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RECEIVED 10 December 2025

REVISED 09 March 2026

ACCEPTED 10 March 2026

PUBLISHED 01 April 2026

CITATION

Panigrahy M, Panda N, Priyadarshini S,
Gupta AK, Nayak A, Padhan K,
Mohanty S, Dash M, Sahoo SK, Patro H
and Sethi D (2026) Long-term manurial
endowment on soil culturable bacterial
dynamics, biological properties, and
productivity of cabbage in
acid *Inceptisols*.
Front. Agron. 8:1765116.
doi: 10.3389/fagro.2026.1765116

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Long-term manurial endowment on soil culturable bacterial dynamics, biological properties, and productivity of cabbage in acid *Inceptisols*

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Introduction: Soil culturable bacterial population dynamics is crucial for soil health which suffers due to overexploitation and other unsustainable practices. Long-term manurial endowments are becoming more common as a component of regenerative agriculture linked to crop productivity.

Methods: The present study was undertaken to give an insight into regenerative agriculture. A total of 10 manurial practices formulated with integrating soil test-based inorganic fertilizers (STD), farmyard manure (FYM), vermicompost (VC), consortia biofertilizers (BFs), lime (L), organic I, and organic II were evaluated.

Results: The integrated treatments T8 (STD + VC at 2.5 t ha⁻¹ + BFs + L) significantly enhanced the diversity of beneficial bacterial genera such as *Bacillus*, *Pseudomonas*, *Rhizobium*, *Azotobacter*, *Azospirillum*, and *Alcaligenes*. Biological activities like soil enzyme activities (urease and dehydrogenase), microbial biomass carbon, and nitrogen were synergistically proliferated in T8 (STD + VC at 2.5 t ha⁻¹ + BFs + L). After long-term utilization of STD + VC at 2.5 t ha⁻¹ + BFs + L (T8) MBC, MBN, and DHA were enhanced by 36%, 85%, and 12% over soil test doses of the fertilizer application package. Physiological plant traits, leading to the highest cabbage yield (22 t ha⁻¹), head circumference (42.53 cm), and total chlorophyll content (2.11 mg g⁻¹), demonstrated strong interdependence between microbial health and plant performance. Combining bio-inoculants and liming techniques increased the economic yield of cabbage by 13%-21% at P = 0.05 over control. The antibiotic sensitivity profiling reflected adaptive responses by long-term manurial endowment on soil ecological dynamics. Multivariate analyses, including PCA, regression, and path modelling, confirmed the pivotal role of culturable soil bacterial population dynamics for optimizing both microbial functions and cabbage productivity.

Conclusion: The study underscores the importance of integrating inorganics, organics, bio-inoculants, and strategic chemical amendments for a regenerative agriculture in acid *Inceptisols*.

KEYWORDS

biological properties, cabbage, culturable bacterial population dynamics, path analysis, PCA, regression analysis

1 Introduction

A sustainable farming system integrates efficient use of resources for maintaining soil health, biodiversity, and resilience to climate change. As biodiversity is critical for the soil ecosystem, proper nutrient management strategies should be taken care of for sustainability of the system. Injudicious use of chemical fertilizers and pesticides in modern agriculture has imparted deleterious effects like soil degradation, nutrient depletion, and a decline in soil biodiversity, including beneficial bacterial genera (Rahman, 2015). Feeding a growing population, sustainable soil health management is required by amalgamating bioinoculants and organic and inorganic fertilizers judiciously. Thus, integrated approaches including organics, inorganics, and biostimulants with ameliorating agent liming material leads to sustaining soil biota (Khambalkar et al., 2025). Use of synthetic fertilizers in agriculture has boosted yields (Pandian et al., 2024), but their injudicious use degrades soil structure, destroys microbial diversity, alters pH, and causes pollution and land degradation (Bhatia and Sindhu, 2024). Thus, integrating bioinoculants and organic inputs with appropriate inorganic fertilizer under long-term manurial practice supports soil biota, elevates productivity, and protects the environment for sustainable food security (Zhao et al., 2025).

Long-term manurial endowment involves repeated application of nutrients with amendments and bioinoculants over time. Proper nutrient management strategies of soil ecology lead to enhanced soil organic carbon, microbial biomass, and enzymatic activities (Sethi et al., 2025), which in turn maintain soil biodiversity. They also promote the accumulation of glomalin-related soil proteins (GRSP), contributing to carbon stabilization and soil structure that promotes macroaggregate stability (Yang et al., 2023). Ultimately, long-term manurial practices maintain soil fertility, soil structure stabilization, and soil biodiversity (Li et al., 2023), which are critical for a sustainable agrifood system and regenerative agriculture.

Culturable bacterial population dynamics in agroecosystems is crucial for maintaining a sustainable agrifood system, as diverse communities accelerate the transformation of major nutrients in the rhizosphere zone, decomposition of organic matter, soil structure improvement and stabilization, support of plant health defense mechanisms, etc (Babu et al., 2025). Culturable bacterial population dynamics are gold standards for isolating specific bacterial genera in soil ecosystems. Although they offer a narrow window into the microbial world, called great plate count anomaly, still they accelerate a specific nutrient dynamic in agrifood systems. Thus, culturable bacterial study in rhizosphere ecology confirms the live activeness and involvement in nutrient dynamics. Several studies on long-term manurial practices in cabbage have thus been studied to

reveal the richness of culturable bacterial diversity over conventional practices (Meylinga et al., 2013; Li et al., 2024a; Martin-Cardoso et al., 2024). Certain bacterial taxa, such as *Bacillus* and *Pseudomonas*, are common in cabbage-grown soils and support plant development and soil health (Wei et al., 2023). Environmental factors, such as soil moisture and pH, are also important in determining culturable bacterial diversity (Chen et al., 2023). Overall, the relationship between environmental factors and agricultural methods is critical in influencing the culturable bacterial diversity of cabbage-grown soil (Li et al., 2024b; Mastiholi et al., 2024). Thus, integrating bioinoculants with organics, inorganics, and ameliorants can enrich a soil with a diverse culturable bacterial community that acts as soil's driving force for proper nutrient flow in rhizosphere ecology of the crop. The soil biological properties including soil enzymes and microbial biomass are key indicators of soil fertility in cabbage cultivation (Zhua et al., 2020). The soil dehydrogenase enzyme activity reflects the oxidation and reduction pathways and the soil's capacity to support biochemical processes in the agroecosystem (Zhang et al., 2021). The soil urease enzyme activity is studied to express the N cycle in the agroecosystem. This enzyme helps in catalyzing hydrolysis of urea into ammonium and thereby increases available nitrogen content to crops. This enzyme being a biological indicator of soil health urease is crucial for plant nutrition studies (Luan et al., 2023). Thus, cabbage productivity under long-term manurial practices can be enhanced by adopting improved nutrient management practices and amalgamating bioinoculants and ameliorants under an acidic soil to elevate soil enzyme activities, soil biodiversity, and soil fertility (Dar et al., 2023). However, since soil type and environmental factors maintain soil biodiversity and plant response, optimizing soil biological activities with best nutrient management practices can maximize cabbage productivity. The present study was thus conducted in a long-term manurial experiment for investigating soil culturable bacterial population dynamics and biological properties in a tropical acid soil of India and their influence on cabbage productivity for maintaining sustainable food security. Thus, we hypothesized that amelioration of acidic *Inceptisols* through liming enhances bacterial proliferation which directly regulates other soil biological properties and yield of cabbage.

2 Materials and methods

2.1 Sites and collection of soil samples

The present study was conducted at the Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India, since 2010.

The experimental site is geographically located at 20°15.86'N latitude and 85°48.68'E longitude, at an elevation of 25.9 m above mean sea level (MSL). The initial (before 14 years) experimental soil was acidic in nature (pH 4.75); low in organic carbon content (0.35%), available P (8 kg ha⁻¹), and nitrogen (185 kg ha⁻¹); and medium in available K (187 kg ha⁻¹). The soil was sandy loam in texture and had a bulk density and particle density of 1.35 and 2.42 Mg m⁻³, respectively. After completion of 14 years of experiment (2024), the soil samples were collected from a depth of 0–20 cm at five random places from manurial plots, ensuring minimal disturbance to the rhizosphere ecology of the cabbage crop. A total of 10 soil samples of each treatment were mixed properly, and the sample size was reduced to 500 g by following the quartering method. From each treatment, approximately 200 g of soil samples was stored at 4 °C in a refrigerator for the study of microbial parameters.

2.2 Experimental design

The field experiment was conducted by taking 10 different treatments replicated thrice considering the soil test-based fertilizer/soil test dose (STD), farm yard manure (FYM), vermicompost (VC), biofertilizers (BFs), and lime (L). The treatments were as follows: no external supplements of nutrients, as control plots (T1); soil test-based dose of inorganic fertilizer (N, P, K, and S) (T2); STD+FYM (F) at 5 t ha⁻¹ (T3); STD + vermicompost (VC) at 2.5 t ha⁻¹ (T4); STD + F + biofertilizers (BFs) (T5); STD + VC + BFs (T6); STD + F + L at 0.2 LR (lime requirement) + BFs (T7); STD + VC + L at 0.2LR + BFs (T8); 100% N through FYM and VC (1:1) as organic I (T9); FYM at 5 t ha⁻¹ + VC at 2.5 t ha⁻¹ + poultry manure (PM) at 1 t ha⁻¹ + neem oil cake at 0.5 t ha⁻¹ + BFs as organic II (T10). Farmyard manure (5.0 t ha⁻¹), vermicompost (2.5 t ha⁻¹), poultry manure (1.0 t ha⁻¹), and oil cake (0.5 t ha⁻¹) were applied according to treatment specificity. Consortia biofertilizers (BFs) consisting of *Azotobacter*, *Azospirillum*, and phosphate-solubilizing bacteria (PSB) at a 1:1:1 ratio (at a rate of 12 kg ha⁻¹) were prepared using isolated strains of *Azotobacter vinelandii*, *Azospirillum lipoferum*, and *Bacillus amyloliquefaciens* in a sterilizer vermicompost carrier material. Locally available agricultural wastes like paddy straw, leaf litter, and fruit and vegetable wastes were used in the process of vermicomposting. After 45 days of composting in pits, the earthworm species *Eudrilus eugeniae*, commonly called African nightcrawler, were inoculated into the composting pit for preparation of vermicompost, and after 90 days of composting, the finished product was used as vermicompost. After preparation of vermicompost, it was air-dried and sterilized in autoclave for 25 min at 115-lb pressure. The said sterilized vermicompost was used as a carrier material for preparation of consortia biofertilizer. The consortia biofertilizer was mixed with farmyard manure/poultry manure/vermicompost as per the treatment details and incubated for 7 days at 30% moisture under control laboratory conditions using a BOD incubator for maintaining all the growth parameters. After incubation, the consortia biofertilizer was applied as per the treatments. In lime-applied treatments, incubated organics mixed with calcium silicate (NV 80%) were added at 0.2 LR as a basal mix with the organics to address soil acidity. For cabbage, N-P-K-S was supplied at 150–40–75–45 kg ha⁻¹ using urea, Navaratna diammonium phosphate (DAP), and

MOP following an integrated nutrient management approach to maintain the soil biodiversity and productivity of cabbage. A concise table summarizing cropping sequence, treatment continuity, and liming frequency over 2010–2024 is thus included (Supplementary Tables 1, 2) for an insightful background of the long-term manurial experiment.

2.3 Isolation of culturable soil bacteria

The fresh soil samples were taken for enumerating culturable bacterial population dynamics through the pour plate method, and six dominant bacteria were further quantified by using the selective culture media like *Bacillus* Agar, King's B Media, Yeast Mannitol Agar to Congo red, *Azotobacter* selective media, *Azospirillum* medium, and Mac Conkey Agar with a dilution factor to 10⁻⁵. Distinct colonies were transferred to *Bacillus* agar (B1), King's B (P1), Yeast Mannitol agar with Congo Red (R1), *Azotobacter* agar (A1), *Azospirillum* Medium (A2), and Pikovskaya's Agar (A3). Colony morphology was examined through streaking and spreading to isolate pure cultures, which were then preserved on specific agar slants for further analysis. Although the plate count method has several drawbacks, e.g., it only represents culturable bacterial count and it is not a true representative of bacterial diversity, this method was still adopted in this study as it is used widely for biological characterization of the agricultural soil.

2.4 Morphological and biochemical characterization of isolated culturable soil bacteria

Gram staining was performed on colonies from nutrient agar using standard methods described by Yasin and Al-Mayaly, (2020). Biochemical tests were used for the specific identification of bacteria, such as methyl red (MR), Voges-Proskauer (VP), nitrate (NI), motility (MT), urease hydrolysis (UR), Simmons citrate (SC), oxidase (OX), triple sugar iron (TSI), catalase (CA), and indole (IN). It was performed by using the VITEK 2 COMPACT System (bioMérieux, France) at generic-level identification of some specific bacteria, which were then subjected to Gram staining (Yasin and Al-Mayaly, 2020).

2.5 Antibiotic sensitivity test of isolated culturable soil bacteria

A different antibiotic sensitivity test (AST) was undertaken under laboratory conditions by using the Kirby-Bauer disk diffusion technique (Hudzicki, 2009). As soil is a reservoir of microbes and an evolutionary hot spot of resistant traits, antibiotic sensitivity test directly linked with soil ecological resilience and antimicrobial resistance ecology. Isolated organisms were grown in culturable media along with the antibiotics. Bacterial taxa like *Bacillus* were treated with tetracycline, clindamycin, erythromycin, and chloramphenicol.

Pseudomonas was treated to amoxicillin, cefoperazone, cefixime, and other related antibiotics. *Rhizobium* was tested against gentamycin, vancomycin, and chloramphenicol. *Azotobacter* was tried against tetracycline, chloramphenicol, ampicillin, and streptomycin. *Azospirillum* was investigated for gentamycin, penicillin, and kanamycin. *Alcaligenes* was tested against

tetracycline, chloramphenicol, penicillin, and ciprofloxacin. A loopful of culture was spread evenly on plates containing solidified media. Antibiotic bio-discs were placed on the surface, and zone formation was measured after 24 h at 28 ± 1 °C. A clear zone around the disc where the bacteria growth was inhibited was recorded to find out the zone of inhibition by measuring its diameter carefully. The zone diameter was compared over a standard chart to categorize the bacteria as susceptible, intermediate, and resistant to antibiotics.

2.6 Soil microbial biomass assay

Fresh soil samples were collected at the maximum cabbage growth stage without disturbing the rhizospheric activities for study of biological parameters. Soil microbial biomass carbon (SMBC) and soil microbial biomass nitrogen (SMBN) were measured on an equal set of fumigated and non-fumigated soil samples for 24 h, and the contents were measured using the fumigation–extraction method as described by Wu et al. (1990). The SMBC and SMBN were calculated by using Equations 1, 2, respectively. The basal soil respiration was quantified using $\text{CO}_2\text{-C g}^{-1}$ of soil after 24 h. The amount of organic carbon in the soil was measured using the wet digestion method developed by Walkley and Black (1934).

$$\text{Microbial Biomass C}(C_{min}) = 2.64 \times E_c \quad (1)$$

where EC refers to the difference in extractable organic C between the treatments; 2.64 is the proportionality factor for biomass C released by fumigation extraction.

$$\text{Microbial Biomass N}(N_{min}) = \frac{FN}{0.54} \quad (2)$$

where FN is the difference between N extracted from fumigated and non-fumigated samples and 0.54 is the fraction of microbial biomass N released by the fumigation extraction process.

2.7 Soil enzyme assay

2.7.1 Urease activity

The study used the method given by Kandeler and Gerber (1988) to measure urease activity using urea as the substrate. In a 100-ml conical flask, 5 g of fresh field soil sample and 5 ml of urea solution were taken and incubated at 37 °C for 5 h. A solution of 50 ml of 2 M KCL–PMA (potassium chloride–phenyl mercuric acetate) mixture was added to it after the incubation period followed by stirring for 1 h. Using Whatman No. 42 filter paper, it was filtered to get a red-colored supernatant. A UV-Vis spectrophotometer (Agilent Cary 3500 Compact UV-Vis) at wavelength 527 nm was used to measure the soil sample's red color intensity. The final result was expressed in μg triphenyl formazan (TPF) g^{-1} soil day^{-1} .

2.7.2 Dehydrogenase activity

Dehydrogenase activity in air-dried soil was assessed using the Casida et al. (1964) method. 20 g of air-dried field soil samples was mixed with 20 g of calcium carbonate, and 6 g of this mixture was then transferred into a sterilized test tube. A solution of 2,3,5-triphenyl tetrazolium chloride (TTC) at 3% aqueous solution was

added to the test tubes. After mixing, the test tube with a lid was incubated at 37 °C for 24 h in a BOD incubator. After 24 h, it was taken out and filled with 10 ml of methanol followed by shaking for 1 min. The reddish-brown color developed was then measured at 485 nm using a UV-Vis spectrophotometer (Agilent Cary 3500 Compact UV-Vis). The final result was expressed in $\mu\text{g NH}_4^+ - \text{N g}^{-1}$ soil 2 h^{-1} .

2.8 Growth and yield of cabbage

Growth parameters like chlorophyll-a, b and total content (mg g^{-1} fresh leave) at the maximum growth stage of cabbage were determined using the 80% acetone method, following Yoshida et al. (1971). Chlorophyll-a, Chlorophyll-b, and total chlorophyll were calculated by using Equations 3–5, respectively. The diameters of the five best cabbage heads were measured horizontally with a meter scale, and the mean values were recorded for recording the head circumference (cm). An electric balance was used to weigh the cabbage heads, and total biomass (t ha^{-1}) was measured at the time of maturity (110 days after sowing the seed of cabbage).

$$\begin{aligned} \text{Chlorophyll - a (mg g}^{-1} \text{ frsh leave)} \\ = 12.7 (A_{663}) - 2.69 (A_{645}) \times \left(\frac{V}{100 \times W} \right) \end{aligned} \quad (3)$$

$$\begin{aligned} \text{Chlorophyll - b(mg g}^{-1} \text{ frsh leave)} \\ = 22.9 (A_{645}) - 4.68 (A_{663}) \times \left(\frac{V}{100 \times W} \right) \end{aligned} \quad (4)$$

$$\begin{aligned} \text{Total Chlorophyll (mg g}^{-1} \text{ frsh leave)} \\ = 20.2 (A_{645}) - 8.02 (A_{663}) \times \left(\frac{V}{100 \times W} \right) \end{aligned} \quad (5)$$

2.9 Statistical analysis

According to Gomez and Gomez (1984), growth and yield parameters of cabbage, soil bacterial diversity, and microbial activities were analyzed statistically by using the randomized block design (RBD). The least significant difference (LSD) at 5% significance was calculated only when the “F” test showed significant variance. It was performed using the Statistical Package for Social Sciences (SPSSv.21), and regression analysis and biplot analysis were developed between treatment means and different growth, yield, and biological parameters using RStudio (R 3.6.0+) (Kronthaler and Zollner, 2021).

3 Results

3.1 Isolation and morphological and biochemical characterization of culturable bacterial genera

From the laboratory study using different growth media for isolation of culturable bacteria from cabbage soil, it was confirmed

that beneficial culturable bacteria like genera *Bacillus* (B1), *Pseudomonas* (P1), *Rhizobium* (R1), *Azotobacter* (A1), *Azospirillum* (A2), and *Alcaligenes* (A3) were present in the experimental soil of crop cabbage. Isolated culturable bacterial plates were further streaked for morphological characterization using the gram staining method (Table 1; Figures 1, 2), and results confirmed that all the genera have the characteristics of bacteria. For identification of culturable bacteria, morphological

and biochemical characteristics play a key role. It helps to describe bacterium physical features, size, arrangement, and appearance. The metabolic activity and physiology of bacterium are identified through production of enzymes and response to different chemicals (Subudhi et al., 2020). Thus, laboratory-incubated culturable bacteria plates of all the genera were further studied for their conformity by using biochemical tests under the VITEK 2 COMPACT system, and results confirmed all the genera as culturable bacteria as obtained from the plate count isolation study (Table 2).

TABLE 1 Morphological characterization of the recovered culturable bacteria from selected media.

Types of media	Isolated code	Colony color	Gram staining
Bacillus agar base media	B1	Green	+ve, rod-shaped, spore-forming
King's B media	P1	White	-ve, rod-shaped
Yeast Mannitol Agar with Congo red	R1	Pink	-ve, rod-shaped
<i>Azotobacter</i> agar	A1	White	-ve rod-shaped
<i>Azospirillum</i> Medium	A2	White	-ve rod-shaped
Pikovskaya's agar	A3	White	-ve rod-shaped

B1, *Bacillus*; P1, *Pseudomonas*; R1, *Rhizobium*; A1, *Azotobacter*; A2, *Azospirillum*; A3, *Alcaligenes*.

3.2 Antibiotic sensitivity test response of isolated culturable bacteria genera

As a routine microbiological study, antibiotic sensitivity test (AST) of the isolated culturable beneficial bacteria genera was conducted with specific concentration of antibiotic disc (mentioned in brackets), and results of the experimental plots are presented in this section. Culturable bacterial isolates like B1 (*Bacillus*) were susceptible to antibiotics like tetracycline (30 $\mu\text{g ml}^{-1}$) but resistant to erythromycin (15 $\mu\text{g ml}^{-1}$), clindamycin (2 $\mu\text{g ml}^{-1}$), and chloramphenicol (30 $\mu\text{g ml}^{-1}$); isolate P1 (*Pseudomonas*) had moderate imipenem sensitivity and is resistant to cephamycin (30 $\mu\text{g ml}^{-1}$) and cefazolin (30 $\mu\text{g ml}^{-1}$); isolate R1 (*Rhizobium*) was resistant to vancomycin (30 $\mu\text{g ml}^{-1}$) and chloramphenicol (30 $\mu\text{g ml}^{-1}$) but sensitive to gentamycin (10 $\mu\text{g ml}^{-1}$); isolate A1 (*Azotobacter*) was sensitive to streptomycin (10 $\mu\text{g ml}^{-1}$) but resistant to tetracycline (10 $\mu\text{g ml}^{-1}$), chloramphenicol (30 $\mu\text{g ml}^{-1}$), and

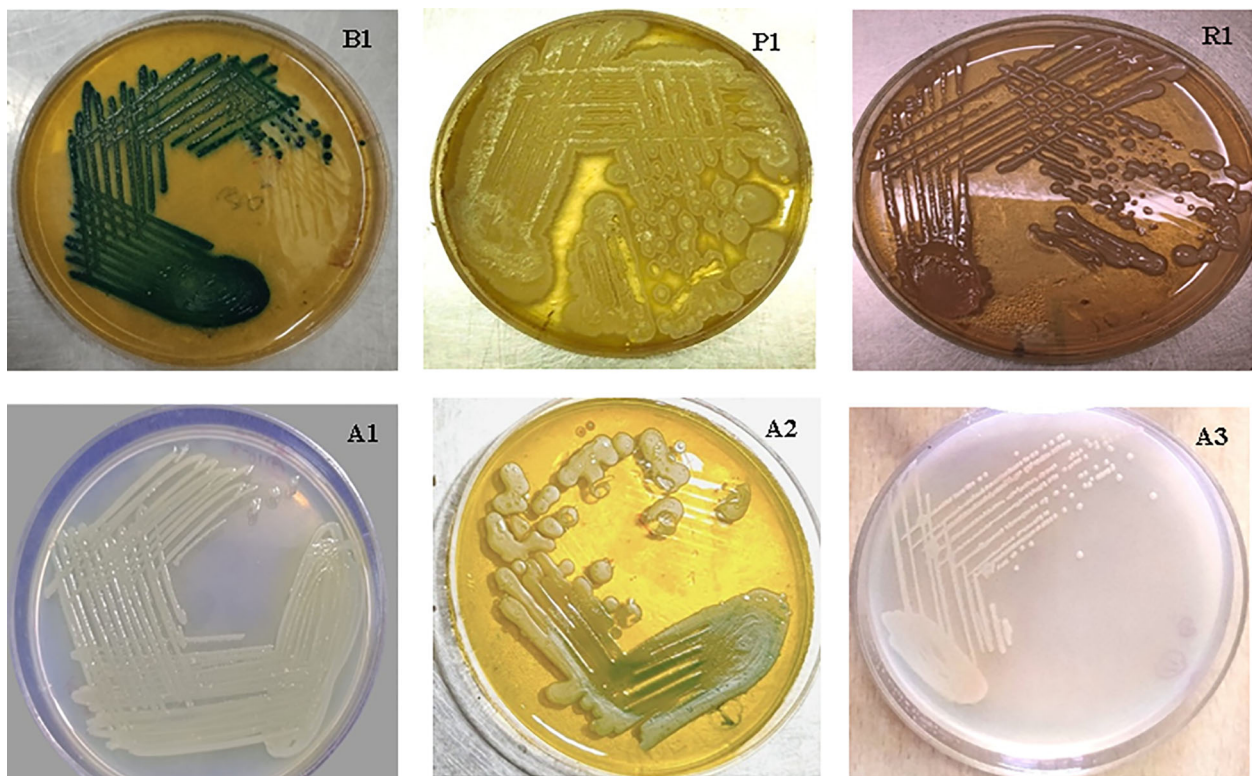


FIGURE 1

Streaking of the isolated colony on the selective media. B1, *Bacillus*; P1, *Pseudomonas*; R1, *Rhizobium*; A1, *Azotobacter*; A2, *Azospirillum*; A3, *Alcaligenes*.

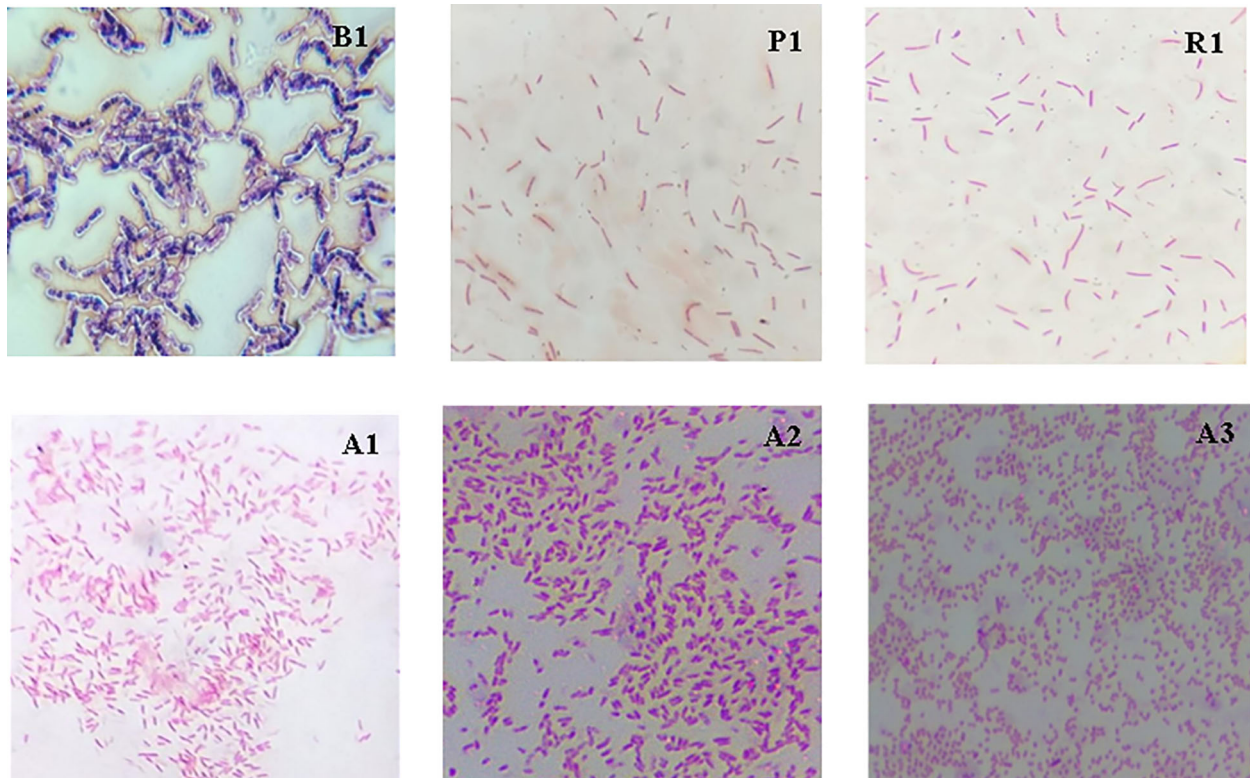


FIGURE 2
Gram Staining picture of the bacteria isolated from different selective media. B1, *Bacillus*; P1, *Pseudomonas*; R1, *Rhizobium*; A1, *Azotobacter*; A2, *Azospirillum*; A3, *Alcaligenes*.

ampicillin ($10 \mu\text{g ml}^{-1}$); isolate A2 (*Azospirillum*) was susceptible to kanamycin ($30 \mu\text{g ml}^{-1}$) but resistant to gentamycin ($10 \mu\text{g ml}^{-1}$) and penicillin ($10 \mu\text{g ml}^{-1}$); and isolate A3 (*Alcaligenes*) was resistant to penicillin ($10 \mu\text{g ml}^{-1}$), tetracycline ($30 \mu\text{g ml}^{-1}$), and chloramphenicol ($30 \mu\text{g ml}^{-1}$) but susceptible to ciprofloxacin ($5 \mu\text{g ml}^{-1}$) (Table 3). This test helps to identify the ability of bacteria as susceptible, intermediate, or resistant to an antibiotic.

TABLE 2 Biochemical characterization of the recovered culturable bacterial isolates from different selective media.

Biochemical test	B1	P1	R1	A1	A2	A3
Methyl red	-	-	-	-	+	+
Voges-Proskauer	-	-	-	-	-	-
Nitrate	-	-	+	-	+	+
Motile	M	M	M	M	M	M+F
Urease	+	+	+	-	-	-
Simmons citrate	+	+	+	+	+	+
Oxidase	+	+	+	+	+	+
Starch hydrolysis	-	-	+	-	+	+
Triple sugar iron	K/K	K/K	A/A + Gas	K/K	A/A	K/A + Gas
Catalase	+	+	+	+	+	+
Indole	-	-	-	-	+	+

M, motile; M+F, motile + fermented; K/K, alkaline; A, acidic; K/A, alkaline slant and acidic butt; A/A, acidic slant and acidic butt; B1, *Bacillus*; P1, *Pseudomonas*; R1, *Rhizobium*; A1, *Azotobacter*; A2, *Azospirillum*; A3, *Alcaligenes*.

As one health concept is an interdisciplinary approach starting from soil linked to plants, animals, and finally human health and wellbeing, a sustainable natural resource approach amalgamating different sources of nutrients in agrifood systems leads to a better crop production under a greater level of antibiotic resistance soil bacteria (Athul et al., 2022).

3.3 Culturable bacterial diversity in cabbage soil

Population dynamics of the isolated culturable bacteria up to the genus level from different treated plots of the cabbage experimental field were investigated. Although culturable bacterial population dynamics study has limitations over molecular approaches, isolation of culturable bacterial genera still gives information on very specific genera involved in nutrient dynamics. Their presence confirmed the activity and involvement of specific genera in nutrient transformation under agrifood systems. The initial biomass population of culturable soil bacteria, viz., *Bacillus*, *Pseudomonas*, *Rhizobium*, *Azotobacter*, *Azospirillum*, and *Alcaligenes*, was recorded at 41.23, 6.39, 2.05, 0.92, 4.59, and $1.01 (\times 10^5 \text{ cfu g}^{-1} \text{ dry soil})$, respectively. At the maximum growth stage of cabbage, the population of isolated culturable bacteria, including *Bacillus*, *Pseudomonas*, *Rhizobium*, *Azotobacter*, *Azospirillum*, and *Alcaligenes*, in surface soil under the influence of long-term manurial endowment ranged from 29.33 to 49.00, 05.00 to 10.03, 01.33 to 04.09, 00.13 to 04.55, 00.25 to 22.36, and 01.00 to 04.00 ($\times 10^5 \text{ cfu g}^{-1} \text{ dry soil}$), respectively (Table 4).

TABLE 3 Antibiotic sensitivity test (AST) of isolated culturable bacteria.

Antibiotic test	B1	P1	R1	A1	A2	A3
Tetracycline	29 mm	–	–	20 mm	–	12 mm
Clindamycin	15 mm	–	–	–	–	–
Erythromycin	26 mm	–	–	–	–	–
Chloramphenicol	17 mm	–	27 mm	15 mm	–	14 mm
Imipenem	–	22 mm	–	–	–	–
Cephameycin	–	15 mm	–	–	–	–
Cefazolin	–	20 mm	–	–	–	–
Gentamycin	–	–	34 mm	–	20 mm	–
Vancomycin	–	–	23 mm	–	–	–
Ampicillin	–	–	–	10 mm	–	–
Streptomycin	–	–	–	28 mm	–	–
Penicillin	–	–	–	–	13 mm	18 mm
Kanamycin	–	–	–	–	28 mm	–
Ciprofloxacin	–	–	–	–	–	24 mm

B1, *Bacillus*; P1, *Pseudomonas*; R1, *Rhizobium*; A1, *Azotobacter*; A2, *Azospirillum*; A3, *Alcaligenes*—zone diameter (mm): susceptible, ≥ 17 mm; intermediate, 14–16 mm; resistant, ≤ 13 mm. No or small zone formation indicates resistant against the bacteria (based on minimum inhibitory concentrations (MICs) or zone diameters following EUCAST guidelines).

The lime-integrated package of practices with inorganics and organics (T8) had a higher impact on these beneficial culturable bacterial dynamics over the non-integrated package of practices. Proper integration of inorganic and organic bioinoculants with ameliorants like liming material under acid soil helps in creating a congenial environment for proliferation of the bacterial population (Athul et al., 2022). Among only organic-treated plots, organic practice II (T10) where combo inputs like FYM at 5 t ha^{-1} + VC at 2.5 t ha^{-1} + poultry manure (PM) at 1 t ha^{-1} + neem oil cake at 0.5 t ha^{-1} + BFs were applied preserved a greater *Bacillus* population over others compared with organic practice I (T9), where 100% N through FYM and VC at 1:1 was applied (Table 4).

3.4 Microbial activities in cabbage soil

Different microbial activities like basal respiration, organic carbon, respiration quotient, MBC, and MBN were studied in cabbage soil. The initial soil basal respiration, organic carbon, respiration quotient, MBC, and MBN were $67.1 \text{ mg CO}_2 \text{ g}^{-1} \text{ soil}$, 0.35%, 0.32 q CO_2 , $172.0 \text{ } \mu\text{g C g}^{-1} \text{ soil}$, $50.29 \text{ } \mu\text{g N g}^{-1} \text{ soil}$, $24.00 \text{ } \mu\text{g TPF g}^{-1} \text{ soil day}^{-1}$, and $45.39 \text{ } \mu\text{g NH}_4^+ \text{-N g}^{-1} \text{ soil } 2 \text{ h}^{-1}$, respectively. This study showed that applying balanced inorganic fertilizers (T2) increased basal respiration (BR) by 11% compared with the control plots (T1). Adding FYM (T3) to T2 results in a 12% further increase in BR, whereas combining vermicompost (T4) and FYM + biofertilizers (T5) also boosts BR. The highest BR (37%) was observed when FYM, lime, and biofertilizers were applied with inorganic fertilizers (Jian et al., 2022). Soil organic carbon (SOC) ranged from 0.55% to 0.65%, with an 18% rise under inorganic fertilizers and a 32% increase when integrated with vermicompost, lime, and biofertilizers. T7 and T8 (STD+FYM/VC+Lime+BFs) showed superior SOC performance and the lowest respiration quotient ($\text{qCO}_2 = 0.35$). T10, receiving only organics (FYM, VC, PM, neem cake, and BF), recorded the highest qCO_2 value of 0.53.

The absence of inorganic fertilizer leads to a higher respiration quotient, indicating less efficient microbial activity (Purohit et al., 2020). Similar observations are consistent with earlier studies, indicating that microbial acclimatization to environments with limited organic substrates results in a shift from growth-oriented metabolism to maintenance respiration, which may ultimately contribute to carbon losses from the soil (Malik et al., 2018; Batista et al., 2022). In comparison, T7 and T8 showed a 23% reduction in qCO_2 versus T10. FYM with STD (T3) also reduced the respiration quotient compared with the control plots (Table 5).

Soil microbial biomass carbon (MBC) as influenced by long-term manurial endowment practices in cabbage varied from 123.5 to $219.9 \text{ } \mu\text{g C g}^{-1}$. Only the inorganic source of nutrient application through STD increased MBC by 23% over the control plots. Adding FYM (T3) and biofertilizers (T5) to inorganic fertilizers further enhanced MBC, but vermicompost with STD (T4) reduced it by 2.3% from T3 (Padbhushan et al., 2021). Organically managed treatments showed lower microbial carbon than integrated ones. Microbial biomass nitrogen (MBN) ranged between 38.8 and $96.4 \text{ } \mu\text{g N g}^{-1}$ in cabbage with different nutrient sources. The highest was recorded with the treatment (T8) where STD+VC+Lime+BFs was applied. Inorganic fertilizers alone increased MBN by 21% over control plots. However, its integration with organics, bioinoculants, and ameliorants like liming material elevated its activity by enhancing microbial dynamics, affecting soil respiration and cabbage productivity at T8 where STD+VC+Lime+BFs was applied with an integration (Bandita, 2023).

3.5 Soil enzymes activities in cabbage soil

Soil enzymes are the biological catalysts released into the soil ecosystem by the microorganisms, soil fauna, and plant root exudates (Tabatabai, 1994). Their activities reflect overall biological functioning of the soil ecosystem. As soil health

TABLE 4 Long-term manuring endowment on culturable soil bacterial population dynamics in cabbage.

Treatments	Details	<i>Bacillus</i>	<i>Pseudomonas</i>	<i>Rhizobium</i>	<i>Azotobacter</i>	<i>Azospirillum</i>	<i>Alcaligenes</i>
		(×10 ⁵ cfu g ⁻¹ dry soil)					
T ₁	Control	29.33	05.00	01.33	00.23	03.02	01.00
T ₂	STD	40.66	05.67	01.67	00.13	00.25	01.23
T ₃	STD+FYM at 5 t ha ⁻¹	43.67	08.14	03.04	01.21	05.23	02.13
T ₄	STD+ vermicompost (VC) at 2.5 t ha ⁻¹	43.00	07.33	02.83	01.32	07.23	02.52
T ₅	STD+ FYM + biofertilizer (BFs)	45.83	09.45	03.45	02.04	08.32	03.10
T ₆	STD+VC+BFs	45.67	08.43	03.26	02.38	12.00	03.25
T ₇	STD+ FYM + Lat 0.2LR + BFs	48.70	09.82	04.06	02.87	18.85	03.95
T ₈	STD+ VC +lime at 0.2LR +BFs	49.00	10.03	04.09	04.55	22.36	04.00
T ₉	100% N through FYM and VC (1:1)	42.00	07.15	02.15	03.00	21.23	03.85
T ₁₀	FYM at 5 t ha ⁻¹ +VC at 2.5 t ha ⁻¹ + poultry manure (PM) at 1 t ha ⁻¹ + neem oil cake at 0.5 t ha ⁻¹ + BFs	47.00	07.56	02.89	02.71	13.31	01.94
	Initial (×10 ⁵ cfu g ⁻¹ dry soil)	41.23	6.39	2.05	0.92	4.59	1.01
	LSD (p= 0.05)	2.75	0.71	0.35	1.20	6.49	1.00

TABLE 5 Long-term manuring endowment on soil biological properties in cabbage.

Treatments	Details	Basal respiration (mg CO ₂ g ⁻¹ soil)	Organic carbon (%)	Respiration quotient (q CO ₂)	MBC (μg C g ⁻¹ soil)	MBN (μg N g ⁻¹ soil)	Dehydrogenase (μg TPF g ⁻¹ soil day ⁻¹)	Urease (μg NH ₄ ⁺ -N g ⁻¹ soil 2 h ⁻¹)
T ₁	Control	54.9	0.55	0.44	123.5	38.8	24.12	33.74
T ₂	STD	61.4	0.57	0.38	161.7	52.1	24.66	39.11
T ₃	STD+FYM at 5 t ha ⁻¹	69.9	0.58	0.39	180.5	54.8	25.82	41.65
T ₄	STD+ vermicompost (VC) at 2.5 t ha ⁻¹	74.5	0.59	0.40	184.8	62.8	26.21	41.51
T ₅	STD+ FYM + biofertilizer (BFs)	72.0	0.61	0.37	196.8	74.6	25.62	59.77
T ₆	STD+VC+BFs	74.5	0.62	0.38	197.4	81.2	26.16	62.55
T ₇	STD+ FYM + L at 0.2LR + BFs	75.5	0.65	0.35	215.6	95.7	27.36	62.61
T ₈	STD+ VC + lime at 0.2LR +BFs	77.0	0.67	0.35	219.9	96.4	27.61	63.87
T ₉	100% N through FYM and VC (1:1)	70.0	0.55	0.43	164.6	59.9	26.89	47.78
T ₁₀	FYM at 5 t ha ⁻¹ +VC at 2.5 t ha ⁻¹ + poultry	75.0	0.58	0.45	165.7	61.9	26.59	49.26

(Continued)

TABLE 5 Continued

Treatments	Details	Basal respiration	Organic carbon	Respiration quotient	MBC	MBN	Dehydrogenase	Urease
		(mg CO ₂ g ⁻¹ soil)	(%)	(q CO ₂)	(μg C g ⁻¹ soil)	(μg N g ⁻¹ soil)	(μg TPF g ⁻¹ soil day ⁻¹)	(μg NH ₄ ⁺ -N g ⁻¹ soil 2 h ⁻¹)
	manure (PM) at 1 t ha ⁻¹ + neem oil cake at 0.5 t ha ⁻¹ + BFs							
	LSD (p= 0.05)	14.36	0.042	0.044	33.62	7.59	2.18	5.85
	Initial	67.1	0.35	0.32	172.5	50.29	24.00	45.39

depends on biological functioning of the ecosystem, the soil enzyme activity assay serves as a reliable and sensitive soil health indicator. In the present study, along with soil bacterial diversity, soil enzyme activities were also thus studied to validate the results. Soil enzyme activities like dehydrogenase activity (DHA) and urease activity were studied in cabbage soil. Based on soil test results, dehydrogenase activity (DHA) was lowest in control plots and highest in the fully integrated treatment (T8: STD + VC + lime + BFs). The combination of organics, biofertilizers, lime, and inorganic fertilizers enhanced DHA significantly (Purohit et al., 2019) from 24.12 to 27.61 μg TPF g⁻¹ soil day⁻¹. Highest DHA was recorded with T8 27.61 (μg TPF g⁻¹ soil day⁻¹). Among the organic treatments, organic II practices (T10) showed better improvement over organic I (T9)-treated plots in terms of dehydrogenase enzyme activities. Urease enzyme activity at the maximum growth stage of cabbage was studied in different manurial practices. The response of different manurial practices on urease enzyme activities ranged from 33.74 to 63.87 μg NH₄⁺-N g⁻¹ soil 2 h⁻¹; the highest was recorded in the fully integrated package (T8). Control plots (T1) recorded the lowest urease enzyme activities. Application of ameliorants like lime along with biofertilizers positively influenced urease enzyme activities. Treatments receiving organic I (T9) treatments had higher urease activity over treatments receiving the organic II package of practices (T10), indicating differential effects of organic strategies on urease enzyme activities in cabbage soil (Sahoo, 2022).

3.6 Long-term manurial endowment on growth and yield of cabbage.

At 60 days after planting (DAP), total chlorophyll ranged from 1.12 mg g⁻¹ (control) to 2.11 mg g⁻¹ (T8). Overall, chlorophyll-b was higher than chlorophyll-a, and integrated nutrient use improved chlorophyll content (Table 6). The head circumference of cabbage ranged from 16.26 cm (100% N) to 43.40 cm (FYM+VC 1:1), with the largest heads in the STD+VC+Lime+BF treatment. This combination of lime, vermicompost, biofertilizers, and chemical fertilizers showed a 6.8% increase in head size. Plants with only organic input failed to form heads. Economic yield varied from 2.50 to 37.33 t ha⁻¹, highest in STD+FYM+Lime+BFs and lowest in T9. Inorganic fertilizers enhanced yield by 21%, highlighting the benefit of integrating organics with chemical inputs (Sajib et al., 2015).

3.7 Relationship between different biological and yield parameters of cabbage

The effects of long-term manuring endowment on yield, growth, and biological traits were evaluated by using regression lines, principal component analysis (PCA), and correlation coefficients (r) using a correlogram. Regression lines (R²), PCA, and correlation coefficients (r) were calculated for yield, MBC, MBN, and microbial populations. These values, shown in Table 7, highlighted variable interdependence. A strong positive correlation was found between microbial populations (*Rhizobium*, *Bacillus*, and *Pseudomonas*) and MBC and MBN levels. PCA was employed to study the influence of manurial endowment on bacterial population, biological properties, and yield of cabbage.

3.8 Regression analysis

Regression analysis revealed that specific bacterial populations had a significant impact on key soil biological parameters. *Rhizobium* alone had a beneficial effect on SOC (R² = 0.282, p < 0.01) and MBC (R² = 0.594, p < 0.001), whereas *Bacillus* and *Rhizobium* showed significant positive impacts on basal respiration (R² = 0.657, p < 0.05). MBN variation was strongly influenced by *Rhizobium* and *Alcaligenes* (R² = 0.804, p < 0.001). *Pseudomonas* had a beneficial effect on DHA and urease activities and a substantial negative effect on respiration quotient (R² = 0.282, p < 0.01).

The regression analysis of yield parameters indicated that soil biological properties highly impacted plant performance (Table 7). Head weight was negatively affected by the respiration quotient (R² = 0.143). Chlorophyll content showed a strong positive association with microbial biomass nitrogen (MBN) (R² = 0.623), emphasizing the role of nitrogen availability in enhancing chlorophyll levels. The respiration quotient had a negative effect on head circumference (R² = 0.575), whereas microbial biomass carbon (MBC) had a positive effect, suggesting a balance between microbial activity and plant growth. Leaf weight was positively related to MBC and negatively related to the respiration quotient (R² = 0.634), highlighting the dual impact of microbial biomass and soil respiration on plant biomass. Specific beneficial bacterial

TABLE 6 Effect of long-term manuring endowment on growth and yield of cabbage.

Treatments	Details	Chlorophyll at 60 days after planting			Head circumference (cm)	Head weight (t ha ⁻¹)	Leaf weight (t ha ⁻¹)
		Chl. a	Chl. b (mg g ⁻¹)	Total			
T ₁	Control	0.38	0.74	1.12	24.06	05.50	05.00
T ₂	STD	0.60	0.59	1.19	34.13	17.25	05.50
T ₃	STD+FYM at 5 t ha ⁻¹	0.52	1.11	1.63	36.86	18.33	17.25
T ₄	STD+ vermicompost (VC) at 2.5 t ha ⁻¹	0.54	1.24	1.78	37.93	19.50	18.33
T ₅	STD+ FYM + biofertilizer (BFs)	0.54	1.17	1.71	40.20	20.15	19.50
T ₆	STD+VC+BFs	0.46	1.27	1.73	41.00	21.67	20.15
T ₇	STD+ FYM + L at 0.2LR + BFs	0.53	1.38	1.91	42.53	22.00	21.67
T ₈	STD+ VC +Lime at 0.2 LR +BFs	0.58	1.13	2.11	43.40	00.45	22.00
T ₉	100% N through FYM and VC (1:1)	0.44	1.11	1.55	16.26	00.49	00.45
T ₁₀	FYM at 5 t ha ⁻¹ +VC at 2.5 t ha ⁻¹ + poultry manure (PM) at 1 t ha ⁻¹ + neem oil cake at 0.5 t ha ⁻¹ + BFs	0.49	1.12	1.61	17.26	01.44	00.49
	LSD (p= 0.05)	0.052	0.088	0.14	12.9	0.51	0.51

populations significantly influenced the yield parameters of the plant. Head weight was positively affected by *Alcaligenes*, *Rhizobium*, and *Bacillus*, whereas *Azospirillum* and *Azotobacter* had a negative impact ($R^2 = 0.847$). Chlorophyll content showed a strong positive relationship with *Rhizobium* and *Alcaligenes* ($R^2 = 0.778$), suggesting their key roles in promoting photosynthetic capacity. Head circumference was significantly enhanced by *Rhizobium* and *Alcaligenes* but negatively influenced by *Azospirillum* ($R^2 = 0.640$). Similarly, leaf weight increased with higher *Rhizobium* and *Alcaligenes faecalis* populations but decreased with *Azospirillum* ($R^2 = 0.768$).

3.9 Principal component analysis

The study employed principal component analysis (PCA) to investigate the differences in bacterial populations among various manurial treatments. A 76.08% of the overall variance in the dataset was explained by the first principal component (PC1), and another 13.19% by the second component (PC2), for a total of 89.26% of the variability. This suggested that two dimensions can adequately capture the majority of the variations in bacterial populations (Figure 3).

All six bacterial species, namely, *Bacillus*, *Pseudomonas*, *Rhizobium*, *Azotobacter*, *Azospirillum*, and *Alcaligenes*, showed strong positive loadings on PC1, suggesting a high degree of correlation among them. The bacteria most strongly associated with PC1 were *Azotobacter* (loading = 0.913), *Alcaligenes* (loading = 0.904), and *Pseudomonas* (loading = 0.900), indicating that these species

contribute significantly to the differentiation among treatments. Additionally, this analysis revealed that treatments 1 and 2 were linked to reduced bacterial populations; treatments 7 and 8 were positioned on the positive side of PC1, indicating a higher bacterial abundance. Along PC2, treatment 9 was different, indicating that it affects certain aspects of the structure of the bacterial population. Lower contributions to Dim.1 indicate that treatments like 5 and 4 have less of an impact on driving variability (Figure 3A).

The first principal component (PC1) accounted for 59.09% of the total variance, whereas the second principal component (PC2) explained 14.58%, cumulatively capturing 73.67% of the total variability. This suggests that the first two major components successfully described a significant amount of the variation in biological activity.

The variables microbial biomass nitrogen (MBN), urease activity, and microbial biomass carbon (MBC) had strong positive loadings on PC1, suggesting they are the dominant contributors to the differences among treatments. Specifically, MBN (loading = 0.925), urease (loading = 0.913), and MBC (loading = 0.892) were the most influential variables along this axis. PC2 was mainly managed by dehydrogenase activity (DHA) (loading = 0.732) and soil organic carbon (SOC) (loading = -0.456), indicating that these variables provide an additional dimension of biological variability. According to categorical analysis, PC1 was positively correlated with treatments 7 and 8, suggesting that these treatments had higher levels of total biological activity. Treatments 1 and 2, on the other hand, were situated on PC1's negative side, suggesting comparatively less

TABLE 7 Regression equations of different biological parameters and cabbage yield parameters.

Parameters	Regression equation	R ²
Basal respiration	Basal respiration=32.563***+0.656**×(<i>Bacillus</i>) + 3.265*×(<i>Rhizobium</i>)	0.657
SOC	SOC=0.507***+0.031**×(<i>Rhizobium</i>)	0.282
Respiration quotient	Respiration quotient=0.503***−0.014**×(<i>Pseudomonas</i>)	0.282
MBC	MBC=106.896***+25.774***×(<i>Rhizobium</i>)	0.594
MBN	MBN=15.437**+12.976***×(<i>Rhizobium</i>) + 5.580*×(<i>Alcaligenes faecalis</i>)	0.804
Dehydrogenase	DHA=21.004***+0.649*×(<i>Pseudomonas</i>)	0.187
Urease	Urease=16.302**+3.353***×(<i>Pseudomonas</i>) + 3.441**×(<i>Azotobacter</i>)	0.757
Head weight	Head weight=42.807**−76.470*×(respiration quotient)	0.143
Chlorophyll	Chlorophyll =0.759***+0.013***×(MBN)	0.623
Head circumference	Head circumference=42.071*+0.153**×(MBC)−92.453**×(respiration quotient)	0.575
Leaf weight	Leaf weight=14.561ns+0.149***×(MBC)−72.522**×(respiration quotient)	0.634
Head weight	Head weight=−14.644*−0.900**×(<i>Azospirillum</i>)+8.307***×(<i>Alcaligenes faecalis</i>) +4.948**×(<i>Rhizobium</i>)−7.087***×(<i>Azotobacter</i>) +0.350*×(<i>Bacillus</i>)	0.847
Chlorophyll	Chlorophyll=0.799***+0.187***×(<i>Rhizobium</i>)+0.110**×(<i>Alcaligenes faecalis</i>)	0.778
Head circumference	Head circumference=9.546*+7.203***×(<i>Rhizobium</i>)−1.408***×(<i>Azospirillum</i>)+6.985**×(<i>Alcaligenes faecalis</i>)	0.640
Leaf weight	Leaf weight=−11.077***+6.670***×(<i>Rhizobium</i>)−1.065***×(<i>Azospirillum</i>)+6.239***×(<i>Alcaligenes faecalis</i>)	0.768

***p < 0.001, **p < 0.01, *p < 0.05.

biological activity. With greater DHA and SOC contributions, treatments 9 and 10 stood out along PC2 (Figure 3B).

Together, the first principal component (PC1) and second component (PC2) explained 92.47% of the total variability, with PC1 accounting for 69.05% and PC2 for 23.41%. This suggests that the first two components adequately reflect the majority of the variation in the yield data. The yield factors that contributed most to PC1 were leaf weight (loading = 0.975) and head circumference (loading = 0.942), indicating their strong influence on treatment differentiation. Strong positive loadings on PC1 for head weight (loading = 0.706) and chlorophyll content (loading = 0.652) additionally aided in the separation along this axis. Chlorophyll

content (loading = 0.715) and head weight (loading = -0.636) had the greatest effects on PC2, suggesting that these factors contribute more dimensions of yield variability. Treatments showed distinct patterns in the PCA space. Treatments 7, 6, and 5 were positively associated with PC1, indicating superior yield characteristics, particularly in terms of head circumference and leaf weight. In contrast, treatments 1, 2, 9, and 10 were negatively associated with PC1, reflecting relatively lower yield performances. Treatment 8 showed a strong positive association with PC2, largely managed by chlorophyll content and head weight of cabbage (Figure 3C).

3.10 Correlation analysis

Correlation analysis revealed a strong positive relationship among microbial populations, particularly between *Rhizobium* and *Pseudomonas* ($r = 0.98$) and between *Bacillus* and *Rhizobium* ($r = 0.87$). This positive relationship among culturable bacteria revealed a positive soil biological activity, as evidenced by the strong correlations found between them and the biological parameters, viz., basal respiration, microbial biomass carbon (MBC), and microbial biomass nitrogen (MBN). *Rhizobium* ($r = 0.95$) and *Pseudomonas* ($r = 0.91$) exhibited a substantial positive correlation with chlorophyll concentration, establishing a connection between microbial abundance and plant physiological characteristics. The majority of soil and microbial indicators showed a negative correlation with the respiration quotient, indicating that higher microbial presence leads to better respiration efficiency. In general, enhanced soil health and yield metrics were strongly linked to microbial populations (Figure 4).

3.11 Path analysis (structural equation model)

A path analysis (structural equation model) was also employed for depicting culturable bacterial population influence on biological properties and growth parameters in cabbage (Figure 5). It was analyzed that basal respiration ($\beta = 0.48$, $p < 0.001$) and urease activity ($\beta = 0.41$, $p < 0.001$) were significantly impacted positively by *Bacillus* among the microbial communities, suggesting that it plays a role in boosting nitrogen cycling and soil metabolic activity. The *Pseudomonas* significantly improved soil organic carbon (SOC) ($\beta = 0.35$, $p = 0.003$) and dehydrogenase activity (DHA) ($\beta = 0.27$, $p = 0.022$), suggesting its contribution to carbon sequestration and overall soil biological activity. *Azotobacter* had a strong positive effect on microbial biomass carbon (MBC) ($\beta = 0.42$, $p < 0.001$), whereas *Azospirillum* significantly increased microbial biomass nitrogen (MBN) ($\beta = 0.29$, $p = 0.012$). *Alcaligenes* was positively associated with DHA ($\beta = 0.25$, $p = 0.028$). A negative correlation between *Rhizobium* and the respiration quotient ($\beta = -0.21$, $p = 0.042$) suggests that it may have an impact on how effectively the soil system utilizes carbon.

The components of plant yield were then greatly impacted by the biological parameters. Chlorophyll content was significantly impacted by basal respiration ($\beta = 0.26$, $p = 0.018$), suggesting that increased soil respiration leads to greater plant physiological activity. The SOC directly increased head weight ($\beta = 0.31$, $p = 0.006$), highlighting the role that soil carbon plays in biomass

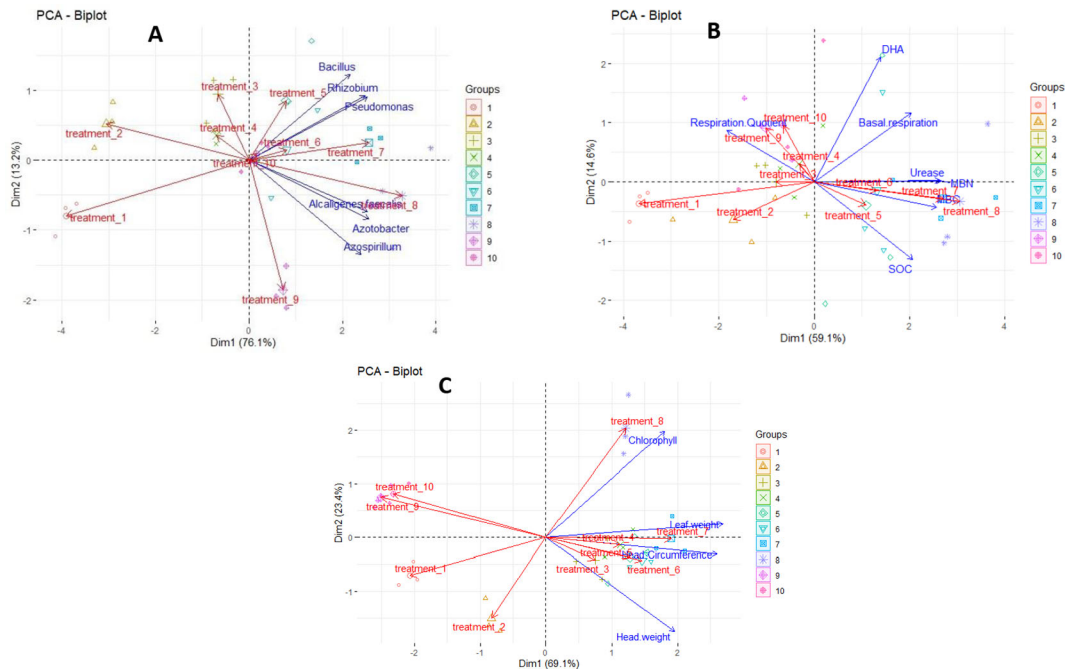


FIGURE 3 PCA biplot showing relationships between (A) treatments and bacterial population, (B) treatments and biological parameters, and (C) treatments and yield parameters of cabbage.

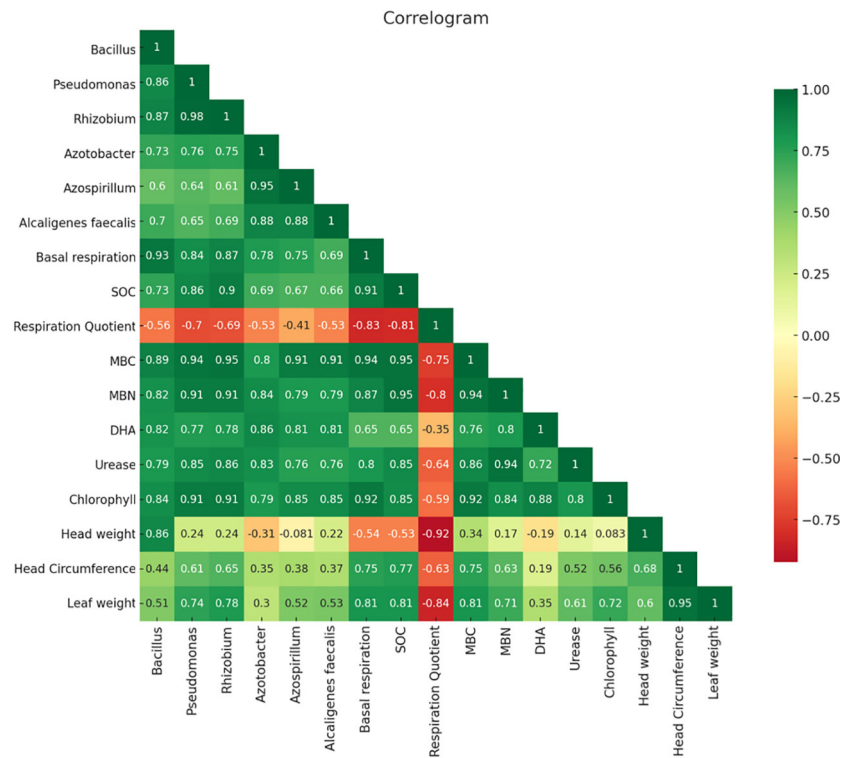
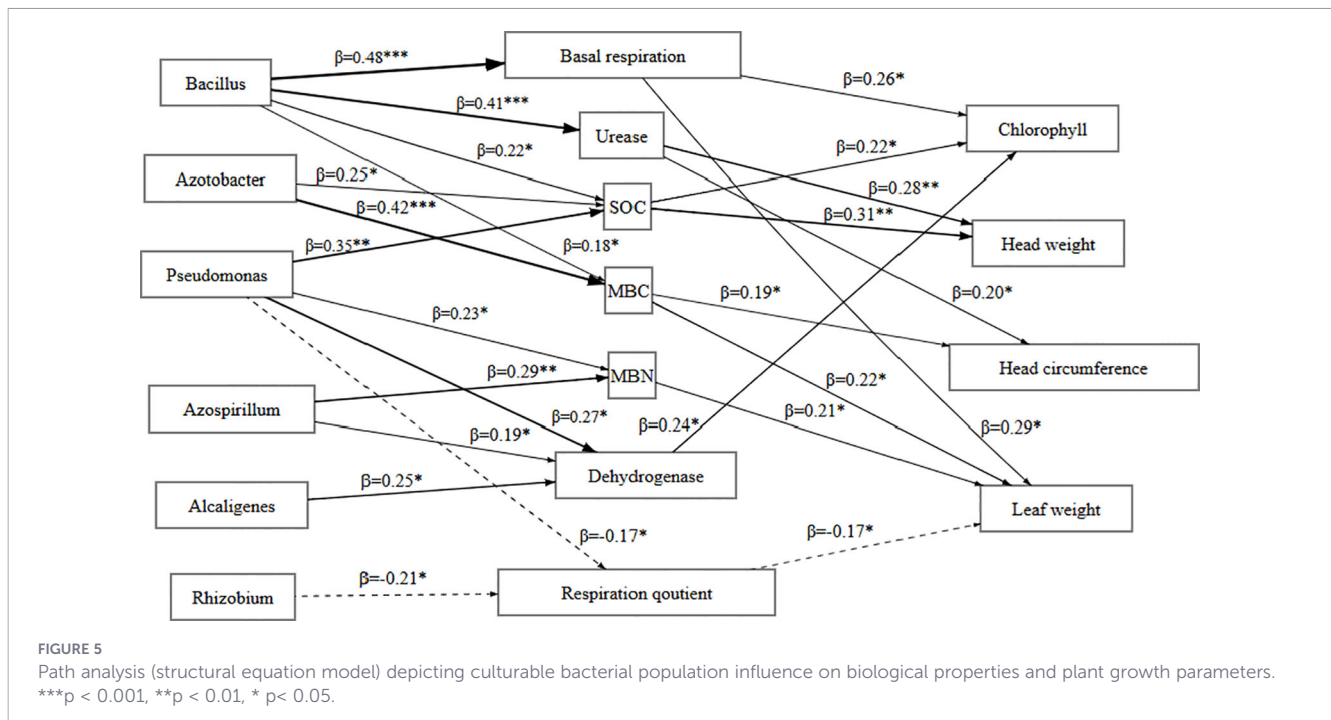


FIGURE 4 Correlogram showing correlation between different culturable bacterial populations, and biological and yield parameters of cabbage.

accumulation. While urease activity significantly improved head weight ($\beta = 0.28, p = 0.008$) and head circumference ($\beta = 0.20, p = 0.042$), MBC was positively correlated with leaf weight ($\beta = 0.22, p = 0.032$). Also, DHA and MBN had a favorable impact on leaf weight

and chlorophyll concentration, respectively. Leaf weight was negatively impacted by the respiration quotient ($\beta = -0.17, p = 0.034$), indicating that biomass allocation may be constrained by increased carbon-use inefficiency.



4 Discussion

Efficient plant nutrient management under different agroecosystems plays a pivotal role in influencing nutrient cycling, soil health, and overall crop productivity (Kabato et al., 2025). From the present study, it was confirmed that beneficial culturable soil bacteria like *Bacillus*, *Pseudomonas*, *Rhizobium*, *Azotobacter*, *Azospirillum*, and *Alcaligenes* are predominant in different experimental plots of cabbage under long-term manurial endowment practices. These culturable soil bacteria colonize in the rhizosphere of the crop and mobilize the plant nutrients through metabolic pathways involving different enzymes and biostimulants (Igiehon et al., 2024). Although limitations are there for culturable microorganisms in soil biodiversity and ecosystem functioning, they help in the study of nutrient transformation, use of native isolates as biostimulants and bioagents, and bioremediation of polluted soils in agricultural production systems (Subudhi et al., 2020; Chen et al., 2023). The present findings thus corroborate the presence of culturable soil bacteria vis-a-vis cabbage productivity under long-term manurial practices.

Antibiotic sensitivity test (AST) of these culturable soil bacteria, viz., *Bacillus*, *Pseudomonas*, *Rhizobium*, *Azotobacter*, *Azospirillum*, and *Alcaligenes*, plays an important role as environmental reservoirs for antibiotic resistance genes (ARGs) enabled them to grow under natural and stressed environments (Ouyang et al., 2024). ARGs in soil are commonly driven into the ecosystem through manure, sewage, and waste water application in agriculture (Zhang et al., 2018). Its presence in soil serves as a hotspot for dissemination of resistance through horizontal gene transfer and poses significant health risks via food chain transmission. Thus, ARGs serve as a vital one health indicator. Interestingly, its estimation in soil focuses on how culturable soil bacteria respond well to specific antibiotics (resistant, intermediate, or susceptible) to evaluate environmental health assessment for potential impacts on crop production, and its subsequent risks of

transferring resistance to humans via the food chain against injudicious agricultural practices. A sustainable natural resource management approaches in agrifood systems can thus give a better crop production option under a greater level of antibiotic resistance soil bacteria (ARB). It is thus vital for identifying which antibiotics are effective against culturable soil bacteria in agricultural field soils for rhizobacterial activities vis-a-vis human health (Zhao et al., 2025).

The plant growth-promoting rhizobacteria (PGPR) properties of these culturable soil bacteria like nutrient mineralization, release of biostimulants, secretion of siderophores, and resistance against different antibiotics depend on active biomass dynamics (Luan et al., 2023). Although culturable bacterial population dynamics study has limitations over molecular approaches and metagenomics, isolation of culturable bacterial population can be used for providing information on very specific genera's involvement in a particular nutrients' dynamics under any agroecosystem (Mastiholi et al., 2024). The influence of long-term manurial endowment practices enhanced the biomass of the culturable bacterial population under the lime-integrated package of practices with inorganics and organics (T8) over the non-integrated package of practices. As a result of this, a congenial environment was created under acid soil ecosystems (Athul et al., 2022) and their PGPR activities enhanced cabbage productivity by increasing the nutrient concentration in an active pool. It was observed that *Rhizobium* biomass alone had a beneficial effect on SOC whereas *Bacillus* and *Rhizobium* showed significant positive impacts on basal respiration. Interestingly, yield parameters like head weight of cabbage were positively affected by culturable bacteria *Alcaligenes*, *Rhizobium*, and *Bacillus*, whereas *Azospirillum* and *Azotobacter* had a negative impact on it. Photosynthetic activity in cabbage taking chlorophyll content into account showed a strong positive relationship with *Rhizobium* and *Alcaligenes* population, suggesting their key roles in promoting the photosynthetic capacity of cabbage. Similarly, leaf weight increased with higher *Rhizobium* and *Alcaligenes faecalis*

population; however, it decreased with the *Azospirillum* population in cabbage. Thus, the presence of culturable soil bacterial, viz., *Bacillus*, *Pseudomonas*, *Rhizobium*, *Azotobacter*, *Azospirillum*, and *Alcaligenes*, significantly contributed in growth and yield under different manurial treatments in cabbage (Khambalkar et al., 2025; Kronthaler and Zollner, 2021; Li et al., 2024a, Li et al., 2024b).

Microbial biomass is directly linked to biological activities like basal respiration, organic carbon, respiration quotient, MBC, and MBN in cabbage soil ecology. Soil microbial biomass is a slow-release fertilizer. It acts as a crucial plant nutrient pool in soil. It helps in degrading the organic matter fraction into mineral plant-accessible nutrients for better plant uptake (Athul et al., 2022; Sahoo, 2022). Thus, integrated nutrient management practices under long-term manurial endowment thus improved soil respiration and microbial activities more effectively than only inorganic and organic treatments. Regression study showed a better relationship on MBN with culturable bacteria like *Rhizobium* and *Alcaligenes*. As soil enzymes are the biological indicators, released into the soil ecosystem by the microorganisms, soil fauna, and plant root exudates (Tabatabai, 1994), study on soil dehydrogenase and urease reflected overall biological functioning of the cabbage soil ecology (Sahoo, 2022), enhancing the growth and yield of cabbage. The majority of soil and microbial indicators showed a negative correlation with the respiration quotient, indicating that higher microbial presence leads to better respiration efficiency. Thus, soil biological parameters greatly influenced the cabbage growth like head circumference and yield under acid soil ecosystems. The MBC had a positive effect on it, suggesting a balance between microbial activity and plant growth. Leaf weight was positively correlated with MBC and negatively with the respiration quotient, highlighting the dual impact of microbial biomass and soil respiration on plant biomass. Long-term manurial treatment (T8) where an amalgamation of inorganics, organics, biostimulants, and ameliorating agent were imposed, showed a strong relationship with chlorophyll content and head weight of cabbage (Padbhushan et al., 2021), expressing a synergistic impact on cabbage growth and productivity under acid *Inceptisols*.

To correlate the culturable soil bacteria with biological properties, interestingly it was concluded that basal respiration and urease activity were significantly impacted with a dominated *Bacillus*-populated soil among the microbial communities. A balanced relationship among the microbial community and their activity played a pivotal role in boosting nutrient availability to cabbage via different soil metabolic processes (Meylinga et al., 2013; Wei et al., 2023). Significant improvement in urease activity under best nutrient management plots (T8) improved cabbage growth parameters like head weight and head circumference, and the improved MBC content in soil enhanced the leaf weight in cabbage under different nutrient management plots. Similarly, the *Pseudomonas* population significantly improved SOC and DHA, suggesting its contribution to carbon sequestration and overall synergistic soil biological activities in cabbage. The SOC directly increased the head weight, highlighting the role of soil carbon in biomass accumulation in cabbage. The culturable *Azotobacter* population had a strong positive effect on MBC, whereas *Azospirillum* significantly increased MBN in cabbage soil. The presence of *Alcaligenes* was positively associated with DHA, suggesting an impact of microbe and enzyme activity effectively. Other biological

parameters like DHA and MBN had a favorable impact on leaf weight and chlorophyll concentration in cabbage.

Over and above, soil amendments like liming materials under acid soil ecosystems acts as a primary driver in modifying the soil ecology particularly the pH of the soil. This change in pH to a neutral level under acidic ecosystems creates microbial functional shifts, favoring a good soil structure that accelerates functional microbial groups in intensifying the specific nutrients' transformation which collectively translated into improved crop productivity in cabbage (Purohit et al., 2019, Purohit et al., 2019; Sahoo, 2022; Athul et al., 2022).

5 Conclusion

Under long-term manurial endowment in acid *Inceptisols*, combined application of soil test-based inorganic fertilizers (STD), lime (L), consortia biofertilizers (BFs), and organic manures such as farmyard manure (FYM) or vermicompost (VC) ensured highest growth characteristics like head circumference, chlorophyll content, and economic yield of cabbage. The application of ameliorant (lime) under acid soil reaction with biofertilizers and FYM, amalgamating with STD, had the most beneficial effect on basal respiration which significantly enhanced culturable bacterial diversity and improved biological properties such as microbial biomass carbon, microbial biomass nitrogen, and soil enzyme activities like urease and dehydrogenase activities. Thus, integration of FYM, lime, BFs, and vermicompost with inorganic fertilizers showed a strong correlation between soil biological properties and cabbage productivity under acid *Inceptisols*.

Data availability statement

The original contributions presented in the study are included in the article/Supplementary Material. Further inquiries can be directed to the corresponding author.

Author contributions

MP: Methodology, Project administration, Validation, Data curation, Writing – review & editing, Writing – original draft, Formal analysis. NP: Supervision, Conceptualization, Writing – original draft, Investigation, Writing – review & editing, Visualization, Software. SP: Writing – original draft, Resources, Visualization, Validation, Writing – review & editing, Funding acquisition. AG: Validation, Formal analysis, Supervision, Methodology, Writing – review & editing, Writing – original draft. AN: Project administration, Formal analysis, Writing – review & editing, Methodology, Writing – original draft. KP: Writing – original draft, Resources, Supervision, Methodology, Writing – review & editing, Investigation. SM: Writing – original draft, Software, Data curation, Investigation, Methodology, Writing – review & editing. MD: Validation, Writing – review & editing,

Writing – original draft, Data curation, Software. SS: Writing – review & editing, Supervision, Writing – original draft, Investigation, Formal analysis, Data curation, Validation. HP: Supervision, Writing – original draft, Visualization, Formal analysis, Writing – review & editing. DS: Writing – review & editing, Writing – original draft, Software, Visualization, Conceptualization, Supervision, Validation.

Funding

The author(s) declared that financial support was not received for this work and/or its publication.

Acknowledgments

All authors are highly thankful to the ICAR, New Delhi, and Odisha University of Agriculture and Technology, Bhubaneswar, India, for providing financial and infrastructure facility to conduct the experiment.

Conflict of interest

The author(s) declared that this work was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Supplementary material

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fagro.2026.1765116/full#supplementary-material>

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