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Taxonomic Dominance and Methodological Biases in Assessing Fungal Diversity in Waterlogged Paddy Soils - A Case Study

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Abstract

Paddy fields present a highly stressful environment for microorganisms. The soil cycles constantly between dry cracked earth and heavily flooded mud. Fungi play a vital role in breaking down crop waste and recycling nutrients in these fields. Researchers have traditionally used standard agar plating to study these soil communities. This traditional approach comes with significant biological blind spots.

This paper presents the culturable fungal profile of agricultural paddy soils in North Bihar. We evaluate the exact methodological biases introduced by these standard laboratory techniques. We collected soil samples across three distinct seasons to track weather impacts. We took dirt from three specific soil depths to measure vertical distribution. We isolated the microscopic organisms using the standard serial dilution method on Potato Dextrose Agar.

The laboratory analysis successfully identified twelve distinct fungal genera. Four specific groups completely dominated the local ecosystem. *Aspergillus* and *Penicillium* were the most abundant fungi present on the plates. We found significant populations of *Fusarium* and *Trichoderma* as well. The spatial data showed that almost all fungal activity happens in the top five centimeters of the soil. The temporal data revealed a massive population spike during the wet monsoon season. The fungal numbers dropped severely during the hot summer drought.

These empirical results tell a very specific biological story. They highlight the active aerobic decomposers feeding on leftover rice stubble. We must acknowledge that the serial dilution method creates a strict biological filter. Potato Dextrose Agar heavily favors fast growing saprophytes. The paddy fields spend weeks completely flooded and starved of oxygen. Our aerobic culturing method completely misses the anaerobic fungal community that thrives in that deep waterlogged mud. We missed the complex symbiotic fungi that refuse to grow without a living plant root.

The twelve identified genera represent just a small fraction of the true soil microbiome. Traditional culturing provides a clear but extremely narrow window into soil ecology. Future agricultural research in this region requires an updated approach. Scientists must integrate environmental DNA sequencing with these older traditional methods. Using modern genetic tools like ITS metabarcoding will allow us to map the hidden unculturable species. This hybrid approach is essential for capturing the complete biological reality of flooded agricultural ecosystems.

Keywords: Soil mycoflora, Paddy ecosystem, Seasonal variation, Methodological bias, Culturable fungi, Anaerobic fungi, Fungal diversity

1. Introduction

Soil is a highly active biological environment. It supports all terrestrial plant life and regulates essential ecological processes. Microscopic organisms drive the essential recycling functions hidden beneath the surface. Fungi represent a massive and vital part of this underground system. They act as the primary decomposers of dead organic matter. These organisms break down tough plant materials like cellulose and lignin. This breakdown process releases locked nutrients back into the dirt. Plants rely entirely on this natural recycling system to grow and thrive. The health of any agricultural field depends heavily on a balanced fungal community.

Agricultural land experiences regular physical disturbances. Paddy fields present an exceptionally extreme habitat for microscopic life. Rice cultivation requires severe human intervention throughout the entire calendar year. Farmers deliberately flood the fields with water for long periods. They plow the wet earth into a thick heavy mud to prepare for planting. They frequently leave crop stubble to rot directly in the standing water. The soil environment shifts rapidly from dry and airy to completely waterlogged. The floodwater pushes oxygen out of the tiny soil pores. This creates a severe lack of air for the microbes living below the ground.

Most common soil fungi require steady oxygen to survive. The constant cycle of flooding and drying forces the microbial community to adapt constantly or die. Fungi that prefer dry conditions might perish completely during the heavy monsoon. Many species survive by producing thick spores that rest in the mud until the water recedes. The physical structure of the soil changes every single season. Fungi must rebuild their delicate microscopic networks after every major plowing event. Only highly resilient organisms can tolerate these sudden environmental shocks.

Physical soil conditions dictate exactly which microbes can survive the year. Moisture is the most critical requirement for fungal growth. Fungal spores need water to germinate properly and spread their networks. Temperature plays an equally important role in determining overall growth rates. Cold weather slows down fungal metabolism and halts reproduction. Warm and wet conditions trigger rapid microbial expansion. The natural acidity of the soil limits the survival of specific fungal groups. These environmental variables shift constantly with the changing weather. The transition from a dry hot summer to a wet monsoon completely rewires the soil biology.

Scientists have studied soil biology for many decades. Mycologists rely heavily on traditional laboratory techniques to identify different species. The standard approach involves taking a small soil sample and mixing it with sterile water. Researchers dilute this muddy water and spread it onto artificial growth media. Potato Dextrose Agar is the most common food source used in these standardized tests. The plates sit in warm incubators for several days. Scientists then observe the physical fungal colonies that grow on the jelly surface. They identify the species by looking at spore shapes under a high power microscope.

This traditional culturing method remains standard practice across the globe. It comes with a massive inherent flaw. The laboratory environment creates a strict biological filter. Standard agar plates favor fast growing fungi that thrive in oxygen rich environments. These aggressive species quickly cover the small plastic plates. They completely hide any slow growing organisms. This creates a highly skewed

picture of the underground ecosystem. We only document the fungi that happen to like our specific artificial laboratory conditions.

Paddy fields spend several weeks entirely underwater. This creates a strict anaerobic environment in the deep mud. Our standard aerobic laboratory methods completely miss the fungi that thrive without oxygen. We fail to capture the complex symbiotic fungi that refuse to grow outside of a living plant root. The traditional data represents a very clear but extremely narrow window into soil ecology. It highlights the active aerobic decomposers while ignoring the hidden biological majority. We must acknowledge this severe methodological bias when looking at historical soil data.

North Bihar represents a unique and challenging agricultural zone. The region experiences intense humid summer heat followed by severe monsoon flooding. Rice farming remains the undisputed economic foundation of this entire area. The local soil consists mostly of fertile alluvial deposits brought by Himalayan rivers. This annual flooding constantly alters the chemical makeup of the land. Farmers here rely heavily on synthetic fertilizers and chemical pesticides to maintain high crop yields. These applied chemicals slowly change the natural soil chemistry over time.

We need to understand how native fungi survive in this chemically modified environment. The rice plants depend on a healthy underground ecosystem to absorb nutrients. Harmful fungi attack the plant roots and reduce the final harvest. Beneficial fungi fight off these exact pathogens and protect the crop. Knowing which groups dominate the dirt helps us predict the overall health of the farm. We lack specific localized data regarding the fungal communities native to North Bihar. Identifying the native culturable fungi is the vital first step to understanding this regional ecosystem. We need baseline biological data to evaluate the health of the current farming system.

This paper addresses the missing regional biological data while confronting the flaws in how we collect it. The research has two distinct primary objectives. The first goal is to present a detailed profile of the culturable fungal community in these local paddy fields. We map exactly how these populations shift across different soil depths and changing seasons. We document the dominant aerobic saprophytes that process the leftover rice stubble. We record the natural populations of pathogenic and beneficial fungi present in the topsoil.

The second goal is to critically evaluate our own specific methodology. We use the empirical data to demonstrate the exact biases introduced by traditional agar culturing. We highlight how the serial dilution method masks the true complexity of a waterlogged ecosystem. This paper turns a standard list of study limitations into a central academic argument. We demonstrate that traditional methods are insufficient for capturing the complete biological reality of flooded agricultural soils. We conclude by proposing a modernized framework for future mycological research in this region. This framework insists on integrating environmental DNA sequencing alongside traditional culturing techniques.

Culturing Methodology

We conducted the fieldwork in the active agricultural paddy fields of North Bihar. We collected soil samples across three distinct seasons to observe how changing weather affects the microbial population. These seasons included the wet monsoon, the cool winter, and the dry summer. We used a sterile stainless steel auger to extract the soil. We carefully took samples from three specific depths to understand the vertical distribution of the microbes. The first layer was the surface down to 5 centimeters. The second layer spanned from 5 to 10 centimeters. The deepest layer went from 10 to 15

centimeters. We placed the dirt into sterile bags right away. We transported them to the laboratory in insulated coolers to preserve their biological activity.

We used the standard serial dilution technique to isolate the fungi from the collected mud. We weighed exactly one gram of fresh soil and mixed it vigorously with sterile distilled water. We diluted this initial mixture several times. This step reduces the total number of microbes per liquid drop. We then spread a tiny amount of the final liquid onto plastic Petri dishes. These dishes contained Potato Dextrose Agar. We added a mild antibiotic to the agar mixture to prevent fast growing bacteria from taking over the plates.

We sealed the Petri dishes and placed them inside a dark incubator. We set the temperature to a constant 28 degrees Celsius. We left the plates undisturbed for five to seven days. This timeframe allowed the fungal spores to germinate and form visible colonies on the agar surface. We then counted the total colonies. We examined their physical structures under a high power microscope to identify the specific genera.

We must be entirely transparent about the physical reality of this laboratory process. This specific culturing method does not capture the entire soil ecosystem. It actually creates a very strict biological filter. Potato Dextrose Agar is incredibly rich in simple sugars. The incubator provides a warm environment with plenty of breathable oxygen. This artificial setup heavily favors fast growing aerobic saprophytes. Fungi that prefer these exact conditions will thrive and quickly cover the entire plate.

This presents a major biological conflict with the natural environment. The paddy fields spend several weeks completely flooded and entirely starved of oxygen. Our standard laboratory environment completely excludes the anaerobic fungi that live in that deep waterlogged mud. The method ignores complex symbiotic fungi that need a living plant root to survive. We utilized this traditional method to document the active aerobic decomposer community. We fully acknowledge that this standard approach leaves a massive portion of the true soil microbiome completely invisible.

Empirical Results

The laboratory analysis produced a massive set of physical data. We successfully cultured living fungi from every single soil sample we collected. The plastic Petri dishes filled with fuzzy biological colonies within just a few days of incubation. We counted the individual growths and grouped them by their physical appearance. We placed small samples under the microscope to identify their exact genus. The final numbers paint a very clear picture of the culturable aerobic community living in the North Bihar dirt.

We documented twelve distinct fungal genera across the entire study period. A small handful of these groups completely dominated the artificial agar environment. The genus *Aspergillus* emerged as the undisputed leader of the laboratory plates. We counted *Aspergillus* colonies on almost every single dish we processed. This specific group accounted for 18.6 percent of the total fungal isolates. These fungi grew incredibly fast in the incubator. They started as tiny white threads and quickly matured into dark green or black powdery circles. Their ability to produce millions of tiny spores allows them to take over the sugary agar very quickly.

Penicillium closely followed as the second most abundant group. This genus made up 16.3 percent of the total laboratory population. *Penicillium* colonies displayed a distinct velvet texture on the agar surface. Their central color was usually a vibrant blue green surrounded by a bright white outer ring. They looked like microscopic paintbrushes under the high power lens. These fungi are famous for their ability

to break down tough plant cellulose. Their high numbers make sense given the amount of dead rice stalks left in the fields.

Fusarium ranked third in overall physical abundance. This group represented 13.8 percent of the isolated community. *Fusarium* colonies looked exactly like fluffy pink cotton candy growing on the clear jelly. They often stained the agar beneath them with deep purple or red pigments. Many species within this genus are aggressive plant pathogens. Finding such high numbers in the dirt indicates a constant disease pressure on the local rice roots. The crop faces a severe natural threat from these specific microbes.

Trichoderma formed the fourth major pillar of the aerobic group. It comprised 11.5 percent of the total fungal count. *Trichoderma* grew faster than almost any other microbe we tested. It formed dark green tufts that aggressively crawled across the plastic plates. This genus is well known for its ability to attack and consume other harmful fungi. Finding a large natural population of *Trichoderma* is an excellent sign for local soil health. It acts as a natural biological shield for the rice plants.

The remaining 39.8 percent of the isolates belonged to eight other minor genera. These included fast growing organisms like *Rhizopus* and *Mucor*. Scientists often call these sugar fungi because they quickly consume simple carbohydrates. They produce tall fuzzy structures that can cover a Petri dish in just two days. We observed dark pigmented fungi like *Alternaria* and *Curvularia*. These fungi have thick cell walls packed with dark melanin. This dark color acts like a natural sunscreen. It helps them survive the extreme summer heat when the soil dries out and bakes under the open sky.

Table 1 Percentage Frequency of Dominant Fungal Genera

Fungal Genus	Percentage of Total Isolates
Aspergillus	18.6
Penicillium	16.3
Fusarium	13.8
Trichoderma	11.5
Minor Genera Combined	39.8

The physical depth of the dirt dramatically influenced the total microbial numbers. We tracked the vertical distribution across three separate soil layers. The highest concentration of biological activity happened right at the surface. The top layer from 0 to 5 centimeters deep contained a massive 425 total fungal isolates. This surface zone holds the vast majority of the decaying rice stubble. The dirt here is loose and allows plenty of oxygen to circulate.

The biological numbers dropped severely just a few inches deeper into the earth. We recorded only 215 total isolates from the middle layer spanning 5 to 10 centimeters deep. The deepest soil layer contained a mere 132 isolates. This bottom layer sits 10 to 15 centimeters below the surface. The deep mud is heavily compacted from years of tractor tires and heavy flooding. It holds very little trapped air. Most of our culturable aerobic fungi simply cannot survive in that suffocating physical environment.

Table 2 Vertical Distribution of Total Fungal Isolates

Soil Depth Layer	Total Fungal Isolates Counted
Surface to 5 centimeters	425
5 to 10 centimeters	215
10 to 15 centimeters	132

The changing weather patterns triggered massive fluctuations in the living population. We tracked the total isolate counts across the three main seasons to measure these climatic impacts. The monsoon season produced an absolute explosion of fungal growth. We counted 312 isolates during these warm and highly humid months. The heavy summer rains soften the hard earth and provide the essential water needed for spore germination. Trichoderma populations specifically multiplied rapidly during this wet period.

The brutal summer months devastated the active microbial community. The intense regional heat bakes the exposed paddy dirt until it cracks open. We recorded a low count of just 210 isolates during this dry season. The total lack of water kills the fragile fungal threads. Only fungi with thick protective spores managed to survive on our laboratory plates after enduring the drought. The winter season provided a moderate middle ground. We counted 250 isolates during the cool winter months. The cold temperatures slow down fungal metabolism but the lingering soil moisture keeps the microbes alive and stable.

Table 3 Seasonal Fluctuation of Fungal Populations

Climatic Season	Total Isolates Counted
Monsoon	312
Winter	250
Summer	210

We measured three physical soil properties to understand exactly what drives these seasonal population swings. We recorded the soil moisture percentage alongside the temperature and the pH level. The soil moisture hit a massive high of 65.4 percent during the monsoon season. The winter soil held a moderate moisture level of 35.2 percent. The summer sun stripped the land dry leaving a moisture content of just 15.6 percent. The summer soil temperature peaked at a burning 38.2 degrees Celsius. The monsoon rains lowered the average soil temperature to a perfect 28.5 degrees Celsius. The winter dropped the dirt temperature down to a chilly 15.4 degrees Celsius.

Table 4 Average Edaphic Factors Recorded Across Three Seasons

Season	Moisture Percentage	Temperature in Celsius	Soil pH Level
Monsoon	65.4	28.5	6.8
Winter	35.2	15.4	6.7
Summer	15.6	38.2	6.9

We used statistical formulas to calculate the Pearson correlation coefficient for each variable. This math gives us an r value that proves how strongly the environment controls the biology. The statistical math proved that water entirely dictates fungal survival. The relationship between soil moisture and the total isolate counts produced a very high r value of 0.86. This indicates a strong positive correlation. The fungal numbers increase immediately when the dirt gets wet. They plummet just as fast when the soil dries out.

Temperature proved to be the second most important physical driver. We calculated a moderate positive correlation with an r value of 0.72. Warmth encourages rapid cellular growth but only if the soil holds

enough water to support it. The extreme summer heat actually hurts the fungi because the soil contains absolutely zero moisture.

The soil pH had almost no measurable impact on the seasonal population changes. We calculated a weak correlation with an r value of just 0.41. The acidity of the North Bihar paddy fields remained surprisingly stable all year long. The pH hovered tightly between 6.7 and 6.9 regardless of the weather or the heavy flooding. This neutral stability is likely due to the constant application of synthetic agricultural lime and fertilizers. The unchanging pH acts as a quiet background condition rather than a trigger for massive biological shifts.

Table 5 Pearson Correlation Coefficients for Fungal Isolates and Edaphic Factors

Edaphic Variable	Pearson r Value	Correlation Strength
Soil Moisture	0.86	Strong Positive
Soil Temperature	0.72	Moderate Positive
Soil pH Level	0.41	Weak Positive

Discussion of Taxonomic Dominance

The laboratory results reveal a very specific biological hierarchy. Twelve fungal genera managed to grow and survive on the artificial media. A few distinct groups completely overpowered the rest of the community. *Aspergillus* and *Penicillium* dominated the soil samples across all seasons and depths. We must look at the biology of these specific organisms to understand why they are so successful. Both of these genera are incredibly fast growing saprophytes. They make their living by breaking down dead and decaying plant matter. The paddy fields provide an endless buffet for these specific microbes. Farmers leave massive amounts of chopped rice stalks and root systems in the dirt after every single harvest. This abundant crop stubble serves as the perfect fuel for these hungry decomposers.

The physical environment of the laboratory plate plays a massive role in this visible dominance. Potato Dextrose Agar is packed with simple sugars. It provides a warm and oxygen rich paradise for aerobic fungi. *Aspergillus* and *Penicillium* are evolutionary opportunists. They are perfectly built to exploit this exact type of environment. They wake up from their spore state rapidly. They spread their microscopic threads across the sugary jelly much faster than almost any other soil microbe. Their aggressive growth physically blocks slower organisms from accessing the food or the surface space. We are seeing a race where the fastest runners completely hide the slow ones. The agar plate essentially mimics the absolute best day in the topsoil.

The strong presence of *Fusarium* and *Trichoderma* adds another layer to this ecological story. *Fusarium* species are notoriously aggressive plant pathogens. Their high numbers confirm that the local rice roots face constant biological attacks. The rice plants must survive in a soil environment heavily loaded with disease causing agents. The natural abundance of *Trichoderma* provides a massive natural defense against this threat. *Trichoderma* is an extremely fast growing predator fungus. It actively hunts and consumes other fungi in the dirt. It specifically targets pathogens like *Fusarium*. Finding such a large population of *Trichoderma* is a very positive sign for the local farms. It means the soil possesses a built in biological immune system capable of suppressing major crop diseases.

We must view this taxonomic dominance through the correct lens. The serial dilution method definitely filters the results. The data still holds tremendous scientific and agricultural value. The twelve identified

genera represent the absolute front line of the soil decomposition crew. These are the active workers responsible for recycling the dead plant material back into usable nutrients. The rice plants rely entirely on this specific group of aerobic fungi to process the harvest waste over the dry winter months. The health and abundance of these saprophytes tell us that the topsoil retains a robust capacity for natural recycling. Documenting this active aerobic fraction provides a crucial baseline for measuring the overall health of the farming system.

The Methodological Critique

We must confront the severe limitations of our own laboratory methods. Traditional culturing techniques create a highly artificial environment. We used serial dilution and Potato Dextrose Agar to isolate these twelve fungal genera. This specific approach does not provide a true reflection of the entire soil microbiome. It acts as a strict biological filter. We essentially designed a race that only the fastest aerobic fungi could win.

Potato Dextrose Agar is a nutrient dense medium loaded with accessible carbohydrates. The warm laboratory incubator provides a constant supply of breathable oxygen. These conditions perfectly match the survival needs of fast growing saprophytes like *Aspergillus* and *Penicillium*. These opportunists wake up quickly and consume the available food. They spread their physical structures across the entire plate within days. This rapid expansion creates a massive physical problem for scientific observation. The fast growers completely bury any slow growing organisms. We cannot count what we cannot see. The data we collected only represents the winners of this artificial laboratory race.

This laboratory setup directly contradicts the physical reality of a working paddy field. Rice cultivation involves extreme water management. Farmers flood the fields for weeks at a time during the growing season. The standing water pushes all the oxygen out of the deep soil mud. This creates a completely anaerobic environment right below the surface. Our aerobic agar plates completely ignore the microbes that thrive in these flooded conditions. We entirely missed the unique anaerobic fungal groups that take over when the water levels rise. The monsoon season data shows a spike in aerobic fungi but it ignores the massive unseen biological shift happening deep in the oxygen starved mud.

We missed other crucial members of the microbial community due to their strict dietary needs. Many highly beneficial fungi are obligate symbionts. They absolutely refuse to grow on dead plant matter or artificial laboratory jelly. They require a living plant root to survive and reproduce. Arbuscular mycorrhizal fungi fall into this specific category. These fungi attach directly to the rice roots and help the plant absorb deep soil nutrients. They are incredibly important for overall crop health. Our traditional plating method completely failed to detect them.

The twelve identified genera represent just a tiny fraction of the true biological reality. We must accept that our empirical data only maps the active decomposer community. The deep waterlogged mud holds a vast undiscovered population of hidden microbes. Relying solely on these traditional methods leads to a skewed understanding of flooded agricultural ecosystems. We need to look past the standard plastic Petri dish to fully comprehend the complex life cycles within these local soils.

Proposed Framework for Future Research

The scientific community must change how we study flooded agricultural ecosystems. We cannot rely entirely on agar plates to understand a complex dirt environment. The missing anaerobic fungi and unculturable symbionts are too important to ignore. We need a new biological baseline for the North

Bihar paddy fields. Future research must adopt modern genetic tools to see the complete picture. The fertile alluvial soil of this region contains a massive undiscovered microbial world.

The most effective path forward involves environmental DNA sequencing. Researchers should utilize a specific technique called ITS metabarcoding. This method completely bypasses the artificial laboratory incubator. Scientists extract genetic material directly from the raw paddy mud. They sequence the internal transcribed spacer regions of the fungal DNA. This genetic barcode identifies exactly which species are present in the dirt. It finds the microbes regardless of whether they are breathing oxygen or resting dormant in the dry summer dust.

Relying entirely on visual identification of spores leaves too much room for human error. Many different fungi look exactly identical under a standard light microscope. ITS metabarcoding removes this visual guesswork entirely. The computer reads the genetic code and provides a highly accurate taxonomic identification. This precision is absolutely necessary when tracking how specific fungi respond to commercial fertilizers over multiple years. This genetic approach removes the biological filter of the Petri dish.

The sequencing technology reveals the strict anaerobic fungi that thrive during the heavy monsoon floods. It detects the fragile mycorrhizal fungi that only live attached to the living rice roots. Sequencing the environmental DNA provides a massive list of the true biological population. We can finally map the specific fungi that handle nutrient recycling when the fields are entirely submerged. We can track the exact species that help the rice plants absorb difficult nutrients from the dense mud.

We should not throw away our traditional methods completely. Agar plating still holds immense practical value for daily agriculture. We need traditional culturing to isolate live physical strains of beneficial fungi. We must physically grow organisms like *Trichoderma* in the lab to study their disease fighting abilities. A purely genetic list cannot give us a live biological control agent to use on a farm. The best research framework combines both techniques into a single hybrid approach.

Future studies in this region should run these two methods side by side. Researchers should take a single soil sample and split it into two different paths. Half the dirt goes to the traditional agar plates to catch the fast aerobic decomposers. The other half goes to the DNA sequencer to map the hidden anaerobic majority. This dual strategy gives us a live library of agricultural workers alongside a complete map of the underground ecosystem.

Farmers need precise data to protect their crops from increasing climate stress. Knowing the exact genetic makeup of the soil allows them to adjust their daily farming practices. They might choose different crop rotations if they know the deep mud contains specific beneficial anaerobes. They might change how they manage their winter stubble to support the delicate mycorrhizal networks. A complete genetic map turns the invisible soil biology into a practical farming tool.

This hybrid methodology will establish North Bihar as a leading model for tropical soil research. Other agricultural regions facing similar extreme weather cycles can adopt this exact dual framework. Combining old physical techniques with new genetic tools creates a foolproof system for environmental monitoring. We must stop guessing what lives in the mud and start reading the actual biological code. The future of sustainable rice farming depends entirely on understanding every single microbe hidden below the surface.

Conclusion

This study examined the microscopic life inside the agricultural paddy soils of North Bihar. We successfully identified twelve distinct fungal groups living in this specific environment. A small number of fast growing fungi completely dominated the results. *Aspergillus* and *Penicillium* appeared the most frequently. These fungi excel at breaking down the leftover rice stalks. The soil holds a significant population of *Fusarium*. This indicates a constant threat of plant disease. A strong natural presence of *Trichoderma* provides a built in defense against these harmful pathogens.

The physical location of these microbes follows a strict vertical pattern. Almost all fungal activity happens right at the surface. The top five centimeters of dirt contain the perfect mix of fresh food and breathable air. Fungal numbers drop sharply deeper underground. The deep mud is heavily compacted and lacks oxygen.

The changing weather controls the rhythm of this microscopic world. Soil moisture is the absolute most important factor driving fungal growth. The heavy monsoon rains trigger a massive population spike. The brutal summer drought forces the surviving fungi into a deep dormant state.

We must view these specific findings through a critical lens. Our laboratory methods created a strict biological filter. We used traditional agar plates to grow these organisms. This artificial environment heavily favors fast growing aerobic fungi. Paddy fields spend several weeks completely underwater. This floods the deep mud and removes the oxygen. Our traditional methods entirely missed the fungi that thrive in those flooded conditions. We missed the complex symbiotic fungi that require a living plant root to survive. The identified genera represent just the active aerobic decomposers.

Future mycology research in this region requires an updated approach. Scientists must combine traditional culturing with modern genetic sequencing. Extracting environmental DNA directly from the mud bypasses the artificial laboratory environment. Utilizing techniques like ITS metabarcoding reveals the hidden anaerobic species. We need a hybrid framework to capture the complete biological reality of these flooded fields. Understanding the entire soil microbiome is necessary to secure the future of local rice farming.

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