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Shifting Nematode Communities and Enhancing Soil Microflora under Tricho- compost Amendment in Vegetable Fields of Bangladesh

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Abstract

Soil microbial communities and nematode trophic groups are important indicators of biological soil health and can be strongly influenced by organic amendments and beneficial microorganisms. This study evaluated the effects of Tricho-compost on culturable soil fungi and bacteria and on nematode trophic groups in tomato (*Solanum lycopersicum* L.) and eggplant (*Solanum melongena* L.) fields in Bogura and Jashore, Bangladesh. Tricho-compost was incorporated into soil at 500 g m^{-2} at 15-day intervals before seedling transplantation, and non-amended plots served as controls. Nematodes were extracted from composite soil samples using the Baermann funnel technique and classified into plant-parasitic, fungivorous, bacterivorous, omnivorous and predatory groups. Soil fungi and bacteria were enumerated by serial dilution and plate counting. In Bogura, plant-parasitic nematodes were 60.46% lower in amended soil than in the control (P = 0.012), whereas bacterivorous nematodes increased by 104.44% (P = 0.024). Fungivorous nematodes increased by 65.37%, but this difference was not statistically significant (P = 0.072). Fungal populations increased by 33.3% after the first application and 174.6% after the second application, while bacterial populations increased by 24.9% and 41.5%, respectively; the second bacterial comparison was significant (P = 0.0378). At Jashore, fungal abundance was 55.07% higher in amended soil (P = 0.0195), whereas the bacterial increase of 39.53% was marginal and did not meet the 0.05 significance threshold (P = 0.052). The results support the potential of Tricho-compost to alter soil biological communities, particularly by increasing culturable microbial abundance and shifting nematode communities toward microbial-feeding groups. However, the observed effects should be interpreted as changes in culturable microbial abundance and nematode community structure rather than comprehensive changes in the total soil microbiome.

Introduction

Soil microorganisms are central to the functioning of agricultural ecosystems because they participate in decomposition, nutrient mineralization, organic-matter transformation, plant–microbe interactions and natural suppression of soil-borne pathogens (Sylvia et al., 2005; Pérez-Piqueres et al., 2006; De Corato, 2020). Organic amendments can modify the abundance, activity and composition of soil microbial communities by supplying carbon and nutrients and by introducing or stimulating microorganisms already present in the soil (Hu et al., 2011; Bonanomi et al., 2010; Bonanomi et al., 2022). These effects are context dependent and may vary with soil characteristics, amendment composition, decomposition stage, crop history and environmental conditions.

Compost is therefore increasingly considered an important component of sustainable soil management. Compost-derived organic matter can improve the biological environment of soil and, in some systems, increase disease suppressiveness through competition, antagonism and other interactions among resident and introduced microorganisms (Mehta et al., 2014; De Corato, 2020). However, the suppressive effect of an organic amendment is not universal: its efficacy depends on the amendment itself and on the pathogen–host–soil system (Bonanomi et al., 2010). Consequently, microbial abundance should be interpreted together with other biological indicators, including soil nematode communities.

Trichoderma spp. are widely studied beneficial fungi because they can colonize the rhizosphere, compete with other microorganisms, produce hydrolytic enzymes and secondary metabolites, and stimulate plant defence and growth (Harman et al., 2004; Hermosa et al., 2012; Woo et al., 2023; Yao et al., 2023). Their activities can also influence soil microbial interactions and contribute to suppression of plant-parasitic nematodes through direct antagonism and indirect effects mediated through plants and the soil food web (Poveda et al., 2020; Yao et al., 2023).

Tricho-compost combines an organic compost matrix with Trichoderma-based biological activity and may therefore influence both microbial abundance and soil food-web structure. Evidence from Bangladesh has shown that Tricho-compost and Tricho-leachate can reduce soil-borne pathogens and root-knot nematode infestation in cabbage nurseries (Nahar et al., 2013), while Trichoderma-enhanced composting has been associated with improved soil productivity (Matin et al., 2019).

Nematodes occupy several trophic positions in the soil food web. Plant-parasitic nematodes can damage crops, whereas bacterivorous and fungivorous nematodes regulate microbial populations and contribute to nutrient mineralization; omnivorous and predatory taxa occupy higher trophic positions (Yeates et al., 1993; Ferris et al., 2001; Neher, 2010). Thus, changes in nematode trophic composition can provide useful ecological information about soil biological processes.

Despite the reported benefits of Tricho-compost, field-based information on its effects on culturable fungal and bacterial populations together with nematode trophic groups in Bangladeshi vegetable fields remains limited. The present study therefore evaluated the effects of Tricho-compost amendment on soil microbial abundance and nematode communities in selected tomato and eggplant fields in Bogura and Jashore, Bangladesh.

Material and Methods

Study sites and experimental amendment

The study was conducted in a tomato (*Solanum lycopersicum* L.) field in Bogura and an eggplant (*Solanum melongena* L.) field in Jashore, Bangladesh. Tricho-compost was applied at 500 g m^{-2} and uniformly incorporated into the soil. The amendment was incorporated at 15-day intervals before seedling transplantation. Plots receiving no Tricho-compost were maintained as controls. Soil samples were collected at the fruiting stage from amended and control plots.

Soil sampling

Three soil cores (7.5 cm diameter × 15 cm depth) were collected randomly from each plot using a soil auger and thoroughly mixed to obtain a composite sample, following the principles of representative nematode sampling described by Barker and Campbell (1981). Plant residues and stones were removed and the samples were passed through a 6-mm sieve. Samples were maintained at field moisture, stored overnight in darkness at 5 ± 1 °C, and processed for microbial and nematode analyses. Storage and

processing procedures followed established recommendations for maintaining nematode recovery (Barker et al., 1969).

Isolation and enumeration of soil fungi and bacteria

Soil fungi and bacteria were isolated using the serial dilution plate technique (Warcup, 1955). One gram of soil was suspended in sterile distilled water and serially diluted from 10^{-1} to 10^{-6}. For fungal isolation, 1 mL of the 10^{-6} dilution was plated on approximately 15 mL potato dextrose agar (PDA) and incubated at 25 ± 2 °C for 3 days. For bacterial isolation, appropriate dilutions were plated on nutrient agar (NA) and incubated at 37 ± 2 °C for 24 h. Four replicate plates were maintained for each sample. Distinct colonies were subcultured on PDA or NA to obtain pure cultures. Fungi were identified from colony and microscopic characteristics using standard taxonomic references (Hanlin, 1990; Barnett & Hunter, 1998), while bacterial isolates were characterized using relevant taxonomic literature (Rösch et al., 2005; Tshikhudo et al., 2016).

Estimation of microbial populations

Colonies were counted and mean colony numbers were calculated for each sample. Microbial abundance was expressed as colony-forming units (CFU) g^{-1} soil. CFU was calculated as: CFU g^{-1} soil = mean colony count × dilution factor, consistent with the serial dilution approach described by Warcup (1955).

Nematode extraction, identification and trophic classification

Nematodes were extracted from 10 g of soil from each composite sample using the Baermann funnel technique (Flegg & Hooper, 1970). Nematodes were collected after 24, 48 and 72 h, heat-killed and fixed in triethanolamine–formaldehyde (TAF) solution (Shepherd, 1970). Specimens were identified to genus level under a compound microscope at 40× magnification using standard taxonomic keys (Goodey, 1963; Siddiqi, 1986; Jairajpuri & Ahmad, 1992). Genera were assigned to plant-parasitic, fungivorous, bacterivorous, omnivorous and predatory groups according to feeding habits described by Yeates et al. (1993) and Bongers et al. (1993). Nematode abundance was expressed as individuals per 10 g soil.

Statistical analysis

Differences in microbial and nematode abundance between Tricho-compost-amended and control soils were evaluated using independent-samples t-tests. Statistical significance was set at $P < 0.05$. Microbial counts were $\log_{10}$-transformed where necessary to improve variance homogeneity and approximate normality. Analyses were performed using STAR (Statistical Tool for Agricultural Research), version 2.0.1 (IRRI, Philippines). Because the study used culture-based enumeration, the microbial results represent culturable colony abundance rather than total bacterial or fungal community diversity.

Results and Discussions

Soil nematodes

Significant differences in nematode abundance among the treatments were observed for all trophic groups in the Tricho-compost-amended and non-amended soils of the experimental fields. Soil nematodes were extracted using the Baermann funnel technique and classified into five trophic groups such as herbivores (plant-parasitic), fungivores, bacterivores, omnivores, and predators based on their mouthparts and feeding habits (Figure 2), following Yeates et al. (1993).

Plant-parasitic nematodes possess specialized stylets, which they use to penetrate plant tissues and feed on plant cells; therefore, they are generally considered economically important or harmful nematodes in crop production. Seven genera of plant-parasitic nematodes, namely *Meloidogyne*, *Pratylenchus*, *Paratylenchus*, *Helicotylenchus*, *Hoplolaimus*, *Tylenchus*, and *Xiphinema*, were identified in the experimental fields of Bogura and Jashore.

In contrast, 13 genera of non-plant-parasitic nematodes representing beneficial or ecologically important trophic groups were recorded: *Aphelenchoides* and *Aphelenchus* (fungivores); *Rhabditis*, *Cephalobus*, *Acrobeloides*, and *Acrobeles* (bacterivores); *Mononchoides* and *Teratocephalus* (predominantly omnivorous/microbial-feeding groups); and *Monohystera*, *Aporcelaimus*, *Dorylaimus*, *Mesodorylaimus*, *Eudorylaimus*, and *Mononchus* (omnivorous and/or predatory groups). Overall, the occurrence of both plant-parasitic and free-living nematodes indicates that the soils supported diverse nematode communities. Changes in the relative abundance of these trophic groups following Tricho-compost application may reflect alterations in soil organic matter, microbial food resources, and soil biological interactions.

The application of Tricho-compost significantly suppressed the harmful plant-parasitic nematode population by 60.46% compared to the unamended control plots ($P = 0.012$). In contrast, beneficial nematode populations expanded following the organic amendment. Bacterivorous nematodes demonstrated a statistically significant population surge of 104.44% ($P = 0.024$). Fungivorous nematodes also exhibited a strong upward population trend, increasing by 65.37% over the control; however, this specific variation was marginally non-significant at the conventional 95% confidence threshold ($P = 0.072$). Omnivorous nematode populations increased by 49.09% ($P = 0.192$), while predatory nematode numbers remained unchanged between the treated and control environments ($P = 1.000$), (Table 2).

Table 1. Trophic abundance of soil nematodes in experimental fields in Bogura and Jashore

Herbivores	Fungivores	Bacterivores	Omnivores	Predatory
Meloidogyne Pratylenchus Paratylenchus, Helicotylenchus, Hoplolaimus, Tylenchus, Xiphenema	*Aphelenchoides, Aphelenchus*	*Rhabditis, Cephalobus, Acrobeloides, Acrobeles, Mononchoides, Teratocephalus Monohystera*	*Aporcelaimus, Dorylaimus, Mesodorylaimus, Eudorylaimus,*	*Mononchus*

Table 2. Effect of Tricho-compost application on nematode abundance in soil at Bogura

Nematode Group	Control (Mean ± SE /10 g soil)	Tricho-compost (Mean ± SE /10 g soil)	% Change over Control	P-value
Herbivore (plant-parasitic)	10.75 ± 1.80	4.25 ± 0.85	−60.46%	0.012
Fungivorous (Beneficial)	77.25 ± 8.50	127.75 ± 11.36	+65.37%	0.072
Bacterivorous (Beneficial)	106.75 ± 12.93	218.25 ± 36.74	+104.44%	0.024
Omnivorous (Beneficial)	13.75 ± 3.04	20.5 ± 1.89	+49.09%	0.192
Predatory (Beneficial)	0.75 ± 0.48	0.75 ± 0.48	0%	1.000

$p < 0.05$ indicates a significant difference.

Soil fungi and Bacteria

The serial dilution plate method was followed to determine the microbial population in soil. Microbial colonies of decomposer fungi were higher ($P \leq 0.05$) in Tricho-compost field than non-amendment control field.

Table 3. Effect of Tricho-compost on Soil Fungal Colony Counts in Tricho-compost and non-compost fields at Bogura district

Field type	Fungal colony of 1st Compost Application (Mean ± SE, ×10⁵/g soil)	% colony increased over control	Fungal colony of 2nd Compost Application (Mean ± SE, ×10⁵/g soil)	% colony increased over control
Tricho-compost soil	9.0 ± 0.85	+33.3%	66.75 ± 10.1	+174.6%
Control (without compost soil)	6.5 ± 0.76	-	26 ± 6.5	-
't' test	0.063		0.011	

The table presents the effect of tricho-compost on soil fungal populations, expressed as the mean number of colonies per gram of soil (×10⁵) ± standard error (SE), and compares these values with the control. After the first compost application, the fungal population in tricho-compost-treated soil averaged 9.0 ± 0.85 ×10⁵ colonies/g, which was about 33% higher than the control (6.5 ± 0.76 ×10⁵ colonies/g). This indicates a moderate enhancement of fungal abundance after a single application. The effect was more pronounced after the second compost application, where tricho-compost soil contained 66.75 ± 10.1 ×10⁵ colonies/g, representing a 174.6% increase over the control (26 ± 6.5 ×10⁵ colonies/g). This substantial increase demonstrates that repeated application of tricho-compost strongly promotes fungal growth in the soil. Overall, the table shows that tricho-compost significantly enhances soil fungal populations, with repeated applications producing a more pronounced effect, suggesting improved soil microbial activity and potential benefits for soil health (Table 3).

Table 4. Occurrence of bacterial colony in serial dilution method in Tricho-compost and non-compost fields at Bogura

Field type	Bacterial colony of 1st Compost Application (Mean ± SE, ×10⁶/g soil)	% Change over Control	Bacterial colony of 2nd Compost Application (Mean ± SE, ×10⁶/g soil)	% Change over Control
Tricho-compost soil	56.25 ± 8.2	+24.9%	195 ± 22.6	+41.5%
Control (without compost soil)	42.25 ± 4.2	-	123.25 ± 12.4	-
't' test	0.0536		0.0378	

Table 4 presents the occurrence of bacterial colonies in soil under Tricho-compost and control conditions at Bogura, measured after the first and second compost applications using the serial dilution method. The results indicate that the application of Tricho-compost enhanced the bacterial population compared to the non-compost control. After the first application, the mean bacterial count in Tricho-compost-treated soil was 56.25 ± 8.2 ×10⁶/g soil, which is 24.9% higher than the control (42.25 ± 4.2

×10⁶/g soil). Although this increase suggests a positive effect, the t-test value (0.0536) indicates that the difference is marginally non-significant. Following the second application, a more pronounced effect was observed, with the bacterial population rising to 195 ± 22.6 ×10⁶/g soil in Tricho-compost-treated soil compared to 123.25 ± 12.4 ×10⁶/g soil in the control, representing a 41.5% increase. The corresponding t-test value (0.0378) demonstrates that this difference is statistically significant. Overall, the findings suggest that repeated application of Tricho-compost significantly enhances soil bacterial populations, thereby potentially improving soil microbial activity and fertility.

Table 5. Fungal and bacterial populations in Tricho-compost amended and control soils at Jashore experimental field

Field type	Fungal Colonies (Mean ± SE, ×10⁵/g soil)	% Increase over Control	Bacterial Colonies (Mean ± SE, ×10⁶/g soil)	% Increase over Control
Tricho-compost soil	34.5 ± 3.7	+55.07%	149.25 ± 17.5	+39.53%
Control (without compost soil)	15.5 ± 2.6	-	90.25 ± 11.1	-
‘t´ test	0.0195		0.052	

The table presents a comparison of fungal and bacterial colony populations in Tricho-compost-treated soil and control (non-compost) soil. The results clearly show that Tricho-compost application significantly enhances microbial abundance. In the case of fungal colonies, the mean population in Tricho-compost soil was 34.5 ± 3.7 ×10⁵/g soil, which is about 55.07% higher than the control soil (15.5 ± 2.6 ×10⁵/g soil). The t-test value (0.0195) indicates that this increase is statistically significant ($p < 0.05$), confirming a strong positive effect of Tricho-compost on fungal growth (Table 5, Figure 3).

Similarly, for bacterial colonies, the Tricho-compost soil recorded a mean population of 149.25 ± 17.5 ×10⁶/g soil, representing a 39.53% increase over the control (90.25 ± 11.1 ×10⁶/g soil). (Table 5, Figure 3).

Overall, the findings demonstrate that Tricho-compost notably improves soil microbial communities, with a particularly strong and statistically significant effect on fungal populations, while also promoting bacterial growth to a considerable extent.

Microbial Diversity in Tricho-compost-Amended Soil

The genera with the greater number of species in fungi and bacteria were recorded in Tricho-compost applied soil. Fungi genera were *Aspergillus niger*, *A. flavus*, *Glomus* sp., *Penicillium* sp., *Cladosporium* sp., *Rhizopus stolonifer*, *Trichoderma* spp., *Fusarium* sp., *Mucor* sp., *Alternaria* sp., and *Humicola* sp. While bacterial genera were *Pseudomonas* sp. and *Bacillus* sp. in both soil sample fields (Table 6). Pathogenic fungi and bacterial colonies were lower in Tricho-compost applied soil compared to non-applied control

soil. A total microbial colony per gram soil was higher in Tricho-compost application field than control field (Table 6, Figure 3).

Table 6. Microbial Diversity in Tricho-compost-Amended Soil

District	Fungal Species Identified	Bacterial Species Identified
Bogura	*Aspergillus niger*, *A. flavus*, *Glomus* sp., *Penicillium* sp., *Cladosporium* sp., *Rhizopus stolonifer*, *Trichoderma* sp., *Fusarium s*p., *Colletotrichum* sp., *Muco*r sp., *Alternaria* sp., *Humicola* sp.	*Pseudomonas* sp., *Bacillus* sp., *Azotobacter* sp., *Streptomyces* sp., *Paenibacillus* sp., *Micrococcus* sp. *Ralstonia solanacearum*
Jashore	*Aspergillus niger*, *Glomus* sp., *Penicillium* sp., *Cladosporium* sp., *Rhizopus stolonifer*, *Trichoderma* sp., *Fusarium* sp., *Alternaria* sp.	*Pseudomonas* sp., *Bacillus* sp., *Azotobacter* sp., *Streptomyces* sp., *Paenibacillus* sp., *Micrococcus* sp. *Ralstonia solanacearum*

Discussion

The present field observations indicate that Tricho-compost influenced both microbial abundance and nematode trophic structure. Such responses are biologically plausible because compost amendments alter the supply of organic substrates, microbial habitats and nutrient availability, while compost-associated microorganisms may also become established or stimulate indigenous microbial populations (Pérez-Piqueres et al., 2006; Hu et al., 2011; De Corato, 2020). The magnitude and direction of these responses are known to depend on compost characteristics, soil properties and the resident microbial community (Bonanomi et al., 2010; Bonanomi et al., 2022).

The 60.46% reduction in plant-parasitic nematodes in amended soil is consistent with previous reports of nematode suppression following biological and organic management. Nahar et al. (2013) reported substantial reductions in root-knot nematode infestation following Tricho-compost and Tricho-leachate application in cabbage nurseries in Bangladesh. Trichoderma can affect plant-parasitic nematodes through several mechanisms, including direct antagonism, production of bioactive metabolites and enzymes, interference with nematode development, and induction of plant defence responses (Sharon et al., 2001; Poveda et al., 2020; Yao et al., 2023). However, the present study did not directly measure these mechanisms; therefore, the decline in plant-parasitic nematodes should be interpreted as an observed field response rather than direct evidence of nematicidal activity.

The strong increase in bacterivorous nematodes (+ 104.44%; P = 0.024) suggests a shift in the soil food web toward greater availability of bacterial prey or more favorable conditions for bacterial-feeding nematodes. Bacterivorous and fungivorous nematodes are important regulators of microbial populations and nutrient mineralization (Ferris et al., 2001; Neher, 2010). The simultaneous increase in culturable bacteria and bacterivorous nematodes in the amended soil is therefore ecologically

consistent, although the study design does not establish a causal relationship between the two variables.

Fungivorous nematodes increased by 65.37%, but the difference was not statistically significant (P = 0.072). This distinction is important because the numerical increase alone should not be interpreted as a confirmed treatment effect. Similarly, the 49.09% increase in omnivores was non-significant. Predatory nematodes remained unchanged. These results indicate that Tricho-compost did not uniformly increase all higher trophic groups and that responses may be group specific.

Repeated amendment produced a particularly large increase in culturable fungi in Bogura: 33.3% after the first application and 174.6% after the second. The second comparison was significant (P = 0.011). This pattern is compatible with the view that repeated organic inputs can increase microbial substrate availability and modify microbial community structure (Pérez-Piqueres et al., 2006; Hu et al., 2011). The presence of Trichoderma in the cultured isolates is also consistent with the biological component of Tricho-compost and with the recognized capacity of Trichoderma to interact with other microorganisms and the plant rhizosphere (Harman et al., 2004; Woo et al., 2023).

Bacterial abundance also increased following repeated application, but the first increase was marginal (P = 0.0536), whereas the second increase was significant (P = 0.0378). At Jashore, fungal abundance increased significantly, whereas bacterial abundance did not reach the conventional 5% threshold (P = 0.052). The difference between fungal and bacterial responses emphasizes that amendment effects can be taxon specific and site dependent, a pattern widely recognized in studies of organic amendments and soil microbial communities (Bonanomi et al., 2010; Zhang et al., 2022).

The culture based microbial profiles included *Trichoderma*, *Pseudomonas* and *Bacillus*, taxa frequently associated with plant growth promotion, antagonism and rhizosphere competence (Glick, 2012; Harman et al., 2004; Woo et al., 2023). Nevertheless, the present methods measured culturable organisms only and did not use culture independent sequencing. Therefore, the reported list of taxa should not be interpreted as a complete representation of soil microbial diversity. In addition, the detection of *Ralstonia solanacearum* should not by itself be interpreted as evidence of active disease or pathogenicity because disease incidence, virulence and molecular confirmation were not assessed.

The biological mechanisms underlying pathogen suppression by compost are complex and may involve competition for resources, antagonistic microorganisms, antimicrobial compounds, changes in nutrient availability and plant-mediated defence responses (Mehta et al., 2014; De Corato, 2020; Woo et al., 2023). Recent reviews further emphasize that compost-mediated disease suppression is influenced by physical, chemical and biological properties of the amendment and soil environment (De Corato, 2020; Bonanomi et al., 2022). Accordingly, the present findings support Tricho-compost as a promising soil biological amendment, but they do not establish disease suppression directly because pathogen inoculum, disease incidence and crop yield were not quantified.

Overall, the results are consistent with the ecological concept that organic amendments can reshape soil biological communities and potentially improve soil functioning. The strongest evidence in this study is the significant reduction in plant-parasitic nematodes, the significant increase in bacterivorous nematodes, and the increases in culturable fungal and bacterial abundance following repeated amendment. Further studies using replicated multi-season field trials, soil physicochemical measurements, quantitative pathogen assays and culture-independent microbial profiling would be valuable for determining the durability and mechanisms of these effects.

Conclusion

Tricho-compost amendment altered several biological indicators of soil health in the studied vegetable fields of Bangladesh. In Bogura, plant-parasitic nematodes decreased significantly by 60.46%, while bacterivorous nematodes increased significantly by 104.44%. Culturable fungal abundance increased significantly after the second compost application, and bacterial abundance also increased significantly after the second application. At Jashore, fungal abundance increased significantly, whereas the bacterial increase was not significant at $P < 0.05$. These findings indicate that repeated Tricho-compost application can modify soil microbial abundance and nematode trophic structure. The amendment therefore has potential as a component of sustainable soil management; however, claims of biofertilizer or biocontrol efficacy should be validated with crop-growth, yield, pathogen-disease and longer-term soil-health measurements.

Declarations

Author contributions Seema Datta led the study under the supervision of Najmun Naher and Mossammat Shamsunnahar. Seema Datta, Najmun Naher, and Mossammat Shamsunnahar collected the data, isolation the soil microbes and nematodes from soil and identification. Mritunjoy Mojumder created the location map instructed the data and statistical analyses; Seema Datta and Mafruha Afroz wrote the manuscript with help from all authors. All authors have read and approved the final manuscript.

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Data availability Data will be made available on request.

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Ethics, Consent to Participate, and Consent to Publish declarations: Not applicable

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Figures

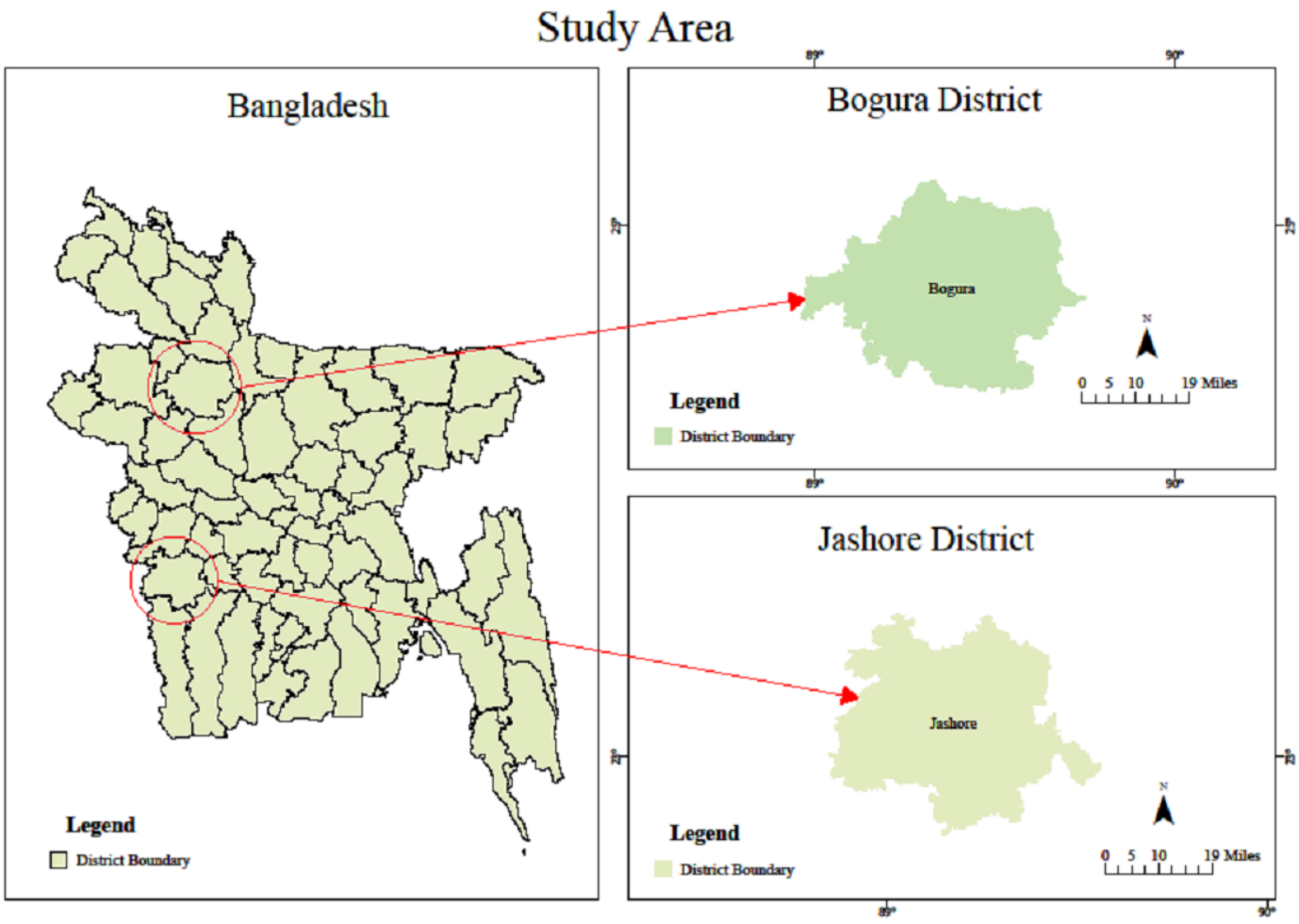


Figure 1

Study areas of experimental sites on map

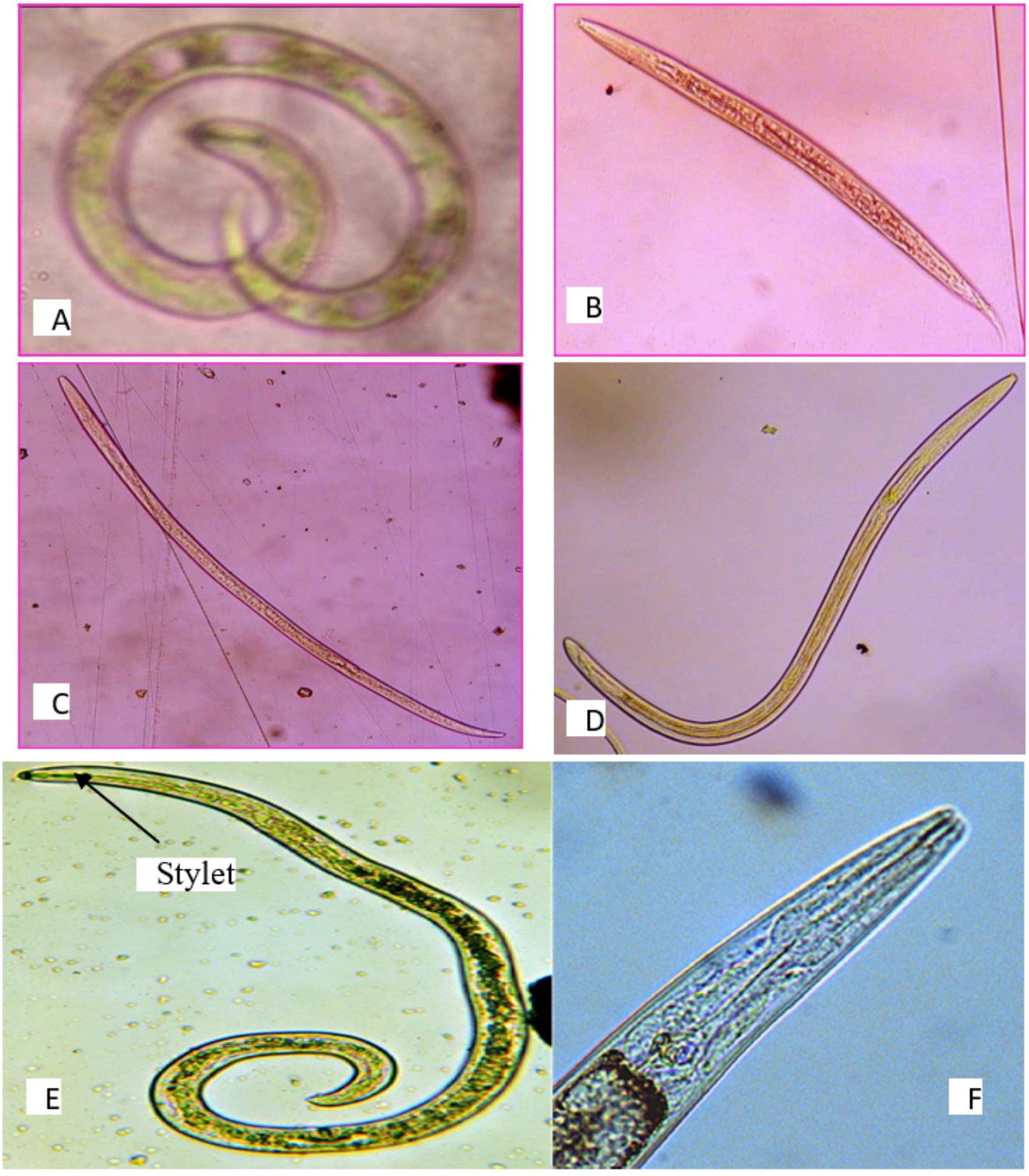


Figure 2

Photograph showing different type of nematode isolated from Tricho-compost soil under compound microscope at 40X; A. Plant parasitic, B. Bacterial feeder, C. Fungal feeder, D. Omnivore, E. Herbivore (with stylet) mouthpart, F. Bacterivore (without stylet) mouthpart.

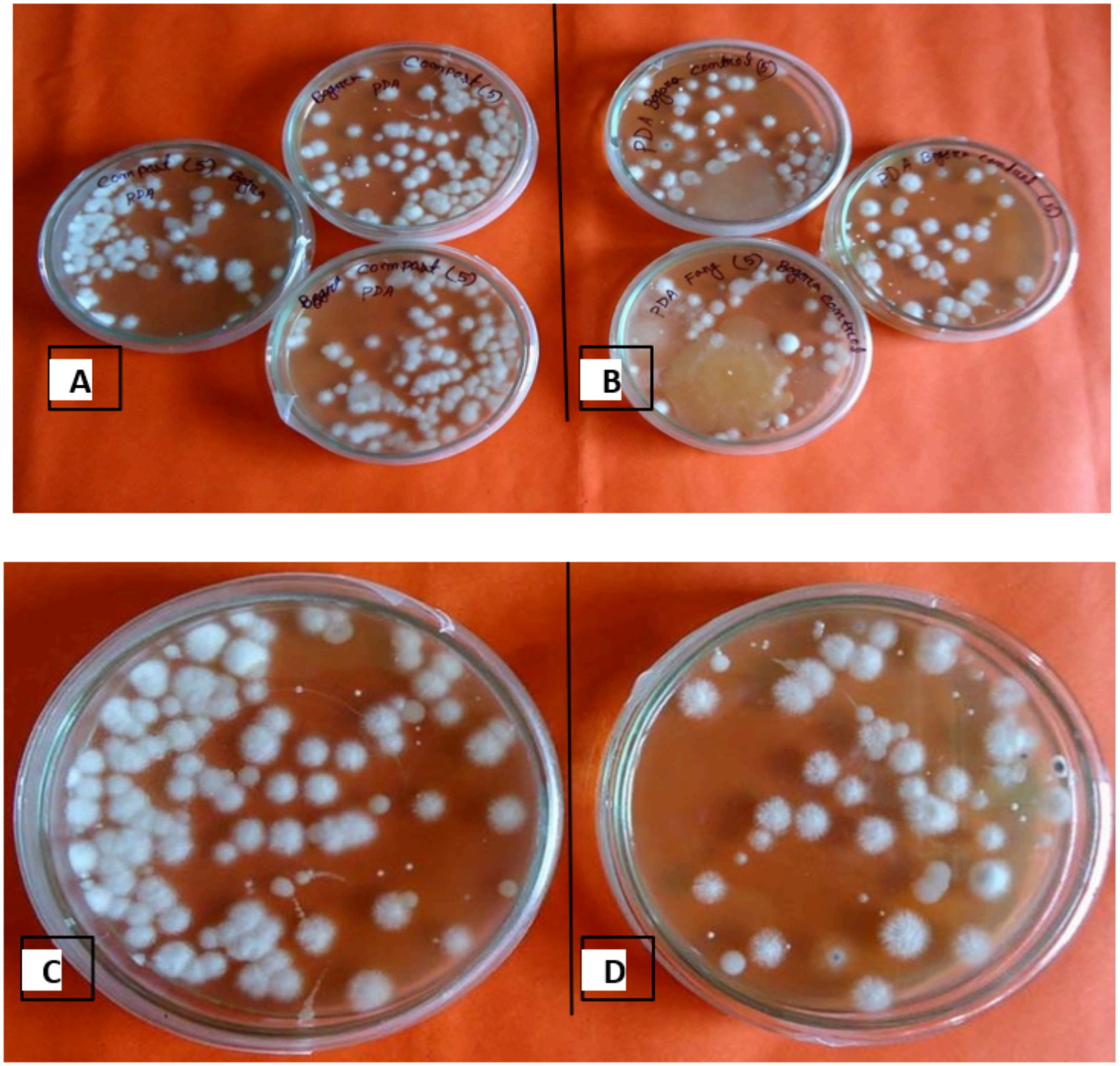


Figure 3

Fungal colony on PDA medium; A and C. Tricho-compost treatment soil, B and D. Control plot (without Tricho- compost).