Research Article

Journal of Agricultural Biotechnology (JOINABT) 5(1), 19-32, 2024

Received: 20-May-2024 Accepted: 12-Jun-2024

homepage: https://dergipark.org.tr/tr/pub/joinabt

https://doi.org/10.58728/joinabt.1486927

SAKARYA UNIVERSITY OF APPLIED SCIENCES

Toprak Kaynaklı Fungal Mikobiomların Çeşitliliği ve Alansal Dağılımının Çevresel Parametreler, Üretim Sistemleri ve Üretim Sezonlarına Göre İncelenmesi

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ÖZ

Kurak bölgeler tarım için önemli alanlardır ve bu alanlarda toprak kaynaklı fungal patojenlerin neden olduğu yıkıcı bitki hastalıkları nedeniyle önemli engellerle karşılaşmaktadırlar. Topraktaki fungusların yapısı ve davranışı ile bunların bu hastalıklarla bağlantısı hakkında bilgi edinmek, hastalıklarla mücadelede etkili yöntemler geliştirmek için çok önemlidir. Bu çalışmanın amacı, yüksek sıcaklıklığa sahip bölgelerde toprakta bulunan fungal çeşitliliğin analizi ve bunların çevre koşulları ve önemli bitki hastalıklarının yaygınlığı arasındaki ilişkiyi aydınlatmaktır. Hastalık salgınlarının görüldüğü tarım alanlarından toprak örnekleri toplandı ve modern teknikler kullanılarak fungus varyeteleri analiz edildi. Bu çalışma, hem faydalı hem de zararlı türleri kapsayan, toprakta yaşayan çok çeşitli fungusları belirledi. Patojenik fungusların, özellikle de basidiomycetes ve ascomycetes türlerinin, hastalık salgınlarının sıkça görüldüğü topraklarda yaygın olduğu keşfedildi ve dolayısıyla bu durum, bunların örnekleme alanlarında hastalık gelişimine önemli katkı sağladıklarını gösteriyor. Sıcaklık, nem ve toprak koşulları da fungal topluluğun yapısını ve hastalık dinamiklerini etkiledi. Bu bulgular, bitki hastalıklarının tahmin edilmesinde ve yönetilmesinde toprak kaynaklı fungus mikobiyomunun önemini vurgulamaktadır. Şiddetli bitki hastalıklarını azaltmak ve bu yerlerdeki tarımsal sürdürülebilirliği korumak için entegre hastalık yönetimi, toprak kökenli funguslar, konukçu bitkiler ve çevre koşulları arasındaki karmaşık etkileşimleri içermelidir. Fungal patofizyolojisini anlamak ve hedefe yönelik hastalık önleme v[1]e kontrol önlemleri geliştirmek için daha fazla çalışmaya ihtiyaç duyulmaktadır.

Keywords: Toprak, Fungal mikrobiyomlar, Çevre, Alansal dağılım, Teşhis, Faydalı fungus

Unraveling the diversity and spatial distribution of Soil-borne Fungal Mycobiomes with response to environmental parameters, cropping schemes and cropping seasons

ABSTRACT

The arid zones are vital agricultural areas, yet they encounter substantial obstacles due to destructive plant diseases caused by soil-borne fungal pathogens. Gaining knowledge about the structure and behavior of the fungus community in the soil and its connection to these ailments is crucial for developing efficient ways to manage the diseases. This study aimed to examine the fungal communities found in soil in areas with high temperatures and multiple cropping schemes. The main objectives of this study were to provide insight into the relationship between these fungal communities, environmental circumstances, and the occurrence of severe plant diseases. Soil samples were collected from agricultural fields exhibiting disease outbreaks, and the fungus diversity was analyzed using modern techniques. The results of this study revealed a diverse array of soil-dwelling fungi, encompassing both beneficial and detrimental species. The presence of pathogenic fungi, specifically

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basidiomycetes and ascomycetes, in soils where disease outbreaks occur frequently suggests that they play a substantial role in the development of these diseases. Temperature, moisture, and soil conditions also affected fungal community structure and disease dynamics. These findings highlight the importance of soil-borne fungus mycobiome in forecasting and managing plant diseases. To reduce severe plant diseases and preserve agricultural sustainability in these areas, integrated disease management must include the complex interactions between soil fungus, plant hosts, and environmental conditions. To understand fungal pathophysiology and develop targeted disease preventive and control measures, a comprehensive study is required.

Keywords: Soil, Fungal mycobiomes, Cropping schemes, Environment, Spatial distribution, Characterization, Beneficial fungi

1. Introduction

The only way to categorize the soil health is by measuring the soil quality and its fertility which is considered as most important characteristics of ecosystem of soil. The integrated approaches to maintain the fitness of soil health assumes that it's a living system and soil health results from the interface via diverse practices and possessions having significant conclusion on actions of soil microbiota. All the soils having distinct characteristics are categorized by employing chemical, biological and physical properties but implementation to ecological changes obsessed by the processes of natural selection are exceptional to later one [1, 2].

The soil-borne fungal mycobiome are the leading inhabitants of soil because of having maximum plasticity and their ability to adopt several forms of inadequate and adverse circumstances [3]. These soil-borne fungal mycobiome have significant potential to yield the wide range of extracellular enzymes, have capacity to breakdown the available organic matter, disintegrating the constituents of soil and amendable the stability of carbon and other nutrients [4].

The role of fungi in terms of converting the organic matter into organic acids, carbon dioxide and biomass is significant. Many species of fungi hold the substantial potential to perform as an effective bio-absorbent of many toxic metals which includes copper, zinc, cadmium, lead and mercury by gathering them in their fruiting bodies. Although such elements can constrain their growth and distress the reproduction [5, 6]. The activity and diversity of many fungal species is controlled by several biotic (plants and other living organisms) and abiotic (soil, moisture, temperature, pH, structure, and salinity) factors [7, 8]. It has concluded from many studies that fungal mycobiome can alive in almost every environment and have significant potential to live in soils having wide range of pH and temperature [9, 10].

The diversity of soil-borne fungal mycobiome can be restricted under natural conditions by unsuitable environmental factors including the biotic and abiotic conditions, tillage system, nutrient resources and microbial interfaces which prevent the occurrence or survival of species in the environment [11]. It is concluded from many previous studies that research on microbial activity in various circumstances is

mandatory to uplift the knowledge about ecology of its biogenesis and must be evaluated in linking with the existing environmental settings including biotic and abiotic elements [12, 14]. The most key phase of such type of experiments is development and selection of important indicators and mechanisms for evaluating the activity of soil-borne microbes and their biodiversity, so that the most reproducible and consistent results should be obtained [15, 16]. The soil-borne fungal mycobiome are consist of bio diversified group of agricultural soils and execute the various imperative ecosystem functions including the effect of health of plants [17]. In contradiction to this, soil-borne fungal species also play a beneficiary role for plant health in soils [18, 19]. Many studies on fungal biodiversity indicated that distribution, definition of role in agricultural ecosystems and identification of such species sometimes become an important issue [19, 20].

The assessment of and diversity of soil-borne fungal species and function diversity of soil can enable a superior indulgent of their natural and ultimate role and influence of health of agricultural plants. It has been revealed from many studies that several natural elements i.e. biological activities, organic matter contents, soil moisture, climate change, tillage practices, cropping pattern and scheme, biomass contents, irrigation, fertilization and physiochemical and biological properties of soil can considerably effect the biodiversity of soil-borne fungal microbiomes community [21, 22]. Keeping in view the importance of such fungal microbiomes, a detailed survey was conducted to isolate, identify and characterize the soil-borne fungal species associated with agricultural crops of south Punjab, Pakistan. The primary aim of present study was to elucidate the correlation between fungal communities, environmental conditions, and prevalence of severe plant diseases in arid zones with multiple cropping patterns. These fungal species were classified on the basis of their already established literature.

2. Research Methodology

2.1 Collection of soil samples

A detailed survey was conducted in Muzaffargarh district of south Punjab to collect the soil samples. This district has versatile range of cropping pattern including agricultural crops, forests and rangeland. The four tehsils of this district i.e. Alipur, Jatoi, Kotaddu and Muzaffargarh were selected for collection of soil samples. From every location, ten soil samples including agricultural crops and forests were collected from 20 cm depth during four seasons for further study. The soil debris was removed from each collected sample. The collected samples were preserved in airtight polythene bags to avoid the contaminations. All the collected samples were brought into plant pathology laboratory for further analysis.

2.2 Isolation of soil-borne fungal microorganisms

All the collected samples were dried under natural sunlight and contaminations were removed. All the obtained samples were sieved twice to remove the large stones and debris. The 10gram oven dried soil/sample was used for each sample for further analysis. The samples were converted into liquid form by performing a series of dilutions in sterile distilled water for each sample. The first dilution was undergoing about half an hour in Thermolyne AROS160 shaker to break the soil specks. The one-gram soil was mixed in nine ml sterile distill water to make the sample homogenous. All the samples were diluted up to (10^{-3}) with the following procedure. The one ml of (10^{-3}) dilution sample was shifted into its corresponding petri dish having the media of Potato dextrose agar (PDA). The streptomycin was used in each sample to inhibit the growth of bacteria and other contaminants. The replications were performed for each corresponding samples. All the Petri plates containing its corresponding sample with PDA were incubated in incubation chamber at 25°C for 6-7 days [23-25]. The soil washing technique was performed in parallel for each collected sample. The twenty-gram oven dried soil sample was engaged in glass funnel with muslin cloth. All these samples were washed firstly in two liter of tap water and its outflow was collected in another funnel. The whole process was repeated two times. The outflow was shifted into a sterile petri plates having Czapek (Dox) agar media with 30mg/l streptomycin. All the petri plates were allowed to incubate at 25°C for 6-8 days for further growth of soil-borne fungal microbes [26, 27].

2.3 Identification of Soil-borne fungal microbes and enumeration of fungal counts

The specimens were transferred to sterilized petri dishes for subsequent analysis. The cultured fungi were mounted on slides for identification. The slides, which were covered with a cover slip, were dyed using lactophenol-cotton blue in order to identify and quantify the fungal colony structures..The identification and measurement of fungal structure with its colony morphology, spore formation and spore characteristics were examined under microscope and compared with already published literatures, identification keys and reference books [28-39]. The fungal counts were measured on the basis of colony appearance on each designated plate.

3. Results and Discussion

The area selected for sampling consist of four seasons and have major cash crops including cotton, wheat, sugarcane, maize, rice and horticultural crops. All the samples were collected from different crops and forests situated in district Muzaffargarh. All the corresponding samples were incubated at 25°C in incubation chamber for growth of soil-borne fungal microbiomes. It was observed that many fungal diseases are prevailing in this area and causing devastating diseases in many crops, vegetables and horticultural crops.

Table. 1 The mean values of atmospheric temperature, surface temperature, and soil moisture in the designated region at the moment the samples were acquired.

Season	AT **(ºC)**	ST **(ºC)**	SM **%**
Winter -21	20	9.8	25.2
Spring-22	25	14.1	23.5
Summer-22	38	29	18.1
Autmn-22	29	20	23.7

AT=Atmospheric temperature, ST= Soil temperature, SM= Soil moisture

The environmental parameters including atmospheric temperature, soil temperature and soil moisture were measured in all sampling areas during four seasons as shown in table 1. The environmental parameters like atmospheric temperature during winter season was more favorable for soil-borne microbiomes affecting the multiples crops like wheat, sugarcane, maize, mung bean and pearl millet. This district has versatile agricultural vegetation which are grown in winter seasons. The horticultural crops including Mango, Citrus, Pomegranate, Guava, Strawberry, Potato, Pepper, Chilly, and other multiple vegetables. All the agricultural crops which are sown in this district were showing some type of fungal diseases symptoms in winter seasons. The spring season was moderate in that year so, a less disease incidence was observed. There were a few soil-borne fungal microbiomes which were identified in spring season. It might be a less favorable environmental conditions were present during that season. The summer and autumn season was most favorable for soil-borne fungal microbiomes. There were multiple fungal species present during the summer and autumn season. Abiotic variables such as soil pH, nutrient availability, and temperature play a significant role in shaping fungal communities. Soil water availability is a significant component that can greatly impact the fungal community. This impact can occur either directly or indirectly through its effect on plant performance. When there is a water deficit, it leads to changes in root design and the types of substances released by the roots [40].

A number of metrics, including size, elevation, color, surface, opacity, edge, and shape, were utilized in order to ascertain the colony characteristics of the soil-borne fungal microbial isolates. The Gram's stain, the motility test, the spore stain, the capsule stain, the catalase test, the oxidase test, the methyl red test, the indole test, the starch hydrolysis, the citrate utilization, the sugar fermentation, and the oxygen relationship were the experiments that were used to determine the cellular characteristics of the isolates. The amount and diversity of soil microorganisms, which are essential to terrestrial ecosystems, can reveal information about the fertility of the soil as well as the effectiveness of biotransformation. Nevertheless, the mechanisms involved in the formation of microbial communities in agricultural soils are intricate and contingent upon factors such as crop structure, land use, and management techniques [41-43].

The colonial morphology of the fungal isolates on the plates was used to characterize the isolates. When attempting to accurately characterize the isolates, various parameters were taken into consideration. These parameters included the color of the colonies, the nature of the hyphae, the look of the colonies, and the growth rates. Additionally, the isolates were subjected to microscopic inspection. Observation of reproductive and vegetative structures were made. Microscopy was used to examine the characteristics of spores, sporangia, hyphae branching, and the presence of septa. The fungi were examined microscopically using the protocols outlined by Samson and Van 1998 [44].

The identified soil-borne fungal microbial isolates were included *Trichophyton rubru, Fusarium oxysporum, Aspergillus niger, Penecillium chrysogenum, Rhizopus oryzae, Aspergillus flavus, Mucor hiemalis. Tilletia indica, Tilletia horrida, Nevossia indica, Helmenthosporium oryzae, Puccinia recondite, Puccinia oryzae, Puccinia graminis tritici, Puccinia glumarum, Erysiphe graminis tritici, Gibberella zeae, Rhizoctonia solani, Phytophthora spp., Pythium spp. Verticillium spp., Sclerotinia spp., Phoma spp., Thielaviopsis basicola, Macrophomina phaseolina, Cylindrocarpon spp., Trichoderma harzianum, Humicola grisea, Absidia, Circinella, Cunninghamella echinulate, Mucor spp.,* and *Verticillium lecanii*.. There are certain elements which can creates the problem during the isolation, identification and characterization of soil-borne mycobiomes. An additional complicated element arises from the possibility of finding both spores and mycelium in a single soil sample, which are likely to be removed together during the extraction procedure [45, 46]. Multiple studies were conducted on the spatial distribution and temporal persistence of extraradical mycelia of a basidiomycete fungus called *Hebeloma cylindrosporum*. It was revealed from many reports that they could detect the presence of 100 basidiospores in 0.5 g of soil for this particular species.

The prevalence of fungal isolates with response to cropping seasons was measured. The main 10 type of fungal species during all growing seasons were identified and listed in table 2. The *Rhizoctonia solani* was observed in grains, corn, tobacco and in multiple vegetables. The symptoms severity was more severe in agronomic crops. The other fungal species which were in severe form including *Phytophthora infestans, Tilletia indica, Sclerotinia spp, Pythium spp, Macrophomina phaseolina, Trichoderma harzianum, Verticillium lecanii, Helmenthosporium oryzae* and *Puccinia recondite* as shown in table 2. Different soil biotic communities can be impacted by agricultural management techniques, which could lead to differences in the production and function of farmlands. Nevertheless, the impact of agricultural practices on microbial diversity and function is very intricate. Further work is needed to determine the general validity of this result across various soil types and climatic circumstances. Furthermore, when examining microbial communities under different fertilization treatments or crop rotations, it is possible to identify significant high-dimensional biomarkers that can effectively differentiate between these communities. This

exploration of soil-borne mycobiome has the potential to contribute to sustainable agricultural productivity and plant protection [47, 48].

Table 2. The season wise distribution of soil-borne fungal isolates from the correspondent samples of every location.

Sample units	Fungal isolates	Seasons			
		Summer-22	Autmn-22	Spring-21	Winter-21
A1	*Rhictonia solani*	+ve	_ve	+ve	+ve
A2	*Phytophthora infestans*	+ve	-ve	-ve	+ve
A3	*Tilletia indica*	-ve	-ve	+ve	+ve
A4	*Sclerotinia spp*	+ve	+ve	-ve	-ve
A5	*Pythium spp*	+ve	+ve	+ve	+ve
A6	*Macrophomina phaseolina*	+ve	-ve	-ve	+ve
A7	*Trichoderma harzianum*	+ve	+ve	+ve	+ve
A8	*Verticillium lecanii*	-ve	-ve	+ve	+ve
A9	*Helmenthosporium oryzae*	+ve	+ve	+ve	+ve
A10	*Puccinia recondite*	+ve	+ve	+ve	+ve

+ve means the presence of fungal species while _ve means the absence of fungal specie in designated areas. These fungal species were identified during all four cropping seasons.

This study also focused on the colonial morphology, cellular morphology, and biochemical properties of the soil-borne fungal microbiome isolates. These characteristics of every fungal species were measured on the basis of its colony appearance under microscope which are shown in table 3. The fungal counts of every isolate was almost same in size but differ in structure and other morphological characters. The fungal counts of *Rhizoctonia solani, Pythium spp., Macrophomina phaseolina, Trichoderma harzianum, Helmenthosporium oryzae,* and *Puccinia recondite* were $1.5X10^5$ while *Phytophthora infestans, Tilletia indica, Sclerotinia spp., Verticillium lecanii* were $1.4X10^5$. The bacterial and other soil-borne microbiomes were discarded at the time of isolation and purification. The fungal counts were measured during dilution process in number of colonies per one gram. A method for quantifying the concentrations of viable fungal spores in soil was involved combining a defined quantity of soil with distilled water, transferring a portion of this mixture onto agar plates, incubated them for a specific duration, and thereafter enumerated the colonies that developed on the plates. The melon plants exhibited comparable symptoms, but were infested by distinct soil-borne fungal diseases across various studied sites and cropping seasons. These infections included *Plectosphaerella melonis*, *P. cucumerina*, *Fusarium solani*, *Macrophomina phaseolina*, and *Monosporascus cannonballus. Olpidium bornovanus* and O. virulentus with two distinct species were identified through the use of bait plants and NGS analysis [49]. This study also revealed the impact of plant species identity and drought on the richness and composition of both the overall and pathogenic fungal population that is linked to the roots of 16 distinct grassland plant species. This experiment was placed in a common garden setting in the Netherlands [50].

Table. 3 Fungal colonies and its counts (cfu/g) of each sample from the designated locations.

Sr. No.	Fungal isolates	Fungal counts (cfu/g)
1	*Rhizoctonia solani*	$1.5X10^5$
2	*Phytophthora infestans*	$1.4X10^5$
3	*Tilletia indica*	$1.4X10^5$
4	*Sclerotinia spp.*	$1.4X10^5$
5	*Pythium spp.*	$1.5X10^5$
6	*Macrophomina phaseolina*	$1.5X10^5$
7	*Trichoderma harzianum*	$1.5X10^5$
8	*Verticillium lecanii*	$1.4X10^5$
9	*Helmenthosporium oryzae*	$1.5X10^5$
10	*Puccinia recondite*	$1.5X10^5$

The *Rhizoctonia solani* is a fungus that was identified from soil and have different forms, such as mycelium (the fungus's vegetative body), sclerotia (dense masses of hyphae that act as survival structures), and conidia (asexual spores) as shown in table 4. The cellular morphology of *Rhizoctonia solani* can exhibit variability based on factors such as environmental circumstances and growth stage. The *Phytophthora infestans* is a type of pathogen known as an oomycete. It has been shown to cause a disease called late blight in plants, and it was more destructive in potatoes and tomatoes. It mostly spreads through structures such as sporangia and zoospores, rather than producing visible colonies in the conventional manner. *Tilletia indica* is a pathogenic fungus that causes Karnal bunt disease in wheat. The impact of it was noticed on the kernels of wheat plants, resulting in interior imperfections rather than the formation of apparent colonies on the outer surfaces. The *Sclerotinia spp*. is a type of fungus that was identified causing numerous plant diseases, such as white mold, in crops like beans, lettuce, and sunflowers. This fungus usually develops soft, white mycelium on infected plant tissues and can generate solid, black sclerotia. *Pythium spp*. is an aquatic and soil-borne fungi that have been shown to cause a range of plant diseases, including damping-off, root rot, and seedling blight. These organisms are distinguished by their hyphae that do not have septa and their capacity to generate sporangia that contain zoospores. The taxonomic study of fungus employs standardized processes, and presents an explanation of general practices in phenotypic approaches. This focuses specifically on micro-fungi due to the impracticality of providing an exhaustive account of approaches for all fungi [51]. The isolation methods for many types of micro-fungi, such as basal fungi, hyphomycetes, coelomocytes, ascomycetes, plant diseases, soil fungi, air-borne fungus, epiphytes, and endophytes, have significant importance. Sporulating cultures are valuable for elucidating the morphological traits of significant fungus. However, these traits may be absent or challenging to see on natural substrates, making it difficult to establish connections between the same fungal species based on their sexual and asexual forms [52, 53].

Macrophomina phaseolina is a pathogenic fungus responsible for causing illnesses like charcoal rot in a range of plant species, including soybeans, maize, and cotton. It commonly invades the vascular system of

plants and generates microsclerotia, which aid in its survival and dissemination in the soil. *Trichoderma harzianum* is a fungus species widely used in agriculture as a biocontrol agent to combat plant diseases. It is renowned for its quick proliferation and capacity to generate enzymes that can break down the cell walls of other fungus, rendering it a potent adversary against many plant ailments. *Verticillium lecanii*, or *Lecanicillium lecanii*, is a fungus employed as a biological agent to combat insect pests like aphids, whiteflies, and scale insects. The organism has distinct fluffy colonies and generates conidia to disperse and infect insect hosts. *Helminthosporium oryzae* is a pathogenic fungus that invades rice plants, resulting in distinct lesions on the leaves, stems, and panicles. The main mode of transmission is by conidia that are generated on diseased plant tissues. *Puccinia recondita* is a pathogenic fungus that invades wheat plants, resulting in the formation of rust-colored pustules on various above-ground plant structures such as leaves and stems. This organism has the ability to reproduce through both sexual and asexual means, generating urediniospores and teliospores. It was revealed from the study of [54] that *P. exigua* (45*%), F. nygamai* (25%), *Rhizoctonia solani* (19%), and *F. camptoceras* (11%), were the most common fungal pathogens. The *P. exigua*, *F. nygamai*, *F. camptoceras*, and *R. solani* infected injured and unwounded seedlings with varying degrees of disease severity (DS). *R. solani* was the most harmful fungus on wounded and unwounded Roselle seedlings, followed by *P. exigua*. The least pathogenic fungus, *F. camptoceras*, infected only unwounded seedlings but not damaged plants [55, 56].

Table 4. The cellular shapes, colonial opacity, colonial surface, cellular arrangement, cellular morphology and colonial morphology of identified fungal isolates.

Fungal isolates	**cellular shape**	**colonial opacity**	**colonial surface**	**cellular arrangment**	**cellular moprphology**	**colonial morphology**
Rhictonia solani	Cross-wall	Typically opaque or whitish in color	Often felty or cottony	Multicellular with septate or aseptate hyphae	Hyphae forming mycelium, sclerotia, and conidia	circular or irregular
Phytophthora infestans	Ovoid or spherical	N/A*	N/A*	Multicellular	Hyphae, zoospores	N/A*
Tilletia indica	Spherical to subspherical	N/A*	N/A*	Teliospores within sori	Teliospores, hyphae	N/A*
Sclerotinia spp	compact masses	Opaque	fluffy or cottony	Multicellular	Hyphae, sclerotia	Circular or irregular
Pythium spp	Non-septate multinucleate	transparent translucent	Slimy-mucoid	Non-septate	Hyphae, zoospores	Spreading
Macrophomina phaseolina	Septate hyphae, microsclerotia	N/A*	N/A*	Septate, microsclerotia	Hyphae, microsclerotia	N/A*

Trichoderma harzianum	Septate hyphae, conidiophores	Opaque-white	Woolly cottony	Septate hyphae, conidiophores	Hyphae, conidiophores, conidia	Spreading
Verticillium lecanii	Septate hyphae, conidiophores	Opaque-white	Fluffy-cottony	Septate hyphae, conidiophores	Hyphae, conidiophores, conidia	Spreading
Helmenthosporium oryzae	Septate hyphae	N/A*	N/A*	Septate hyphae	Hyphae, conidia, conidiophores	N/A*
Puccinia recondite	Oblong urediniospores, hyphae	N/A*	N/A*	Septate hyphae	Urediniospores, teliospores, hyphae	N/A*

*Note N/A=not available because every fungal isolate affects the plants in a differential way so some information is not available.

4. Conclusion

Disease control in experimental zones, where agriculture is essential to the economy, requires understanding soil-borne fungal community dynamics. This study reveals the numerous critical results in the soil-borne fungal mycobiome that link fungal diversity to catastrophic plant diseases. First, this study found a variety of soil-borne fungal mycobiome in arid agricultural soils. This diversity includes beneficial and harmful fungus, showing the soil microbial community's delicate balance. Environmental factors like temperature, moisture, and soil qualities also affected fungal community structure and disease dynamics. The hot and arid environment promote the growth of detrimental fungus, increasing crop disease risk. The study's major findings and its conclusion underscore the relevance of understanding soil-borne fungus communities in minimizing plant diseases.

5. Declaration

5.1 Competing interests:

No competing interest exists for this study between author and institution.

5.2 Authors Contributions

Muhammad Arif; Conceptualization, designing of experiment, methodology, analysis, resources, supervision, execution, writing initial and final draft

5.3 Ethics Committee Approval

No ethics committee approval/permit was required for this study because this study does not involve any humans or animal’s participation.

5.4 Acknowledgment

There is no person or institution contributing to this research other than the authors. Author declare that no conflict of interest exists.

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