



ORIGINAL PAPER

Integrating organic fertilizer strategies for optimizing mulberry crop production and soil health resilience: A pathway to sustainable agriculture

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Received: 14 September 2025 / Accepted: 27 November 2025
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Abstract

Concerns regarding the detrimental effects of synthetic fertilizers on soil quality and environmental sustainability have emphasized the necessity of integrating organic fertilization strategies into crop management. This research work evaluates the effects of various organic fertilizers specifically cow dung and vermicompost, both individually and in combination with recommended NPK on the growth, yield, and leaf quality of three mulberry (*Morus alba* L.) varieties, along with an assessment of soil health and microbial characteristics. Field experiments demonstrated that combined organic treatments, particularly T8 (cow dung + vermicompost), significantly enhanced mulberry leaf yield (up to 116.6 t ha⁻¹ year⁻¹), chlorophyll content, and soluble proteins when compared to conventional NPK fertilization. Soil quality also improved, with increased levels of total carbon, nitrogen, and available phosphorus observed under organic treatments, as well as elevated soil enzyme activities and microbial biomass. Phospholipid fatty acid (PLFA) profiling indicated a rise in microbial diversity in organic plots, with the very first identification of beneficial bacterial strains (*Rosellomorea marisflavi*, *Arthrobacter* spp., *Priestia megaterium*, and *Bacillus marisflavi*) in the sericultural field, further supporting the role of organic amendments in promoting plant growth. Overall, the findings underscore the advantages of organic fertilization in enhancing mulberry productivity and restoring soil health, presenting a sustainable approach to sericulture practices.

Keywords Mulberry (*Morus alba*) · Organic amendment · Sericulture productivity · Soil microbiota · Soil resilience · Sustainable agriculture

1 Introduction

As of now, the global population stands at 7.6 billion, and it is expected to rise to 8.6 billion by 2030 and 9.7 billion by 2050 (Poveda 2021). In response to this projected growth,

various intensive agricultural methods have been proposed and are currently being implemented to meet the increasing demand for agricultural products (Dahiya et al. 2024). Historically, the main strategies for intensifying agricultural output have included large-scale water use, intensive ploughing, and the excessive use of synthetic fertilizers, herbicides, and pesticides (Han et al. 2021). While these intensive farming practices can yield significant crop outputs, the over-reliance on chemical inputs has led to detrimental effects on the environment, biodiversity, soil health, and long-term sustainability (Ayamba et al. 2023a and b; Philippot et al. 2024). Recent studies emphasize the necessity for substantial changes in agricultural practices to minimize the impact on the environment while satisfying the demands of the expanding population (Ahmed 2021; Ahammed et al. 2025). The adoption of organic fertilizers is increasingly favoured as agricultural systems worldwide transition toward more sustainable and ecologically resilient methods (Summuna et al. 2020). Organic fertilizations, such as vermicompost and farmyard manure, not only supply essential nutrients but

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also enhance microbial activity, enrich soil organic content, as well as improve water retention capacity and soil structure (Bamdad et al. 2022; Afrin and Shilpi 2023; Imran 2024; Sande et al. 2024; Xing and Wang 2024).

The primary food source for *Bombyx mori* L. silkworms is the mulberry tree (*Morus alba* L.), which is a foundational crop within agro-ecosystems dedicated to sericulture. The yield of cocoons and the quality of raw silk are closely tied to the productivity and quality of mulberry leaves. To achieve sustainable mulberry production, it is crucial to enhance soil fertility and manage nutrients effectively (Fig. 1). Although chemical fertilizers may provide short-term increases in production, they can adversely affect soil microbiota and disrupt nutrient cycling over time (Zhou et al. 2022). In contrast, integrated nutrient management which combines organic and inorganic sources has been shown to sustain crop yields while improving the biological and biochemical properties of the soil (Al-Maliki et al. 2021; Yuan et al. 2023; Wang et al. 2025).

Recent studies indicate that the amendment of organic fertilizers enhances photosynthetic efficiency, boosts the nutritional content of leaves, and improves various physiological traits in plants. These improvements are vital for enhancing silkworm nutrition and the overall quality of silk production (Ju et al. 2022; Nguyen et al. 2024). Furthermore,

organic inputs significantly increase microbial biomass carbon (MBC) and nitrogen (MBN), and enzymatic activity, which positively influences the structure of microbial communities (Al-Maliki et al. 2021). This leads to enhanced nutrient availability and greater disease prevention (Fall et al. 2022; Liu et al. 2023a and b; Bortolot et al. 2024). Despite these well-established advantages, there is a notable lack of field-level data regarding the relative effectiveness of different organic fertilizers, especially in relation to mulberry cultivars grown across diverse ecological environments. Additionally, research in sericulture often falls short in providing comprehensive assessments of soil health indicators that include physico-chemical, biological, and microbiological factors.

The present study explores the impact of different organic fertilizer treatments on the growth of mulberry plants, the quality of their leaves, and the health of the soil across three mulberry genotypes, both independently and in conjunction with inorganic fertilizers. To gain a comprehensive understanding of sustainable mulberry agriculture, the research also examines soil biochemical functionality and microbial diversity. The findings are intended to guide the effective management of organic fertilizers in sericulture systems, ultimately promoting long-term productivity, soil resilience, and ecological sustainability.



Fig. 1 Mulberry cultivation during experimental study. **a** Cuttings of mulberry stem prepared for plantation, **b** Pre-treatment (anti-fungal) of cuttings prior to plantation, **c** new mulberry saplings after

15 days of plantation, **d** preparation of different fertilizers, **e** application of fertilizers in the mulberry field, **f** mature mulberry plants after 60 days of pruning, **g** harvesting of mulberry leaves

2 Methodology

2.1 Description of study area

Field experimentation was conducted from March 2023 to September 2024 (successive two seasons) at a mulberry farm in Nabagram block, Murshidabad district, West Bengal, India. The site was chosen based on rainfall patterns, soil quality, and landscape characteristics, which are vital for crop production. This region is known for its sericulture and high-quality mulberry silk production.

The study area is located in the lower Gangetic plains, which is influenced by sub-tropical humid climate, with the average annual precipitation of 1300–1500 mm and 27 °C temperature recorded from the year 2012 to 2022. Peak rainfall occurs from June to September, accounting for over 70% of total annual precipitation.

During the experimental period meteorological data such as temperature, relative humidity and precipitation were recorded from the Meteorological Station, Government of West Bengal, Murshidabad, India. All these meteorological factors showed low inter-annual variation, while moderate seasonal fluctuation was observed (Supplementary Fig. 1). In the 2023, annual precipitation was 1101 mm, with approximately 75% concentrated between June and September. In the 2024, annual precipitation was recorded 1141 mm. For both the consecutive years, a slightly earlier onset of the monsoon (late May) was recorded along with more even precipitation across the months of June–August. The average temperature was recorded as 27–28 °C for the both consecutive years with highest and lowest values in the month of June (31.5 °C) and December (16 °C) respectively. Moreover, the seasonal variability in relative humidity was observed between 50 to 89%. These seasonal fluctuations in meteorological factors likely contributed to variances in soil moisture and nutrient cycling among seasons, which were accounted for by randomization and blocking within the experimental design.

The topography of the study site is predominantly flat, punctuated by some isolated highlands that reach elevations of 25–30 m (Fig. 2a). The watershed area is primarily associated with small seasonal streams. During the summer months, these water channels are typically dry; however, in the rainy season, they connect in an organized stream order flowing southward, which directs water to the lowland areas (Fig. 2b).

The soil of the Murshidabad district is classified as an alluvial soil, and the values of total nitrogen (TN), total phosphorus (TP), total potassium (TK), and pH in soil (0–25 cm) were recorded as 606 kg ha⁻¹, 92 kg ha⁻¹, 106 kg ha⁻¹ and 7.08, respectively.

2.2 Experimental designs

The present investigation was conducted to evaluate the potential of organic fertilizers on mulberry (*Morus alba* L.) crop production, soil health and microbiota. Three different varieties (S1, S1635 and C2038) of mulberry were selected and raised in the experimental field with 60 cm × 60 cm spacing following the pit system of cultivation under irrigated conditions.

2.2.1 Fertilizer treatment

We had prepared our experimental field by a randomized block design with eight fertilizer treatments and three independent replicates (blocks) per treatment (total 24 experimental plots) based on previous related research with befitting modifications (<https://www.fao.org/4/x9895e/x9895e04.htm>). Each plot was prepared with an area of 100 m² (10 m X 10 m). The eight treatments were, **T1**: absolute control (without any fertilizer treatment), **T2**: with recommended dose of NPK for irrigated mulberry cultivation (350 kg N + 140 kg P₂O₅ + 120 kg K₂O ha⁻¹ year⁻¹, five split doses), **T3**: vermicompost (8 tons ha⁻¹ year⁻¹, two split doses), **T4**: cow dung (10 tons ha⁻¹ year⁻¹, two split doses), **T5**: NPK: vermicompost: cow dung ([115 kg N + 50 kg P₂O₅ + 40 kg K₂O] ha⁻¹ year⁻¹ of T2: 4 tons ha⁻¹ year⁻¹: 5 tons ha⁻¹ year⁻¹), **T6**: NPK: cow dung ([115 kg N + 50 kg P₂O₅ + 40 kg K₂O] ha⁻¹ year⁻¹ of T2: 8 tons ha⁻¹ year⁻¹), **T7**: NPK: vermicompost ([115 kg N + 50 kg P₂O₅ + 40 kg K₂O] ha⁻¹ year⁻¹ of T2: 6 tons ha⁻¹ year⁻¹) and **T8**: vermicompost: cow dung (8 tons ha⁻¹ year⁻¹: 10 tons ha⁻¹ year⁻¹). Other agricultural operations (irrigation, pruning, pest control) were performed uniformly across all plots throughout the experimental period as recommended for the irrigated mulberry cultivation. Treatments were randomly assigned to plots within each block using a random number table to reduce allocation bias. The blocks were oriented perpendicular to the main soil or moisture gradient to minimize environmental variation. A buffer zone of 1 m (uncropped alley) was maintained between adjacent plots and 2 m between blocks to limit edge effects and prevent nutrient movement. Within-plot sampling involved collecting composite subsamples from at least five randomly selected locations per plot, combining them to form a single representative sample for laboratory analyses. For all analyses, the experimental plot was considered the primary experimental unit.

2.2.2 Field sampling and study of crop yield

Phenological data, including plant height, stem width, number of leaves per branch, and leaf length, were recorded every 15 days as per Sadat et al. (2017a) until the experiment

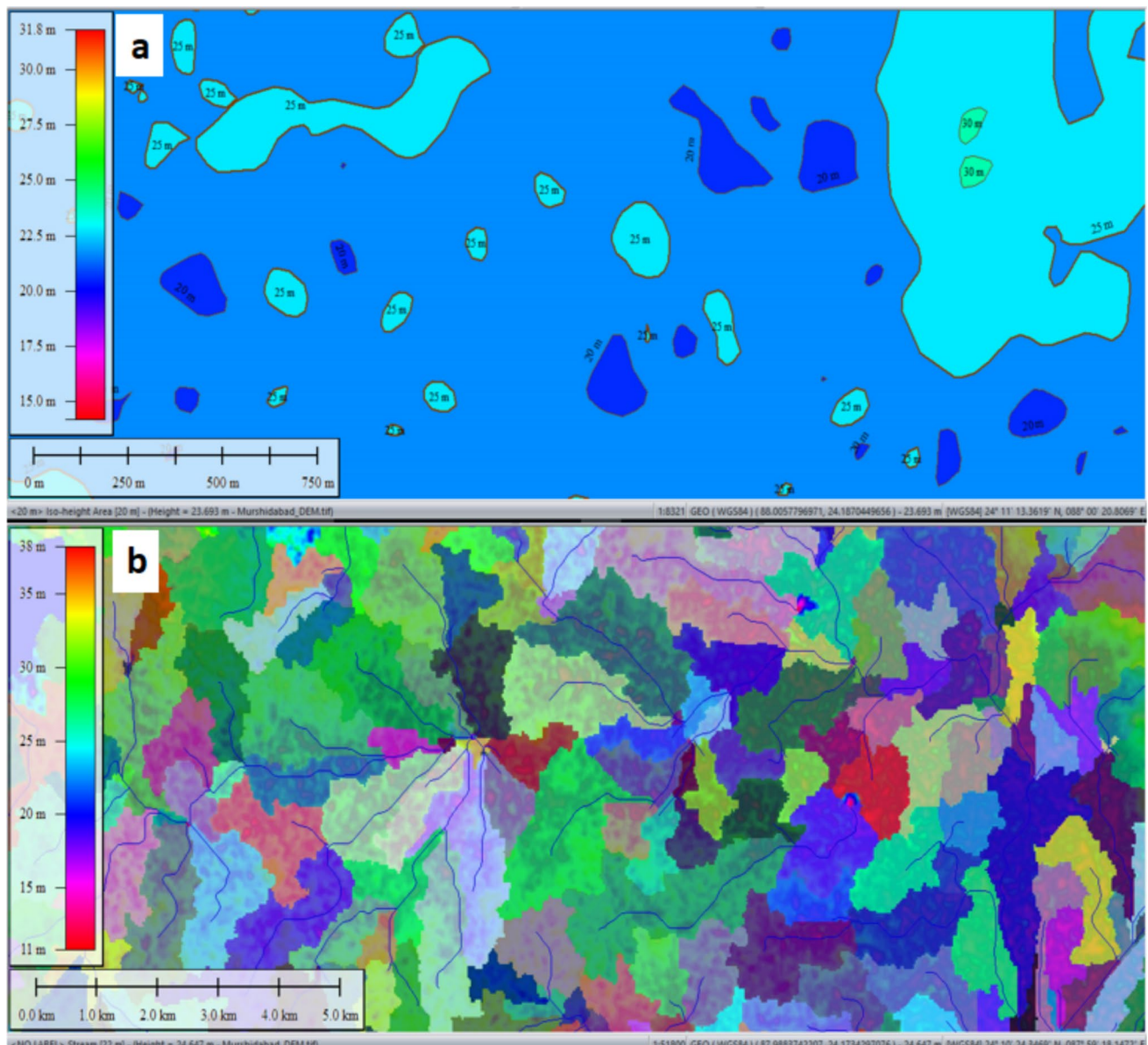


Fig. 2 GIS mapping of the study area September 2023. **a** Topography showing elevation of land forms, **b** watershed area associated with small seasonal streams

concluded. Three crops were harvested annually, pooling data for yield computations. Mulberry leaves for phytochemical analysis were collected from the second crop 60 days post-pruning. Total moisture content, relative water content, total soluble protein, total soluble sugar, and chlorophyll content of leaves were estimated using modified standard protocols (Sadat et al. 2017b).

2.2.3 Study of soil health and soil microbiota

To determine the soil health three soil samples (20 cm depth) from each experimental plot were collected on 15th June 2024. For physico-chemical properties of the soil, pH value,

electric conductivity (EC), cation exchange capacity (CEC), total carbon (TC), total organic carbon (TOC), total nitrogen (TN), available nitrogen (AN), total phosphorus (TP), available phosphorus (AP), total potassium (TK), exchangeable Na, K, Mg and Ca were examined.

Soil samples were extracted in double-distilled water (1:2.5 soil/water) and allowed to stand for 30 min before measuring pH and EC with a glass electrode (Zhou et al. 2022). CEC was determined calorimetrically using hexaminecobalt (III) chloride extraction (Zhou et al. 2022). The Dumas dry-combustion method was employed to measure TC and TN with a PerkinElmer 2400 Series CHNS/O Analyzer. Soil TOC was assessed using the $K_2Cr_2O_7$ - H_2SO_4

method, AN through alkaline hydrolysis diffusion, and TP content with the colorimetric molybdenum blue method after a mixed acid extraction. Soil AP was measured after sodium bicarbonate extraction at pH 8.5. TK content was determined by flame photometry following $\text{H}_2\text{SO}_4\text{--H}_2\text{O}_2$ digestion (Zhou et al. 2022). Exchangeable Na, Mg, K, and Ca concentrations were analysed by ICP-OES after extraction with 1.0 mol L^{-1} ammonium acetate (Zhou et al. 2022).

To determine the soil enzyme activity, soil samples (air-dried) were passes through a 2 mm sieve. The soil enzymes activity including sucrase, urease, nitrite reductase, catalase, β -1,4-glucosidase and polyphenol oxidase were examined spectrophotometrically using soil enzyme kits (Suzhou Comin Biotechnology Company Limited, China).

To determine soil microbial biomass carbon (MBC) and nitrogen (MBN), 50 g of fresh soil samples from each experimental plots were used following chloroform fumigation extraction method. 25 g soil sample was extracted with 50 ml solution of K_2SO_4 (0.5 mol L^{-1}). The remaining 25 g soil sample was fumigated using chloroform for 24 h at ambient temperature. Then the residual chloroform was removed and biomass was extracted. All extractions were diluted upto five folds TOC was measured (multi N/C 3100, Analytik Jena, Germany, TOC-L Total Organic Carbon Analyzer, Shmiazdu). Similarly, TN was also measured for each samples following chloroform fumigation extraction method. MBC and MBN was calculated using the formula:

$$\begin{aligned} \text{MBC} &= (\text{TOC}_F - \text{TOC}_{NF})/k_{EC} \\ \text{MBN} &= (\text{TN}_F - \text{TN}_{NF})/k_{EN} \end{aligned}$$

where,

TOC_F	total organic carbon of fumigated sampl
TOC_{NF}	total organic carbon of non-fumigated samples
TN_F	total nitrogen of fumigated samples
TN_{NF}	total nitrogen of non-fumigated samples
k_{EC}	conversion factors for carbon were set at 0.45
k_{EN}	conversion factors for nitrogen were set at 0.54.

To assess biomass of different soil microbial groups, phospholipid fatty acid (PLFA) study was executed following Bossio et al. (1998). Freeze dried soil samples were used to extract lipids in the chloroform–methanol-citrate buffer mixture (1:2:0.8, v/v/v). The PLFAs were then screened in Agilent 6850 gas chromatograph with the MIID Sherlock 6.03 software with the internal standard set at PLFA 19:0.

2.2.4 Molecular identification of soil bacteria

For the molecular identification, pure culture of soil bacteria was prepared using different selective culture media viz., Aleksandrow medium, Ashby's manitol agar, Jensen's

medium, Pikovskaya's agar and Thiosulfate medium. All the five isolates were named as ALK(S1), ASH(S1), JEN(S1), PIKO(S1) and THIO(S1) respectively. Universal primers 27F and 1492R were used for 16S rDNA amplification (Mao et al. 2012).

Contamination-control and validation procedures were rigorously conducted during bacterial isolation and molecular analysis to ensure the reliability of the data. Sterile blank controls, including no-template PCR reactions and un-inoculated media plates, were incorporated at each stage of DNA extraction and amplification to monitor for contamination; no amplification products were observed. All media, reagents, and consumables underwent pre-sterilization by autoclaving at 121°C and 15 psi for 15 min and were handled under aseptic conditions within a laminar flow cabinet. For isolate validation, each morphologically distinct colony underwent three successive streaking until uniform colony morphology was achieved, with purity confirmed microscopically before DNA extraction. PCR products were assessed by gel electrophoresis on 1% agarose to verify expected amplicon size of approximately 1.5 kb and specificity. Sanger chromatograms were manually reviewed for double peaks or ambiguous bases. Negative-control sequences were also examined to confirm the absence of spurious reads.

Purified 16S rDNA was sequenced utilizing the Sanger sequencing technique. Both strands of the sequenced nucleotides were aligned using Sequence Scanner 2.0 (<http://www.sequence-scanner-software.software.informer.com/2.0/>) to obtain the partial or complete sequence of the 16S rDNA from the isolates. The acquired 16S rDNA sequence was submitted to the NCBI database (<https://www.ncbi.nlm.nih.gov/nucleotide/>) and Basic Local Alignment Search Tool (BLAST) was used for the identification of the closest type strains. From the NCBI database, all the nearest type strains corresponding to the isolated bacterial strains were downloaded to perform multiple sequence alignment with the Contig Assembly Program (CAP3) via multiple sequence alignment software. Then, the phylogenetic trees were constructed through neighbor-joining (NJ) method, with evolutionary distance calculated based on the Kimura 2 parameter model. Bootstrap investigation for phylogenetic trees was conducted through resampling performed 1000 times to validate each clade of the phylogenetic tree. NCBI accession numbers for the 16S rDNA sequences of ALK(S1), ASH(S1), JEN(S1), PIKO(S1), and THIO(S1) were PX116960, PX063811, PX063770, PX063775, and PX116884, respectively.

2.3 Statistical analysis

All recorded data were analyzed using a randomized complete block design (RCBD) model, treating the treatment as a fixed

effect and the block as a random effect. The statistical analyses were conducted using KyPlot version 6.0 beta 15 (64-bit). Results are presented as mean $\pm$ standard deviation ($n = 3$, where n represents the number of replicate plots per treatment). Before analysis, the data were assessed for normality using the Shapiro–Wilk test and for homogeneity of variances with Levene's test. If these assumptions were violated, the data were transformed (using $\log_{10}$ or square-root transformations) until they met the necessary criteria. The results are reported in their original units after back-transformation. Outliers, defined as values greater than 3 standard deviations from the mean, were verified against the raw field records before being removed. A two-way analysis of variance (ANOVA) was conducted according to the RCBD model following the equation:

$$y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij}$$

where,

y_{ij} observation from treatment i in block j ,
 μ is the overall mean, τ_i treatment effect,
 β_j block effect,
 ϵ_{ij} random error for the observations

When ANOVA indicated significant treatment effects ($p < 0.05$), we conducted post-hoc mean separation using Duncan's Multiple Range Test (DMRT). The relationships among soil physico-chemical properties, microbial, and plant variables were evaluated using Spearman's correlation coefficients and principal component analysis (PCA).

3 Results

3.1 Response of mulberry plants towards organic fertilizer treatment

Both the phenological and phytochemical parameters of all three varieties (S1, S1635 and C2038) of mulberry plants were tested against different fertilizer treatments.

3.1.1 Growth and yield

Present study revealed that all mulberry plant varieties showed variable development in phenological characters and leaf yield in respect to the different fertilizer treatment strategies (Supplementary Table 1). Highest growth in plant height was recorded for all three plant varieties for the T8 i.e., application of cow dung and vermicompost as 403 ± 11.5 cm, 322 ± 8 cm and 373 ± 10.5 cm respectively for the mulberry variety S1, S1635 and C2038, respectively. Maximum stem width of S1 plant was recorded in T6 treatment while S1635 and C2038 plants showed

maximum stem width for T5 and T8 treatment respectively. Highest value for number of leaves per branch of S1, S1635 and C2038 were recorded in T3, T6 and T8 treatment respectively. Moreover, the most valuable attribute leaf yield showed higher production in T5, T6, T7 and T8 treatments (Fig. 3a-c). However, for all the varieties highest leaf production was recorded in the T8 treatment that ranges from 88.0 ± 4.0 to 116.6 ± 12.5 t ha⁻¹ year⁻¹.

Principal Component Analysis (PCA) was performed to evaluate the multivariate relations between the leaf yield of S1, S1635 and C2038 mulberry varieties and the different fertilizer treatments strategies (T1-T8). The PCA biplot (Fig. 3d) shows both loading vectors of mulberry varieties and distribution of treatments on the first two principal components (PC1 and PC2). PCA showed that PC1 and PC2 together contributed to 99.93% (PC1, 99.71% and PC2, 0.22%).

3.1.2 Leaf quality parameters

Present study concerned to evaluate the physiological and phytochemical changes in leaf of the three mulberry varieties revealed that these attributes varied significantly due to the different fertilizer treatment strategy (Supplementary Table 2). During the study maximum moisture content (74.00%–76.73%), relative water content (80.57%–88.60%), total chlorophyll (3.86 mg g⁻¹– 3.94 mg g⁻¹), chlorophyll-a (2.60 mg g⁻¹– 2.65 mg g⁻¹), total soluble protein (35.57 mg g⁻¹– 39.87 mg g⁻¹) and total soluble sugar (24.30 mg g⁻¹– 29.97 mg g⁻¹) were recorded in the plot T8. Whereas, highest concentration of chlorophyll-b (1.26 mg g⁻¹– 1.36 mg g⁻¹) was noticed in the plants cultivated in T5 plots.

Leaf protein content is the most important attribute in connection to the quality silk production by the silkworms. 39.74% increase in leaf protein content (Fig. 4) was recorded in the mulberry plants cultivated in the T8 plot treated with cow dung and vermicomposed in comparison to untreated plot (T1), while only 10.86% improvement was observed in plants cultivated with recommended NPK dose (T2) only. Moreover, present study showed that leaf protein content does not significantly differ between the groups T3-T4, and T5-T7.

3.2 Response of soil towards organic fertilizer treatment

3.2.1 Soil physico-chemical properties

In the present study total 14 physico-chemical properties of the soil were examined (Table 1). Eleven soil variables were affected significantly by organic fertilizer treatment compared with inorganic fertilizer. Moreover, all variables showed significant correlations among them (Supplementary Table 3). Organic fertilizer treatments resulted into significant changes

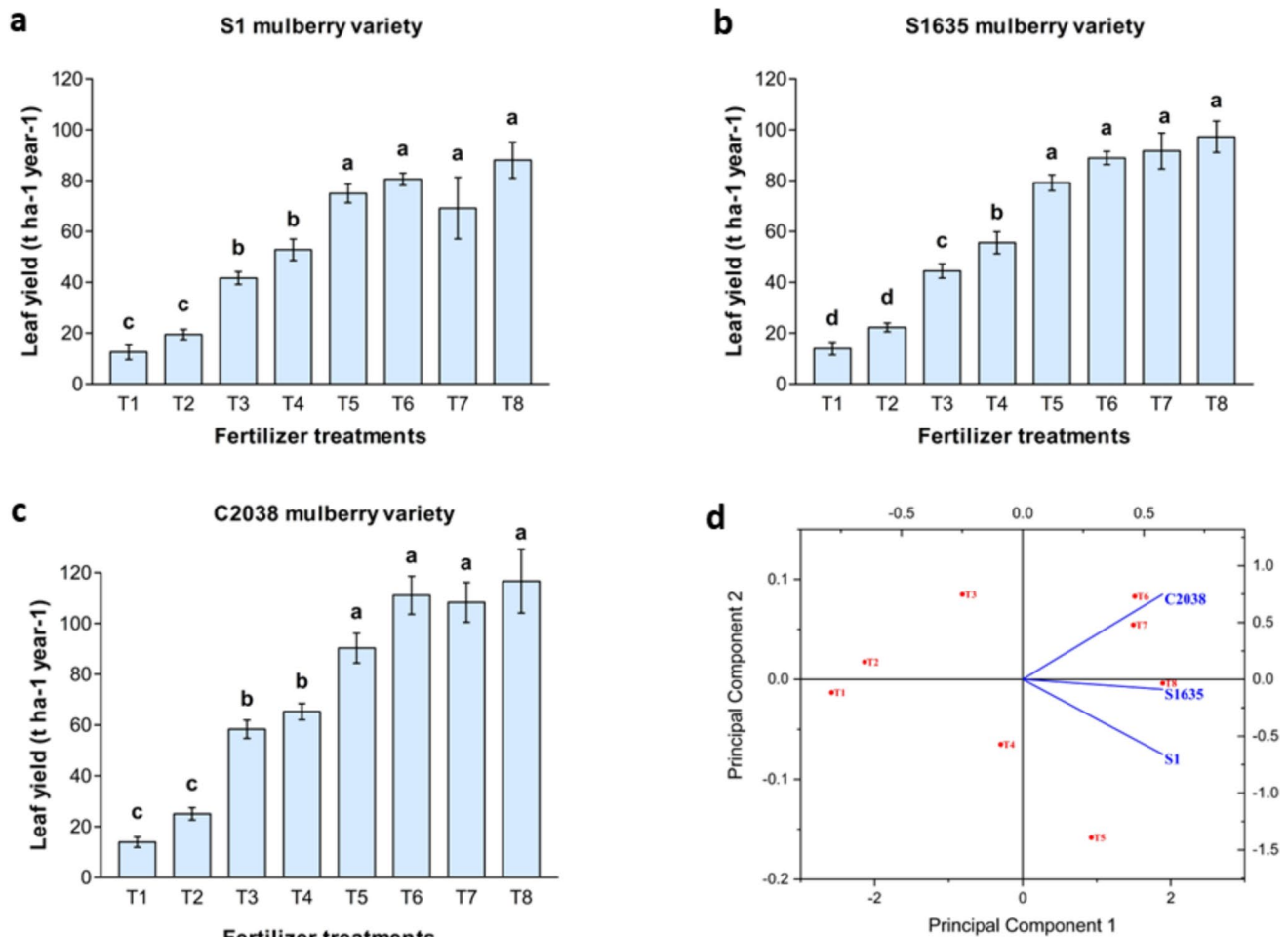


Fig. 3 Mulberry leaf yield ($\text{t ha}^{-1} \text{ year}^{-1}$) during experimental period. **a** S1 mulberry variety, **b** S1635 mulberry variety, **c** C2038 mulberry variety, **d** Principal Component Analysis (PCA) of leaf

yield. The lowercase letters above the column indicate significant differences between groups (p value < 0.05) by Duncan's Multiple Range Test

in total carbon (TC) and total organic carbon (TOC), total nitrogen (TN), available nitrogen (AN), total phosphorus (TP) and available phosphorus (AP) in the fertilizer treatment strategies T3, T4, T5, T6, T7 and T8, in comparison to T1 and T2. Application of organic fertilizer improved total carbon (TC) of soil from 20.6% to 40.7% versus unfertilized (T1) soil and 16.9%–36.4% versus chemical fertilizer (T2) treatments. Total organic carbon (TOC) also showed same improvement as total carbon (TC) following organic fertilizer treatments. Moreover, present investigation revealed that total carbon (TC) and total organic carbon (TC) of the experimental plots were increased maximum in T8 treatment (where no chemical fertilizers were used) in contrast unfertilized (T1) and chemical fertilizer (T2) treatments.

Total nitrogen (TN) and available nitrogen (AN) contents of soil in organic fertilizer treated plots were improved significantly from 64.1%–78.3%, 18.0%–28.1%,

68.7%–72.8%, 34.0%–38.2% respectively with compared to unfertilized field (T1) and the field treated with recommended inorganic fertilizer (T2). However, no significant difference was recorded for total nitrogen (TN) and available nitrogen (AN) contents of soil between different combinations of organic fertilizer treatments (T3 to T8). In comparison to inorganic fertilizer (T2) treatment, total phosphorus (TP) and available phosphorus (AP) content in T8 plot showed highest increase of 41.1% and 118.0% respectively, followed by the treatment strategies T7, T5, T6, T3 and T4. Total potassium (TK) content of soil remains more or less unaffected across all the experimental plots.

Compared with the unfertilized plot, the inorganic fertilizer treated plot showed an increase in soil acidity by 3.36%, while the organic fertilizer treatment revealed significantly improved soil pH by 4.23% to 5.69% ($p < 0.05$), respectively in contrast to the chemical fertilizer treated (T2) plot. The exchangeable

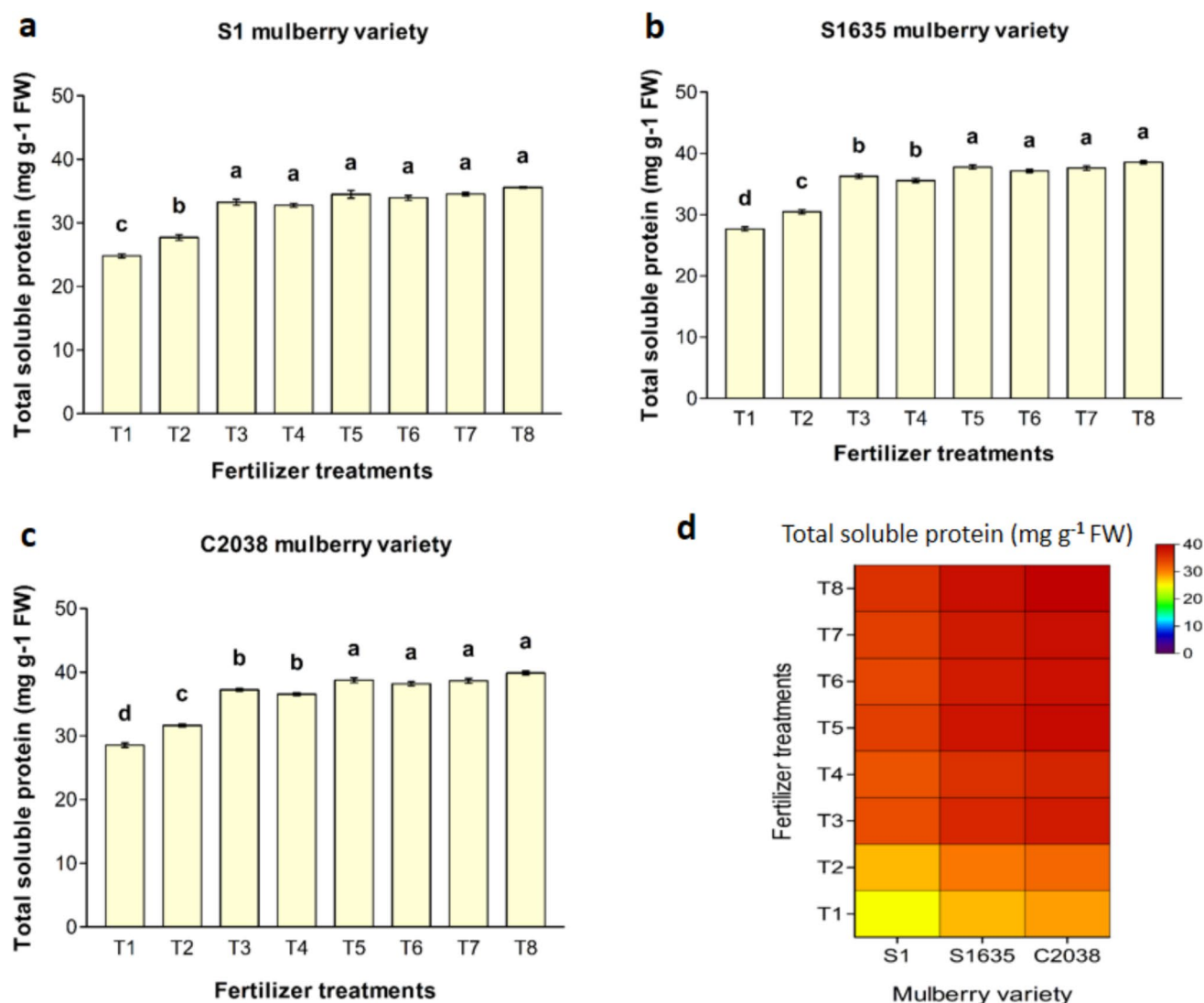


Fig. 4 Total soluble protein content (mg g⁻¹ FW) of mulberry leaf. **a** S1 mulberry variety, **b** S1635 mulberry variety, **c** C2038 mulberry variety, **d** Heat map of leaf protein content. The lowercase letters

above the column indicate significant differences between groups (p value < 0.05) by Duncan's Multiple Range Test

Ca content upon organic fertilizer treatment was significantly ($p < 0.05$) improved by 6.13% to 6.48%, than in the recommended inorganic fertilizer treated plot. Whereas, no significant changes in the exchangeable Mg and cation exchange capacity (CEC) were recorded among different organic fertilizer (T3-T8) treatments and inorganic fertilizer treatment (T2) plots. Moreover, exchangeable Na and K contents in the organic fertilizer amended plots significantly increased up to 112.1% and 103.9%, compared with inorganic fertilizer.

3.2.2 Enzymatic activity of soil

Organic fertilizer treatment strategies resulted in significant alterations in the soil enzyme activity at different experimental plots (Table 2). Likewise, all enzymatic activities have a

significant correlation between them (Supplementary Table 4). Compared to the inorganic fertilizer treated (T2) plot, soil enzyme activity augmented in organic fertilizer treated (T3-T8) plots by 48.25%–59.14%, 28.26%–39.71.4%, 38.78%–91.73%, 27.54%–43.45%, and 85.13%–113.25% respectively, for soil sucrose, urease, soil nitrite reductase, soil catalase, soil β -1,4-glucosidase activity. While polyphenol oxidase activity was significantly ($p < 0.05$) reduced to 19.25 mg d⁻¹ g⁻¹ in the organic fertilizer treated plot (T8) with a per cent reduction of 90.39% compared to inorganic fertilizer treatment (T2) strategy.

3.2.3 Biological characteristics of soil

Application of organic fertilizer significantly ($P < 0.001$) improved MBC, MBN and PLFA levels of the soil (Table 3).

Table 1 Soil chemical variables under each soil fertilizer management practice. Different letters following the means $\pm$ standard deviation indicate significant differences between groups (p value < 0.05) by Duncan's Multiple Range Test

Soil chemical index	T1	T2	T3	T4	T5	T6	T7	T8
Total carbon (g kg ⁻¹)	13.93 $\pm$ 0.34 ^{abcdef}	14.37 $\pm$ 0.38 ^{abcdef}	16.80 $\pm$ 0.38 ^{abcde}	17.33 $\pm$ 0.98 ^{abcd}	17.47 $\pm$ 0.75 ^{abc}	18.30 $\pm$ 0.91 ^{ab}	18.25 $\pm$ 2.15 ^{ab}	19.60 $\pm$ 1.24 ^a
Total organic carbon (g kg ⁻¹)	8.23 $\pm$ 0.31 ^d	8.90 $\pm$ 0.40 ^{cd}	12.60 $\pm$ 0.32 ^{bc}	12.23 $\pm$ 0.38 ^{bc}	14.60 $\pm$ 0.49 ^{ab}	14.70 $\pm$ 0.60 ^{ab}	15.27 $\pm$ 0.69 ^{ab}	16.83 $\pm$ 1.28 ^a
Total N (g kg ⁻¹)	0.92 $\pm$ 0.06 ^c	1.28 $\pm$ 0.01 ^b	1.51 $\pm$ 0.03 ^a	1.53 $\pm$ 0.07 ^a	1.52 $\pm$ 0.08 ^a	1.55 $\pm$ 0.08 ^a	1.59 $\pm$ 0.08 ^a	1.64 $\pm$ 0.08 ^a
Available N (mg kg ⁻¹)	48.33 $\pm$ 3.90 ^b	60.46 $\pm$ 7.90 ^b	83.56 $\pm$ 11.43 ^a	80.93 $\pm$ 5.54 ^a	82.73 $\pm$ 10.10 ^a	86.93 $\pm$ 6.76 ^a	83.76 $\pm$ 4.56 ^a	83.53 $\pm$ 13.20 ^a
Total P (g kg ⁻¹)	0.85 $\pm$ 0.05 ^c	0.90 $\pm$ 0.13 ^{bc}	1.04 $\pm$ 0.08 ^{ab}	1.07 $\pm$ 0.05 ^{ab}	1.04 $\pm$ 0.09 ^{ab}	1.17 $\pm$ 0.15 ^a	1.25 $\pm$ 0.11 ^a	1.27 $\pm$ 0.09 ^a
Available P (mg kg ⁻¹)	50.40 $\pm$ 9.90 ^c	56.33 $\pm$ 9.60 ^c	105.67 $\pm$ 14.15 ^{ab}	101.86 $\pm$ 14.30 ^{ab}	107.33 $\pm$ 7.10 ^{ab}	104.66 $\pm$ 11.68 ^{ab}	108.10 $\pm$ 5.55 ^{ab}	122.83 $\pm$ 14.29 ^a
Total K (g kg ⁻¹)	18.77 $\pm$ 0.75 ^b	19.13 $\pm$ 0.45 ^b	18.83 $\pm$ 0.65 ^b	19.20 $\pm$ 0.60 ^b	19.47 $\pm$ 0.40 ^b	19.46 $\pm$ 0.30 ^b	19.57 $\pm$ 0.80 ^b	19.70 $\pm$ 0.46 ^b
Exchangeable Na (mg kg ⁻¹)	272 $\pm$ 28.5 ^c	257 $\pm$ 27.8 ^c	354 $\pm$ 96.7 ^b	352 $\pm$ 78 ^b	466 $\pm$ 105 ^a	467 $\pm$ 95 ^a	468 $\pm$ 86 ^a	524 $\pm$ 75 ^a
Exchangeable K (mg kg ⁻¹)	339 $\pm$ 34.04 ^c	397 $\pm$ 37.16 ^c	599 $\pm$ 36.89 ^b	588 $\pm$ 38.10 ^b	592 $\pm$ 29.61 ^b	776 $\pm$ 68.70 ^a	761 $\pm$ 37.90 ^a	842 $\pm$ 103.50 ^a
Exchangeable Ca (mg kg ⁻¹)	4960 $\pm$ 236 ^c	4842 $\pm$ 205 ^c	5140 $\pm$ 224 ^{bc}	5139 $\pm$ 258 ^{bc}	5140 $\pm$ 241 ^{bc}	5142 $\pm$ 205 ^{bc}	5147 $\pm$ 230 ^{bc}	5156 $\pm$ 195 ^{bc}
Exchangeable Mg (mg kg ⁻¹)	1015 $\pm$ 24.53 ^b	1130 $\pm$ 26.31 ^a	1160 $\pm$ 14.43 ^a	1153 $\pm$ 15.58 ^a	1165 $\pm$ 15.57 ^a	1163 $\pm$ 23.67 ^a	1174 $\pm$ 25.98 ^a	1187 $\pm$ 24.25 ^a
cation exchange capacity (cmol kg ⁻¹)	16.45 $\pm$ 0.23 ^c	18.63 $\pm$ 0.45 ^b	19.70 $\pm$ 0.55 ^{ab}	19.24 $\pm$ 0.42 ^{bc}	19.71 $\pm$ 0.37 ^{ab}	18.83 $\pm$ 0.22 ^{bc}	19.78 $\pm$ 0.38 ^{ab}	19.95 $\pm$ 0.18 ^a
pH	7.08 $\pm$ 0.06 ^b	6.85 $\pm$ 0.07 ^c	7.14 $\pm$ 0.01 ^{ab}	7.16 $\pm$ 0.04 ^{ab}	7.15 $\pm$ 0.02 ^{ab}	7.19 $\pm$ 0.05 ^{ab}	7.18 $\pm$ 0.05 ^{ab}	7.24 $\pm$ 0.04 ^a
Electric conductivity (μ S cm ⁻¹)	319 $\pm$ 63 ^b	458 $\pm$ 88 ^{ab}	493 $\pm$ 82 ^{ab}	434 $\pm$ 39 ^{ab}	492 $\pm$ 45 ^{ab}	438 $\pm$ 58 ^{ab}	511 $\pm$ 88 ^{ab}	600 $\pm$ 76 ^a

Table 2 Soil enzyme activity under each soil fertilizer management practice. Different letters following the means $\pm$ standard deviation indicate significant differences between groups (p value < 0.05) by Duncan's Multiple Range Test

Soil enzyme activity	T1	T2	T3	T4	T5	T6	T7	T8
Sucrase (mg d ⁻¹ g ⁻¹)	1.81 $\pm$ 0.01 ^d	2.57 $\pm$ 0.01 ^c	3.87 $\pm$ 0.03 ^{ab}	3.81 $\pm$ 0.01 ^{ab}	3.87 $\pm$ 0.01 ^{ab}	3.83 $\pm$ 0.01 ^{ab}	3.84 $\pm$ 0.01 ^{ab}	4.09 $\pm$ 0.012 ^a
Urease (μ g d ⁻¹ g ⁻¹)	631.3 $\pm$ 25.7 ^c	744.6 $\pm$ 20.4 ^b	989 $\pm$ 6.5 ^a	955 $\pm$ 21.7 ^a	1018 $\pm$ 7.2 ^a	940.3 $\pm$ 18.4 ^a	998.6 $\pm$ 10.2 ^a	1040.3 $\pm$ 19.3 ^a
nitrite reductase (μ mol d ⁻¹ g ⁻¹)	3.49 $\pm$ 0.12 ^d	4.47 $\pm$ 0.37 ^c	7.41 $\pm$ 0.28 ^{ab}	6.76 $\pm$ 0.27 ^{ab}	7.46 $\pm$ 0.45 ^{ab}	6.83 $\pm$ 0.31 ^{ab}	6.32 $\pm$ 0.22 ^{ab}	8.57 $\pm$ 0.45 ^a
Catalase (μ mol d ⁻¹ g ⁻¹)	18.4 $\pm$ 0.30 ^c	17.72 $\pm$ 0.52 ^c	22.83 $\pm$ 0.2 ^{ab}	22.60 $\pm$ 0.47 ^{ab}	23.83 $\pm$ 0.40 ^{ab}	22.75 $\pm$ 0.26 ^{ab}	23.48 $\pm$ 0.25 ^{ab}	25.42 $\pm$ 0.96 ^a
β -1,4-glucosidase (μ mol d ⁻¹ g ⁻¹)	16.2 $\pm$ 0.75 ^b	12.37 $\pm$ 0.37 ^c	24.77 $\pm$ 0.45 ^a	22.90 $\pm$ 0.26 ^a	25.53 $\pm$ 0.40 ^a	23.58 $\pm$ 0.20 ^a	25.20 $\pm$ 0.70 ^a	26.38 $\pm$ 0.66 ^a
polyphenol oxidase (mg d ⁻¹ g ⁻¹)	34.62 $\pm$ 1.86 ^a	36.65 $\pm$ 0.56 ^a	20.56 $\pm$ 0.62 ^b	22.82 $\pm$ 1.55 ^b	22.98 $\pm$ 0.89 ^b	24.50 $\pm$ 1.86 ^b	23.28 $\pm$ 0.60 ^b	19.25 $\pm$ 0.75 ^b

The experimental study showed that MBC level increased 185.02%–197.78% in the organic fertilizer treated plots (T3–T8) in comparison to untreated plots (T1), while only 94.67% increase was recorded in the plots (T2) treated with chemical fertilizers alone. Similar improvement was also observed for soil MBN level, with the highest increase of 271.17% in the plots (T8) treated with cow dung and vermicompost.

PLFA analysis also showed a considerable improvement in biomass of total soil microbiota, bacterial community, arbuscular mycorrhizae fungi (AMF), fungi (non-AM), actinomycetes, anaerobes, eukaryotes and methanotrophs. We have recorded highest increase of 197.78%, 212.22%, 171.05%, 148.86%, 221.31%, 225.64%, 196.25% and 315.62% biomass of total soil microbiota, bacterial community, fungi (non-AM), AMF, actinomycetes, anaerobes, eukaryotes and methanotrophs respectively in the organic fertilizer (T8) treated soils in comparison to the chemical fertilizer treated (T2) plot (Supplementary Fig. 2). 94.21%, 205.98%, 148.50%, 263.75% and 371.87% improvements of biomass of total soil microbiota, bacterial community, anaerobes, eukaryotes and methanotrophs were recorded respectively in the T2 plot, while 90.68%, 74.30% and 54.50% decrease in the arbuscular mycorrhizae fungi (AMF), fungi (non-AM), actinomycetes groups were also observed in the same soil.

3.2.4 Molecular identification of soil bacteria

The 16S rDNA gene sequencing revealed the prevalence of five bacterial strains in the experimental plots (Supplementary Table 5). The five isolates were identified as the strains *Rosellomorea marisflavi* ALK(S1), *Arthrobacter* sp. ASH(S1), *Arthrobacter* sp. JEN(S1), *Priestia megaterium* PIKO(S1), and *Bacillus marisflavi* THIO(S1). Phylogenetic analysis base on the 16S rDNA point out that closest relative to the isolated strains ALK(S1), ASH(S1), JEN(S1), PIKO(S1), and

THIO(S1) were *Rosellomorea marisflavi* EB110 with 99.85% similarity, *Arthrobacter* sp. FMS 60 m D8 with 99.46% similarity, *Arthrobacter* sp. MRHB1-161 with 99.91% similarity, *Priestia megaterium* SIN-22 with 100.00% similarity and *Bacillus marisflavi* PBBW2 with 99.29% similarity respectively (Fig. 5).

4 Discussion

Our current study demonstrates that the application of organic fertilizer amendments, particularly the combination of cow dung and vermicompost, remarkably improves both the yield and quality of mulberry leaves compared to the application of inorganic fertilizers alone. These improvements are allied with substantial elevation in soil total organic carbon, nitrogen, and phosphorus levels, as well as increased enzymatic activities, including sucrase, catalase, urease and β -1,4-glucosidase. This specifies an improved dynamic nutrient cycling process between cultivated plants and the agro-ecosystem. Furthermore, the use of organic amendments nurtures a diverse and balanced soil microbial community (Supplementary Fig. 2), evidenced by augmented microbial biomass and the emergence of beneficial taxa such as *Rosellomorea marisflavi*, *Priestia megaterium*, *Bacillus marisflavi*, and *Arthrobacter* spp. that are testified here for the first time from a sericultural ecosystem.

4.1 Integration of microbial and biochemical responses

Organic fertilizer amendment significantly boosted mulberry leaf productivity compared to exclusive inorganic fertilizer treatment, underscoring the crucial role of biochemical and microbial feedback mechanisms in nutrient cycling. The combination of cow dung and vermicompost produced improved and more consistent results than either inorganic or organic inputs used

Table 3 Soil biological characteristics under each soil fertilizer management practice. Different letters following the means $\pm$ standard deviation indicate significant differences between groups (p value < 0.05) by Duncan's Multiple Range Test

Soil biological activity	T1	T2	T3	T4	T5	T6	T7	T8
MBC ($\mu\text{g C g}^{-1}$)	293.47 $\pm$ 3.50 ^d	571.30 $\pm$ 4.16 ^c	836.45 $\pm$ 7.20 ^b	825.74 $\pm$ 4.36 ^b	835.55 $\pm$ 2.68 ^b	839.21 $\pm$ 4.25 ^b	832.85 $\pm$ 3.42 ^b	873.92 $\pm$ 5.10 ^a
MBN ($\mu\text{g C g}^{-1}$)	29.35 $\pm$ 1.35 ^d	81.61 $\pm$ 4.78 ^c	92.98 $\pm$ 3.23 ^b	91.75 $\pm$ 3.45 ^b	104.44 $\pm$ 5.28 ^a	104.90 $\pm$ 3.39 ^a	104.10 $\pm$ 4.75 ^a	109.24 $\pm$ 2.42 ^a
Total microbial biomass (nmol g^{-1})	5240.62 $\pm$ 72.31 ^d	10201.84 $\pm$ 85.52 ^c	14936.65 $\pm$ 93.81 ^b	14745.50 $\pm$ 87.12 ^b	14920.65 $\pm$ 103.40 ^b	14985.96 $\pm$ 94.85 ^b	14872.45 $\pm$ 115.48 ^b	15605.75 $\pm$ 95.80 ^a
Bacteria (nmol g^{-1})	2805.30 $\pm$ 36.30 ^f	8583.07 $\pm$ 75.53 ^c	8397.38 $\pm$ 82.50 ^d	8244.2 $\pm$ 64.92 ^e	9467.05 $\pm$ 49.82 ^a	9574.52 $\pm$ 78.65 ^a	9436.60 $\pm$ 49.64 ^a	8757.93 $\pm$ 95.53 ^b
Gram-bacteria (nmol g^{-1})	1768.71 $\pm$ 18.50 ^h	7137.69 $\pm$ 65.52 ^a	4719.98 $\pm$ 38.95 ^f	4534.24 $\pm$ 42.65 ^g	5759.31 $\pm$ 38.90 ^b	5627.22 $\pm$ 64.52 ^c	5197.92 $\pm$ 45.96 ^d	5071.86 $\pm$ 53.76 ^e
Gram + bacteria (nmol g^{-1})	1036.59 $\pm$ 15.78 ^e	1445.38 $\pm$ 26.25 ^d	3677.40 $\pm$ 18.84 ^c	3709.96 $\pm$ 26.45 ^c	3707.74 $\pm$ 34.88 ^c	3947.30 $\pm$ 22.59 ^b	4238.68 $\pm$ 35.85 ^a	3686.07 $\pm$ 24.75 ^c
Anaerobes (nmol g^{-1})	251.55 $\pm$ 7.80 ^g	624.76 $\pm$ 5.62 ^d	784.17 $\pm$ 13.45 ^b	690.80 $\pm$ 7.28 ^c	420.75 $\pm$ 17.10 ^e	407.61 $\pm$ 8.75 ^e	379.24 $\pm$ 12.90 ^f	819.30 $\pm$ 18.38 ^a
Actinomycetes (nmol g^{-1})	509.38 $\pm$ 7.11 ^e	231.65 $\pm$ 4.13 ^f	1601.20 $\pm$ 13.56 ^c	1670.66 $\pm$ 10.50 ^a	1529.35 $\pm$ 8.98 ^d	1625.97 $\pm$ 6.40 ^b	1674.63 $\pm$ 11.46 ^a	1635.48 $\pm$ 9.12 ^b
Fungi (non-AM) (nmol g^{-1})	1078.52 $\pm$ 16.22 ^g	277.49 $\pm$ 14.08 ^h	2718.47 $\pm$ 12.50 ^a	2632.07 $\pm$ 16.37 ^c	2056.04 $\pm$ 9.72 ^d	1898.72 $\pm$ 6.93 ^e	1754.94 $\pm$ 14.88 ^f	2684.18 $\pm$ 14.88 ^b
arbuscular mycorrhizae (AM) fungi (nmol g^{-1})	493.66 $\pm$ 8.06 ^e	45.91 $\pm$ 12.18 ^f	1147.13 $\pm$ 15.26 ^d	1206.18 $\pm$ 6.84 ^c	1126.49 $\pm$ 9.92 ^d	1122.44 $\pm$ 13.74 ^d	1289.44 $\pm$ 16.20 ^b	1338.97 $\pm$ 13.07 ^a
Eukaryotes (nmol g^{-1})	79.65 $\pm$ 6.28 ^e	290.76 $\pm$ 12.90 ^a	156.83 $\pm$ 5.82 ^d	197.58 $\pm$ 9.38 ^c	183.52 $\pm$ 10.30 ^c	235.27 $\pm$ 7.80 ^b	240.93 $\pm$ 6.95 ^b	237.20 $\pm$ 4.55 ^b
Methanotrophs (nmol g^{-1})	31.96 $\pm$ 4.90 ^e	151.01 $\pm$ 2.85 ^a	131.44 $\pm$ 7.50 ^b	109.11 $\pm$ 4.25 ^b	137.26 $\pm$ 7.60 ^b	121.38 $\pm$ 2.90 ^b	96.67 $\pm$ 5.22 ^b	132.64 $\pm$ 6.25 ^b

independently. This finding reflects a synergistic improvement in soil structure and release of nutrients. Under organic management system, there was a prominent increase in microbial biomass and enzymatic activities, including sucrase, catalase, urease and β -1,4-glucosidase (Türkay et al. 2024). These soil activities indicate strengthening of biogeochemical cycling of carbon and nitrogen, which supports plant nutrition and metabolism in the rhizosphere (Li et al. 2021; Wang et al. 2023; Chaudhary et al. 2025a, b). Additionally, the increase in total organic carbon and cation exchange capacity indicates an improvement in the soil nutrient retention capacity and micro-habitat quality, which consequently promotes microbial growth. These findings align with previous research that showed how organic amendments enhance beneficial soil microbial communities, boost enzymatic activity, and improve nutrient bioavailability (Zhang et al. 2022; Lemanowicz et al. 2024a, b). The enhanced activities of sucrase and β -1,4-glucosidase indicate accelerated carbon turnover and the decomposition of organic matter, while the enhancements in nitrite reductase and urease point to better nitrogen mineralization efficiency (Wang et al. 2023; Yuan et al. 2025a, b). Collectively, these microbial and biochemical responses demonstrate how organic fertilizers pledge a self-reinforcing cycle of organic matter decomposition, nutrient mobilization, and microbial activation, an ecological mechanism vital for sustaining long-term soil fertility.

4.2 Mechanistic link between soil processes and mulberry yield

The findings of the present research work collectively indicate a tightly coupled relationship between microbial amelioration, soil biochemical functionality, and plant productivity, establishing a systems-level understanding of the fertilizer–soil–plant continuum i.e., from belowground processes to aboveground productivity. Organic inputs provided substrates that trigger the soil microbial metabolism, which sequentially enhanced soil enzyme activities and nutrient transformation particularly those of carbon, nitrogen, and phosphorus (Javed et al. 2021; Li et al. 2021; Zhang et al. 2022; Wang et al. 2023; Purwin et al. 2024). Elevated sucrase and β -1,4-glucosidase activities indicate accelerated carbon turnover, providing readily available energy substrates that support microbial proliferation and rhizosphere respiration (Li et al. 2023a and b). Simultaneously, increased nitrite reductase and urease activities enhance nitrogen mineralization and transformation, improving ammonium and nitrate availability for mulberry uptake (Wang et al. 2023; Kaur et al. 2023a). The resulting improvement in nitrogen and phosphorus availability directly supported chlorophyll synthesis, photosynthetic performance and protein accumulation in mulberry leaf system (Hannet et al. 2021). Higher chlorophyll contents and soluble sugar detected under combined organic treatments suggest improved photosynthetic

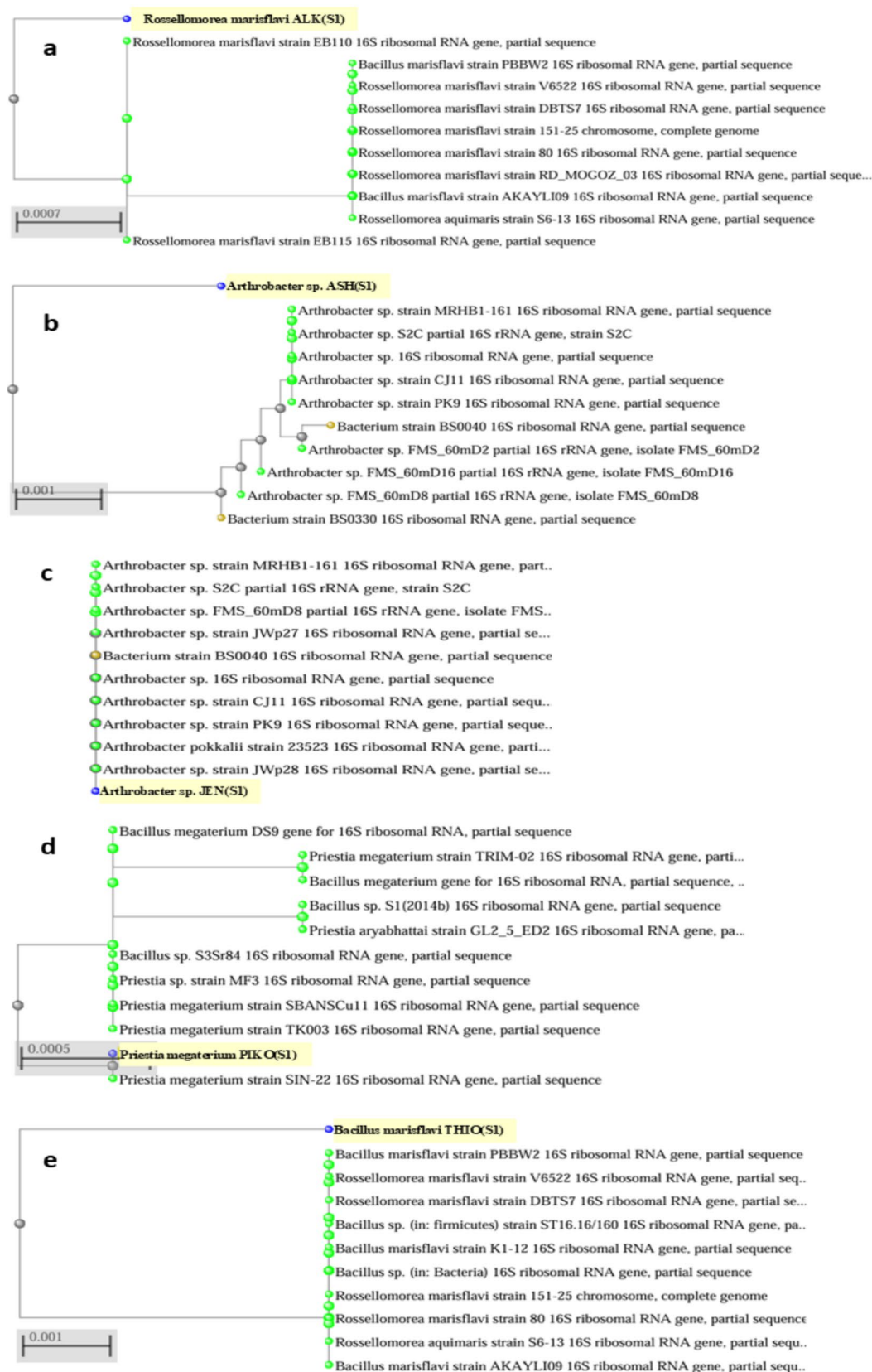


Fig. 5 Phylogenetic tree of the bacterial isolates. **a** *Rossellomorea marisflavi* ALK(S1), **b** *Arthrobacter* sp. ASH(S1), **c** *Arthrobacter* sp. JEN(S1), **d** *Priestia megaterium* PIKO(S1), **e** *Bacillus marisflavi* THIO(S1)

efficiency and osmotic regulation in plant, which collectively augment leaf biomass. Previous works suggested that such improvements in plant system were correspond to improved microbial diversity and functional stability in organic amended soils (Bharti et al. 2021; Hu et al. 2024a and b). Moreover, PCA study validated these linkages by differentiating organic fertilizer amended treatments from conventional fertilizer management practice based on the yield of mulberry leaf and their quality traits. The clustering of high-performing treatments with enhanced biochemical and microbial parameters supports a systems-level interaction, where soil biology mediates plant nutrient acquisition and yield. Additionally, the improved microbial consortia, including *Rossellomorea*, *Priestia*, *Bacillus*, and *Arthrobacter*, likely acted as functional bio-catalysts that promote nutrient solubilization and modulate redox dynamics, thereby reinforcing biochemical feedback loops in the rhizosphere (Bharti et al. 2021; Li et al. 2022; Yang et al. 2022). These interactions collectively improved root nutrient acquisition efficiency and photosynthetic capacity, ultimately translating into higher leaf biomass and enhanced leaf biochemical quality (Liu et al. 2023a and b; Pan et al. 2024). This mechanistic linkage between microbial activation, soil enzymatic dynamics, and mulberry physiological performance underscores the systemic integration of biological, chemical, and plant processes under organic nutrient management (Li et al. 2021; Zhang et al. 2022).

4.3 Comparison with previous studies

Our findings are consistent with several reports indicating the benefits of organic or integrated fertilizer management in improving both the soil health and crop yield performance (Sridevi et al. 2024; Sande et al. 2024; Shi et al. 2025). Hu et al. (2024a, b a and b; 2025a and b) reported that organic inputs lengthen photosynthetic duration and delays leaf senescence, which sequentially associated with the increased chlorophyll content and protein synthesis. Also, Ayamba et al. (2023a, b) and Imran (2024) observed that the application of organic fertilizers augments total carbon and nitrogen pools in soil, improving nutrient efficiency. Our results also confirm previous reports that long-term application of inorganic fertilizers alone can disturb microbial balance, leads to the enrichment of fast-growing Gram-negative bacterial populations while suppressing beneficial Gram-positive bacteria, fungi and actinomycetes (Devi et al. 2021; Kaur et al. 2023a and b). The repossession of soil microbial balance under organic amendments consistent with the report of Walia et al. (2025), who recorded an improved bacterial-fungal ratios and AM fungal activity following farm treatments with organic manure and compost. Moreover, identification of *Rossellomorea marisflavi*, *Priestia megaterium*, *Bacillus marisflavi*, and *Arthrobacter*

spp. as key microbial taxa in organically enriched soils represents a novel contribution to sericultural microbiology. These taxa are well documented as plant growth-promoting rhizobacteria (PGPR) with capabilities for phosphate solubilization, nitrogen fixation, and stress alleviation (Xu et al. 2023; Chhetri et al. 2022; Saha et al. 2023; Zhang et al. 2021; Sun et al. 2024). A comprehensive literature search across NCBI databases, Web of Science and Scopus revealed no prior reports documented the presence of *Rossellomorea marisflavi*, *Priestia megaterium*, *Bacillus marisflavi*, or *Arthrobacter* spp. in mulberry rhizosphere or sericultural soils. Earlier studies involving *R. marisflavi* and *B. marisflavi* have been confined largely to saline or coastal environments (Yoon et al. 2005; Yang et al. 2022; Xu et al. 2023; Saha et al. 2023), whereas *Priestia megaterium* has been widely reported in maize and wheat systems (Zhang et al. 2021) but not within mulberry agro-ecosystems. Likewise, *Arthrobacter* species also have been reported from rice system and medicinal plant rhizospheres (Chhetri et al. 2022; Niu et al. 2025). To the best of our knowledge, there are no former reports of these bacterial genera being associated with mulberry cultivation system, confirming the novelty of the current findings. Report of these bacterial genera in the mulberry cultivation system expands the known ecological distribution of these genera beyond saline or cereal-based systems, representing their adaptability and potential utility in sustainable sericulture.

4.4 Implications for eco-friendly sericulture

This study offers valuable insights into how organic nutrient management can enhance resilient soil ecosystems, ultimately supporting the productivity of mulberry plants. By improving the structure of microbial communities and boosting enzymatic activity, organic fertilizers not only restore soil fertility but also enhance the biochemical quality of leaves (Javed et al. 2021; Chauhan et al. 2022; Rajesaheb et al. 2025). These two factors are essential for the health of silkworms and the yield of cocoons. The combination of microbial and biochemical indicators provides a practical framework for assessing soil health in sericulture-based agroecosystems (Kan et al. 2024; Kapoor et al. 2025). Future research should focus on validating these microbial indicators on a larger scale in the field, as well as conducting long-term monitoring of soil carbon dynamics under ongoing organic management practices (Pan et al. 2020; Kapoor et al. 2025).

Overall, this research improves our understanding by demonstrating how organic amendments influence the relationship between soil microbiota, biochemical cycling, and plant productivity. This insight highlights both the ecological and economic benefits of reducing chemical inputs and encouraging the recycling of organic resources in mulberry-based farming systems.

5 Conclusion, limitations and future directions

The present investigation substantiated the initial hypothesis by demonstrating that the integration of organic fertilizers specifically, the combined application of cow dung and vermicompost markedly enhances mulberry yield, leaf quality, and soil health in comparison to conventional NPK fertilization. These enhancements are evident through increased photosynthetic efficiency, elevated protein and sugar concentrations in the leaves, and the augmentation of soil nutrient reserves and beneficial microbial populations. Collectively, these findings underscore the efficacy of organic amendments as a sustainable approach to fortifying mulberry-based sericulture systems. This study provides the first molecular evidence of *Rosellomorea marisflavi*, *Priestia megaterium*, *Bacillus marisflavi*, and *Arthrobacter* spp. within the sericultural soil ecosystem, expanding the current understanding of microbial diversity and its role in sustainable mulberry cultivation.

In addition to improving productivity, this study demonstrates that organic fertilizers contribute to soil resilience by increasing enzymatic activity, microbial diversity, and populations of plant growth-promoting rhizobacteria. These improvements support sustainable silk production and align with broader agricultural objectives such as reducing chemical inputs, enhancing carbon sequestration, and fostering ecosystem services. The findings offer strong justification for incorporating organic fertilizer practices into agricultural management and policy, both in sericulture and in other crop systems, aiming to balance yield with ecological sustainability. From a policy perspective, incorporating organic nutrient management into regional agricultural development programs can encourage low-cost, resource-efficient practices that enhance farmer livelihoods while minimizing environmental harm. Establishing incentives for on-farm composting, promoting organic certification, and sharing knowledge through sericulture extension networks can help smallholders adopt these practices more quickly.

Although the findings indicate significant benefits of organic fertilizer application, few limitations remain. The study was conducted under short-term field conditions, and long-term trials are required to assess the cumulative effects of organic amendments on yield stability, soil fertility, and carbon storage. Additionally, the research focused on three mulberry varieties within a single ecological context, which limits the generalizability of the results to other agro-climatic zones.

Future research should prioritize multi-location and long-duration field experiments, including farmer-participatory trials, to validate the scalability of organic nutrient management. Integrating biofertilizers with organic amendments is likely to enhance nutrient efficiency and plant resilience.

Furthermore, employing advanced omics-based approaches such as metagenomics, transcriptomics, and metabolomics can clarify the mechanistic roles of soil microbes in nutrient cycling and stress adaptation. These insights will inform the development of region-specific, policy-relevant guidelines for sustainable nutrient management that support both agricultural productivity and environmental sustainability. Finally, translating scientific insights into practical guidelines is crucial for the effective integration of organic nutrient management within national sericulture missions and climate-smart agriculture frameworks. This requires collaboration among researchers, policymakers, and farmer cooperatives to ensure that these strategies are implemented successfully.

Supplementary Information The online version contains supplementary material available at <https://doi.org/10.1007/s44447-025-00116-6>.

Acknowledgements Imtiaz Ahammed would like to acknowledge Swami Vivekananda Merit-cum-Means Scholarship (WBP211619782449), Govt. of West Bengal.

Authors' contributions Conceptualization, A.S.; Methodology, I.A., J.N. and A.S.; Investigation, I.A. and P.C.; Data analysis: B.D., D.S., J.N. and A.S.; Writing- original draft: I.A.; Writing- review and editing: J.N. and A.S.; Supervision, A.S.

Funding The authors declare that no funds, grants, or other support were received during the preparation of this manuscript.

Data availability The datasets generated and/or analysed during the current study are available from the corresponding author upon reasonable request. 16S rDNA sequences of the ALK(S1), ASH(S1), JEN(S1), PIKO(S1), and THIO(S1) bacterial isolates are accessible in NCBI portal with accession numbers PX116960, PX063811, PX063770, PX063775, PX116884, respectively.

Code availability Not applicable.

Declarations

Ethics approval Not applicable.

Consent to participate Not applicable.

Consent for publication Consent for publication (for Fig. 1) was taken in written.

Competing interest The authors have no relevant financial or non-financial interests to disclose.

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