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ASSESSMENT OF THE IMPACT OF DIFFERENT CROPPING SEQUENCES ON SOIL MICROBIAL POPULATIONS (BACTERIA, FUNGI, AND ACTINOMYCETES) AND ENZYMATIC ACTIVITY ACROSS VARYING SOIL DEPTHS IN WESTERN UTTAR PRADESH

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ABSTRACT
This investigation was conducted to evaluate the influence of different cropping systems and soil depths on soil microbial properties. Soil samples were collected from different cropping sequences at three depths: 0–15, 15–30, and 30–45 cm. The samples were analyzed for microbial populations (bacteria, fungi, and actinomycetes), microbial biomass carbon (MBC), and dehydrogenase activity. The results showed that both cropping sequence and soil depth significantly influenced soil microbial characteristics. All microbial parameters were recorded to be highest in surface layer (0–15 cm) and declined progressively with increasing depth due to reduced organic matter availability. Bacterial populations ranged from 3.6×10^6 to 5.1×10^8 CFU g^{-1} soil, with the highest average values under maize–wheat and sugarcane–mustard–ratoon–rice systems. Fungal populations varied from 1.5×10^4 to 8.2×10^4 CFU g^{-1} soil, while actinomycetes ranged from 1.7×10^4 to 7.4×10^4 CFU g^{-1} soil, both recording maximum populations in the maize–wheat system. Microbial biomass carbon ranged from 223 to 385 µg g^{-1} in surface soil, with the highest values under maize–wheat and sugarcane–cucumber cropping sequences. Dehydrogenase activity ranged from 62 to 81 µg TPF g^{-1} day^{-1}, with maximum activity in the maize–wheat system. Overall, maize- and sugarcane-based cropping systems supported greater microbial abundance and activity than other cropping sequences.

KEYWORDS: Cropping Sequences; Dehydrogenase Activity; Microbial Biomass Carbon; Soil Depth; Soil Microbial Population.

INTRODUCTION
The increasing population, urbanization, and industrialization in India have reduced per capita land availability from 0.14 ha to an expected 0.09 ha by 2030, making it essential to enhance productivity through intensified and diversified cropping systems. Cropping systems, which include crop sequences and management practices over time, are now focused on both productivity and sustainability. In the Indo-Gangetic Plains (IGP), major systems such as rice–wheat, maize–wheat, and sugarcane-based systems dominate, with rice–wheat alone covering about 10 million hectares. However, continuous cereal-based systems have resulted in declining productivity, nutrient imbalances, and pest pressure (1,2). Inclusion of legumes and green manuring has shown significant benefits; for example, green manuring with *Sesbania* increased soil organic carbon from 0.29% to 0.45% over six years (3), while long-term studies at Pantnagar reported increases of 15 kg ha^{-1} nitrogen and 13.8 kg ha^{-1} available phosphorus with legume incorporation. Diversified systems like rice–legume rotations have also been found to improve productivity and sustainability compared to continuous rice–wheat systems (4). Additionally, microbial properties are enhanced under diversified systems, with higher microbial biomass carbon and enzyme activity reported in rice–legume systems than in rice–wheat systems (5).

MATERIALS AND METHODS
The present investigation on soil properties under different cropping sequences in Muzaffarnagar and Ghaziabad districts was conducted by collecting soil samples from 20 locations at three depths (0–15, 15–30, and 30–45 cm). The study area lies in the Indo-Gangetic Plains with subtropical climatic conditions, characterized by hot summers (up to 42–44°C), cold winters (3–4°C), and annual rainfall of about 681–714 mm. Soil samples were collected using an auger, air-dried, sieved (2 mm), and properly labelled for analysis. Microbial populations were estimated using the standard serial dilution and spread plate technique. Bacterial populations were enumerated on nutrient agar medium and incubated at 28 ± 1°C for 48–72 hours (6,7). Fungal populations were estimated on Rose Bengal Streptomycin Agar using the serial dilution plate technique and incubated for 3–7

days. Actinomycetes populations were determined on Kenknight and Munaier's medium and incubated for approximately 7 days (8). Microbial biomass carbon (MBC) was determined using the chloroform fumigation–extraction method (9). Dehydrogenase activity was measured following Page *et al*. method based on the reduction of triphenyl tetrazolium chloride (TTC) to triphenyl formazan (TPF), which was estimated spectrophotometrically at 485 nm (10). The study also included the collection of field-level information such as cropping system, fertilizer use, irrigation practices, residue management, and farmers' feedback to support the interpretation of microbial populations, microbial biomass carbon, and enzymatic activity under different cropping sequences and soil depths.

RESULTS AND DISCUSSION

Effect of Cropping Sequences on Bacterial Population

The bacterial population differed significantly among cropping sequences and soil depths (Table 1 and Fig. 1.1). At 0–15 cm soil depth, the highest bacterial population (6.4×10^8 count g^{-1} soil) was recorded under the sugarcane–mustard–ratoon–rice cropping sequence, whereas the lowest population (4.6×10^6 count g^{-1} soil) was observed under the rice–berseem cropping sequence. The higher bacterial population under the sugarcane–mustard–ratoon–rice sequence was due to continuous addition of crop residues, greater biomass production, an extensive root system and higher organic carbon accumulation. These conditions provided a continuous supply of carbon and energy to soil microorganisms, resulting in greater bacterial growth and multiplication. Doran and Parkin reported that continuous incorporation of crop residues improves soil organic matter and enhances microbial growth and activity (11). Similarly, Masto *et al.*, observed that residue-rich cropping systems sustain a higher bacterial population because of increased organic carbon availability (12).

At 15–30 cm soil depth, the bacterial population ranged from 2.7×10^4 to 6.2×10^5 count g^{-1} soil, while at 30–45 cm depth, it ranged from 2.0×10^2 to 6.2×10^2 count g^{-1} soil, indicating a significant decline with increasing soil depth. The reduction in bacterial population with increasing soil depth was associated with lower organic carbon content, reduced root density, limited aeration and decreased availability of readily decomposable organic substrates in the subsurface layers. Surface soils receive continuous inputs of plant residues and root exudates, creating favourable conditions for microbial proliferation. Alexander reported that bacterial populations are concentrated in the surface soil because of higher organic matter content and favourable environmental conditions (7). Likewise, Brady and Weil explained that microbial abundance decreases rapidly below the plough layer owing to reduced carbon availability and diminished root influence (13). Similar depth-wise reductions in bacterial populations were also reported by Ghosh *et al.* (14).

Among the remaining cropping sequences, maize–wheat also recorded a comparatively higher bacterial population (4.4×10^8, 4.5×10^6 and 4.2×10^2 count g^{-1} soil at 0–15, 15–30 and 30–45 cm depths, respectively). Similarly, maize–potato, sugarcane–cucumber and urd–wheat maintained relatively higher bacterial populations than rice-based cropping systems. The higher bacterial population in these cropping systems was attributed to greater rhizosphere activity and continuous addition of decomposable crop residues. In the case of urd–wheat, the inclusion of a leguminous crop enhanced biological nitrogen fixation, improved soil fertility and stimulated microbial activity. Adekulne *et al.* reported that soil microbial population and diversity are directly influenced by soil organic matter and biological activity. Their findings demonstrated that increased organic matter input promotes microbial proliferation and improves soil biological health (15).

In contrast, rice–berseem and rice–wheat recorded comparatively lower bacterial populations across all soil depths. The lower bacterial population in these cropping systems resulted from comparatively lower residue retention and reduced organic matter accumulation, which limited the availability of carbon substrates required for bacterial growth. Consequently, microbial multiplication remained comparatively low throughout the soil profile. Overall, the present investigation demonstrated that bacterial population was strongly influenced by cropping sequence and soil depth. Residue-rich and diversified cropping systems maintained higher bacterial populations, whereas bacterial abundance consistently decreased with increasing soil depth because of reduced organic carbon availability and lower biological activity.

Effect of Cropping Sequences on Fungal Population

The fungal population varied significantly among different cropping sequences and soil depths (Table 2 and Fig. 2.1). At 0–15 cm soil depth, the highest fungal population (8.2×10^4 count g^{-1} soil) was recorded under the maize–wheat cropping sequence, whereas the lowest fungal population (1.4×10^4 count g^{-1} soil) was observed under the urd–wheat cropping sequence. The higher fungal population under the maize–wheat cropping sequence was attributed to greater crop biomass production, continuous incorporation of crop residues, extensive root biomass and favourable soil environmental conditions. Fungi play a vital role in the decomposition of complex organic compounds such as cellulose, hemicellulose and lignin; therefore, cropping systems producing higher biomass provide abundant substrates for fungal growth and multiplication. Masto *et al*. reported that soils receiving higher quantities of crop residues and organic inputs maintain significantly greater microbial populations and biological activity (12). Similarly, Ghosh *et al.* observed higher fungal biomass and microbial activity in diversified cropping systems because of enhanced organic matter accumulation and favourable rhizosphere conditions (14).

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The fungal population varied significantly among different cropping sequences and soil depths (Table 2 and Fig. 2.1). At 0–15 cm soil depth, the highest fungal population (8.2 × 10^4 count g^{-1} soil) was recorded under the maize–wheat cropping sequence, whereas the lowest fungal population (1.4 × 10^4 count g^{-1} soil) was observed under the urd–wheat cropping sequence. The higher fungal population under the maize–wheat cropping sequence was attributed to greater crop biomass production, continuous incorporation of crop residues, extensive root biomass and favourable soil environmental conditions. Fungi play a vital role in the decomposition of complex organic compounds such as cellulose, hemicellulose and lignin; therefore, cropping systems producing higher biomass provide abundant substrates for fungal growth and multiplication. Masto *et al*. reported that soils receiving higher quantities of crop residues and organic inputs maintain significantly greater microbial populations and biological activity (12). Similarly, Ghosh *et al.* observed higher fungal biomass and microbial activity in diversified cropping systems because of enhanced organic matter accumulation and favourable rhizosphere conditions (14).

Among the remaining cropping sequences, sugarcane–cucumber, rice–sugarcane and maize–potato also recorded comparatively higher fungal populations. The fungal populations under these cropping systems were 6.3 × 10^4, 4.4 × 10^4 and 4.2 × 10^4 count g^{-1} soil, respectively, in the surface layer, with comparatively higher populations also maintained at deeper soil depths. The comparatively higher fungal population under these cropping systems resulted from continuous addition of organic residues, greater root biomass and sustained availability of decomposable organic substrates. These conditions enhanced fungal colonization and decomposition processes, thereby improving overall microbial activity in the soil. Subba Rao emphasized that soil fungi are highly dependent on organic substrates and therefore occur in greater abundance in soils receiving continuous organic matter inputs (16).

In contrast, the urd–wheat, rice–wheat, rice–wheat–urd and sugarcane–mustard–ratoon–rice cropping sequences recorded comparatively lower fungal populations across all soil depths. The lower fungal population in these cropping systems was associated with reduced availability of decomposable organic substrates and comparatively less favourable soil conditions for fungal proliferation. Limited organic residue inputs restricted the supply of carbon and energy required for fungal growth, resulting in comparatively lower fungal abundance.

A consistent decline in fungal population was observed with increasing soil depth under all cropping sequences. At 15–30 cm soil depth, the fungal population ranged from 1.5 × 10^2 to 7.4 × 10^2 count g^{-1} soil, while at 30–45 cm depth it ranged from 1.0 × 10^2 to 7.3 × 10^2 count g^{-1} soil. For example, under the maize–wheat cropping sequence, the fungal population declined from 8.2 × 10^4 count g^{-1} soil in the surface layer to 7.3 × 10^2 count g^{-1} soil at 30–45 cm depth, whereas under the rice–berseem cropping sequence it decreased from 2.07 × 10^4 to 1.5 × 10^2 count g^{-1} soil.

The reduction in fungal population with increasing soil depth was due to lower organic carbon content, reduced root exudation, poor aeration and limited nutrient availability in the subsurface layers. Surface soils continuously receive plant residues and root exudates, which serve as major sources of carbon and energy for fungal growth and activity, whereas deeper layers contain comparatively fewer substrates for microbial proliferation. Alexander reported that fungal populations are concentrated in the upper soil layers because of greater availability of organic matter and favourable environmental conditions (7). Brady and Weil explained that microbial abundance decreases rapidly with increasing soil depth because of reduced carbon availability and diminished root influence (13). Likewise, Paul reported that lower root density and reduced nutrient availability in subsurface soils significantly restrict microbial growth (17). Nannipieri *et al.* further highlighted that the distribution of soil microbial communities is closely associated with the distribution of organic carbon throughout the soil profile (18).

Overall, the present investigation demonstrated that fungal population was strongly influenced by both cropping sequence and soil depth. Cropping systems producing greater biomass and higher residue returns, particularly maize–wheat, sugarcane–cucumber and rice–sugarcane, maintained significantly higher fungal populations, whereas fungal abundance consistently declined with increasing soil depth because of reduced organic carbon availability and less favourable environmental conditions. These findings highlight the importance of residue management and diversified cropping systems in sustaining soil fungal communities and improving overall soil biological health.

Effect of Cropping Sequences on Actinomycetes Population

The actinomycetes population varied significantly among different cropping sequences and soil depths (Table 3 and Fig. 3.1). At 0–15 cm soil depth, the highest actinomycetes population (7.4 × 10^4 count g^{-1} soil) was recorded under the maize–wheat cropping sequence, whereas the lowest population (1.7 × 10^4 count g^{-1} soil) was observed under both the rice–wheat and urd–wheat cropping sequences.

The higher actinomycetes population under the maize–wheat cropping sequence was attributed to greater biomass production, continuous incorporation of crop residues and higher accumulation of soil organic matter. Crop residues served as a continuous source of carbon and energy, creating favourable conditions for the growth and multiplication of actinomycetes. These microorganisms actively decompose resistant organic compounds such as cellulose, chitin and lignin derivatives, thereby contributing to nutrient cycling and soil organic matter turnover. Goodfellow and Williams reported that actinomycetes are abundant in soils containing high levels of

organic substrates and play an important role in the decomposition of complex organic materials (19). Similarly, McCarthy and Williams observed that the abundance of actinomycetes increases significantly in soils receiving continuous organic residue inputs because of enhanced substrate availability (20).

Among the remaining cropping sequences, sugarcane–cucumber and maize–potato also maintained comparatively higher actinomycetes populations, recording 6.7×10^4 and 6.1×10^4 count g^{-1} soil, respectively, in the surface layer.

The higher actinomycetes population under these cropping systems resulted from greater residue return, extensive root systems and increased soil organic matter accumulation. Continuous supply of plant residues promoted the decomposition of resistant organic compounds and sustained microbial activity throughout the growing season. Acosta-Martínez *et al.* reported that diversified cropping systems receiving higher organic residue inputs maintain greater microbial abundance and biological activity than conventional cropping systems (21). Likewise, Larkin demonstrated that crop rotation and residue management significantly improve actinomycetes populations and enhance overall soil microbial activity (22).

In contrast, the rice–wheat, urd–wheat and rice–wheat–urd cropping sequences recorded comparatively lower actinomycetes populations, with surface soil values of 1.7×10^4, 1.7×10^4 and 2.0×10^4 count g^{-1} soil, respectively.

The comparatively lower actinomycetes population under these cropping systems was associated with lower accumulation of resistant organic residues and reduced substrate availability. Limited organic matter inputs restricted the supply of carbon required for the growth and proliferation of actinomycetes, resulting in comparatively lower microbial populations.

A consistent decline in actinomycetes population was observed with increasing soil depth under all cropping systems. At 15–30 cm soil depth, the population ranged from 1.5×10^2 to 6.5×10^2 count g^{-1} soil, whereas at 30–45 cm depth it ranged from 1.2×10^2 to 6.6×10^2 count g^{-1} soil. For example, under the maize–wheat cropping sequence, the actinomycetes population declined from 7.4×10^4 count g^{-1} soil in the surface layer to 6.6×10^2 count g^{-1} soil at 30–45 cm depth, while under the rice–berseem cropping sequence it decreased from 2.0×10^4 to 1.3×10^2 count g^{-1} soil.

The decline in actinomycetes population with increasing soil depth resulted from lower organic carbon content, reduced oxygen availability and diminished root activity in subsurface soils. Surface soils receive continuous additions of crop residues and root exudates and possess better aeration, thereby providing favourable conditions for actinomycetes growth and activity. In contrast, deeper soil layers contain lower concentrations of organic substrates and reduced oxygen availability, which restrict microbial proliferation. Atlas and Bartha reported that actinomycetes are concentrated in the upper soil horizons because of favourable aeration and greater organic matter availability (23). Similarly, Sylvia *et al.* observed that soil actinomycetes are most abundant in biologically active surface soils where organic carbon concentration and root activity are highest (24).

Overall, the present investigation demonstrated that the actinomycetes population was strongly influenced by cropping sequence and soil depth. Cropping systems characterized by higher biomass production and continuous residue return, particularly maize–wheat, sugarcane–cucumber and maize–potato, maintained significantly higher actinomycetes populations. In contrast, actinomycetes abundance declined consistently with increasing soil depth because of reduced organic carbon availability, limited aeration and lower root activity. These findings highlight the importance of residue management and diversified cropping systems in sustaining actinomycetes populations and improving soil biological health.

Effect of Cropping Sequences on Microbial Biomass Carbon (MBC)

The microbial biomass carbon (MBC) varied significantly among different cropping sequences and soil depths (Table 4 and Fig. 4.1). At 0–15 cm soil depth, the highest MBC (385.0 µg g^{-1} soil) was recorded under the maize–wheat cropping sequence, followed closely by sugarcane–cucumber (383.0 µg g^{-1} soil) and maize–potato (359.5 µg g^{-1} soil). In contrast, the lowest MBC (223.0 µg g^{-1} soil) was observed under the rice–wheat cropping sequence.

The higher microbial biomass carbon under the maize–wheat, sugarcane–cucumber and maize–potato cropping systems was attributed to greater biomass production, continuous incorporation of crop residues, extensive root systems and higher organic carbon inputs. Crop residues and root exudates served as readily available sources of carbon and energy for soil microorganisms, thereby enhancing microbial growth and biomass accumulation. Jenkinson and Ladd identified microbial biomass carbon as a sensitive indicator of soil organic matter dynamics and biological activity and reported that continuous organic matter inputs substantially increase microbial biomass (25). Similarly, Powlson *et al.* observed that cropping systems receiving greater quantities of organic residues maintain significantly higher microbial biomass carbon because of increased substrate availability for microbial growth (26).

Among the remaining cropping sequences, rice–berseem, rice–mustard, rice–sugarcane and sugarcane–mustard–ratoon–rice also maintained comparatively higher MBC values than conventional cereal-based systems throughout the soil profile.

The comparatively higher MBC under these cropping systems resulted from continuous organic matter addition, improved rhizosphere activity and enhanced soil biological processes. Greater residue return promoted microbial proliferation and increased the accumulation of microbial biomass carbon. Sparling reported that

microbial biomass carbon is closely associated with soil organic carbon status and responds positively to residue incorporation and improved soil management practices (27). Likewise, Gregorich *et al.* demonstrated that continuous incorporation of crop residues enhances microbial biomass carbon and improves overall soil biological health (28).

The rice–wheat, urd–wheat and rice–wheat–urd cropping systems recorded comparatively lower MBC values. Surface soil MBC under these systems was 223.0, 233.0 and 255.5 µg g^{-1} soil, respectively, with a similar trend observed at deeper soil depths.

The comparatively lower microbial biomass carbon under these cropping systems was associated with lower residue return and reduced organic carbon availability. Limited carbon substrates restricted microbial growth and biomass development, resulting in comparatively lower MBC values throughout the soil profile.

A progressive decline in microbial biomass carbon was observed with increasing soil depth under all cropping systems. At 15–30 cm soil depth, the MBC ranged from 150.0 to 180.0 µg g^{-1} soil, whereas at 30–45 cm depth it ranged from 76.0 to 108.5 µg g^{-1} soil. For example, under the maize–wheat cropping sequence, MBC declined from 385.0 µg g^{-1} soil in the surface layer to 87.5 µg g^{-1} soil at 30–45 cm depth, while under the rice–berseem cropping sequence it decreased from 287.5 µg g^{-1} soil **to** 85.0 µg g^{-1} soil.

The reduction in microbial biomass carbon with increasing soil depth resulted from decreasing organic carbon content, lower root density, reduced availability of microbial substrates and diminished biological activity in the subsurface layers. Surface soils continuously receive crop residues and root exudates, which provide favourable conditions for microbial growth and biomass accumulation, whereas deeper soil layers contain limited carbon sources and reduced microbial activity. Anderson and Domsch reported that microbial biomass is concentrated in the surface soil because of higher concentrations of organic substrates and favourable environmental conditions (30). Similarly, Wardle observed that microbial biomass carbon declines markedly in subsurface soils owing to reduced organic matter and microbial activity (31). Smith and Paul also reported that the availability of organic carbon is the principal factor regulating microbial biomass distribution throughout the soil profile (32).

Overall, the present investigation demonstrated that microbial biomass carbon was strongly influenced by cropping sequence and soil depth. Cropping systems characterized by greater biomass production and continuous residue return, particularly maize–wheat, sugarcane–cucumber and maize–potato, maintained significantly higher microbial biomass carbon than the other cropping systems. In contrast, MBC consistently declined with increasing soil depth because of reduced organic carbon availability, lower root activity and less favourable conditions for microbial growth. These findings emphasize the importance of diversified cropping systems and effective residue management in sustaining microbial biomass carbon and improving long-term soil biological health.

Effect of Cropping Sequences on Dehydrogenase Enzyme Activity

The dehydrogenase enzyme activity varied significantly among different cropping sequences and soil depths (Table 5 and Fig. 5.1). Irrespective of cropping sequence, the highest dehydrogenase activity was recorded in the surface soil (0–15 cm), followed by 15–30 cm and 30–45 cm soil depths, indicating a consistent decline in enzyme activity with increasing soil depth. Among all the cropping sequences, the maize–wheat system recorded the highest dehydrogenase activity (81 µg TPF g^{-1} soil day^{-1}) in the surface soil, followed closely by the sugarcane–cucumber cropping sequence (80 µg TPF g^{-1} soil day^{-1}). In contrast, comparatively lower enzyme activity was observed under the rice–berseem, rice–wheat and urd–wheat cropping systems.

The higher dehydrogenase activity observed under the maize–wheat and sugarcane–cucumber cropping systems was associated with greater biomass production, continuous incorporation of crop residues, extensive root biomass and enhanced microbial activity. Continuous addition of organic residues increased soil organic carbon and supplied readily available carbon sources for soil microorganisms, resulting in greater intracellular enzyme activity. Dehydrogenase is an intracellular enzyme closely associated with living microbial cells; therefore, its activity directly reflects the intensity of microbial metabolism in soil. Casida *et al.* reported that dehydrogenase activity is a reliable indicator of total microbial oxidative activity and is strongly influenced by soil organic matter and microbial abundance (33).

Among the remaining cropping systems, maize–potato, rice–mustard and rice–sugarcane also maintained comparatively higher dehydrogenase activity throughout the soil profile than the conventional cereal-based cropping systems.

The comparatively higher enzyme activity under these cropping systems resulted from continuous residue incorporation, improved rhizosphere activity and greater microbial biomass. Enhanced root growth and organic matter accumulation stimulated microbial metabolism, thereby increasing dehydrogenase enzyme activity. Saha *et al.* reported that residue incorporation and integrated crop management practices significantly increase soil enzyme activities by improving microbial biomass and substrate availability (34). Likewise, Kumar *et al.* demonstrated that diversified cropping systems with higher organic matter inputs maintain greater dehydrogenase activity than less diversified cropping systems (35).

A progressive decline in dehydrogenase enzyme activity was observed with increasing soil depth under all cropping systems. For example, under the maize–wheat cropping sequence, the mean dehydrogenase activity declined from 79.5 µg TPF g^{-1} soil day^{-1} at 0–15 cm depth to 36.5 µg TPF g^{-1} soil day^{-1} at 15–30 cm depth and further to 22.0 µg TPF g^{-1} soil day^{-1} at 30–45 cm depth. Similarly, under the rice–berseem cropping sequence,

the activity decreased from 62.0 to 26.5 and 13.5 µg TPF g^{-1} soil day^{-1}, respectively. A similar decreasing trend was observed under all other cropping systems.

The decline in dehydrogenase activity with increasing soil depth resulted from lower organic carbon content, reduced microbial biomass, decreased root density and limited availability of readily decomposable organic substrates in subsurface soils. Surface soils continuously receive plant residues and root exudates, which provide favourable conditions for microbial growth and enzyme synthesis, whereas deeper soil layers contain lower concentrations of organic substrates and reduced microbial activity. Singh *et al.* reported that dehydrogenase activity decreases markedly with increasing soil depth because of reduced microbial abundance and lower soil organic carbon (36). Similarly, Casida *et al.* observed that soil enzyme activity is closely related to the distribution of viable microorganisms and declines substantially below the surface soil (33). Saha *et al.* also reported that surface soils consistently exhibit higher dehydrogenase activity than subsurface soils because of greater biological activity and organic matter accumulation (34).

Overall, the present investigation demonstrated that dehydrogenase enzyme activity was strongly influenced by cropping sequence and soil depth. Cropping systems characterized by greater biomass production and continuous residue return, particularly maize–wheat, sugarcane–cucumber and maize–potato, maintained significantly higher dehydrogenase activity than the other cropping systems. In contrast, enzyme activity consistently declined with increasing soil depth because of reduced organic carbon availability, lower microbial biomass and less favourable conditions for microbial metabolism. These findings highlight the importance of diversified cropping systems and efficient residue management in sustaining soil enzymatic activity, improving microbial functioning and maintaining long-term soil biological health.

CONCLUSION

The present study clearly demonstrates that cropping sequences and soil depth significantly influence soil microbial populations and enzymatic activity in the Indo-Gangetic plains of Western Uttar Pradesh. Across all cropping systems, surface soil (0–15 cm) consistently recorded the highest values of bacterial, fungal, and actinomycetes populations, as well as microbial biomass carbon and dehydrogenase activity. These parameters declined progressively with increasing soil depth (15–30 and 30–45 cm), primarily due to reduced organic matter and nutrient availability in subsurface layers. Among the different cropping systems, maize–wheat and sugarcane-based systems (especially sugarcane–cucumber and sugarcane–mustard–ratoon–rice) exhibited higher microbial populations and enzymatic activity. For instance, maize–wheat recorded the highest bacterial population (4.4×10^8 g^{-1} soil), actinomycetes population (7.4×10^4 g^{-1} soil), microbial biomass carbon (385 µg g^{-1}), and dehydrogenase activity (81 µg TPF g^{-1} day^{-1}). In contrast, relatively lower values were observed under cereal-dominated systems such as rice–wheat and urd–wheat.

The findings suggest that diversified and high-biomass cropping systems enhance soil biological health by improving microbial activity and organic matter content. Therefore, adoption of diversified cropping sequences, inclusion of legumes, and residue management practices can play a crucial role in maintaining soil fertility, improving nutrient cycling, and ensuring long-term agricultural sustainability.

Overall, the study highlights that soil biological properties are sensitive indicators of soil health and should be considered in designing sustainable cropping systems for improved productivity in the region.

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Author's contribution

VD and AS conceptualized the study, analyzed and curated the data. VS supervised the work, developed the methodology, and reviewed the manuscript. VD, AS, PN and VS prepared the final draft and performed revisions.

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Table-1: Bacteria (count g^{-1}soil) at various soil depths under different cropping sequence

Locations	Cropping Sequence and depth (cm)			Locations	Cropping Sequence and depth (cm)		
	Rice- Barseem				**Rice - Mustard**		
	0-15	15-30	30-45		0-15	15-30	30-45
Purkazi (M)	3.6×10^{6}	4.1×10^{4}	2.1×10^{2}	Baghra (M)	1.3×10^{7}	2.5×10^{4}	2.0×10^{2}
Sadar (M)	4.8×10^{6}	4.3×10^{4}	2.6×10^{2}	Charthawal (M)	3.5×10^{7}	3.0×10^{4}	2.2×10^{2}
Mean	4.6×10^{6}	4.2×10^{4}	2.3×10^{2}	Mean	3.1×10^{7}	2.7×10^{4}	2.0×10^{2}
Rice-Wheat				**Rice-Wheat-Urd**			
Shahpur (M)	4.2×10^{6}	4.4×10^{4}	4.8×10^{2}	Rajapur (G)	4.9×10^{6}	5.6×10^{4}	5.3×10^{2}
Khatauli (M)	5.3×10^{6}	5.1×10^{4}	4.7×10^{2}	Bhojpur (G)	4.7×10^{6}	6.5×10^{4}	5.6×10^{2}
Mean	4.7×10^{6}	4.7×10^{4}	4.3×10^{2}	Mean	6.4×10^{6}	6.2×10^{4}	5.6×10^{2}
Rice-Sugarcane				**Maize-Potato**			
Jansath (M)	5.1×10^{6}	6.5×10^{4}	6.1×10^{2}	Loni (G)	5.5×10^{7}	5.0×10^{4}	4.5×10^{2}
Morna (M)	5.5×10^{6}	6.2×10^{4}	6.5×10^{2}	Muradnagar (G)	6.0×10^{7}	6.5×10^{4}	5.5×10^{2}
Mean	5.2×10^{6}	6.3×10^{4}	6.2×10^{2}	Mean	5.7×10^{7}	6.1×10^{4}	5.5×10^{2}
Maize-Wheat				**Sugarcane-Cucumber**			
Bhojpur (G)	4.0×10^{8}	4.2×10^{5}	3.8×10^{2}	Budhana (M)	6.2×10^{7}	6.0×10^{4}	5.3×10^{2}
Muradnagar (G)	5.1×10^{8}	5.5×10^{5}	4.5×10^{2}	Jansath (M)	7.5×10^{7}	6.8×10^{4}	6.0×10^{2}
Mean	4.4×10^{8}	4.5×10^{5}	4.2×10^{2}	Mean	6.8×10^{7}	6.4×10^{4}	5.5×10^{2}
Sugarcane-Mustard-Ratton-Rice				**Urd-Wheat**			
Sadar (M)	4.9×10^{6}	5.6×10^{4}	5.3×10^{2}	Loni (G)	4.2×10^{6}	4.4×10^{4}	4.8×10^{2}
Baghra (M)	4.7×10^{6}	6.5×10^{4}	5.6×10^{2}	Bhojpur (G)	5.3×10^{6}	5.1×10^{4}	4.7×10^{2}
Mean	6.4×10^{6}	6.2×10^{4}	5.1×10^{2}	Mean	4.6×10^{6}	4.7×10^{4}	4.5×10^{2}

Table-2: Fungi (count g^{-1}soil) at various soil depths under different cropping sequence

Locations	Cropping Sequence and depth (cm)			Locations	Cropping Sequence and depth (cm)		
	Rice- Barseem				**Rice - Mustard**		
	0-15	15-30	30-45		0-15	15-30	30-45
Purkazi (M)	1.8×10^4	1.3×10^2	1.0×10^2	Baghra (M)	2.5×10^4	3.0×10^2	2.3×10^2
Sadar (M)	2.2×10^4	2.0×10^2	1.7×10^2	Charthawal (M)	3.5×10^4	3.6×10^2	3.1×10^2
Mean	2.07×10^4	1.8×10^2	1.5×10^2	Mean	3.1×10^4	3.2×10^2	2.7×10^2
Rice-Wheat				**Rice-Wheat-Urd**			
Shahpur (M)	1.3×10^4	1.5×10^2	1.0×10^2	Rajapur (G)	1.7×10^4	1.5×10^2	1.2×10^2
Khatauli (M)	1.6×10^4	1.8×10^2	1.0×10^2	Bhojpur (G)	1.6×10^4	1.6×10^2	1.2×10^2
Mean	1.5×10^4	1.7×10^2	1.0×10^2	Mean	1.7×10^4	1.5×10^2	1.2×10^2
Rice-Sugarcane				**Maize-Potato**			
Jansath (M)	4.7×10^4	4.6×10^2	3.8×10^2	Loni (G)	4.0×10^4	4.5×10^2	3.8×10^2
Morna (M)	5.1×10^4	5.0×10^2	4.2×10^2	Muradnagar (G)	4.5×10^4	4.7×10^2	3.6×10^2
Mean	4.4×10^4	4.4×10^2	3.7×10^2	Mean	4.2×10^4	4.3×10^2	3.5×10^2
Maize-Wheat				**Sugarcane-Cucumber**			
Bhojpur (G)	8.0×10^4	7.9×10^2	7.5×10^2	Budhana (M)	6.2×10^4	6.5×10^2	5.9×10^2
Muradnagar (G)	7.9×10^4	7.5×10^2	7.0×10^2	Jansath (M)	6.5×10^4	6.4×10^2	5.5×10^2
Mean	8.2×10^4	7.4×10^2	7.3×10^2	Mean	6.3×10^4	6.4×10^2	5.7×10^2
Sugarcane-Mustard-Ratton-Rice				**Urd-Wheat**			
Sadar (M)	1.7×10^4	1.5×10^2	1.2×10^2	Loni (G)	1.3×10^4	1.5×10^2	1.0×10^2
Baghra (M)	1.6×10^4	1.6×10^2	1.2×10^2	Bhojpur (G)	1.6×10^4	1.8×10^2	1.0×10^2
Mean	1.7×10^4	1.5×10^2	1.2×10^2	Mean	1.4×10^4	1.6×10^2	1.0×10^2

Table-3: Actinomycetes (count g^{-1}soil) at various soil depths under different cropping sequence

Locations	Cropping Sequence and depth (cm)			Locations	Cropping Sequence and depth (cm)		
	Rice- Barseem				**Rice - Mustard**		
	0-15	15-30	30-45		0-15	15-30	30-45
Purkazi (M)	1.5×10^4	1.2×10^2	1.1×10^2	Baghra (M)	2.6×10^4	2.7×10^2	2.3×10^2
Sadar (M)	2.7×10^4	2.3×10^2	1.8×10^2	Charthawal (M)	3.7×10^4	3.4×10^2	2.9×10^2
Mean	2.0×10^4	1.7×10^2	1.3×10^2	Mean	3.3×10^4	2.9×10^2	2.5×10^2
Rice-Wheat				**Rice-Wheat-Urd**			
Shahpur (M)	1.5×10^4	1.7×10^2	1.2×10^2	Rajapur (G)	2.0×10^4	1.8×10^2	1.4×10^2
Khatauli (M)	1.9×10^4	1.6×10^2	1.2×10^2	Bhojpur (G)	2.0×10^4	1.9×10^2	1.5×10^2
Mean	1.7×10^4	2.4×10^2	1.2×10^2	Mean	2.0×10^4	1.8×10^2	1.2×10^2
Rice-Sugarcane				**Maize-Potato**			
Jansath (M)	3.5×10^4	3.2×10^2	2.8×10^2	Loni (G)	6.1×10^4	6.4×10^2	4.0×10^2
Morna (M)	5.0×10^4	4.2×10^2	3.8×10^2	Muradnagar (G)	5.2×10^4	6.6×10^2	4.8×10^2
Mean	4.0×10^4	3.5×10^2	3.2×10^2	Mean	6.1×10^4	6.5×10^2	4.6×10^2
Maize-Wheat				**Sugarcane-Cucumber**			
Bhojpur (G)	7.5×10^4	7.0×10^2	6.5×10^2	Budhana (M)	6.5×10^4	6.4×10^2	4.2×10^2
Muradnagar (G)	7.6×10^4	6.1×10^2	5.8×10^2	Jansath (M)	7.0×10^6	5.0×10^4	4.0×10^2
Mean	7.4×10^4	6.0×10^2	6.6×10^2	Mean	6.7×10^4	5.7×10^2	4.1×10^2
Sugarcane-Mustard-Ratton-Rice				**Urd-Wheat**			
Sadar (M)	2.0×10^4	1.8×10^2	1.4×10^2	Loni (G)	1.5×10^4	1.7×10^2	1.2×10^2
Baghra (M)	2.0×10^4	1.9×10^2	1.5×10^2	Bhojpur (G)	1.9×10^4	1.6×10^2	1.2×10^2
Mean	2.0×10^4	1.8×10^2	1.2×10^2	Mean	1.7×10^4	1.5×10^2	1.2×10^2

Table-4: Microbial biomass carbon (μg^{-1}g soil) at various soil depths under different cropping sequence

Locations	Cropping Sequence and depth (cm)				Locations	Cropping Sequence and depth (cm)			
	Rice- Barseem					**Rice - Mustard**			
	0-15	15-30	30-45	Mean		0-15	15-30	30-45	Mean
Purkazi (M)	290	150	90	176.6	Baghra (M)	358	170	95	207.6
Sadar (M)	285	170	80	178.3	Charthawal (M)	300	190	110	200.0
Mean	287.5	160.0	85.0	-	Mean	329.0	180.0	102.5	-
Rice-Wheat					**Rice-Wheat-Urd**				
Shahpur (M)	226	155	77	152.6	Rajapur (G)	293	153	79	151.0

Khatauli (M)	240	145	75	153.3	Bhojpur (G)	218	160	85	154.3
Mean	233.0	150.0	76.0	-	Mean	255.5	156.5	82.0	-
Rice-Sugarcane					**Maize-Potato**				
Jansath (M)	300	150	75	175.0	Loni (G)	368	170	125	221.0
Morna (M)	322	175	87	194.6	Muradnagar (G)	351	190	92	211.0
Mean	311.0	162.5	81.0	-	Mean	359.5	180.0	108.5	-
Maize-Wheat					**Sugarcane-Cucumber**				
Bhojpur (G)	380	190	87	219.0	Budhana (M)	371	180	85	212.0
Muradnagar (G)	390	170	88	216.0	Jansath (M)	395	169	125	229.6
Mean	385.0	180.0	87.5	-	Mean	383.0	174.5	105.0	-
Sugarcane-Mustard-Ratton-Rice					**Urd-Wheat**				
Sadar (M)	293	153	79	151.0	Loni (G)	226	155	77	152.6
Baghra (M)	218	160	85	154.3	Bhojpur (G)	240	145	75	153.3
Mean	255.5	156.5	82.0	-	Mean	233.0	150.0	76.0	-

Table-5: Dehydrogenase (µg TPF g^{-1}soil day^{-1}) at various soil depths under different cropping sequence

Locations	Cropping Sequence and depth (cm)				Locations	Cropping Sequence and depth (cm)			
	Rice- Berseem					**Rice - Mustard**			
	0-15	15-30	30-45	Mean		0-15	15-30	30-45	Mean
Purkazi (M)	69	25	15	36.3	Baghra (M)	73	35	22	44.0
Sadar (M)	55	28	12	23.0	Charthawal (M)	75	45	17	45.6
Mean	62.0	26.5	13.5	-	Mean	72.7	32.7	18.0	-
Rice-Wheat					**Rice-Wheat-Urd**				
Shahpur (M)	60	35	16	37.0	Rajapur (G)	62	25	10	32.3
Khatauli (M)	67	32	12	37.0	Bhojpur (G)	75	28	13	38.6
Mean	63.5	33.5	14.0	-	Mean	68.5	26.5	11.5	-
Rice-Sugarcane					**Maize-Potato**				
Jansath (M)	65	25	15	30.3	Loni (G)	77	40	21	46.0
Morna (M)	62	23	16	33.6	Muradnagar (G)	72	42	18	44.0
Mean	63.5	24.0	15.5	-	Mean	74.5	41.0	19.5	-
Maize-Wheat					**Sugarcane-Cucumber**				
Bhojpur (G)	81	28	21	43.3	Budhana (M)	80	42	28	50.0
Muradnagar (G)	78	45	23	48.6	Jansath (M)	78	40	30	49.3
Mean	79.5	36.5	22.0	-	Mean	79.0	41.0	29.0	-
Sugarcane-Mustard-Ratton-Rice					**Urd-Wheat**				
Sadar (M)	62	25	10	32.3	Loni (G)	60	35	16	36.00
Baghra (M)	75	28	13	38.6	Bhojpur (G)	67	32	12	37.00
Mean	68.5	26.5	11.5	-	Mean	63.5	33.5	14.0	-

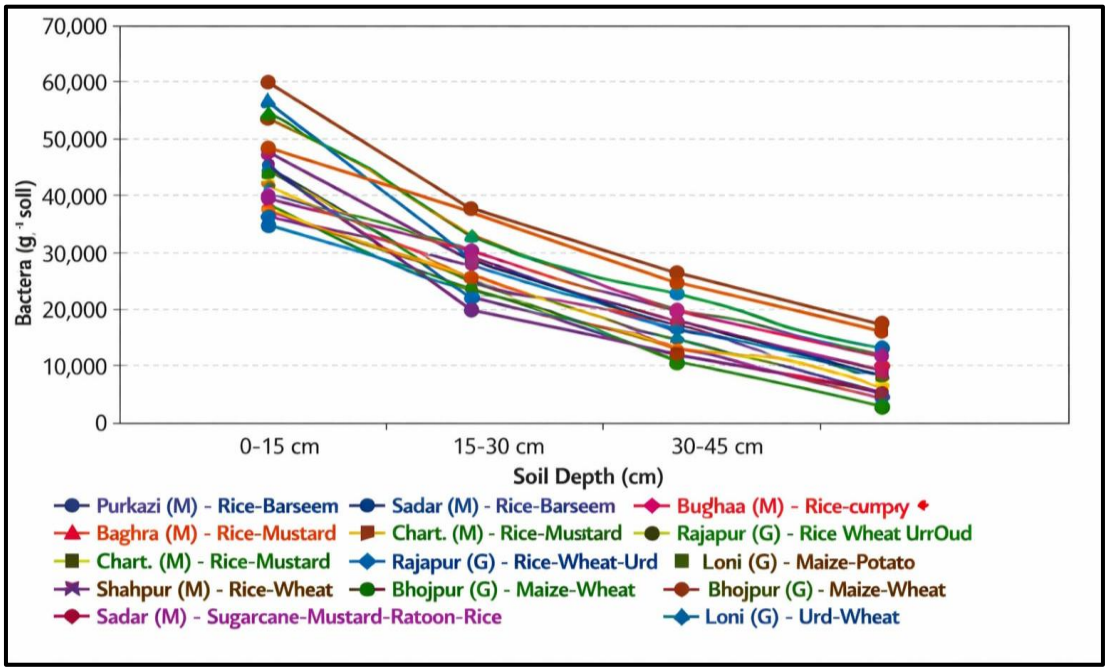

Fig. 1.1 Bacterial count at various soil depth under different cropping sequence

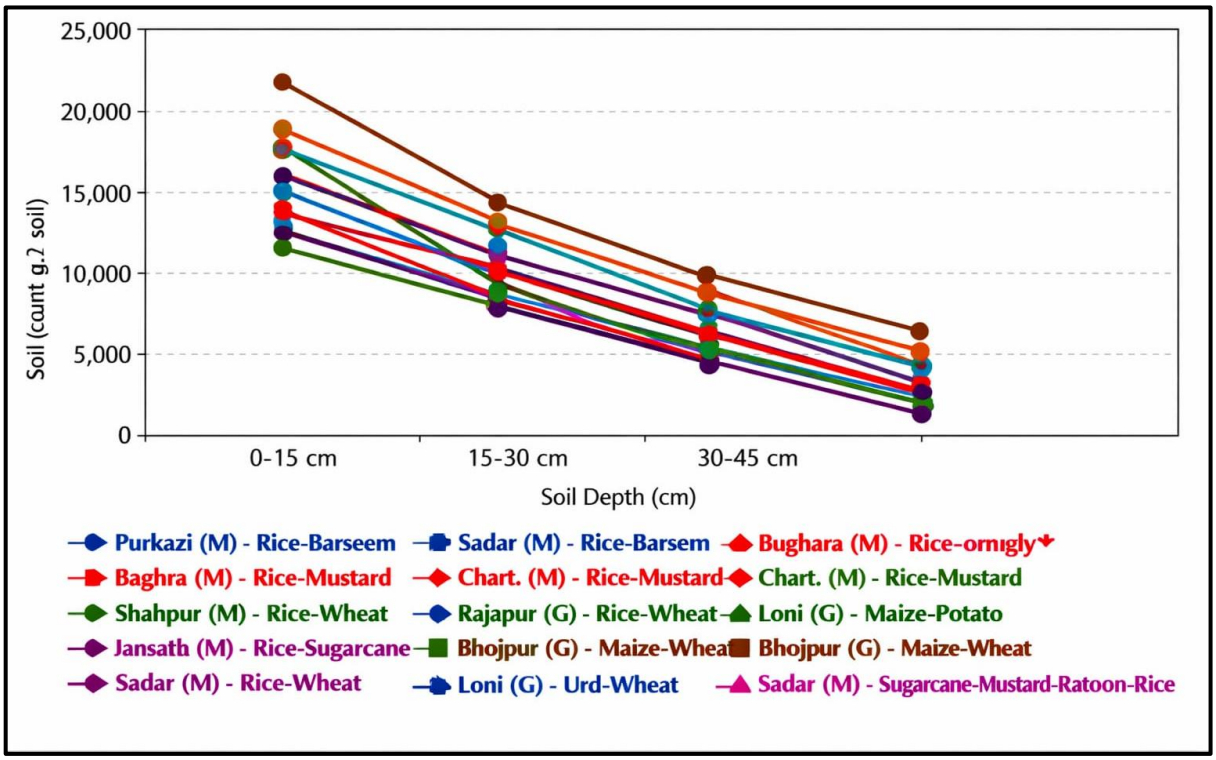

Fig. 2.1 Fungal count at various soil depth under different cropping sequence

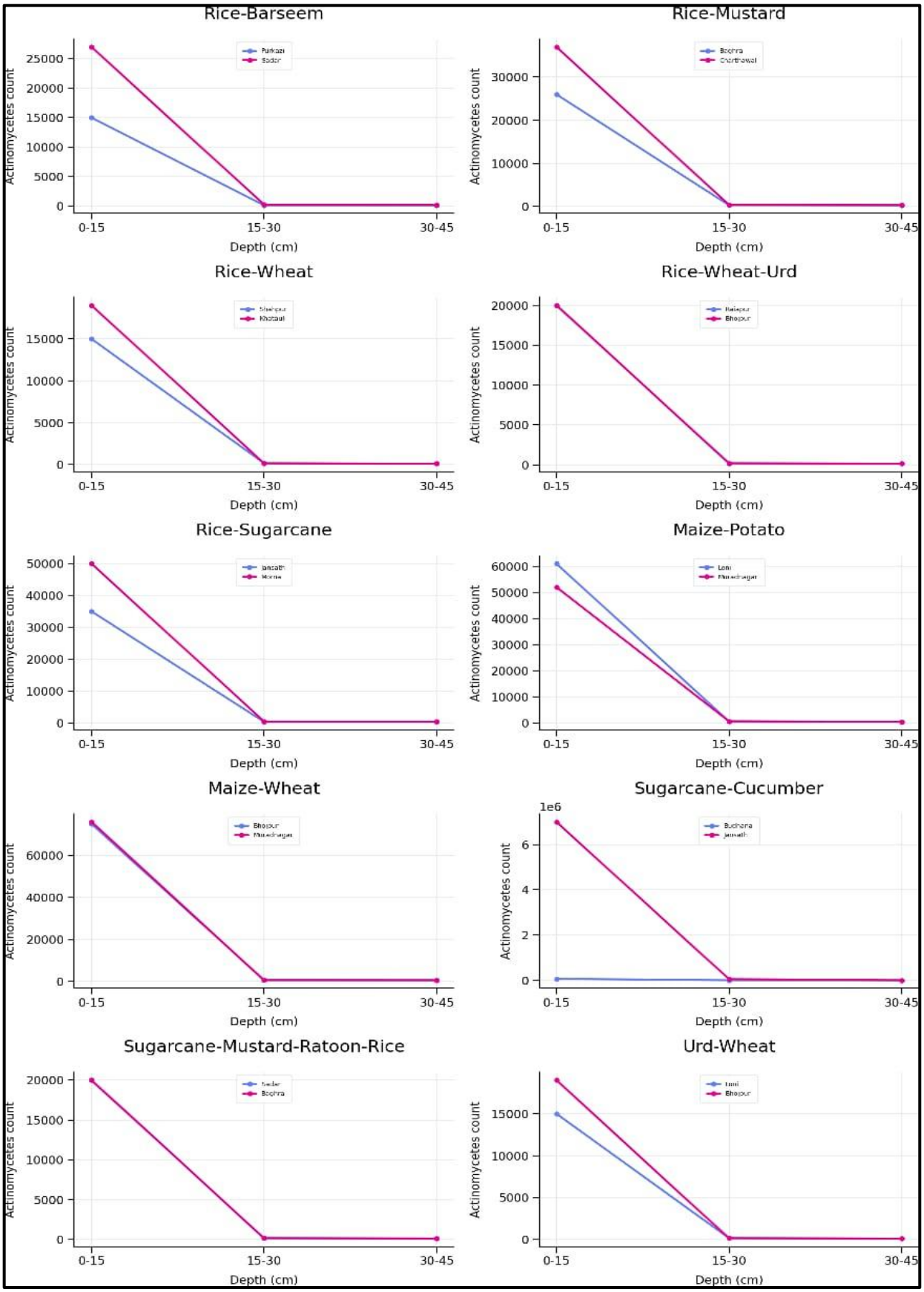

Fig. 3.1 Actinomycetes count at various soil depth under different cropping sequence

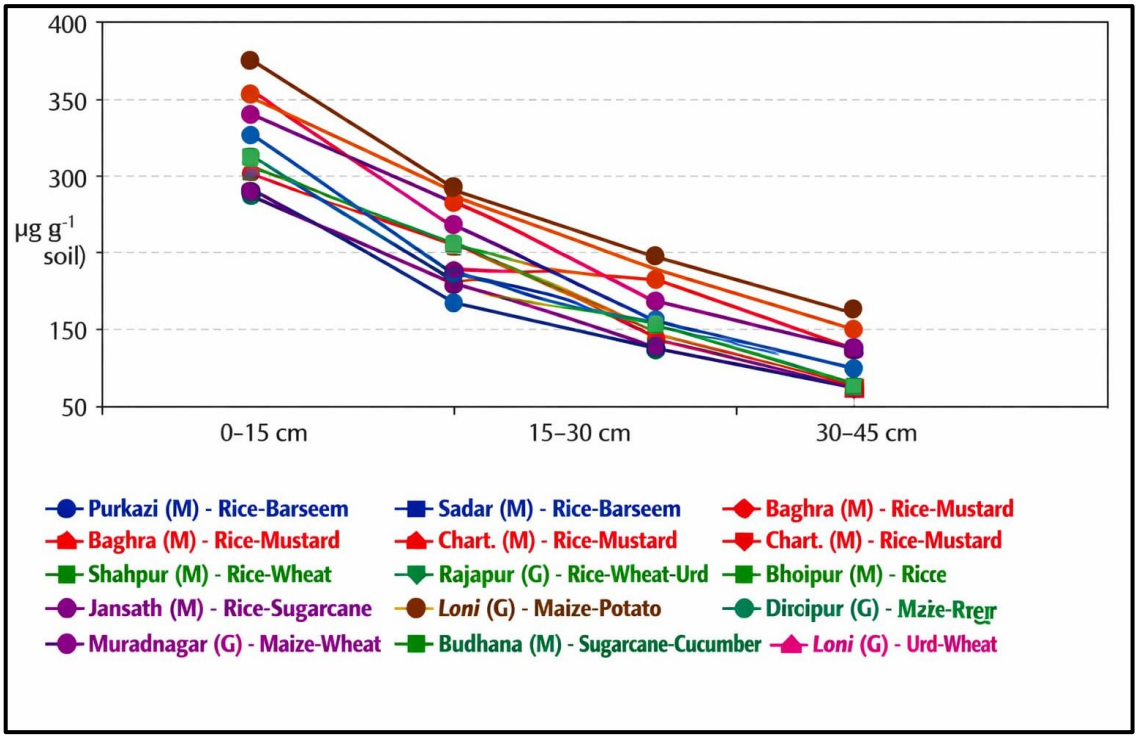

Fig. 4.1 Microbial Biomass Carbon at various soil depth under different cropping sequence

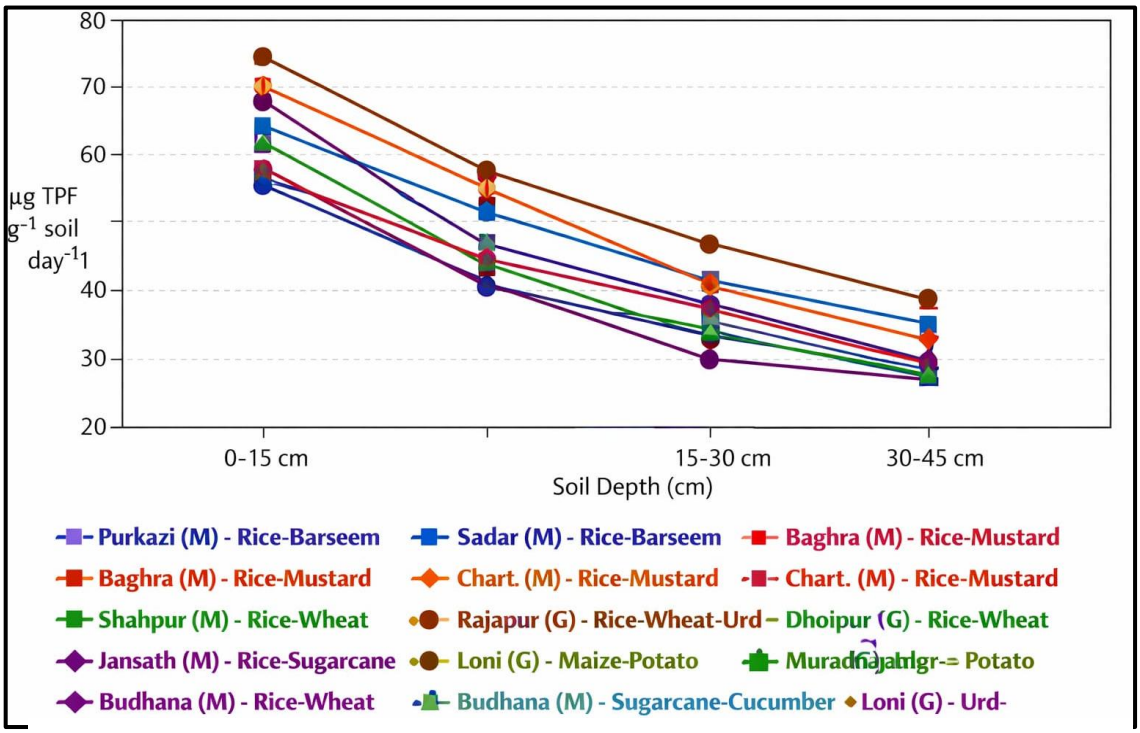

Fig. 5.1 Dehydrogenase activity at various soil depth under different cropping sequence