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Response of bio-inputs on microbes under organic cultivation

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Abstract

A field investigation was carried out during *kharif* season of 2019-20 and 2020-21 at Centre for Organic Agriculture Research and Training field, Department of Agronomy, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. The results after experiment indicated that, the combined application of vermiwash @ 10% with compost @ 3 t ha⁻¹ and neem cake @ 500 kg ha⁻¹ observed significantly highest population of bacteria (173.67 and 144.41 CFU 10⁻⁴ g⁻¹ at flowering and 96.87 and 88.45 CFU 10⁻⁴ g⁻¹ at harvest stage), fungi (18.28 and 17.18 CFU 10⁻³ g⁻¹ at flowering and 12.78 and 11.99 CFU 10⁻³ g⁻¹ at harvest stage) and actinomycetes (15.05 and 14.03 CFU 10⁻⁴ g⁻¹ at flowering and 10.61 and 8.32 CFU 10⁻⁴ g⁻¹ at harvest stage) during 2019-20 and 2020-21 respectively.

Keywords: Cotton, biomanuring, bacteria, fungi and actinomycetes

Introduction

Soil harbors dynamic population of microorganisms which play major role in decomposition of organic matter and transformation of plant nutrients. The availability of organically bound nitrogen through transformation in soil to the plant mainly depends on the population of microorganisms, which is influenced by the application of inorganic fertilizers and organic manures. The microbial biomass, which is the total mass of bacteria, fungi, actinomycetes, algae and protozoa present in soil, serves as a temporary sink for nutrients including nitrogen and can be consider as an index of soil fertility (Ingle *et al.*, 2014) ^[3]. Microbial population accounts for only 1-3 per cent of soil organic carbon but it is the eye of the needle through which all the organic material that enters the soil must pass through (Jenkinson 1988) ^[4]. Any management practice that influences microbial communities in soil may be expected to produce changes in soil enzyme level (Perucci and Scarponi 1983) ^[8]. Microorganisms regulate the nutrient flow in the soil by assimilating nutrients and producing soil biomass and converting C, N, P, and S to mineral forms (mineralization) (Jenkinson and Ladd 1981, Wani and Lee 1995) ^[5, 11].

Bacteria bring about a number of changes and biochemical transformation in the soil and thereby directly or indirectly help in the nutrition of plants. The important transformation and processes in which soil bacteria play vital role are decomposition of cellulose and other carbohydrates, nitrification, denitrification, ammonification, biological fixation of atmospheric nitrogen (symbiotic and non-symbiotic), oxidation and reduction of sulphur and iron compounds. All these processes play a significant role in plant nutrition.

The soil microfauna is the most living part of soil mainly responsible for decomposition and nutrient stabilization in soil. Fungi perform important services related to water dynamics, nutrient cycling and disease suppression. Along with bacteria, fungi are important as decomposers in the soil food web, converting organic material into usable forms. Further, it have higher C content (10:1) C:N ratio and less nitrogen (N = 10%) in their cells than bacteria. Fungus help recycle both nitrogen and phosphorus to plants. Due to their smaller size and much greater surface area, fungus can efficiently scavenge for N and P better than plant root hairs and greatly increase the plant root nutrient extraction efficiency. Many plants are associated with certain species of both bacteria and fungus to increases nutrient extraction from the soil. Actenomycetes, generally anaerobic bacteria noticed for a filamentous and branching growth pattern that results, in most forms, in an extensive colony or mycelium, therefore is an important microagent responsible for the process of soil aggregation.

Material and Methods

The composite soil samples from each plot were collected at flowering and at harvest during both the years of study and used for estimating fungi, actinomycetes and bacteria population using serial dilution technique. The media were prepared and sterilized in autoclave. The soil samples were kept in oven at the same time for gravimetric moisture determination. 1 g soil sample was taken in 9 ml sterilized water in the test tube, stirred well and serial dilution were made up to 10^{-8} (Wollum, 1982, Dingra and Sinclair, 1993, Sharma, 1995)^[12, 2, 9].

Bacteria count (cfu 10⁻⁴ g⁻¹)

The serially diluted supernatant (1 ml) of 10⁻⁴ was taken with pipette and spread over into petriplates filled with potato dextrose agar (PDA) medium. Rose bengal was added in PDA medium to check the growth of bacteria.

Fungi count (cfu 10⁻³ g⁻¹)

The serially diluted supernatant (1 ml) of 10⁻³ was taken with pipette and spread over into petriplates filled with nutrient agar (NA) medium. Antifungal natamycin was added in NA medium to check the growth of fungus.

Actinomycetes count (cfu 10⁻⁴ g⁻¹)

The serially diluted supernatant (1 ml) of 10⁻⁴ was taken with pipette and spread over into petriplates filled with Munairs and Kenknight's medium.

The poured plates (NA, PDA and Munairs and Kenknight) were incubated at 24 + 1 °C for 72 hours. The fungi, actinomycetes and bacteria colonies (cfu) developed were counted.

Result and Discussion

Bacterial count (CFU 10⁻⁴ g⁻¹)

It has been mentioned in many of the literature that management practice greatly influence the bacterial population, hence the study of bacterial population was undertaken to find out the influence of various organic treatments over the bacterial population in rainfed vertisols and presented in Table 1. The mean of bacterial colonies observed to be 160.36 and135.93 CFU 10^{-4} g⁻¹ at flowering and 89.30 and 81.50 CFU 10^{-4} g⁻¹ at harvest stage of crop during the year of 2019-20 and 2020-21 respectively.

Values of bacterial population obtained with various biomanuring treatments revealed significant differences among treatments. During the year of 2019-20, there was more population growth of bacterial colonies in soil with organics, uppermost count at flowering and at harvest was recorded with combined application of vermiwash with compost and neem cake 173.67 and 96.87 CFU 10^{-4} g⁻¹ in 2019-20 and 144.41 and 88.45 CFU 10^{-4} g⁻¹ in 2020-21 which was statistically significant over alone application of nutrients like jivamrut, cow dung slurry, vermicompost and control and being on par with combined application of jivamrut, cowdung slurry (T₄ and T₅) and alone application of compost and vermiwash (T₇ and T₃) during both the year of study.

Greater soil aggregation associated with compost, neem cake and vermiwash along with adequate moisture might have resulted more colonization by the bacterial. The present results are accordance with those of Chang *et al.*, (2010) ^[1], Nakhro and Dkhar (2010) ^[7], Singh *et al.*, (2012) ^[10] and Mallesha and Rao (2017)^[6].

Fungi count (CFU 10⁻³ g⁻¹)

The data regarding of fungal count recorded during the present experiment are placed in Table 1. The mean of fungal colonies was observed to be 16.83 and 15.73 CFU 10^{-3} g⁻¹ at flowering and at harvest it was 11.66 and 10.93 CFU 10^{-3} g⁻¹ during 2019-20 and 2020-21 respectively.

Values of fungal population obtained with various biomanuring treatments recorded changes among different treatments. During the year of 2019-20, there was more growth of fungal colonies in soil than the 2020-21. Maximum count recorded with combined application of vermiwash along with compost and neem cake was 18.28 and 17.18 CFU 10^{-3} g⁻¹ at flowering and 12.78 and 11.99 CFU 10^{-3} g⁻¹ at harvest during the both years of study which was closely followed by combined split application of vermiwash and compost during 2019-20 and 2020-21 respectively. Combined application of vermiwash found superseded over alone and combined application of jivamrut (T₁ and T₄), cow dung slurry (T₂), vermicompost (T₈) and control (T₉) during both successive years of investigation.

The organic manure helps to maintain the organic carbon and nutrient status of soil. The carbon acts as a source of carbon and energy for microbes and ferments organics that results in quick build up of microflora and fauna. This results into activation of soil microflora that are present in soil. Analogous data were given by Chang *et al.*, (2010)^[1], Nakhro and Dkhar (2010)^[7], Singh *et al.*, (2012)^[10] and Mallesha and Rao (2017)^[6].

Actinomycetes count (CFU 10⁻⁴ g⁻¹)

In the present investigation the study of actinomycetes was undertaken with special reference to find out effect of alone and combined application of different organic nutrient sources. The findings on number of actinomycetes colonies are presented in Table 1. The average number of actinomycetes colonies was obtained to be 13.70 and 12.86 CFU 10^{-4} g⁻¹ at flowering and at harvest stage of crop it was 9.27 and 6.80 CFU 10^{-4} g⁻¹ during both consecutive years of experimentation.

Actinomycetes colony forming units differ significantly with sources of nutrients. During the year of 2019-20 there was more growth of actinomycetes colonies in soil with combined application, noteworthy count recorded with split application of vermiwash together with compost and neem cake was 15.05 and 14.03 CFU 10^{-4} g⁻¹ at flowering and 10.61 and 8.32 CFU 10^{-4} g⁻¹ at harvest stage of cotton crop followed by cow dung slurry in combination of compost and neem cake (T₅) and alone application of compost @ 10 t ha⁻¹ (T₇) during 2019-20. The trend was found similar for the successive year of study.

This might be due to the presence of easily metabolizable compounds at the beginning of the crop was also under active growth phase releasing higher amounts of root exudates, supporting numerous and diverse micro flora. The significant increase in microbial population was observed with the addition of organic manures in combination with liquid organic manure at various growth stages of cotton. The present data are in accordance with the findings of Chang *et al.*, $(2010)^{[1]}$ and Singh *et al.*, $(2012)^{[10]}$.

Table 1: Microbial population at flowering and at harvest stage as influenced by different treatment in cotton crop during 2019-20 and 2020-21.

| Treatment | Bacterial count CFU 10 ⁻⁴ g ⁻¹ 2019-20 | | Fungi count CFU 10 ⁻³ g ⁻¹ 2019-20 | | Actinomycetes count CFU 10 ⁻⁴ g ⁻¹ 2019-20 | | Bacterial count CFU 10 ⁻⁴ g ⁻¹ 2020-21 | | Fungi count CFU 10 ⁻³ g ⁻¹ 2020-21 | | Actinomycetes count CFU 10 ⁻⁴ g ⁻¹ 2020-21 | |
|---|--|-------|--|-------|--|-------|--|-------|---|-------|---|------|
| | At . | At | At . | At | At . | At | At . | At | At . | At | At . | At |
| T ₁ : Application of Jivamrut (10%) in four equal splits 20,40,60 and 80 DAS | 145.67 | 86.39 | 15.37 | 11.01 | 12.27 | 8.02 | 129.10 | 79.08 | 14.26 | 10.13 | 11.54 | 5.44 |
| T ₂ : Application of Cow dung slurry (10%) in four equal splits 20,40,60 and 80 DAS | 150.33 | 87.62 | 15.97 | 11.22 | 13.36 | 8.57 | 134.40 | 80.31 | 14.86 | 10.34 | 12.59 | 6.05 |
| T ₃ : Application of Vermiwash (10%) in four equal splits 20,40,60 and 80 DAS | 169.73 | 91.69 | 17.32 | 11.93 | 13.94 | 9.62 | 139.91 | 84.52 | 16.17 | 11.23 | 13.06 | 7.34 |
| $T_4: T_1 + Compost @ 3 t ha^{-1} + 500 kg ha^{-1} Neem cake$ | 161.27 | 90.38 | 17.07 | 11.67 | 13.82 | 9.35 | 136.59 | 82.39 | 15.93 | 11.01 | 12.94 | 7.07 |
| $T_5: T_2 + Compost @ 3 t ha^{-1} + 500 kg ha^{-1} Neem cake$ | 173.07 | 94.61 | 18.15 | 12.55 | 14.79 | 10.37 | 142.67 | 86.07 | 17.05 | 11.77 | 13.77 | 8.04 |
| T ₆ : T ₃ + Compost @ 3 t ha ⁻¹ + 500 kg ha ⁻¹ Neem cake | 173.67 | 96.87 | 18.28 | 12.78 | 15.05 | 10.61 | 144.41 | 88.45 | 17.18 | 11.99 | 14.03 | 8.32 |
| T ₇ : Application of compost @ 10 t ha ⁻¹ in four equal splits 20,40,60 and 80 DAS | 172.70 | 92.24 | 17.61 | 12.22 | 14.22 | 9.94 | 140.92 | 84.89 | 16.54 | 11.60 | 13.49 | 7.77 |
| T _s : Application of Vermicompost @ 5 t ha ⁻¹ in four equal splits 20,40,60 and 80 DAS | 153.40 | 88.97 | 16.51 | 11.34 | 13.58 | 9.08 | 135.68 | 80.85 | 15.44 | 10.71 | 12.85 | 6.19 |
| T ₉ : Control (Biomulching of sunhemp at 35 DAS) | 143.37 | 75.71 | 15.17 | 10.28 | 12.25 | 7.88 | 119.71 | 66.97 | 14.18 | 9.65 | 11.51 | 5.00 |
| S.Em± | 4.42 | 2.18 | 0.39 | 0.28 | 0.33 | 0.24 | 2.74 | 2.21 | 0.40 | 0.27 | 0.30 | 0.26 |
| CD at 5% | 13.24 | 6.53 | 1.18 | 0.85 | 1.00 | 0.73 | 8.22 | 6.61 | 1.20 | 0.80 | 0.90 | 0.79 |
| General mean | 160.36 | 89.30 | 16.83 | 11.66 | 13.70 | 9.27 | 135.93 | 81.50 | 15.73 | 10.93 | 12.86 | 6.80 |



Plate 1: Microbial population as influenced by different treatment in cotton crop

Conclusion

The combined application of vermiwash @ 10% along with compost @ 3 t ha⁻¹ and neem cake @ 500 kg ha⁻¹ was recorded highest population of fungi, bacteria and actinomycetes during 2019-20 and 2020-21.

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