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SEQUENCE OF MICROORGANISMS IN FIELD SOIL ASSOCIATED WITH RICE STUBBLE DEGRADATION AND SCREENING OF EFFICIENT DEGRADERS

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Stages of degradation of rice stubble determine the sequence of microbial population in soil close to it. At the initial stage bacterial population was found to be dominant. But, at later phase fungi became the most dominant followed by actinomycetes. *Oospora lactis,* which was the most frequent population of the dominant fungi also showed highest efficiency in degrading stubbles under laboratory conditions. *Streptomyces chibaensis,* the most dominant component of the actinomycetes, was also found to be an efficient stubble degrader.

INTRODUCTION

Increased agricultural production in different parts of the world has lead to an increase in agricultural wastes. Such wastes, if recycled through biodegradation by efficient degraders, can cause significant improvment in soil fertility (Chatterjee and Nandi, 1981).

After harvest of rice crops the stubble portions (the major agrowaste in India) left in fields become exposed to the soil microorganisms for degradation. This degradation is greatly influenced by the chemical composition of degrading material as well as the population of degraders. Populations of fungi, actinomycetes and bacteria in soil vary on the basis of their efficiencies to utilize constituents of plant residues during degradation (Eitminaviciute *et. al.* 1976 ; Alexander, 1977).

The present investigation has been aimed in studying the succession of different microflora in field soil with a view to screen dominant degraders of rice stubble.

MATERIALS AND METHODS

Isolation of microorganisms was carried out from rice fields in and around Burdwan, West Bengal. Soils closely associated with stubbles immediately after harvest were collected from several spots in each field, homogenized and a composite sample was prepared. Several such samples collected from different fields at intervals of 15 days till 45 days, during which the stubbles

degraded considerably, were air dried. Twenty plates of a fixed dillution (10^{-4}) were made (Touite, 1969) from each soil sample, ten on malt-agar plus streptomycin (100 units/ml) for isolation of fungi and ten on Krainsky's medium (Touite, 1969) plus aureofungin (0.5 μg/ml) for actinomycetes and bacteria. Gradual change in microbial groups (fungi, actinomycetes and bacteria) with the progress of stubble degradation in flelds was studied on the basis of the percentage of microbial populations. Dominant organisms in the predominant microbial groups (fungi or actinomycetes) in soil were determined after 45 days of crop harvest and expressed as percentage of fungal or actinomycetes population.

In another experiment relative stubble degrading efficiency of the dominant components under laboratory conditions were studied. Spore suspension (2 ml) of more or less equal potency (1.2×10^3 spores/ml) of the organisms (except for *Thielavia terricola* where a suspension of mycelial bits was used as inoculum in absence of asexual spores) was inoculated separately to each flask (250 ml) containing sterilised pieces of stubbles (10g) and distilled water (50 ml), and thoroughly mixed. The flasks were then incubated at 30°C for 90 days with periodic shaking. Parallel sets of control (stubbles + distilled water) was also maintained. Partially degraded stubbles were taken out from flasks, dried at 65°C to constant weight and the extent of degradation was estimated on the basis of loss in dry weight.

RESULTS AND DISCUSSION

Immediately after harvest bacterial population was found to be dominant in soil closed to stubbles (Table 1). It was followed by fungi and actinomycetes in descending order. After 15 days, although the bacterial population showed decrease to certain extent the population of fungi and actinomycetes exhibited marked enhancement. Alexander (1977) also mentioned an increase in decomposing plant material in the first week followed by a decline in their number. Fungal population become highest after 30 days of harvest. Further increase in fungal and actinomycetes populations with simultaneous decrease in bacterial population after 45 days resulted the organisms in the descending sequence of fungi-actinomycetes-bacteria. Martynik and Wladyslam (1979) also recorded a prominent increase of fungi over bacteria and actinomycetes at the later phase of plant material decomposition in soil. Kuester (1979), however, recorded the importance of actinomycetes in colonizing organic matter at the later phase of decomposition.

It became evident that as there was the highest availability of simple sugar in soil during early phase of degradation of organic matter, the bacterial population became dominant (cf. Alexander, 1977). With gradual depletion of the simple sugars there was a gradual decline in bacterial population as only the

resistant carbonaceous compounds were left in decomposing crop residues. Remarkable enhancement in fungal and actinomycetes activities in the later phase made it clear that the secondarily dominant flora were better adopted to utilize the comparatively complex carbon compounds.

Table 1. *Changes in population of microbial groups in field soil associated with degradation of rice stubble*

Nature of microorganisms	Population of microorganisms (%)			
	Days after crop harvest			
	0	15	30	45
Fungi	23.0	37.50	42.96	48.61
Actinomycetes	17.50	20.83	25.19	30.65
Bacteria	59.50	41.67	31.85	20.83

Table 2. *Dominant fungi and actinomycetes in soil associated with rice stubbles after 45 days of harvest*

Fungi		Actinomycetes	
Name	No. of colonies (%)	Name	No. of colonics (%)
Penicillium cyaneum (Bainier and Sartory) Biourge	12.86	*Streptomyces chibaensis* Suzuki Nakamura, Okuma and Tomiyama	55.0
Penicillium waksmani Zaleski	11.42	Other types	45.0
Oospora lactis (Fresenius) Lindau	15.71		
Thielavia terricola (Gilman and Abbott) Emmons	14.29		
Geotrichum candidum Link	14.29		
Aspergillus wentii Wehmer	11.42		
Aspergillus niger Van Tieghem	10.0		
Other types	10.0		

The fungal flora after 45 days of harvest included a number of organisms some of which were dominant (Table 2). Among these, *Oospora lactis* proved to be the most frequent followed by *Geotrichum candidum, Thielavia terricola, Penicillium cyaneum, P. waksmani, Aspergillus wentii,* and *A. niger* in squence. Amongest actinomycetes, *Stretomyces chibaensis* showed the highest population.

All these dominant microorgansms proved to be efficient in degrading rice stubbles. The highest efficiency was shown by *O. lactis* followed by *G. candidum, S. chibaensis, P. waksmani, A. niger, A. wentii, T. terricola* and *P. cyaneum* in descending order.

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