowering stage and after that a continuous decline was observed. Maximum number of colonies of bacteria (117 cfu/g dry soil $\times 10^5$), actinomycetes (35.4 cfu/g dry soil $\times 10^5$) and fungi (77.5 cfu/g dry soil $\times 10^4$) was recorded from rhizosphere of plants attaining flowering stage, with highest R/S values in case of bacteria (7), followed by actinomycetes (3.1) and fungi (2.5).

5) Study on the influence of edaphic factors on rhizosphere (R) and non-rhizosphere (NR) microflora of rice crop revealed highest number of bacteria (52.3 cfu/g dry soil $\times 10^5$) in rhizosphere of cow dung treated soil, actinomycetes (69.4 cfu/g dry soil $\times 10^5$) in alkaline soil and fungi (66.2 cfu/g dry soil $\times 10^4$) in rhizosphere of rice field soil. Similar trend was observed in case of non-rhizosphere soil, except fungi which showed highest number in cow dung treated soil.
Chapter 6

Summary and Conclusion

The effect of soil treatments on root and shoot growth of rice plant showed maximum root length (36.9 cm) in plants grown in cow dung treated soil and shoot length (54.1 cm) in plants grown in rice field soil. Maximum root/shoot ratio (0.88) was observed in plants grown in cow dung treated soil and maximum root (0.20 g\(^{-1}\) plant) and shoot (0.40 g\(^{-1}\) plant) dry weight in plants grown in rice field soil.

The effect of soil treatments on nutrient content of rice plant were analysed. The nitrogen and potassium content in rice plant varied significantly by the application of soil treatments \((P < 0.05)\), but no significant variations were observed in case of phosphorus content. Among the different soil treatments, rice plants grown in cow dung treated soil showed increase in the NPK concentration compared to other soil treatments.

6) Qualitative and quantitative estimation of fungal population in the rhizosphere and non-rhizosphere soils was carried out at different growth stages of the crop. The result reveals occurrence of 25 fungal species belonging to 17 genera in rhizosphere and non-rhizosphere soils studied during the investigation. The results revealed that the species of Aspergillus, Fusarium, Mucor, Penicillium, Rhizopus and Trichoderma occurred in all stages of the crop. The isolated fungal flora exhibited a great deal of diversity in morphological characteristics depending on species composition. The fungal isolates exhibited distinct colony and growth characters including the shape and size.

Quantitatively the highest numbers of colonies were exhibited by species of Aspergillus, Cladosporium, Fusarium, Mucor, Penicillium, and Trichoderma, which occurred in greater numbers in both rhizosphere and non-rhizosphere soils, thus indicating a good degree of adaptation in a Kharif rice ecosystem. In contrast, the species of Alternaria, Cephalosporium, Chaetomium, Helminthosporium, Nigrospora, Pyricularia and Verticillium occurred in lesser number, indicating a lesser degree of proliferation in rhizosphere and non-rhizosphere soils.

Maximum number of fungal colonies was recorded in the flowering stage in rhizosphere soils. Similar was the trend with non-rhizosphere soil. Aspergillus niger

153
recorded the highest number of colonies at the flowering stage (11.3 cfu/ g dry soil × 10^4) in the rhizosphere soil and at seedling stage (7.1 cfu/ g dry soil × 10^4) in non-rhizosphere soil.

R/S values of the rhizosphere and corresponding non-rhizosphere fungal population were computed for some predominant fungus. The R/S values showed wide range of variations throughout the growth stages of rice crop. Values were lower at early growth stages which gradually increased with the progressive growth of the rice plant, reaching the maximum values at flowering and maturity stages for majority of the fungi. At seedling stage maximum R/S values were exhibited by *Mucor hiemalis* (3.4). At tillering stage maximum values were shown by *Aspergillus fumigatus* (2.2). At booting stage *Aspergillus niger* (2.7) showed the highest R/S value. At flowering stage maximum R/S values was recorded by *Fusarium moniliforme* (4.4) and at maturity stage highest R/S values were shown by *Penicillium oxalicum* (3.5).

Cumulative numbers of fungal colonies in rhizosphere and non-rhizosphere soils integrated over five growth stages showed that the number varied from 1.3 to 42.8 cfu × 10^4 in rhizosphere soil and from 1.0 to 20.7 cfu × 10^4 in non-rhizosphere soil. Among the fungal types *Aspergillus niger* showed the highest cumulative number of colonies in rhizosphere and non-rhizosphere soil. Based on quantitative rating scale of the values of colony counts, *Aspergillus niger* was found to be strong colonizers.

7) Studies on rhizoplane mycoflora in the tip, intermediate and crown zone of roots and at five different growth stages of rice revealed a total of 14 genera comprising of 23 species of fungi including one unidentified group. Maximum numbers of species were isolated from the crown zone of the root. The frequency of these species increased with the increase in growth of the rice crop, reaching the peak value at flowering stage.

8) Soil microbial biomass carbon (MBC) and nitrogen (MBN) showed wide variations in the two soil depths (0-10 and 10-20 cm) and at different growth stages of rice. MBC (317 mg kg^-1 dry soil) and MBN (42 mg kg^-1 dry soil) content was maximum at flowering stage in the upper 0-10 cm layer.
Summary and Conclusion

Soil enzyme activities was more in 0-10 cm compared to 10-20 cm depth. In 0-10 cm depth amylase activity was highest at seedling stage (439.25 mg glucose kg\(^{-1}\) soil d\(^{-1}\)). Similarly in upper 0-10 cm layer dehydrogenase activity was more at flowering stage (572.95 mg TPF kg\(^{-1}\) soil d\(^{-1}\)). Similar was the trend with phosphatase activity with maximum during flowering stage (260.64 mg PNP kg\(^{-1}\) soil d\(^{-1}\)).

Soil MBC showed significant correlations (P < 0.01 and 0.05) with MBN (P < 0.05, r = 0.910), dehydrogenase (P < 0.05, r = 0.900), acid phosphatase (P < 0.05, r = 0.951) and alkaline phosphatase (P < 0.05, r = 0.939) activity. MBN is strongly correlated to dehydrogenase (P < 0.01, r = 0.988), acid phosphatase (P < 0.05, r = 0.840) and alkaline phosphatase (P < 0.05, r = 0.881) activity.

There was a positive correlation of soil organic carbon and MBC (R\(^2\) = 0.66, P < 0.05) or MBN (R\(^2\) = 0.73, P < 0.05, and of total nitrogen and MBC (R\(^2\) = 0.88, P < 0.05) or MBN (R\(^2\) = 0.79, P < 0.05) in both the soil depth. Microbial C/N ratio ranged from 7.2 to 7.9 in 0-10 cm layer and 6.4 to 8.8 in 10-20 cm layer. MBC/organic-C varied from 3.5 to 3.9 % and 3.6 to 4.9 %, and MBN/total-N varied from 3.8 to 6.0 % and 4.1 to 6.2 % in 0-10 and 10-20 cm depth respectively.

9) Soil respiration from rhizosphere and non rhizosphere soils at different stages of crop growth during the cropping season revealed maximum rate of soil respiration (41.87 mg CO\(_2\)/kg dry soil/24 hrs) at flowering stage in rhizosphere soil. Minimum rate of respiration (22.13 mg CO\(_2\)/kg dry soil/24 hrs) was observed when the crops were at seedling stage. Similar trend was observed in the case of non-rhizosphere soil with maximum soil respiration (11.17 mg CO\(_2\)/kg dry soil/24 hrs) during the flowering stage of the crop and minimum (8.87) during the seedling stage of the crop.

Studies on soil respiration from three different depth (0-5, 5-10 and 10-15 cm) revealed higher rate of CO\(_2\) evolution from the upper surface layer than subsequent lower layers. The highest CO\(_2\) evolution (12.80 mg CO\(_2\)/kg dry soil/24 hrs) was recorded from the top most layers of soil samples in the month of September. There were significant (P < 0.05) differences between CO\(_2\) evolution with respect to soil depth and month.
10) Studies on seed mycoflora and their relationship with rhizosphere mycoflora showed 20 fungal species belonging to 12 genera from unsterilized rice seeds and 11 species belonging to 7 genera from surface sterilized seeds. Species of *Aspergillus*, *Cladosporium*, *Curvularia*, *Fusarium*, *Penicillium* and *Trichoderma* were the dominant genera recorded during the study.

Study of the root surface mycoflora of the seedlings raised from sterilized seeds in natural soil showed altogether 19 different fungal species belonging to 12 genera. Some of the dominant fungi recorded were *Alternaria alternata*, *Aspergillus candidus*, *A. niger*, *Cladosporium herbarum*, *Curvularia affinis*, *C. lunata*, *Fusarium chlamydosporum*, *Helminthosporium oryzae*, *Mucor hiemalis*, *Penicillium citrinum*, *Trichoderma sp.*, and *Verticillium sp.* Most of the fungi which were recorded in good numbers from the unsterilized seeds were not so frequent on the root surface except *Aspergillus niger* and *Cladosporium herbarum*. This indicated that the above mentioned fungi might have originated from soil.

Study of the root surface mycoflora of the seedlings raised from unsterilized seed in sterilized soil, showed that species like *Fusarium oxysporum*, *Penicillium citrinum*, *Torula sp.* and *Verticillium sp.* were absent in the root surface of the seedlings, thus indicating their soil borne origin. *Aspergillus fumigatus*, *Chaetomium sp.* and *Phoma sp.* which was absent in the root surface of sterilized seeds in natural soil, was found to be predominant in the root surface of unsterilized seeds grown in sterile soil. Thus indicting their seed borne origin.

Study of the root surface mycoflora of the seedlings raised from unsterilized seed in natural soil revealed the presence of all the fungi which were found absent in any of the previous three experiments, with species of *Penicillium*, *Aspergillus*, *Fusarium* and *Trichoderma* being more predominant.

11) Study on effect of root exudates of rice on fungal spore germination, showed increase in the exudation of total soluble carbohydrates, total free amino acids and total phenols with the increase in the age of the rice plant. Maximum exudation of soluble
carbohydrates (16.5 mg/plant), amino acids (9.2 mg/plant) and phenols (49.8 µg/plant) was recorded in 45 days old seedlings.

Root exudates showed a stimulatory effect on the spore germination (%) of the tested fungi. The spore germination percentage increased with the increase in concentration of the exudates. The degree of stimulation was far greater in 100% exudates concentration showing stimulatory effects in most cases. The mean percentage of spore germination increased with the age of the seedlings, except *Fusarium oxysporum* which showed gradual decline in the rate of spore germination. *Aspergillus niger* showed highest mean spore germination percentage.

12) Effect of culture filtrate of some predominant fungi on rice seed germination was analysed. Microbial assay of seed mycoflora showed a total 20 fungal species belonging to 12 genera that remain associated with rice *Aijung* rice seeds. The total per cent incidence of the fungal types was higher in agar plate method carrying potato dextrose agar medium compared to the blotter method. In agar plate method, the highest percentage of occurrence was recorded by *Alternaria alternata* (5.5) in surface sterilized seeds and by *Penicillium oxalicum* (5.2) in unsterilized seeds. In blotter method the highest per cent incidence was recorded by *Alternaria alternata* (4.7) in surface sterilized seeds and *Curvularia affinis* (5.2) in unsterilized seeds.

Study of effect of seed borne fungi on germination and seedling vigour by seed inoculation method revealed that the germination percentage was markedly suppressed to a varying degree by all tested fungi. Maximum per cent inhibition in germination over control was observed in the seeds treated with *Fusarium oxysporum* (28.0) and minimum in seeds treated with inoculums of *Trichoderma viride* (1.8). Maximum decrease in shoot length (7.3 cm) was observed in seeds inoculated with *Fusarium moniliforme* and root length (3.4 cm) in seeds treated with *Chaetomium herbasum*. The mean differences are found to be statistically significant. The highest vigour index (1394.8) of seedling was obtained from seeds inoculated with *Phoma sp.* and the lowest (817.6) was recorded in *Fusarium moniliforme* inoculated seeds.
Study of effect of seed borne fungi on germination and seedling vigour by soil inoculation method showed highest per cent inhibition in germination (30.1%) in the seeds sown in *Rhizopus oryzae* inoculated soils. Lowest inhibition was observed in soil treated with inoculums of *Aspergillus niger* (5.3%). Maximum reduction in shoot length (6 cm) was observed in *Rhizopus nigricans* inoculated soils and root length (3.3 cm) in *Chaetomium herbasum* inoculated soils. The highest vigour index (1038.2) was found in seedling obtained from *Aspergillus flavus* inoculated soils and the lowest (603.5) was recorded from *Fusarium chlamydosporum* inoculated soils.

Study of effect of seed borne fungi on germination and seedling vigour by seed submergence method, showed maximum inhibition in germination (62%) and reduction in seedling vigour (322.7) in seeds soaked treated with culture filtrate of *Aspergillus niger* (62.05%) and minimum inhibition seeds treated with culture filtrate of *Penicillium oxalicum* (28.69%). Maximum reduction in shoot length was due to effect of culture filtrate of *Penicillium oxalicum* (5.5 cm) and root length due to culture filtrate of *Fusarium moniliforme* (3 cm). The highest vigour index (861.9) of seedlings was observed in culture filtrate of *Curvularia affinis* and the lowest (322.7) was recorded in filtrate of *Aspergillus niger*.

A comparison between seed germination per cent as affected by seed borne fungi recorded by the three methods, showed maximum inhibitions seed germination by *Aspergillus niger* (62%) as estimated by seed submergence method and minimum by *Trichoderma viride* (2%) estimated through seed inoculation method.

Data on the effect of culture filtrate of seed borne fungi on seed germination revealed marked inhibition in the rate of seed germination from 7 day to 21 day old filtrate. Filtrates of 100% concentration were found to be more effective in inhibiting seed germination than that of other two concentrations. The inhibitory effect of the filtrates on seed germination decreased with increase in dilution but in no case seed germination was observed more than that of the control.
Studies on the degradation of rice stubbles by soil fungi revealed twenty-seven species belonging to 15 genera (excluding 1 unidentified fungus) that were associated with decomposition of rice stubble. The most diverse fungal flora was obtained from 45-days-old stubble (15 genera, 26 species) with a total colony count of 1166/g dry stubble. The predominant genera were *Aspergillus*, *Penicillium*, *Mucor*, *Helminthosporium* and *Trichoderma*. Data on class wise distribution of fungi revealed that, among the recorded fungi, Deuteromycotina constituted 85.3 % of fungal population followed by Zygomycotina and Ascomycotina respectively.

Maximum degradation ability was shown by *Aspergillus flavus* (9.94%), (22.20%) and (26.30%) in 20, 40 and 60 days after decomposition. Analysis of variance between loss in dry weight and incubation periods showed significant difference in mean at 0.05 level of significance. Maximum lignin degradation was achieved by genus *Aspergillus*. However, with respect to individual fungal species the highest lignin degradation was shown by *Penicillium citrinum* in all three incubation periods. Analysis of variance between percentage of lignin degradation (in dry weight) and (incubation period showed significant difference in mean at 0.05 level of significance. Similarly, maximum degradation of Holocellulose was shown by *Aspergillus flavus* (13.35%) and (35.36%) in 20 and 60 days of incubation and *Aspergillus niger* (22.65%) in 40 days of incubation. Analysis of variance between percentage of holocellulose degradation (in dry weight) and incubation period shows significant difference in mean at 0.05 level of significance.