



RESEARCH ARTICLE

Dynamics of soil mycoflora in different cropping patterns under conservation agriculture system

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Abstract

Cropping systems used in agriculture impact soil health and quality and were initially designed to maximise yield from agricultural systems. However, modern agriculture has become increasingly concerned about the environmental sustainability of these systems. Soil samples were collected from different crop fields under conservation agriculture ecology at Bihar Agricultural University, Sabour, Bhagalpur. The soil samples were collected to a depth of 15 cm and then stored in small, sterile polythene bags for further laboratory studies. During the investigation period, 168 fungal colonies out of 13 fungal species and 6 genera of fungi were recorded. The highest number of fungal species recorded belongs to the phylum Deuteromycotina (159 colonies) and Zygomycotina (7 colonies). The isolation of soil mycoflora was carried out by using methodology, viz., the soil dilution technique and the soil plate technique on Potato dextrose agar (PDA) media and Czapeks' Dox agar (CZA) media supplemented with suitable antibiotics. Identification and characterisation of the mycoflora were made by microscopic morphological characters with the help of a microscope. The fungi identified, isolated and characterised were *Aspergillus niger*, *Aspergillus flavus*, *Aspergillus fumigatus*, *Curvularia clavata*, *Curvularia lunata*, *Fusarium oxysporum*, *Fusarium solani*, *Penicillium chrysogenum*, *Penicillium frequentans*, *Penicillium funiculosum*, *Trichoderma harzianum*, *Trichoderma viride* and *Rhizopus stolonifer*. The variations in soil mycoflora and percentage frequency were recorded.

Keywords: agar media; diversity; mycoflora; pathogen; saprophytes

Introduction

Crop rotation, a type of cropping system, is considered a traditional and practical method for managing agroecosystem biodiversity through the enhancement of soil health, the suppression of pests and disease outbreaks and consequently, the increase in yields (1). The value and efficiency of a crop rotation are determined by several factors, including the crop types used in rotation and the characteristics of the soil (2, 3). Opportunities for the growth of certain soil functional microorganisms can be provided through crop rotations, while disease pressure can be limited by the disruption of the life cycle of soil-borne pathogens associated with specific crops or crop genotypes. Certain crops are regarded as more beneficial in rotations than others, which determines the most effective rotation sequence for maximising soil benefits. More specifically, various residues and root exudates can be produced by different crops, through which soil microbial diversity and activity can be enhanced, along with increases in soil microbial mass and the cycling of carbon and nitrogen (3).

Another important factor to be considered in crop rotation design is whether alternative crops can be utilised by soil-borne

pathogens as hosts or whether the pathogens can remain dormant in the soil over the long term and how such crops respond to disease (4). The application of non-host plants in rotations for the control of soil-borne diseases is viewed as critical for minimising yield losses due to diseases, particularly given that some pathogens can persist in the soil for extended periods as spores or other dormant structures in the absence of their preferred host plant (5). For example, severe *Fusarium* root rot injury observed in pea crops grown in rotation in the Canadian prairie was attributed to a limited soil microbial community and a lower abundance of beneficial bacteria and arbuscular mycorrhizal fungi (6).

Soil microorganisms are found in large numbers in soil. Usually, 1–10 million microorganisms are present per gram of soil, with a dominant number of bacteria and fungi. Soil mycoflora plays a pivotal role in the evaluation of soil conditions and in stimulating plant growth. Soil mycoflora has been beneficial for increasing soil fertility and plant growth as they are involved in several biochemical transformations and mineralisation activities in soils (7). Types of cultivation and crop management practices are found to have a greater influence on the activity of soil mycoflora. Continuous use of chemical fertilisers over a long period may cause an imbalance in soil

mycoflora and thereby indirectly affect the biological properties of soil, leading to soil degradation (8).

Soil bacteria and fungi play pivotal roles in various biochemical cycles (BGC) and are responsible for the cycling of organic compounds (7). Fungi are fundamental to soil ecosystem functioning and contribute more significantly to soil biomass than bacteria, depending upon soil depth and nutrient status. Especially in forest and agricultural soils, fungi play a key role in many essential processes such as organic matter decomposition and elemental release by mineralisation. Fungi are an important component of the soil fungal flora (8). Mycoflora play a focal role in nutrient cycling by regulating soil biological activity. The quantity of organic and inorganic materials in soil directly influences the fungal population. Their distribution is affected by the nature and abundance of organic matter, as well as soil and climatic conditions, surface vegetation and soil texture (9). However, the application of chemical fertilisers and pesticides adversely impacts soil mycoflora, which is vital for maintaining soil fertility and ecological balance (10). The composition and diversity of microorganisms in soil depend on numerous environmental factors, including nutrient availability, moisture, aeration, pH and temperature. The present investigation aims to isolate fungal flora from different crop fields and to observe the percentage contribution of different fungal species (11). Understanding of soil mycoflora is beneficial for farmers, agronomists, researchers and microbiologists, aiding in soil ecosystem conservation, microbial diversity preservation and promoting sustainable agricultural practices.

Therefore, understanding the diversity and dynamics of soil fungal communities under different cropping systems is essential for improving soil health and ensuring sustainable agricultural productivity. Although several studies have highlighted the importance of crop rotation and diversification in shaping soil microbial communities, information on the distribution of soil fungal flora under conservation agriculture systems in eastern Indo-Gangetic plains remains limited. In this context, the present study was undertaken to investigate the diversity and dynamics of soil fungal mycoflora under different cropping patterns practiced in experimental crop fields with different cropping patterns at the Bihar Agricultural College (BAC) farm at Bihar Agricultural University, Sabour. Specifically, the

objectives of the study were to isolate and identify soil fungi from different crop fields and to assess the relative occurrence and percentage contribution of different fungal species associated with various cropping sequences. The findings of this study will help improve the understanding of how cropping patterns influence soil fungal communities and contribute to sustainable soil management practices.

Material and Methods

Collection of soil samples

Soil samples were collected from experimental crop fields with different cropping patterns at the BAC farm of Bihar Agricultural University, Bhagalpur. Using core samplers, the samples were collected from a depth of up to 15 cm, placed in sterile bags and transported to the laboratory for further studies. They were stored at 4 °C in the laboratory until examination. This was practiced during January to November (for 3 years), focusing on various crop fields within the conservation agriculture ecosystem. The samples were taken from four symmetrically located points at the corners of a designated square, as well as from the center of the square. Initial collections were performed to standardise the methodology and were not subjected to detailed analysis. The observed microflora from the collected soil samples from different cropping patterns are listed in Table 1.

Isolation of soil mycoflora

The soil mycoflora were isolated using two methodologies : the soil dilution plate method and the soil plate method (7, 12). Fungal isolation was conducted on various culture media, including potato dextrose agar (PDA) and Czapeks' Dox agar (CZA).

Soil dilution plate method

The soil dilution plate technique was employed for isolating fungi from the soil samples (12). Specifically, 1 g of soil was suspended in 9 mL of distilled water within an Erlenmeyer flask. The suspension was mixed using a wrist-action shaker at 120 rpm for 1 hr to ensure a uniform distribution of soil particles (Fig. 1).

Subsequently, the soil suspension was diluted in tenfold increments, from 10^{-3} to 10^{-5} . A volume of 1 mL from each dilution was pipetted onto different melted and cooled culture media: PDA and CZA, both supplemented with 1 % Streptomycin to inhibit

Table 1. List of mycoflora from soil samples at different stages of cropping pattern

Code	Cropping pattern	Soil sample collection		
		Before	During	After
A	1 st Crop (Maize)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Pf, Pfu, Th, Tv	Ccl, Clu, Pf, Pfu, Rs, Tv
	2 nd Crop (Wheat)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Ccl, Clu, Pf, Pfu, Th, Tv	Ccl, Clu, Pf, Pfu, Rs, Tv
B	1 st Crop (Soybean)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Pf, Pfu, Th, Tv	An, Afl, Pf, Pfu, Rs, Tv
	2 nd Crop (Maize)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Pf, Pfu, Th, Tv	Ccl, Clu, Pf, Pfu, Rs, Tv
C	1 st Crop (Maize)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Pf, Pfu, Th, Tv	Ccl, Pch, Pfu, Tv
	2 nd Crop (Mustard)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Pf, Pfu, Th, Tv	Afl, Rs, Tv
D	1 st Crop (Maize)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Pf, Pfu, Th, Tv	Ccl, Pch, Pfu, Tv
	2 nd Crop (Chickpea)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Fo, Pf, Pfu, Th, Tv	An, Afl, Afu, Fo, Pf, Pfu, Tv
E	1 st Crop (Soybean)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Fs, Th, Tv	Ccl, Clu, Pf, Pfu, Tv
	2 nd Crop (Maize)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Pf, Pfu, Th, Tv	Ccl, Clu, Pf, Pfu, Rs, Tv
F	3 rd Crop (Wheat)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Ccl, Clu, Pf, Pfu, Th, Tv	Ccl, Clu, Pf, Pfu, Rs, Tv
	1 st Crop (Maize)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Fs, Th, Tv	Ccl, Pch, Pfu, Tv
G	2 nd Crop (Maize)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Pf, Pfu, Th, Tv	Ccl, Clu, Pf, Pfu, Tv
	1 st Crop (Cowpea)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Fo, Pf, Pfu, Th, Tv	An, Afl, Afu, Fo, Pf, Pfu, Tv
G	2 nd Crop (Radish)	An, Afl, Afu, Fs, Pf, Pfu, Rs	Fs, Pf, Pfu, Th, Tv	An, Afl, Pf, Pfu, Rs, Tv
	3 rd Crop (Field pea)	An, Afl, Afu, Ccl, Fs, Pf, Pfu, Rs	Fo, Fs, Pf, Pfu, Th, Tv	An, Afl, Afu, Fo, Fs, Pf, Pfu, Tv

An: *Aspergillus niger*; Afl: *Aspergillus flavus*; Afu: *Aspergillus fumigatus*; Ccl: *Curvularia clavata*; Clu: *Curvularia lunata*; Fo: *Fusarium oxysporum*; Fs: *Fusarium solani*; Pch: *Penicillium chrysogenum*; Pfu: *Penicillium funiculosum*; Pf: *Penicillium frequentans*; Rs: *Rhizopus stolonifera*; Th: *Trichoderma harzianum*; Tv: *Trichoderma viride*.

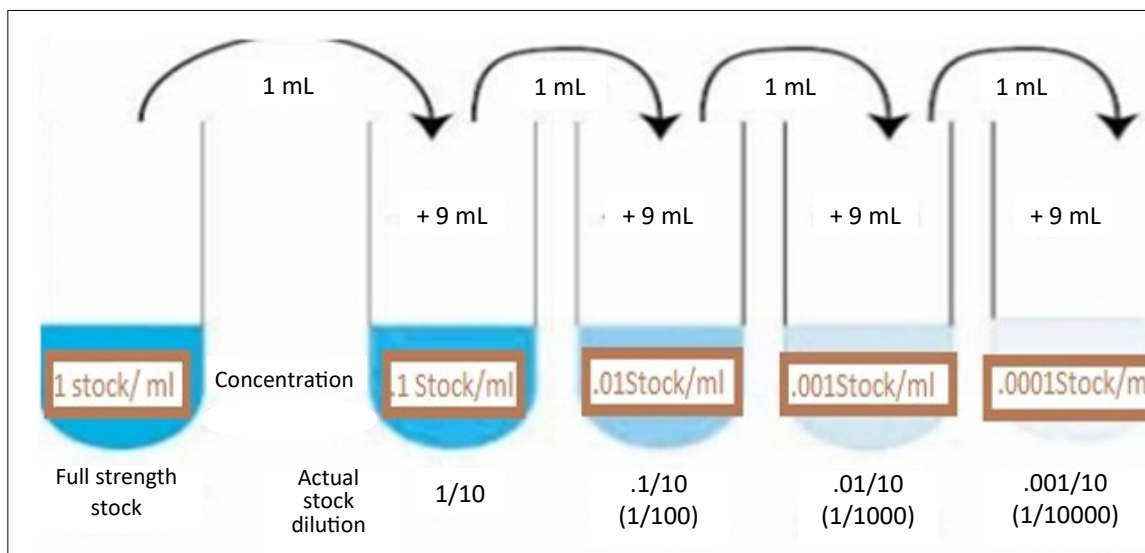


Fig. 1. Preparation of dilution series (soil dilution) for isolation of soil mycoflora through dilution plates technique.

bacterial growth. The pH of the culture media was maintained at 5.5, which is optimal for the growth and sporulation of most fungi. Each medium was prepared in 1 L of distilled water and autoclaved at 120 °C and 15 psi for 20 min. Following incubation, each fungal colony was sub-cultured and preserved on PDA slants for further studies (13).

Soil plate method

Initially, approximately 0.005 g of collected soil is transferred into a sterilised Petri dish. Subsequently, 8–10 mL of cooled medium is added to the dish to facilitate the dispersion of soil particles throughout the agar. For moist soil samples, adequate dispersion is achieved by shaking and rotating the plate prior to the solidification of the agar. In contrast, for very dry soil samples, a drop of sterile water is mixed with the soil in the plate before the addition of the medium. The PDA and CZA, each supplemented with 1 % streptomycin, serve as the isolation media. The inoculated plates are incubated at room temperature (28 ± 2 °C) in an inverted position for a duration of 5–7 days. Three replicates are maintained for each soil sample to ensure reproducibility of results.

Sample collection and sample size

Soil samples were collected from experimental crop fields with different cropping patterns at the BAC farm over a period of 3 years. Samples were collected from 7 different cropping patterns and for each site, 5 subsamples (4 corners and 1 center of a designated square) were taken using a core sampler from a depth of 0–15 cm and combined to form a representative composite sample. The soil samples were transported to the laboratory in sterile bags and stored at 4 °C until analysis. Initial collections were conducted only to standardise the methodology and were not included in the final analysis. Each composite sample was processed in triplicate for fungal isolation using both soil dilution plate and soil plate methods to ensure reproducibility.

Identification of the soil fungi

Fungal morphology was examined using a compound microscope, focusing on the colony characteristics of soil microflora, including color and texture. The structures of conidia, conidiophores and the arrangement of spores were observed microscopically after staining with lactophenol cotton blue (14). Fungal identification was conducted using literature and authentic

manuals (15–17).

Data analysis

The number of micro-flora species was referred to as species diversity. The population density of the micro-flora was expressed as colony forming units (CFU) per gram of soil, adjusted for dilution factors. The percentage contribution of each isolate in the soil was calculated using the following formula:

$$\text{Percentage contribution} = \frac{\text{Total No. of CFU of an individual Species}}{\text{Total No. of CFU of all Species}} \times 100 \quad (\text{Eq.1})$$

Where: CFU = Colony-forming unit.

Results and Discussion

This study investigated the dynamics of soil microflora across 7 distinct crop fields with varying cropping patterns : maize + wheat, soybean + maize, maize + mustard, maize + chickpea, soybean + maize + wheat, maize + maize and vegetable cultivation under conservation agriculture at the BAC farm of Bihar Agricultural University, Bhagalpur.

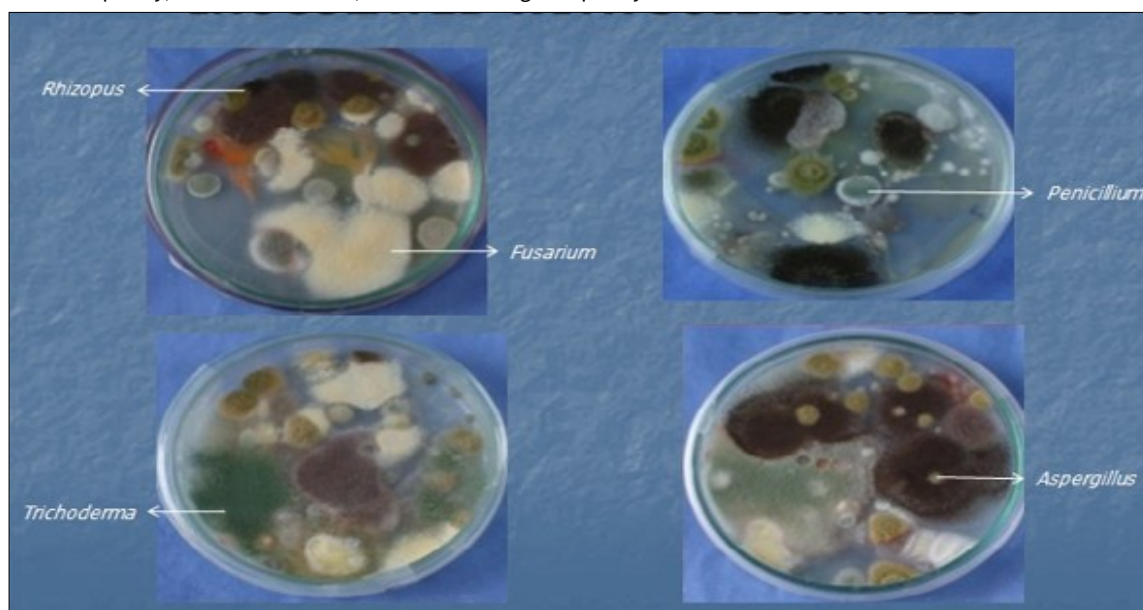
In order to isolate fungal colonies, soil samples were gathered from the corresponding fields using the soil plate and soil dilution plate techniques. For identification purposes, 168 distinct fungal colonies were observed and taxonomically described during the course of the study. According to the findings, the phylum Deuteromycotina accounted for the majority of the fungal species (159 colonies), while the phylum Zygomycotina had a smaller representation (7 colonies). Fourteen fungal colonies were also still unidentified. *Fusarium oxysporum*, *Fusarium solani*, *Aspergillus niger*, *Aspergillus flavus*, *Aspergillus fumigatus*, *Curvularia clavata*, *Curvularia lunata*, *Penicillium chrysogenum*, *Penicillium frequentans*, *Penicillium funiculosum*, *Trichoderma harzianum*, *Trichoderma viride* and *Rhizopus stolonifer* were among the fungal species that were identified (Fig. 2, Table 2).

Soil samples were collected from the respective crop fields and processed for fungal isolation using the soil plate and soil dilution plate techniques (Fig. 2). The cultured samples produced a wide range of fungal colonies on the growth media, indicating the presence of diverse soil fungal flora. During the course of the

Table 2. Microbial dynamics of different cropping patterns

Soil microflora	Maize + wheat	Soybean + maize	Maize + mustard	Maize + chickpea	Soybean + maize + wheat	Maize + maize	Cowpea + radish + field pea
<i>Aspergillus niger</i>	+++	++++	+++	++	++++	++	++
<i>Aspergillus flavus</i>	++++	+++	++	++++	++++	+	++
<i>Aspergillus fumigatus</i>	++++	++++	-	+++	+++	-	++
<i>Curvularia clavata</i>	++	+	+	++	+	++	+
<i>Curvularia lunata</i>	+++	++	+	+++	+	+	++
<i>Fusarium oxysporum</i>	++	+	+	+	++	+	+
<i>Fusarium solani</i>	+	+	+++	-	++	++	+
<i>Penicillium chrysogenum</i>	+++	++	++	+++	-	++	++
<i>Penicillium frequentans</i>	++	+++	++	++	++	++	++
<i>Penicillium funiculosum</i>	++	++	++	-	-	+	-
<i>Rhizopus stolonifer</i>	+	-	++	-	+	+++	-
<i>Trichoderma harzianum</i>	+++	+++	+	++	++	+	+
<i>Trichoderma viride</i>	++	++	++	+	++	++	++

-: Absent, +: Low frequency, ++ & +++: Moderate, ++++ & +++++: High frequency.

**Fig. 2.** Fungal colonies growing on media inoculated with different soil samples.

investigation, a total of 168 fungal colonies were observed and subjected to taxonomic identification based on their morphological characteristics. The results revealed that the majority of the isolates belonged to the phylum Deuteromycotina, comprising 159 colonies, while only 7 colonies were grouped under the phylum Zygomycotina. In addition, 14 colonies remained unidentified due to indistinct morphological features. The identified fungal species included *F. oxysporum*, *F. solani*, *A. niger*, *A. flavus*, *A. fumigatus*, *C. clavata*, *C. lunata*, *P. chrysogenum*, *P. frequentans*, *P. funiculosum*, *T. harzianum*, *T. viride* and *R. stolonifer*. The colonies exhibited varied morphological characteristics such as differences in colour, texture and growth pattern on the culture media. These variations facilitated the preliminary identification of fungal genera present in the soil samples. The predominance of *Aspergillus*, *Penicillium* and *Trichoderma* species indicates active microbial processes in the soil environment. Such beneficial fungal communities play an important role in organic matter decomposition, nutrient cycling and suppression of soil-borne pathogens. Therefore, the presence of diverse soil fungi highlights the importance of suitable cropping systems in maintaining soil biological health and supporting sustainable and conservation-oriented agricultural practices.

Such beneficial fungal communities play an important role in organic matter decomposition, nutrient cycling and suppression of soil-borne pathogens. Similar dominance of *Aspergillus*, *Penicillium* and *Trichoderma* species in agricultural soils has also been reported by recent studies, which highlighted their role in

improving soil biological activity and crop productivity (18, 19). Diversified cropping systems are known to enhance soil microbial diversity and stability, thereby contributing to sustainable agricultural production (20). Comparable observations regarding the importance of soil fungal diversity for maintaining soil health and crop resilience have also been documented in recent agricultural microbiology studies (21).

The results presented in Table 2 reveal considerable variation in soil microbial population under different cropping patterns. The abundance of soil mycoflora was indicated by the presence of symbols (+ to ++++). Among the fungi, *Aspergillus* species were found to be dominant in most of the cropping systems. *Aspergillus fumigatus* showed the highest occurrence in the soybean + maize system, whereas *A. flavus* was more prominent in maize + wheat and maize + chickpea systems. Beneficial fungi such as *T. harzianum* and *T. viride* were also observed across almost all cropping patterns, indicating favourable soil biological activity. *Fusarium* species showed comparatively lower frequency. The results suggest that diversified cropping systems like soybean + maize + wheat support higher microbial diversity compared to continuous maize cultivation, thereby contributing to improved soil health and sustainability. These findings indicate that diversified and legume-based cropping systems promote a richer and more balanced soil microbial community. Such enhanced microbial activity may improve nutrient cycling, organic matter decomposition and overall soil fertility, thereby supporting

sustainable crop production (22, 23). The five fungal species' microscopic views are further identified and depicted in Fig. 3.

The data presented in Table 3 illustrate the abundance of fungal colonies across various cropping patterns. The highest abundance of fungal colonies was recorded in the maize + wheat cropping pattern, which exhibited a total of 32 colonies. This was followed by the soybean + maize combination with 29 colonies and the soybean + maize + wheat pattern, which had 24 colonies. In contrast, the vegetable fields showed the lowest fungal colony count, totalling only 18.

Additionally, the data also displayed the percentage contributions of different fungal species across all cropping patterns. *Aspergillus niger* and *A. flavus* each accounted for 11.9 %, while *A. fumigatus* contributed 10.1 %. Other significant species included *C. lunata* at 7.7 % and *C. clavata* at 5.9 %. Among the *Fusarium* species, *F. solani* contributed 5.9 % and *F. oxysporum*

accounted for 5.3 %. Furthermore, *P. frequentans* represented 9.5 % and *P. chrysogenum* accounted for 8.3 %. Both *T. viride* and *T. harzianum* contributed 7.7 %, while *P. funiculosum* made up 4.1 %. Lastly, *R. stolonifer* exhibited the lowest contribution at 3.5 %.

Further, Table 3 indicates the occurrence and distribution of soil mycoflora under different cropping patterns. A total of 168 fungal colonies were recorded from all cropping systems. Among the cropping patterns, maize + wheat showed the highest number of colonies, followed by soybean + maize, while the vegetable field recorded the lowest population (18). Among the fungal groups, *Aspergillus* species were dominant with the highest percentage contribution (11.9 % each for *A. niger* and *A. flavus*), followed by *P. frequentans* (9.5 %) and *P. chrysogenum* (8.3 %). *Trichoderma* species were also fairly represented in most cropping systems. In contrast, *R. stolonifer* showed the least contribution (3.5 %).

Table 3. Occurrence of soil mycoflora in different cropping patterns

Code	Crop Field	Total No. of colonies	<i>Aspergillus</i>			<i>Curvularia</i>		<i>Fusarium</i>		<i>Penicillium</i>			<i>Trichoderma</i>		<i>Rhizopus</i>
			An	Afl	Afu	Ccl	Clu	Fo	Fs	Pch	Pf	Pfu	Th	Tv	Rs
A	Maize + Wheat	32	3	4	4	2	3	2	1	3	2	2	3	2	1
B	Soybean + Maize	29	4	3	5	1	2	1	1	2	3	2	3	2	-
C	Maize + Mustard	22	3	2	-	1	1	1	3	2	2	2	1	2	2
D	Maize + Chickpea	23	2	4	3	2	3	1	-	3	2	-	2	1	-
E	Soybean + Maize + Wheat	24	4	4	3	1	1	2	2	-	2	-	2	2	1
F	Maize + Maize Cowpea + Radish + Field pea	20	2	1	-	2	1	1	2	2	3	1	1	2	2
G		18	2	2	2	1	2	1	1	2	2	-	1	2	-
Total		168	20	20	17	10	13	9	10	14	16	7	13	13	6
% Contribution			11.9	11.9	10.1	5.9	7.7	5.3	5.9	8.3	9.5	4.1	7.7	7.8	3.5

An: *Aspergillus niger*; Afl: *Aspergillus flavus*; Afu: *Aspergillus fumigatus*; Ccl: *Curvularia clavata*; Clu: *Curvularia lunata*; Fo: *Fusarium oxysporum*; Fs: *Fusarium solani*; Pch: *Penicillium chrysogenum*; Pf: *Penicillium frequentans*; Pfu: *Penicillium funiculosum*; Th: *Trichoderma harzianum*; Tv: *Trichoderma viride*; Rs: *Rhizopus stolonifera*.

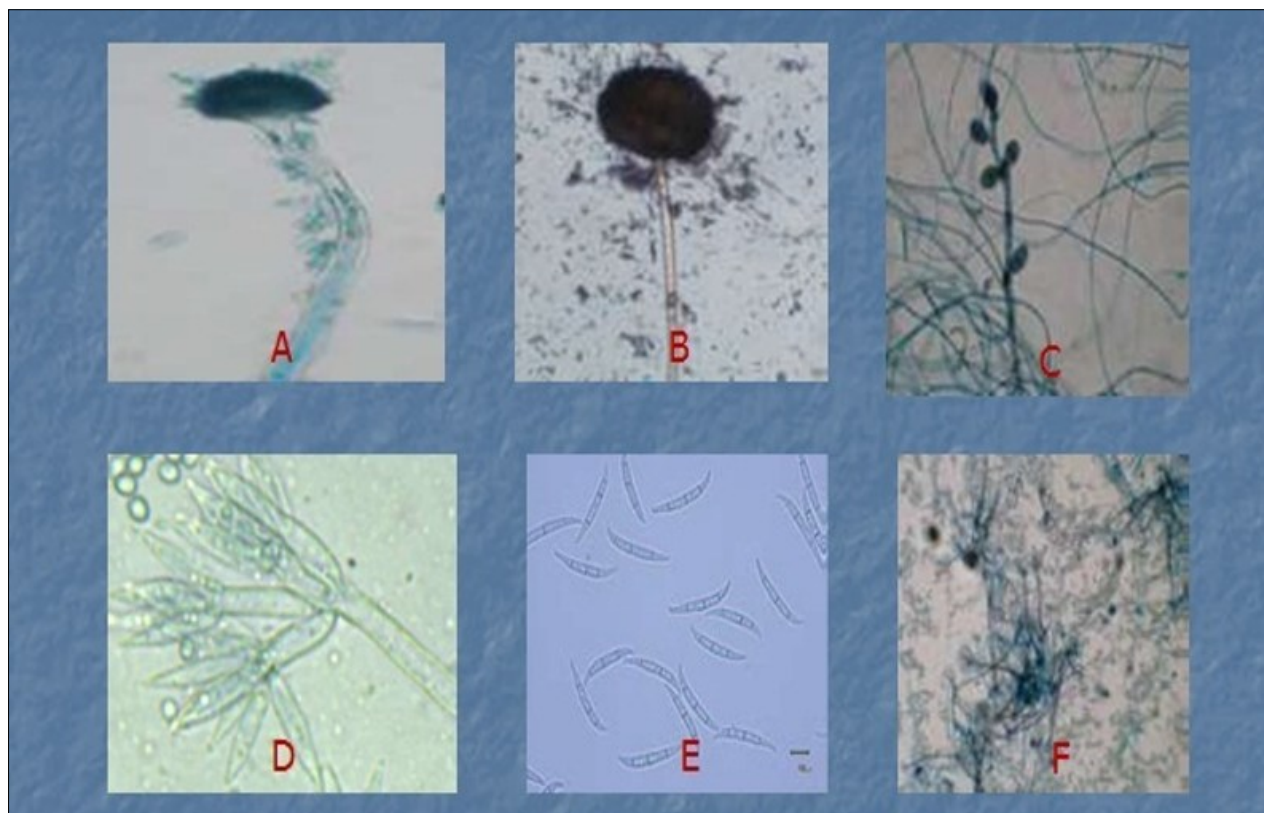


Fig. 3. Microscopic view of fungal isolates. A: *Aspergillus flavus*; B: *Aspergillus niger*; C: *Curvularia clavata*; D: *Penicillium chrysogenum*; E: *Fusarium oxysporum*; F: *Rhizopus stolonifera*.

The results suggest that diversified cropping patterns favour greater fungal diversity and abundance in soil. These findings indicate that mixed and legume-based cropping systems help maintain a balanced soil microbial community and may contribute to improved soil fertility and sustainable crop production. The higher occurrence of beneficial fungi such as *Trichoderma* and *Penicillium* in diversified cropping systems indicates better soil biological activity. Therefore, adoption of suitable crop rotations and mixed cropping practices may enhance microbial diversity and improve soil health in agricultural ecosystems. Similar observations regarding the influence of cropping systems on soil fungal diversity and ecosystem functioning have been reported in recent studies (24, 25).

The findings of this study highlight that diversified cropping patterns enhance the abundance and diversity of beneficial soil fungal flora. Such microorganisms play an important role in nutrient cycling, organic matter decomposition and suppression of soil-borne pathogens. This supports the principles of conservation agriculture, where crop diversification and reduced soil disturbance help maintain soil biological health. Improved microbial activity contributes to better soil fertility, structure and long-term productivity. Therefore, adopting diversified and sustainable cropping systems can strengthen conservation agriculture practices and promote resilient agricultural production.

The results further indicated specific fungal distribution patterns within the cropping systems (Table 3). In the maize + wheat pattern, *Rhizopus* showed the least abundance, with the lowest number of colonies, while *Aspergillus* showed the highest abundance, with other fungi present in moderate quantities. In the soybean + maize pattern, the least abundant species was *Fusarium*, with *Aspergillus* again demonstrating the highest prevalence and other fungi present in moderate amounts. In the maize + mustard cropping pattern, the least abundant fungi were *Curvularia* and *Trichoderma*, while *Aspergillus* exhibited the greatest abundance, with other species moderately represented. Similarly, in the maize + chickpea pattern, the minimum colonies were observed for *Fusarium* and *Trichoderma*, while *Aspergillus* was the most abundant, with other fungi at moderate levels. In the soybean + maize + wheat combination, *Rhizopus* had the fewest colonies, whereas *Aspergillus* showed the highest counts, with other fungi present in moderate numbers. The maize + maize cropping pattern also revealed that *Rhizopus* had the lowest colony count, while *Aspergillus* was the most prevalent, with other fungal species in moderate quantities. Lastly, in the vegetable fields, the least abundant fungi were *Curvularia* and *Trichoderma*, with *Rhizopus* being the most prevalent, alongside other species present in moderate numbers.

The data presented in Table 3 revealed clear variations in the occurrence and distribution of soil fungal mycoflora under different cropping patterns. A total of 168 fungal colonies were recorded across all cropping systems, indicating a diverse fungal community associated with the agricultural soils. Among the cropping patterns, maize + wheat recorded the highest number of colonies, followed by soybean + maize, while the vegetable field showed the lowest population (18). Among the fungal groups, *Aspergillus* species (*A. niger*, *A. flavus* and *A. fumigatus*) were dominant in most cropping systems, contributing the highest percentage of total colonies. Moderate occurrence of *Penicillium*, *Curvularia* and *Trichoderma* species was also observed, while *R. stolonifer* exhibited the least contribution overall. The predominance of *Aspergillus* species may

be attributed to their adaptability to different soil environments and their ability to colonise agricultural soils effectively. Similar dominance of *Aspergillus* and *Penicillium* species in cultivated soils has been reported in recent studies, highlighting their role in organic matter decomposition and nutrient cycling (26).

Further analysis of the cropping systems indicated distinct distribution patterns of fungal species. In maize + wheat, soybean + maize, maize + mustard, maize + chickpea and soybean + maize + wheat systems, *Aspergillus* species showed the highest abundance, while fungi such as *Rhizopus*, *Fusarium*, or *Curvularia* were comparatively less represented. Interestingly, in the vegetable field, *Rhizopus* was comparatively more abundant, whereas *Curvularia* and *Trichoderma* showed lower occurrence. The moderate presence of beneficial fungi such as *T. harzianum* and *T. viride* across several cropping systems indicates favourable soil biological activity and potential suppression of soil-borne pathogens (27). Diversified cropping systems, particularly those involving legumes such as soybean and chickpea, are known to support greater microbial diversity due to improved soil organic matter and root exudates (23, 28). These findings support the concept that crop diversification enhances soil microbial diversity and soil health, thereby promoting sustainable agricultural productivity.

The silent findings of the experiment are in maize + wheat cropping pattern found minimum colonies of *Rhizopus* and maximum colonies of *Aspergillus* and others were moderate in number. In soybean + maize cropping pattern, minimum colonies of *Fusarium* and maximum colonies of *Aspergillus* and others were moderate in number. In maize + mustard cropping pattern, minimum colonies of *Curvularia* and *Trichoderma* and maximum colonies of *Aspergillus* and others were moderate in number. In maize + chickpea cropping pattern, minimum colonies of *Fusarium* and *Trichoderma* and maximum colonies of *Aspergillus* and others were moderate in number. In soybean + maize + wheat cropping pattern, minimum colonies of *Rhizopus* and maximum colonies of *Aspergillus* and others were moderate in number. In maize + maize cropping pattern, minimum colonies of *Rhizopus* and maximum colonies of *Aspergillus* and others were moderate in number. In the vegetable field, minimum colonies of *Curvularia* and *Trichoderma* and maximum colonies of *Rhizopus* and others were moderate in number.

Soil fungal flora are essential components of biodiversity, playing a crucial role in maintaining ecosystem health and functionality. Fungi and bacteria are particularly significant as they actively contribute to nutrient cycling by breaking down organic matter and releasing vital nutrients for plant growth (18). The efficiency of fungi in decomposition processes is influenced by their abundance, diversity and species composition within the soil ecosystem. Every year, large quantities of readily decomposable organic matter, such as crop residues and animal manure, are added to agricultural soils. This influx significantly impacts soil microbial activity and community dynamics (19). Moreover, the specific plant species growing in the soil can modulate the populations and diversity of soil fungi, as different plants provide varying types of organic matter and root exudates that support distinct fungal communities (8).

The studies on diverse crop rotation systems, particularly soybean-maize-maize and maize-soybean-soybean, enhance soil organic carbon, nutrient levels and crop yields compared to monocultures. The rotations also promote greater microbial

diversity and beneficial microbial communities while reducing soil-borne pathogens. These findings emphasise the importance of strategic crop rotations for improving soil health and fertility, offering valuable insights for sustainable agricultural practices. Drought stress and crop rotation patterns affect soil microbial communities and soil organic matter (SOM) was found to be the primary factor influencing both fungal and bacterial community structures under varying agricultural practices. However, a short-term experiment conducted on crop rotation revealed that microbial communities in soils from various plants, excluding barley, exhibited higher alpha diversity compared to reference fallow soil. Vetch had the most significant impact on microbial composition, particularly when grown continuously, while clover also induced notable changes. Other crops demonstrated moderate effects, typically not surpassing intergroup variation.

The diversity of soil fungi is influenced by multiple factors, including environmental conditions, land management practices and ecological interactions. Natural and anthropogenic activities both can adversely affect fungal diversity. For instance, practices such as tillage, pesticide application and land conversion for agriculture can disrupt soil structure and nutrient availability, leading to shifts in fungal species composition. Natural disturbances, such as flooding or drought, can similarly alter the ecological balance within the soil. Such changes can reduce the resilience of fungal communities, making them more susceptible to further disturbances. Furthermore, the loss of fungal diversity can have cascading effects on soil health, impacting processes such as nutrient cycling, organic matter decomposition and plant health.

Understanding the dynamics of soil mycoflora is critical for developing sustainable agricultural practices. Strategies that promote fungal diversity, such as crop rotation, reduced tillage and organic amendments, can enhance soil health and improve nutrient availability for crops. By maintaining a diverse soil fungal flora, farmers can support ecosystem resilience, reduce dependency on chemical fertilisers and foster more sustainable agricultural systems.

Conclusion

The present study revealed significant variation in the occurrence and distribution of soil fungal mycoflora under different cropping patterns in the conservation agriculture system at the Bihar Agricultural College farm of Bihar Agricultural University, Sabour. A total of 168 fungal colonies belonging to several genera, including *Aspergillus*, *Penicillium*, *Curvularia*, *Fusarium*, *Trichoderma* and *Rhizopus*, were isolated from the studied fields. Among these, *Aspergillus* species showed the highest frequency across most cropping systems, while *Rhizopus stolonifer* showed comparatively lower occurrence. Cropping patterns such as maize + wheat and soybean + maize supported higher fungal abundance compared to other systems, whereas vegetable fields recorded the lowest population. The results indicate that diversified cropping systems, particularly those involving legumes, promote greater soil fungal diversity and beneficial microbial activity. These findings highlight the importance of suitable crop rotations in maintaining soil microbial balance and improving soil health under conservation agriculture.

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Authors' contributions

JNS carried out the field experiment, analysed data and prepared the manuscript. The manuscript was overall prepared and modified by MP. RS estimated the population of the pathogenic and saprophytic fungi from the collected soil samples. PS, SK, PB and SS reviewed this article. AG carried out field experiment, analyzed data and finalized the manuscript. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

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