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Isolation and Identification of Soil-Borne Fungi and Their Role in Plant Diseases

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Abstract

Soil-borne fungi are a major constraint on crop production because they survive for years in soil and attack plants below ground, where disease is difficult to detect and control. This paper deals with the isolation and identification of soil-borne fungi and their role in plant diseases. Soil samples were collected from cultivated fields, and fungi were isolated by the serial dilution plate technique on potato dextrose agar and Sabouraud dextrose agar. Isolates were identified on the basis of colony characters and microscopic features, with molecular confirmation by ITS sequencing recommended for doubtful isolates. The isolates included saprophytic genera such as Aspergillus and Penicillium, the beneficial genus Trichoderma, and the pathogenic genera Fusarium, Rhizoctonia, Pythium, Sclerotium and Macrophomina. These pathogens are responsible for vascular wilt, root rot, damping-off, stem rot and charcoal rot, and each persists in soil through resistant structures such as chlamydospores, oospores and sclerotia. The paper also describes the mechanisms of infection and compares cultural, biological, chemical and resistant-variety approaches to management. It concludes that accurate identification of the pathogen is the basis of effective control and that integrated disease management, supported by sustainable soil health practices, offers the most reliable protection of crops.

Keywords: soil-borne fungi; isolation; identification; plant diseases; Fusarium; Rhizoctonia; integrated disease management

1. Introduction

Soil-borne fungi are among the most important biotic constraints on crop production worldwide, because they live in the same soil that supplies plants with water and nutrients and can attack roots, crowns and stems from below ground (Katan, 2017). This paper describes how soil-borne fungi are isolated and identified, and explains how the major genera cause disease and how those diseases can be managed.

Soil-borne fungi are fungi that spend all or a critical part of their life cycle in soil, where they grow as saprophytes on organic matter or survive as dormant structures such as sclerotia, chlamydospores and oospores. Pathogenic members infect plants through roots or the stem base and cause wilts, root rots, damping-off and stem rots (Katan, 2017). Many of these organisms are not fungi in the strict sense: oomycetes such as Pythium are fungus-like but are classified in a separate kingdom, and they are routinely studied together with true fungi because they cause similar diseases (Kamoun et al., 2015).

1.1 Importance of Soil Microorganisms in Agriculture

Soil microorganisms drive nutrient cycling, organic matter decomposition, soil aggregation and the suppression of pathogens, and the soil microbiome is increasingly seen as an extension of plant immunity (Raaijmakers & Mazzola, 2016). Greater soil biodiversity is associated with more stable crop yields and lower dependence on external inputs, which is why microbial diversity is treated as a basis for sustainable agriculture (Bender et al., 2016). Fungi contribute to this through mycorrhizal partnerships, decomposition and antagonism of competitors, while a minority of species act as serious pathogens.

1.2 Diversity and Distribution of Soil-Borne Fungi

Current estimates place global fungal diversity between 2.2 and 3.8 million species, of which only a small fraction has been formally described (Hawksworth & Lücking, 2017). Soil fungal communities vary with climate, soil pH, organic carbon and land use, and the global topsoil survey by Bahram et al. (2018) showed that these environmental factors shape which fungal groups dominate in a given location. Most soil remains poorly characterised, and much of its fungal diversity is still unknown (Fierer, 2017). Cultivated fields typically hold a mixture of saprophytes, beneficial fungi and pathogens whose proportions change with crop sequence, tillage and fertiliser regime.

1.3 Relationship Between Soil Fungi and Plant Health

Plant health depends on the balance between pathogenic and beneficial soil organisms. Where antagonistic microbes are abundant, soils can suppress disease even when the pathogen is present (Schlatter et al., 2017). Where the balance is lost, for example through monoculture or poor drainage, pathogens build up and can cause large yield losses. Emerging fungal and oomycete pathogens are now regarded as a growing threat to global food security (Fisher et al., 2020; Fones et al., 2020). Reliable isolation and identification of the organisms present is therefore the first step towards accurate diagnosis and sound disease management.

2. Review of Literature

The soil-borne pathogens are economically and ecologically important and have been increasing in number and diversity in recent years, as indicated in the recent literature, which has moved from culture-based surveys to combined morphological and molecular surveys. In this section, the key studies reviewed are summarized in table 1.

2.1 Previous Studies on Soil-Borne Fungal Diversity

It was found by large scale surveys that the soil fungal communities are structured by climate, soil chemistry and vegetation. Bahram et al. (2018) compared the diversity and composition of fungi in topsoil from all over the world and revealed that there was a close relationship between environmental gradients and fungal richness and community composition. Fierer (2017) pointed out that the soil microbiome is largely under-characterized and that there is a need for methods to connect taxa to function. Bender et al. (2016) demonstrated that in agricultural soils, diverse soil communities are important for the productivity and ecosystem services of the crop, allowing the purpose of diversity surveying to go beyond the mere cataloguing of species.

2.2 The isolation and identification of fungi.

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Dilution-plating and direct plating of fungi on selective media are still the most common methods for obtaining living-isolates of fungi from soil, and these methods are still widely used because they provide living-isolates for pathogenicity tests (Raja et al., 2017). Morphological identification is based on colony colour, growth rate, hyphal structure and spore form and may not be reliable for closely related species. Lücking et al. (2020) tested the accuracy and precision of DNA-based barcoding in fungi and found that there is no single marker that will identify every fungal group; therefore, multiple lines of evidence should be used for identification.

2.3 Studies on Fungal Pathogens

Soil-borne pathogens are hard to manage due to their ability to survive in soil for several years and to infect below-ground parts where symptoms may not be evident until late in the season (Katan, 2017). For a taxonomy and population biology of Rhizoctonia solani and its involvement in seedling disease of soybean, see Ajayi-Oyetunde and Bradley (2018). Lamichhane et al. (2017) reviewed damping-off diseases caused by Pythium, Rhizoctonia and Fusarium and the options for integrated control. Macrophomina phaseolina is a pathogen of increasing importance in warm and dry regions, and Marquez et al. (2021) described the pathogenicity and control of this pathogen. Fones et al. (2020) and Fisher et al. (2020) have been warning about emerging fungal and oomycete pathogens in food security at a global scale.

2.4 Advances in Fungal Taxonomy and Molecular Identification.

The internal transcribed spacer (ITS) region is now the most widely used barcode for fungi, and curated reference databases like UNITE enhance match reliability, especially for sequences from uncultured or less well-known fungi (Nilsson et al., 2019). ITS is used in addition to protein-coding genes for genera like Fusarium, where ITS alone is not effective to distinguish species. Summerell (2019) commented on the recent reclassifications of the genus, while Geiser et al. (2021) provided evidence using the 19-gene dataset that the Fusarium genus is monophyletic and contains the F. solani species complex.

Table 1. Summary of selected studies on soil-borne fungi, 2015–2023.

Study	Focus	Main finding
Kamoun et al. (2015)	Oomycete pathogens	Ranked the ten most important oomycete plant pathogens, including Pythium species
Raaijmakers & Mazzola (2016)	Soil immunity	Soil microbial communities can protect plants from disease
Bender et al. (2016)	Soil biodiversity	Soil biodiversity supports sustainable crop production
Fierer (2017)	Soil microbiome	Most soil microbial diversity remains uncharacterised
Hawksworth & Lücking (2017)	Fungal diversity	Estimated 2.2–3.8 million fungal species worldwide
Bahram et al.	Global topsoil	Environment shapes soil fungal community

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Study	Focus	Main finding
(2018)		structure
Nilsson et al. (2019)	Molecular identification	UNITE database improves ITS-based identification
Fones et al. (2020)	Emerging pathogens	Emerging fungal and oomycete pathogens threaten food security
Lücking et al. (2020)	DNA barcoding	Barcoding accuracy varies across fungal groups
Geiser et al. (2021)	Fusarium phylogeny	Nineteen genes resolve a monophyletic Fusarium

3. Materials and Methods

The study followed a standard culture-based workflow from field sampling to identification, summarised in Figure 1. Site names, crop details and soil properties in Table 2 are example entries and should be replaced with the details of your own survey.

3.1 Study Area and Soil Sample Collection

Soil samples were collected from cultivated fields in the study area (insert district and state), which has a sub-tropical climate with a hot summer, a monsoon season and a mild winter. Sampling was done after the harvest of the previous crop and again at the vegetative stage of the current crop, so that both resting structures and active pathogen populations could be recovered.

3.2 Selection of Sampling Sites

Six sites were chosen to represent the main crops and soil types of the area. Fields with a recorded history of wilt, root rot or damping-off were included alongside apparently healthy fields, which allows pathogens from diseased plots to be compared with the background community. Site characteristics are given in Table 2.

Table 2. Description of sampling sites (example entries).

Site	Crop	Soil type	Soil pH	Disease history
S1	Chickpea	Sandy loam	7.4	Wilt reported
S2	Wheat	Clay loam	7.8	None
S3	Tomato	Loam	6.9	Damping-off in nursery
S4	Groundnut	Sandy loam	7.1	Stem rot reported
S5	Soybean	Clay	7.6	Root rot reported
S6	Maize	Loam	7.2	None

3.3 Collection and Preparation of Soil Samples

At each site, five sub-samples were taken from the root zone (0–15 cm depth) in a zigzag pattern after removing surface litter, using a sterilised trowel. The sub-samples were mixed into one composite sample of about 500 g, placed in a clean polythene bag, labelled and transported to the laboratory in a cool box. Samples were processed within 24 hours. Stones and plant debris were removed, and the soil was passed through a 2 mm sieve.

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3.4 Isolation of Soil-Borne Fungi

Fungi were isolated by the serial dilution plate technique. Ten grams of sieved soil were suspended in 90 mL of sterile distilled water and shaken for 15 minutes, and serial dilutions were prepared up to 10^{-5}. One millilitre of the 10^{-3} and 10^{-4} dilutions was spread on solidified medium in Petri dishes, with three replicates per dilution. Plates were incubated at 25 ± 2 °C for 5–7 days and checked daily. Colonies were counted and expressed as colony-forming units per gram of dry soil. Distinct colonies were transferred to fresh plates, and pure cultures were obtained by hyphal-tip or single-spore transfer and maintained on slants at 4 °C. Isolates were identified by colony characters and by microscopic examination of mounts in lactophenol cotton blue, using standard taxonomic keys. Doubtful isolates can be confirmed by ITS sequencing and comparison with a curated database such as UNITE (Nilsson et al., 2019; Raja et al., 2017).

3.5 Preparation of Culture Media (PDA and SDA)

Potato dextrose agar (PDA) is a general-purpose medium that supports a wide range of fungi, whereas Sabouraud dextrose agar (SDA) has a lower pH and higher sugar content that favour fungal growth over bacteria. Both media were adjusted to pH 5.6 ± 0.2, autoclaved at 121 °C and 15 psi for 15 minutes, cooled to about 45 °C and amended with an antibiotic to suppress bacteria. The composition is given in Table 3.

Table 3. Composition of the culture media used (per litre of distilled water).

Component	PDA	SDA
Potato infusion	200 g	none
Dextrose	20 g	40 g
Peptone	none	10 g
Agar	15–20 g	15 g
Streptomycin (added after autoclaving)	100 mg	100 mg
Final pH	5.6 ± 0.2	5.6 ± 0.2

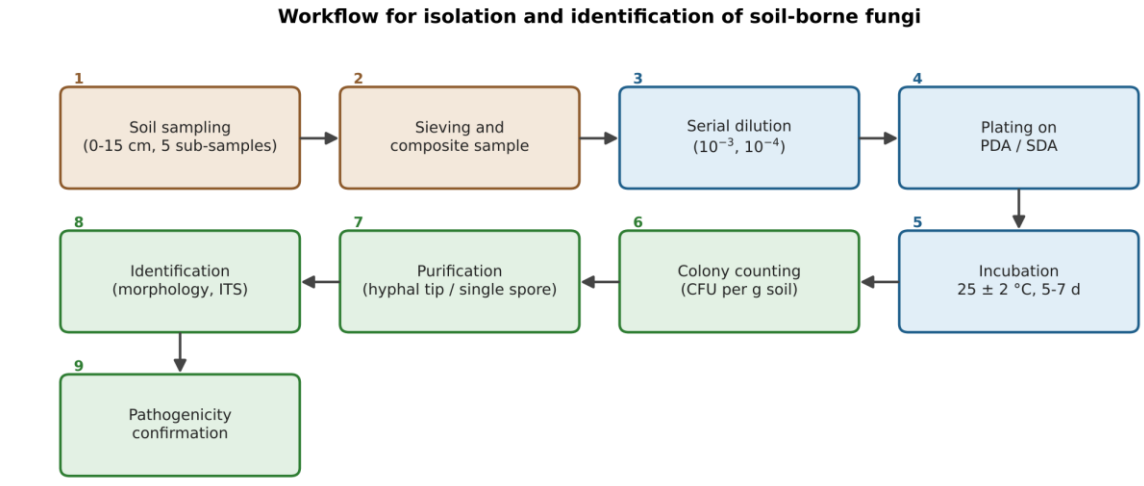


Figure 1. Workflow for the isolation and identification of soil-borne fungi, from sampling to identification and pathogenicity confirmation.

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4. Results and Discussion

Note: the isolate counts in Tables 4–5 and Figures 2–3 are illustrative placeholder values that show how results are reported. Replace them with your own survey data before submission.

The six sites yielded 186 fungal isolates belonging to ten genera or groups, and 72 of them (38.7%) belonged to genera that contain well-known soil-borne plant pathogens.

4.1 Diversity of Soil-Borne Fungal Isolates

Saprophytic genera such as Aspergillus and Penicillium made up the largest share of isolates, which is typical of cultivated soils where fast-growing, sporulating fungi dominate plate counts. Pathogenic genera were less numerous but were present at every site with a disease history. Sites S5 (soybean, root rot) and S3 (tomato, damping-off) gave the most pathogen isolates, and the healthy wheat and maize fields gave the fewest. This agrees with the general finding that soil fungal community composition follows crop, soil and management differences (Bahram et al., 2018). The beneficial genus Trichoderma was also common, and its presence in all but one site suggests natural antagonistic potential, in line with the idea that soil communities can limit pathogen activity (Raaijmakers & Mazzola, 2016).

Table 4. Frequency and distribution of fungal isolates (n = 186, example data).

Genus	Isolates	Relative frequency (%)	Sites present (of 6)
Aspergillus	38	20.4	6
Penicillium	30	16.1	6
Fusarium	27	14.5	5
Trichoderma	22	11.8	5
Rhizoctonia	14	7.5	3
Pythium	12	6.5	3
Sclerotium	10	5.4	2
Macrophomina	9	4.8	2
Alternaria	8	4.3	4
Others (Mucor, Rhizopus)	16	8.6	6

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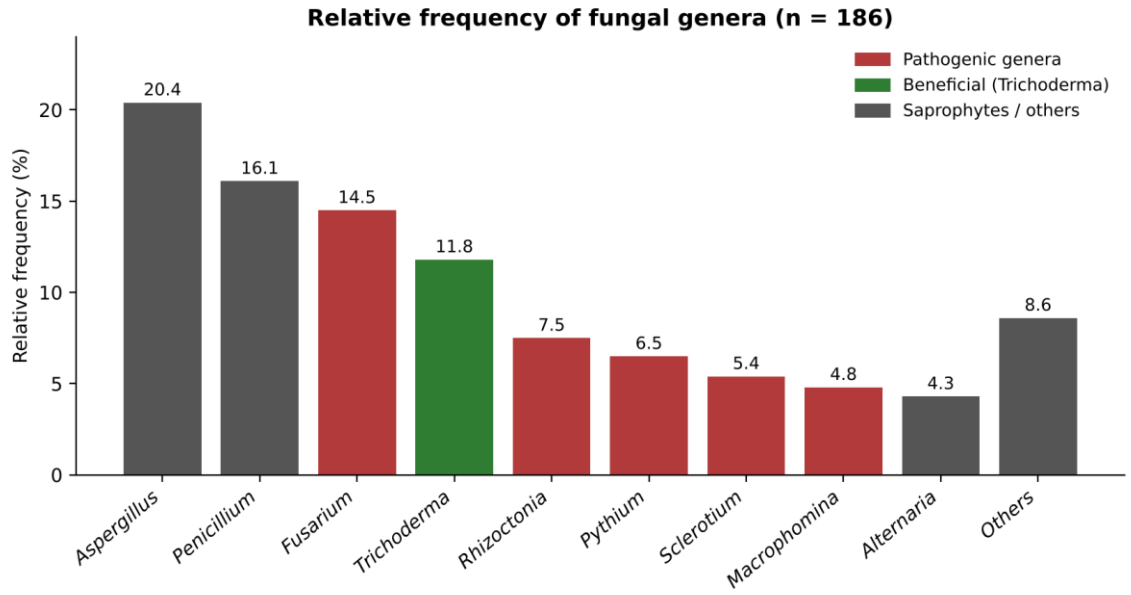


Figure 2. Relative frequency (%) of fungal genera isolated from the six sampling sites.

4.2 Morphological and Cultural Characteristics of Isolated Fungi

Isolates were separated first by colony colour, texture and growth rate on PDA, and then by microscopic features of hyphae and spores. Table 5 lists the characters used to identify the major genera. Species-level separation inside Fusarium and Rhizoctonia is difficult by morphology alone, and molecular confirmation is advisable (Lücking et al., 2020; Summerell, 2019).

Table 5. Cultural and morphological characters of the major genera on PDA.

Genus	Colony on PDA	Microscopic features
Fusarium	White to pink or violet, cottony	Sickle-shaped, septate macroconidia; small microconidia
Rhizoctonia solani	Fast-growing, pale to dark brown	Right-angled branching, constriction at branch base; no spores
Pythium	White, fast-growing, cottony	Coenocytic hyphae; globose sporangia and oospores
Sclerotium rolfsii	White, fan-like mycelium	Round, mustard-seed-like sclerotia; clamp connections
Macrophomina phaseolina	Grey to black	Black microsclerotia; pycnidia with hyaline conidia
Trichoderma	Green, dense, rapid	Branched conidiophores; flask-shaped phialides
Aspergillus	Green, yellow or black, powdery	Conidial heads with swollen vesicle
Penicillium	Blue-green, velvety	Brush-like conidiophores (penicilli)

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4.3 Identification of Major Fungal Genera

Five genera were of particular concern: Fusarium, Rhizoctonia, Pythium, Sclerotium and Macrophomina. Fusarium was identified by its curved, multi-septate macroconidia, and the genus is now defined broadly after multigene phylogenies placed the F. solani complex inside Fusarium (Geiser et al., 2021). Rhizoctonia solani was recognised by right-angled branching and the absence of spores, with anastomosis grouping needed for finer separation (Ajayi-Oyetunde & Bradley, 2018). Pythium produced coenocytic hyphae and oogonia and, as an oomycete, belongs outside the true fungi (Kamoun et al., 2015). Sclerotium rolfsii and Macrophomina phaseolina were identified by their sclerotia and microsclerotia respectively (Marquez et al., 2021).

4.4 Frequency and Distribution of Fungal Isolates

Three patterns stand out in Table 4 and Figure 3. First, the saprophytes Aspergillus, Penicillium and the group of minor genera occurred at all six sites. Second, Sclerotium and Macrophomina were restricted to two sites each, which suggests patchy, field-specific infestation, as expected for pathogens that survive as sclerotia. Third, pathogen load was highest in the clay and loam soils under legumes and vegetables. A single survey cannot separate the effects of crop, soil and disease history, so the site pattern should be read as descriptive and not causal.

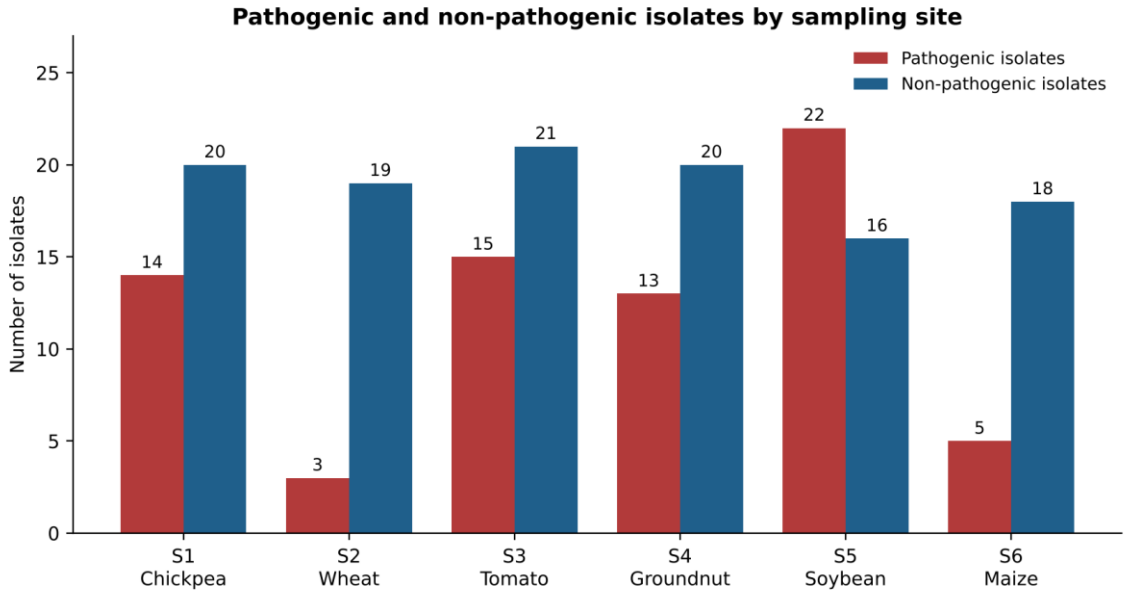


Figure 3. Number of pathogenic and non-pathogenic fungal isolates at each sampling site.

5. Major Soil-Borne Fungi and Their Role in Plant Diseases

Five pathogens account for much of the damage caused by soil-borne fungi and fungus-like organisms, and they differ in the tissues they attack, the structures they use to survive and the conditions that favour them. Table 6 compares them, and the sections below describe each in turn.

Table 6. Major soil-borne pathogens, diseases, hosts and survival structures.

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Pathogen	Main disease	Typical hosts	Survival structure
Fusarium oxysporum	Vascular wilt	Chickpea, tomato, banana, cotton	Chlamydospores
Rhizoctonia solani	Root rot, damping-off, sheath blight	Soybean, potato, rice, vegetables	Sclerotia, mycelium in debris
Pythium spp.	Damping-off, root rot	Seedlings of most crops	Oospores
Sclerotium rolfsii	Stem rot, collar rot	Groundnut, tomato, pulses	Sclerotia
Macrophomina phaseolina	Charcoal rot, dry root rot	Soybean, sorghum, sesame, chickpea	Microsclerotia

5.1 Fusarium Species and Vascular Wilt Diseases

Fusarium oxysporum infects roots, enters the xylem and blocks water transport, which causes yellowing, wilting and vascular browning. Strains are host-specific and are grouped into formae speciales. The fungus survives for many years as chlamydospores, which makes crop rotation a slow remedy (Katan, 2017). Fusarium taxonomy has changed considerably in recent years, and a broad genus concept is now supported by multigene data (Geiser et al., 2021; Summerell, 2019).

5.2 Rhizoctonia solani and Root Rot Diseases

R. solani is a species complex divided into anastomosis groups that differ in host range and virulence. It attacks seeds, seedlings and mature roots and stems, and causes lesions, root rot and damping-off. It survives as sclerotia and as mycelium in plant debris, and it is favoured by cool, wet soil at planting (Ajayi-Oyetunde & Bradley, 2018).

5.3 Pythium Species and Damping-Off Diseases

Pythium species are oomycetes that produce motile zoospores, which swim towards root exudates in saturated soil. They cause pre-emergence and post-emergence damping-off and rot of fine roots, and survive as thick-walled oospores (Kamoun et al., 2015). Damping-off is most severe in cold, waterlogged and poorly drained soil, and it is a leading cause of seedling loss in nurseries (Lamichhane et al., 2017).

5.4 Sclerotium rolfsii and Stem Rot Diseases

S. rolfsii causes collar rot and stem rot, often seen as white mycelial mats and mustard-seed-like sclerotia at the base of the plant. It has a very wide host range and is most active in warm, humid conditions. Its sclerotia remain viable in soil for long periods, so soil-borne inoculum accumulates in fields where susceptible crops are grown repeatedly (Katan, 2017).

5.5 Macrophomina phaseolina and Charcoal Rot

M. phaseolina causes charcoal rot and dry root rot, and the disease is most damaging when drought and high temperature stress the crop. Infected roots and stems show grey-black discolouration from masses of microsclerotia that persist in soil and residue (Marquez et al., 2021). Its importance is expected to increase as warmer and drier seasons become more common (Fones et al., 2020).

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5.6 Mechanisms of Fungal Infection and Disease Development

Soil-borne pathogens follow a common sequence: inoculum survives in soil, germinates in response to root exudates, penetrates the host, colonises tissue and produces new survival structures when the host dies (Figure 4). The pathogens differ in the tools they use at each step. Table 7 compares the main infection strategies. Disease development depends on the pathogen, a susceptible host and a favourable environment, and it is modified by the resident soil microbiome (Raaijmakers & Mazzola, 2016).

Table 7. Infection strategies of the major soil-borne pathogens.

Pathogen	Entry into host	Main virulence factors	Result in the plant
Fusarium oxysporum	Root tips and wounds	Cell-wall-degrading enzymes, effector proteins, fusaric acid	Xylem blockage and wilting
Rhizoctonia solani	Direct penetration by infection cushions	Cell-wall-degrading enzymes, toxins	Tissue maceration, lesions
Pythium spp.	Zoospore encystment on roots	Cell-wall-degrading enzymes, effectors	Rotting of fine roots, seedling collapse
Sclerotium rolfsii	Mycelium on stem base	Oxalic acid, pectinases	Rapid tissue breakdown, collar rot
Macrophomina phaseolina	Roots, through root hairs and wounds	Microsclerotia, toxins, enzymes	Vascular plugging, charcoal rot

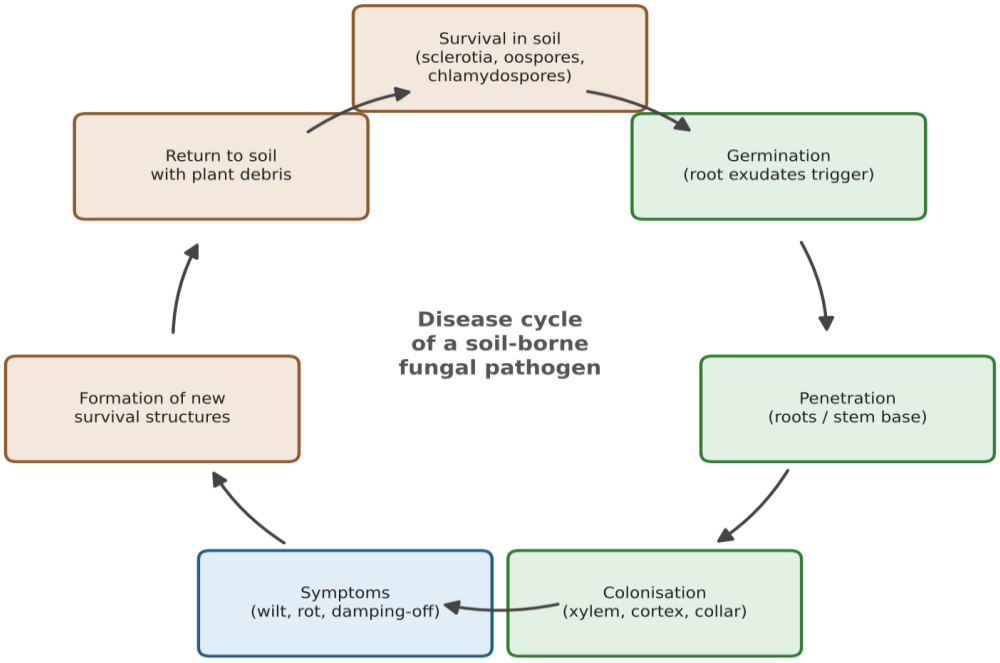


Figure 4. Generalised disease cycle of a soil-borne fungal pathogen.

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6. Management and Control of Soil-Borne Fungal Diseases

No single measure controls soil-borne diseases reliably, because the pathogens persist in soil, infect below ground and are hard to reach with fungicides (Katan, 2017). Effective programmes combine several tactics, compared in Table 8 and brought together in Figure 5.

6.1 Cultural and Agronomic Management Practices

Crop rotation with non-host crops, deep summer ploughing, soil solarisation, balanced fertilisation, good drainage and the use of disease-free seed and transplants all reduce inoculum or make conditions less favourable for infection. Organic amendments can raise microbial activity and suppress some pathogens (Bender et al., 2016). Rotation is least effective against pathogens with long-lived sclerotia or a wide host range, such as Sclerotium rolfsii and Macrophomina phaseolina (Katan, 2017).

6.2 Biological Control Using Antagonistic Microorganisms

Antagonists such as Trichoderma and Bacillus suppress pathogens through competition, antibiosis, parasitism of the pathogen and induced plant resistance, and the relevant mode of action should be understood as well as the field efficacy (Köhl et al., 2019). Mycoparasitism is a well-documented mechanism by which Trichoderma suppresses fungal pathogens (Mukherjee et al., 2022). Biocontrol agents work best as part of an integrated programme, because their performance depends on soil conditions and on how well they establish in the root zone.

6.3 Chemical Management of Soil-Borne Pathogens

Seed treatment and soil drenches with fungicides give useful protection during the vulnerable seedling stage, and fumigants have been used for high-value crops. Chemical control of soil pathogens, however, is costly, can harm non-target soil organisms and may select resistant strains, and several fumigants are restricted for environmental and health reasons (Katan, 2017). Chemicals are therefore best used as a targeted supplement and not as the only control.

6.4 Use of Resistant Plant Varieties

Resistant cultivars are among the most economical and environmentally safe controls, particularly against Fusarium wilt. Resistance can be overcome when pathogen races change, so varieties should be matched to the races present in the field, which depends on accurate identification (Summerell, 2019). Grafting susceptible scions onto resistant rootstocks is a useful option in vegetable production.

6.5 Integrated Disease Management Strategies

Integrated disease management combines clean planting material, resistant varieties, rotation, soil health improvement, biological agents and selective use of fungicides, with decisions guided by monitoring and diagnosis (Lamichhane et al., 2017). The strategy works because each tactic reduces risk by a different route and no single failure leaves the crop unprotected.

Table 8. Comparison of management options for soil-borne fungal diseases.

Option	Main mechanism	Strengths	Limitations
Cultural practices	Reduce inoculum, improve conditions	Low cost, widely applicable	Slow; weak against long-lived sclerotia

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Option	Main mechanism	Strengths	Limitations
Biological control	Antagonism, parasitism, induced resistance	Safe for the environment	Variable field performance
Chemical control	Toxicity to the pathogen	Fast, easy to apply	Cost, resistance risk, non-target effects
Resistant varieties	Host genetic resistance	Economical, durable if races are known	Races may overcome resistance
Integrated management	Combination of the above	Most reliable and robust	Needs planning and monitoring

6.6 Sustainable Approaches to Soil Health Management

Management is shifting from killing pathogens to building soils in which they cannot thrive. Practices such as diverse rotations, cover crops, reduced tillage and organic matter additions raise microbial diversity and can create disease-suppressive soils (Schlatter et al., 2017; Raaijmakers & Mazzola, 2016). Understanding the soil microbiome is expected to make such approaches more predictable (Fierer, 2017).

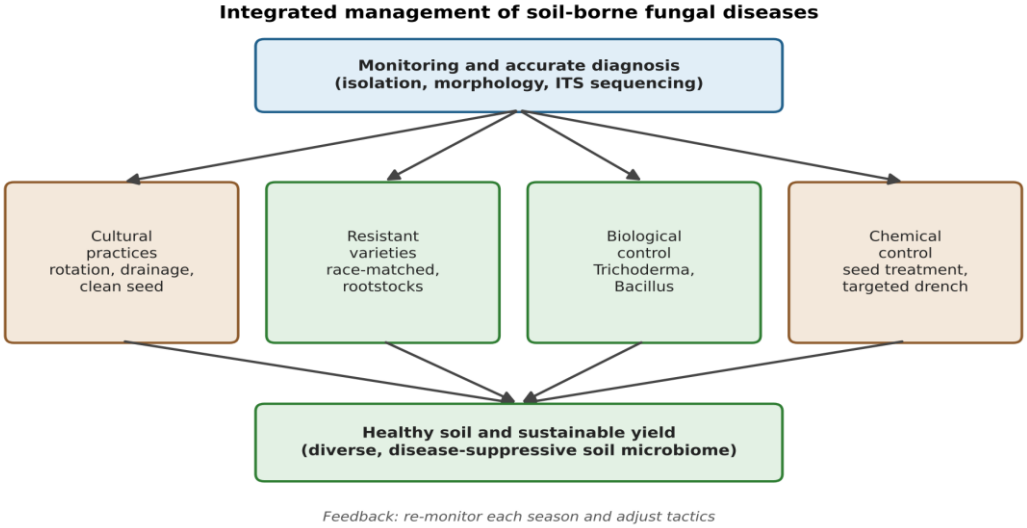


Figure 5. Framework for integrated management of soil-borne fungal diseases.

7. Conclusion

Isolation and identification of soil-borne fungi is essential to good disease management and the most harmful pathogens are better understood both in their biology and their survival.

Saprophytic, beneficial and pathogenic fungi were recovered by dilution on PDA and SDA and the major genera were separated by morphological characters. The pathogens of most concern include Fusarium, Rhizoctonia, Pythium, Sclerotium and Macrophomina (which cause wilt, root rot, damping-off, stem rot and charcoal rot, respectively). These diseases reoccur as a result of resistant structures that survive in the soil.

Correct identification determines which control will be effective; a Fusarium-resistant rotation will not control Sclerotium and resistant varieties have to be for a compatible race of

the pathogen. Morphological characteristics don't help for closely related species, so sequencing of ITS and other genes should be used alongside a curated database.

The results have contributed to integrated management using clean planting material, rotation, resistant varieties, biological agents and well-timed use of chemicals, with soil health as a long-term goal (Lamichhane et al., 2017; Schlatter et al., 2017). The isolation scheme and the character tables given in this paper may be used for routine determinations in diagnostic laboratories and extension services.

7.1 Future Scope of Research

Future work should confirm pathogenicity of isolates by Koch's postulates, add multi-gene sequencing and metabarcoding to capture non-culturable fungi, and test locally adapted biocontrol agents in field trials. Research on how climate change alters the distribution and aggressiveness of soil-borne pathogens is also needed (Fisher et al., 2020; Fones et al., 2020).

References.

1. Ajayi-Oyetunde, O. O., & Bradley, C. A. (2018). Rhizoctonia solani: Taxonomy, population biology and management of Rhizoctonia seedling disease of soybean. Plant Pathology, 67(1), 3–17.
2. Bahram, M., Hildebrand, F., Forslund, S. K., Anderson, J. L., Soudzilovskaia, N. A., Bodegom, P. M., Bengtsson-Palme, J., Anslan, S., Coelho, L. P., Harend, H., Huerta-Cepas, J., Medema, M. H., Maltz, M. R., Mundra, S., Olsson, P. A., Pent, M., Põlme, S., Sunagawa, S., Ryberg, M., … Bork, P. (2018). Structure and function of the global topsoil microbiome. Nature, 560(7717), 233–237.
3. Bender, S. F., Wagg, C., & van der Heijden, M. G. A. (2016). An underground revolution: Biodiversity and soil ecological engineering for agricultural sustainability. Trends in Ecology & Evolution, 31(6), 440–452.
4. Fierer, N. (2017). Embracing the unknown: Disentangling the complexities of the soil microbiome. Nature Reviews Microbiology, 15(10), 579–590.
5. Fisher, M. C., Gurr, S. J., Cuomo, C. A., Blehert, D. S., Jin, H., Stukenbrock, E. H., Stajich, J. E., Kahmann, R., Boone, C., Denning, D. W., Gow, N. A. R., Klein, B. S., Kronstad, J. W., Sheppard, D. C., Taylor, J. W., Wright, G. D., Heitman, J., Casadevall, A., & Cowen, L. E. (2020). Threats posed by the fungal kingdom to humans, wildlife, and agriculture. mBio, 11(3), e00449-20.
6. Fones, H. N., Bebber, D. P., Chaloner, T. M., Kay, W. T., Steinberg, G., & Gurr, S. J. (2020). Threats to global food security from emerging fungal and oomycete crop pathogens. Nature Food, 1(6), 332–342.
7. Geiser, D. M., Al-Hatmi, A. M. S., Aoki, T., Arie, T., Balmas, V., Barnes, I., Bergstrom, G. C., Bhattacharyya, M. K., Blomquist, C. L., Bowden, R. L., Brankovics, B., Brown, D. W., Burgess, L. W., Bushley, K., Busman, M., Cano-Lira, J. F., Carrillo, J. D., Chang, H.-X., Chen, C.-Y., … Zhang, N. (2021). Phylogenomic analysis of a 55.1-kb 19-gene dataset resolves a monophyletic Fusarium that includes the Fusarium solani species complex. Phytopathology, 111(7), 1064–1079.

8. Hawksworth, D. L., & Lücking, R. (2017). Fungal diversity revisited: 2.2 to 3.8 million species. Microbiology Spectrum, 5(4), FUNK-0052-2016.
9. Kamoun, S., Furzer, O., Jones, J. D. G., Judelson, H. S., Ali, G. S., Dalio, R. J. D., Roy, S. G., Schena, L., Zambounis, A., Panabières, F., Cahill, D., Ruocco, M., Figueiredo, A., Chen, X.-R., Hulvey, J., Stam, R., Lamour, K., Gijzen, M., Tyler, B. M., … Govers, F. (2015). The top 10 oomycete pathogens in molecular plant pathology. Molecular Plant Pathology, 16(4), 413–434.
10. Katan, J. (2017). Diseases caused by soilborne pathogens: Biology, management and challenges. Journal of Plant Pathology, 99(2), 305–315.
11. Köhl, J., Kolnaar, R., & Ravensberg, W. J. (2019). Mode of action of microbial biological control agents against plant diseases: Relevance beyond efficacy. Frontiers in Plant Science, 10, Article 845.
12. Lamichhane, J. R., Dürr, C., Schwanck, A. A., Robin, M.-H., Sarthou, J.-P., Cellier, V., Messean, A., & Aubertot, J.-N. (2017). Integrated management of damping-off diseases: A review. Agronomy for Sustainable Development, 37, Article 10.
13. Lücking, R., Aime, M. C., Robbertse, B., Miller, A. N., Ariyawansa, H. A., Aoki, T., Cardinali, G., Crous, P. W., Druzhinina, I. S., Geiser, D. M., Hawksworth, D. L., Hyde, K. D., Irinyi, L., Jeewon, R., Johnston, P. R., Kirk, P. M., Malosso, E., May, T. W., Meyer, W., … Schoch, C. L. (2020). Unambiguous identification of fungi: Where do we stand and how accurate and precise is fungal DNA barcoding? IMA Fungus, 11, Article 14.
14. Marquez, N., Giachero, M. L., Declerck, S., & Ducasse, D. A. (2021). Macrophomina phaseolina: General characteristics of pathogenicity and methods of control. Frontiers in Plant Science, 12, Article 634397.
15. Mukherjee, P. K., Mendoza-Mendoza, A., Zeilinger, S., & Horwitz, B. A. (2022). Mycoparasitism as a mechanism of Trichoderma-mediated suppression of plant diseases. Fungal Biology Reviews, 39, 15–33.
16. Nilsson, R. H., Larsson, K.-H., Taylor, A. F. S., Bengtsson-Palme, J., Jeppesen, T. S., Schigel, D., Kennedy, P., Picard, K., Glöckner, F. O., Tedersoo, L., Saar, I., Kõljalg, U., & Abarenkov, K. (2019). The UNITE database for molecular identification of fungi: Handling dark taxa and parallel taxonomic classifications. Nucleic Acids Research, 47(D1), D259–D264.
17. Raaijmakers, J. M., & Mazzola, M. (2016). Soil immune responses. Science, 352(6292), 1392–1393.
18. Raja, H. A., Miller, A. N., Pearce, C. J., & Oberlies, N. H. (2017). Fungal identification using molecular tools: A primer for the natural products research community. Journal of Natural Products, 80(3), 756–770.
19. Schlatter, D., Kinkel, L., Thomashow, L., Weller, D., & Paulitz, T. (2017). Disease suppressive soils: New insights from the soil microbiome. Phytopathology, 107(11), 1284–1297.
20. Summerell, B. A. (2019). Resolving Fusarium: Current status of the genus. Annual Review of Phytopathology, 57, 323–339.