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By adjusting the local bacterial and protistan populations, organic fertilisation practices reduce fungal plant diseases.

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Research Article

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Abstract

Fungal plant diseases pose a serious concern to global food security and are a growing hazard to commercially significant crop output globally. However, our understanding of the underlying ecological processes and how agricultural management techniques influence the establishment and spread of diseases inside crop microbiomes is inadequate. In sorghum phyllosphere, root endosphere, rhizosphere, and bulk soils obtained from a long-term experiment with various inorganic and organic fertilisation regimes, we described the profiles of possible fungal plant pathogens as well as bacterial and protistan populations. The four sorghum-soil compartments showed different patterns of fungal plant pathogens, and the organic fertilisation regime considerably decreased the variety and proportions of fungal plant pathogens in bulk soils and the rhizosphere. We also discovered that resident bacterial and protistan populations, rather than soil physicochemical factors, were the primary drivers of changes in fungal plant diseases. Sorghum yield and protein levels were substantially correlated negatively with the variety of fungal plant diseases in the rhizosphere and bulk soils. Long-term organic fertilisation regimes were shown to inhibit fungal plant diseases primarily by modifying the resident bacterial and protistan populations, according to structural equation modelling.

KEYWORDS

Protists, organic fertiliser, fungal plant pathogens, crop microbiome, and sustainable agriculture

1 INTRODUCTION

Global food output is expected to significantly decline as a consequence of outbreaks of plant illnesses brought on by soil-borne fungal and oomycete pathogens.¹⁻³ Fungal plant diseases are predicted to become more prevalent at continental or global sizes under future climatic scenarios (such as increasing precipitation and climate warming), with unclear implications for stable agricultural productivity and global food security.^{6, 7} Despite the widespread prevalence of fungal plant diseases in soil and their functional and economic significance, little is known about the critical elements influencing their occurrence in plant-soil systems and effective strategies for controlling their environmental occurrence.⁸ The prevalence and composition of fungal pathogens can be influenced by a variety of edaphic factors and environmental drivers, including soil pH, nutrients, temperature, and precipitation. At the same time, anthropogenic disturbances like fertilisation, tillage, grazing, land-use changes, and pesticide application can also have an impact. In order to predict plant health and performance and to develop focused methods to address the problem of developing crop diseases, it is especially crucial to comprehend how plant infections respond to environmental stress. In different compartments like

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the phyllosphere, rhizosphere, and endosphere, plant-associated microorganisms (also known as the plant microbiome) expand the genomic and metabolic capacities of hosts and play a crucial role in a wide range of vital processes like immune regulation, stress tolerance, and nutrient uptake.^{10, 11} Plant-soil microbiome interactions may be harmful or beneficial. (e.g., fungal plant diseases) to neutral to very helpful (e.g., plant beneficial microorganisms) to the plant,¹² with profound effects on ecosystem functioning, plant performance, and fitness.^{5, 13} More significantly, it is known that plant-associated beneficial microbes play a significant role in strengthening the host's resistance against soil-borne plant pathogens. This may be due to direct antagonism through the production of antibiotics or volatiles, competition with pathogens for niches, induction of systemic or induced resistance through the production of compounds like salicylic acid, or direct predation of pathogenic microbes.^{17–19} Optimising plant-soil-microbe partnerships to improve soil protection against fungal diseases is a viable approach, given the crucial role that plant-microorganism and microorganism-microorganism interactions play in disease suppression. Agricultural management techniques may have a favourable or negative impact on plant-associated microbiomes, leading to changes in the microbiomes' taxonomy and functions. Numerous recent studies have examined the effects of common agricultural management practices (such as inorganic and organic fertilisation regimes) and abiotic factors (such as climatic and edaphic factors) on crop productivity and the structure and functions of microbiomes associated with soil and plants.^{13, 21, 22} However, most of them only addressed bacteria, fungi, and protists (^{21, 23, 24}), and we know very little about how agricultural management methods affect fungal plant diseases in different plant compartments. By altering trophic biological interactions and the relative abundances of pathogenic and beneficial microbes that are expected to affect plant pathogenesis, agricultural management techniques often affect the dynamics of microbial communities. Fertilisation schedules might affect fungal plant diseases either directly by changing the physicochemical characteristics of the soil or indirectly by changing the microbial populations, which are known to be crucial in suppressing plant pathogens.^{12, 15} Therefore, in order to predict the future patterns of fungal plant pathogens under intensive agricultural management, which will ultimately contribute to global food security, a better understanding of the effects of agricultural practices (such as organic and inorganic fertilisation regimes) and particularly biotic factors is crucial. The development of sustainable agricultural systems will greatly benefit from agricultural management strategies that may boost the number of helpful microorganisms while lowering plant pathogens.²⁷ In order to assess the effects of different inorganic and organic fertilisation treatments on the amounts, variety, and compositions of fungal plant pathogens in different sorghum-soil compartments, we collected soil and plant samples from a long-term experimental location. A significant cereal crop that is well suited to dry and semiarid regions, sorghum is used to provide food and biofuel.²⁸ The sustainable production of sorghum is seriously threatened by fungal plant diseases, which are acknowledged as a significant and ongoing barrier to grain production. The variety of fungal pathogens in sorghum crops and the relationships between infections and other elements of sorghum-associated microbiomes are currently poorly understood. In order to understand the ecological processes underpinning the existence of fungal plant diseases in plant and soil systems, we sought to identify the most important biotic and abiotic variables influencing their diversity and abundance. We investigated the hypothesis that organic fertilisation, as opposed to inorganic fertilisation, may help decrease soil-borne fungal infections by altering the native microbial populations.

2 | MATERIALS AND METHODS

2.1 | Site description and sample collection

In September 2019, soil and plant samples were taken at a long-term experimental station located in Don-gyang, Shanxi Province, China (37° 33' 21' N, 112° 40' 2' E). According to USDA soil

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taxonomy, the soil at this location is sandy loam with 86.7% sand, 11.6% silt, and 1.7% clay. It also has a sorghum-maize rotation system. This location has a mean annual temperature of 9.7° C and a mean annual precipitation of 321 mm. In 2011, a randomised block design was used to establish six organic and in-organic fertilisation treatments in triplicate plots (15 × 5 m²/plot): control treatment without fertilisation (CON), nitrogen (N) + phosphorous (P) + potassium (K) (NPK), NPK + organic manure (NPKM), NPK + organic manure + straw (NPKMS), organic manure + straw (MSD). In the NPK treatment, N was administered as urea at a rate of 225 kilogram N per hectare annually, P as diammonium phosphate at a rate of 60 kg P₂O₅ per hectare annually, and K as potassium sulphate at a rate of 60 kg K₂O per hectare annually. At a rate of 45 m³ per hectare, or 100 kilogram N, 56 kg P₂O₅, and 69 kg K₂O per hectare, organic manure in the form of cow dung was applied. 6150 kilograms of straw, or 49 kg N, 11 kg P₂O₅, and 139 kg K₂O per acre, were used in the straw application treatments. The original purpose of this fertilisation experiment was to investigate how different fertilisation regimes affected crop yield and soil fertility. At the sorghum ripening stage, we gathered all plant and soil samples. Five randomly selected soil cores were mixed at a distance of 30 cm from the plants to create a composite bulk soil (0–10 cm) inside each plot. Samples of plant leaves were taken from sorghum plants at a height of around 60 cm above the ground. Samples of rhizosphere soil were taken from the soils that were affixed to the roots of sorghum plants. Every sample was transported on ice to the Fujian Normal University laboratory. Before soil physicochemical parameters were measured, soil samples were sieved to a size of 2 mm and either kept at 4° C or –80° C prior to DNA extraction. As soon as the leaf samples arrived, they were utilised to isolate DNA. Sorghum protein content was evaluated as an indication of sorghum quality, while sorghum yield was recorded as an indicator of sorghum productivity.

2.2 | Soil physicochemical analysis and DNA extraction;

The amount of dissolved organic carbon (DOC) in soil was measured using 0.45 µm filtered water extracts (1:4 of the soil:water ratio). A flow analyser (Skalar) was used to determine the NO[–] and NH⁺–N concentrations of the soil. The combustion technique was used to determine the total nitrogen (TN) and total carbon (TC) of soil samples using an element analyser (Vario MAX C/N). Using a heating-acid-digestion technique, total phosphorus (TP) was extracted and measured using a flow analyser. The DNeasy PowerSoil DNA Isolation kit (Qiagen) was used to extract rhizosphere and bulk soil DNA in accordance with the manufacturer's instructions. As previously mentioned, the DNeasy PowerSoil DNA Isolation kit (Qiagen) was used to extract the genomic DNA of leaf phyllosphere microorganisms from 5.0 g leaf samples. The DNeasy PowerSoil DNA Isolation kit (Qiagen) was used to isolate DNA from 13 sorghum root samples after they had been surface sterilised and crushed with liquid nitrogen. The NanoDrop One spectrophotometer (Thermo Fisher Scientific) was used to measure the concentration and purity of DNA.

2.3 | Amplicon sequencing and bioinformatic analyses:

Using the primers F-TAR-euk454FWD1 and R-TAReukREV3, 30 515F and 806R, 31 and ITS1F and ITS2R, 32, respectively, the eukaryotic 18S ribosomal ribonucleic acid (rRNA) gene, bacterial 16S rRNA gene, and fungal ITS1 region were amplified and sequenced on the Illumina Miseq platform (Illumina). In QIIME.33, raw sequences were quality-filtered to exclude reads with unclear nucleotides, a poor quality score (Q < 20), and a short length (<100 bp). To eliminate all chimeric sequences, we used the USEARCH tool, which is based on the UCHIME algorithm. The Protist Ribosomal Reference (PR2) database was used to taxonomically assign the eukaryotic 18S rRNA gene sequences for protists. 34. Taxonomic assignments for bacteria and fungus were made using the Silva35 and UNITE databases, respectively. Prior to the downstream analysis, bacterial sequences that matched host mitochondria and chloroplasts were eliminated. Operational taxonomic units (OTUs) were found using UPARSE v7.0.1090.37 at a 97% similarity level. Prior to the examination of OTU richness across various compartments and treatments, the number of sequences per sample was rarefied to 47,541 for fungus, 30,828 for protists, and 30,079 for bacteria. The FUNGuild database, which has been extensively used in many recent research, was utilised to forecast potential fungal plant

diseases.4, 5, 9 In this research, potential fungal plant pathogens were categorised into “highly probable” or “probable” categories using a FUNGuild assignment that incorporated the word “pathotroph.”^{9,38} Raw sequences with accession number PRJNA648662 (SRP273724) have been added to the NCBI Sequence Read Archive (SRA).

2.4 | Statistical analyses:

The significant variations in the richness and proportions of possible fungal pathogens across treatments and compartments at $p < 0.05$ were compared using analysis of variance (ANOVA) tests. Principal coordinates analysis (PCoA) based on the Bray-Curtis dissimilarity was carried out using the “vegan” package³⁹ in R to identify the variations in the fungal plant pathogen compositions across treatments and compartments. A multifactorial per-mutational analysis of variance (PERMANOVA) was then used to determine whether the differences were statistically significant. In the subsequent analyses, the change in the compositions of fungal pathogenic communities was represented by the first component (PCoA1). In order to assess the contributions of soil properties, protistan, and bacterial community compositions to the variation in the fungal pathogenic community composition in the “vegan” package, variation partitioning analysis was performed. The “UpSetR” package was used to visualise the variation partitioning result. The impacts of biotic and abiotic variables on the proportions of fungal plant diseases in the “randomForest” package were estimated using random forest analysis. Forty Using R’s “lm” function, we used ordinary least squares (OLS) to investigate the connections between the richness of fungal plant pathogens and sorghum production and protein contents. Using Amos Graphics v22 (IBM Corp.), a structural equation model (SEM) was built to determine the effects of compartments, fertilisation treatments, soil properties, protistan and bacterial community compositions, and sorghum yield and protein contents on the composition of the fungal plant pathogenic community. All potential paths between these parameters were included into the a priori model. The Bentler comparative fit index (CFI), goodness-of-fit index (GFI), and χ^2 test all showed the overall model fit.

3 | RESULTS :

3.1 | Impacts of fertilization on the diversity and community composition of potential fungal plant pathogens:

A total of 4,824,904 high-quality sequences were obtained from amplicon sequencing of the ITS1 region, and the FUNGuild database was used to identify 435 OTUs of potential fungal diseases. The root endosphere had the lowest value of the detected OTU richness of possible fungal plant diseases, whereas bulk soil had the greatest value (Figure 1a). The community structure of fungal plant pathogens was significantly separated across several plant-soil compartments, according to PCoA analysis (Figure 1b). 78.08% of all fungal sequences in the phyllosphere, 44.58% in the root endosphere, 10.25% in rhizosphere soils, and 16.29% in bulk soils were potential fungal plant pathogens (Figure 1c). In each plant compartment, we further described how the diversity and community compositions of possible fungal plant diseases responded to fertilisation treatments (Figure 2). In the phyllosphere and root endosphere, organic fertilisation (including the MS, NPKM, NPKMSD, and NPKMS treatments) did not significantly affect the OTU richness or community compositions of potential fungal plant pathogens; however, in the rhizosphere and bulk soils, it significantly decreased the OTU richness and proportions of fungal plant pathogens and altered their community compositions (Figure 2a-c).

3.2 | Biotic and abiotic factors driving the patterns of potential fungal plant pathogens:

As biotic variables, Spearman’s correlation showed strong relationships between the relative abundances of prominent fungal plant diseases and those of bacterial and protistan taxa (at the

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genus level, top 10 most prevalent genera), but modest correlations with abiotic factors (Figure 3a). The proportions of fungal plant pathogens were best predicted by dominating bacterial and protistan species and less by abiotic variables, according to random forest modelling (Figure 3a). For instance, *Sphingomonas*, *Microbacterium*, *Sandonidae_X*, and *Polymyxa* were the best biotic predictors of *Alternaria*, *Cladosporeum*, and *Epicoccum*; *Streptomyces*, *Sandonidae_X*, *Pseudoplatyophrya*, *Polymyxa*, and *Glissomonadida_Clade-Y_X* were the best predictors of *Fusarium* and *Periconia*; and *Pseudomonas* and *Cercomonas* were the best biotic predictors of *Gibberella* and *Nectria*. Fungal plant pathogens belonging to the phyla Ascomycota, Basidiomycota, and Chytridiomycota displayed extensive positive and negative associations with many taxa belonging to key bacterial phyla and protistan phyla, according to our further study (Figure 3b). Interestingly, *Sandonidae_X* and *Hyphochytrium* exhibited only negative relationships with fungal pathogen taxa, but protistan groupings like *Neoheteromita* and *Polymyxa* had only positive connections. *Blastococcus*, *Curtobacterium*, *Gaialla*, *Lechevalieria*, *Solirubrobacter*, *Lyso-bacter*, and *Skermancella* had negative associations with fungal pathogen taxa, but *Microbacterium*, *Aureimonas*, and *Neorhizobium* were mostly favourably associated. To determine the relative contributions of biotic (bacterial and protistan communities) and abiotic (soil physicochemical qualities) variables on the patterns of fungal plant diseases, variation partitioning analysis was performed (Figure 4). In all four sorghum-soil compartments, the composition of the bacterial and protistan communities explained a greater percentage of the variance in fungal plant pathogens than soil parameters (Figure 4). It's interesting to note that the majority of the variance in fungal plant pathogens in both rhizosphere soils (64%) and bulk soils (51%) was explained by the interplay of soil characteristics, bacterial, and protistan community compositions (Figure 4). The interactions between fertilisation treatments, compartments, soil characteristics, and community compositions of bacteria and protists were subsequently investigated using structural equation modelling (SEM).

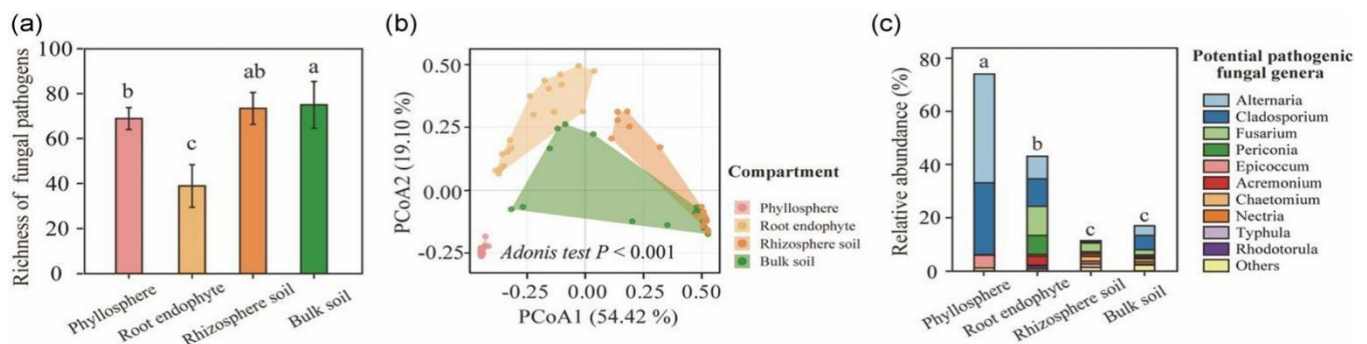


FIGURE 1 Potential fungal plant pathogens' operational taxonomic unit richness in several sorghum-soil compartments (a). The general distribution pattern of possible fungal plant pathogens across several compartments is shown using principal coordinate analysis (PCoA) based on the Bray-Curtis distance (b). Variations in possible fungal plant pathogenic genera' relative abundances across various compartments (c). Significant differences at $p < 0.05$ are indicated by different letters above the boxes.

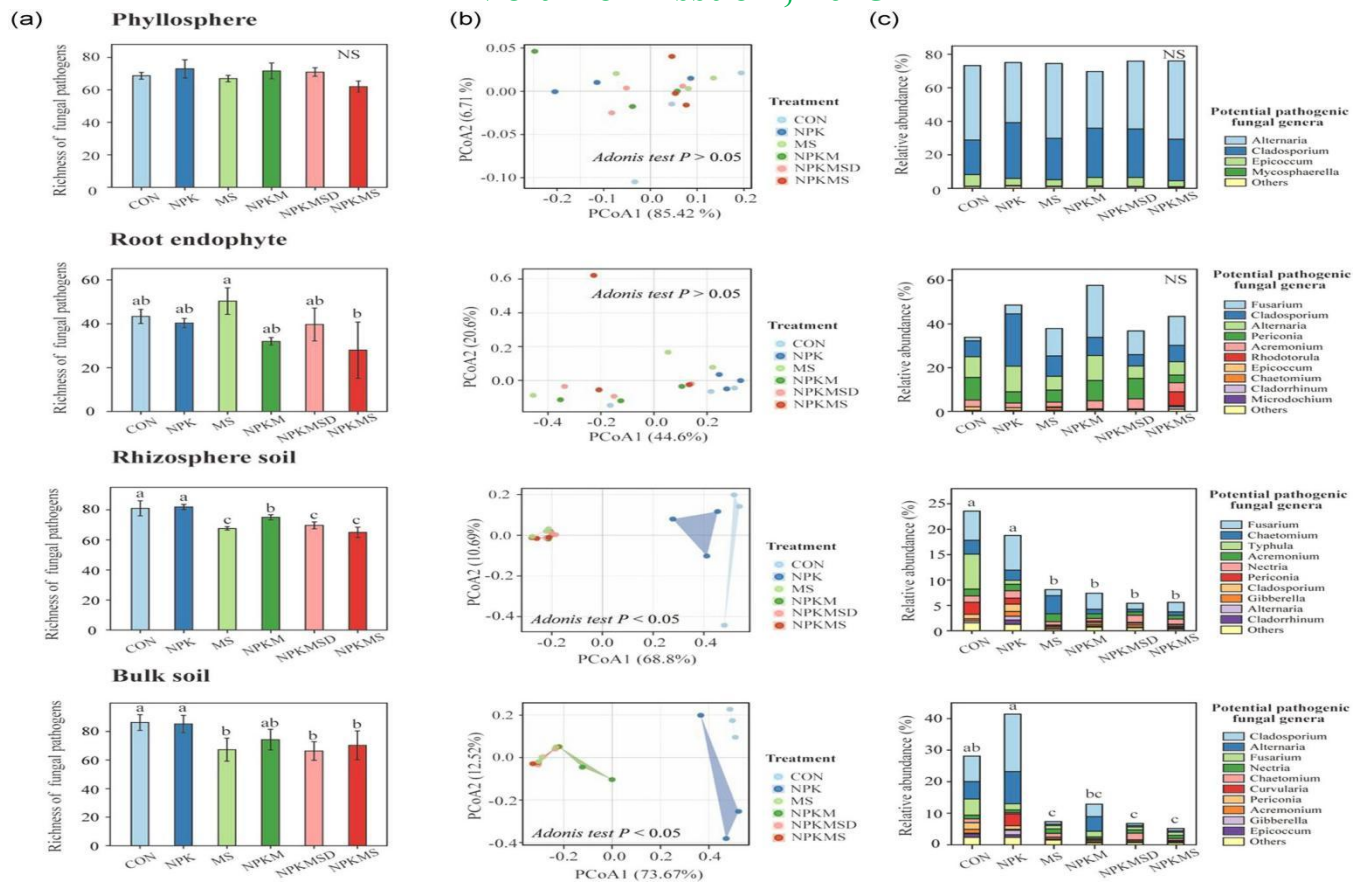


FIGURE 2 Diversity and compositions of fungal plant pathogenic communities across different sorghum

departments. Fungal plant pathogens' operational taxonomic unit richness under various fertilisation conditions (a). The general distribution pattern of the fungal plant pathogenic population in each compartment is shown using principal coordinate analysis (PCoA) classified by fertilisation treatments based on the Bray-Curtis distance (b). Variations in the relative abundances of helpful fungal genera (d) and potentially harmful fungal plant genera (c) throughout fertilisation treatments in various sorghum compartments. Significant differences at $p < 0.05$ and fungal pathogens, together with their effects on sorghum yield and protein levels, are shown by different letters above the boxes (Figure 5). By altering soil characteristics as well as bacterial and protozoan communities, we discovered that fertilisation had a substantial effect on the fungal pathogenic community compositions (Figure 5a). Additionally, sorghum-soil compartments may have a direct or indirect effect on the compositions of fungal pathogenic communities by modifying the compositions of bacterial and fungal communities (Figure 5a). Sorghum yield and protein contents were found to be negatively impacted by fungal pathogens (Figure 5b). This finding was corroborated by negative correlations between the richness of fungal pathogens and sorghum yield and protein contents in both rhizosphere and bulk soils (Figure 6). With the exception of a strong negative association in the root endosphere, no significant correlations were discovered between the richness of fungal pathogens and sorghum production or protein content in the phyllosphere or root endosphere (Figure 6).

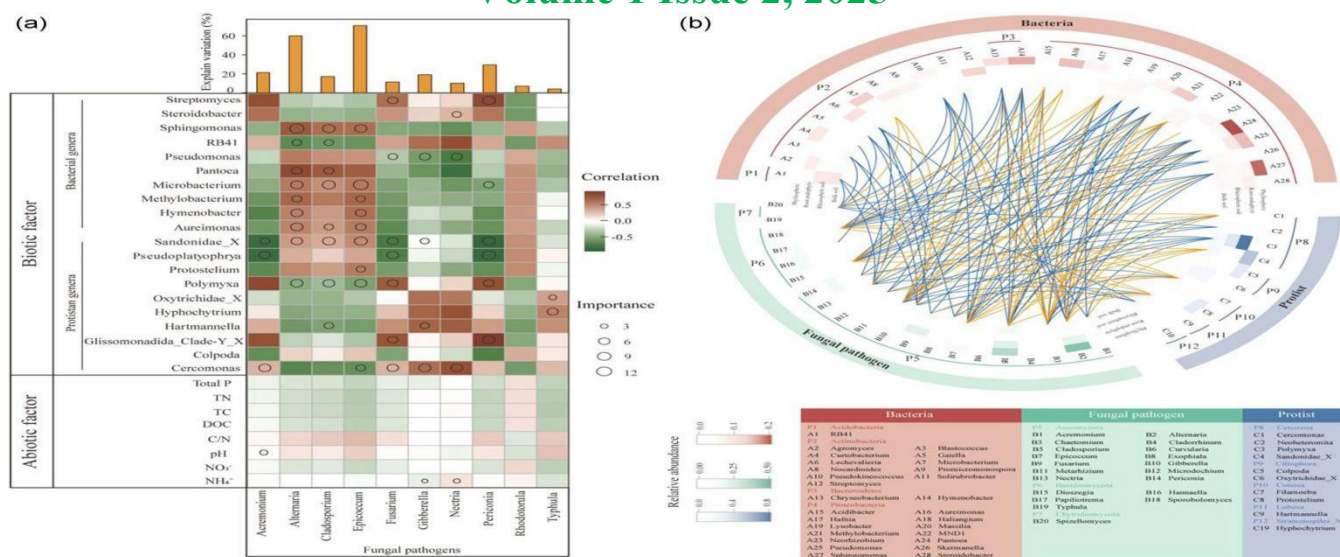
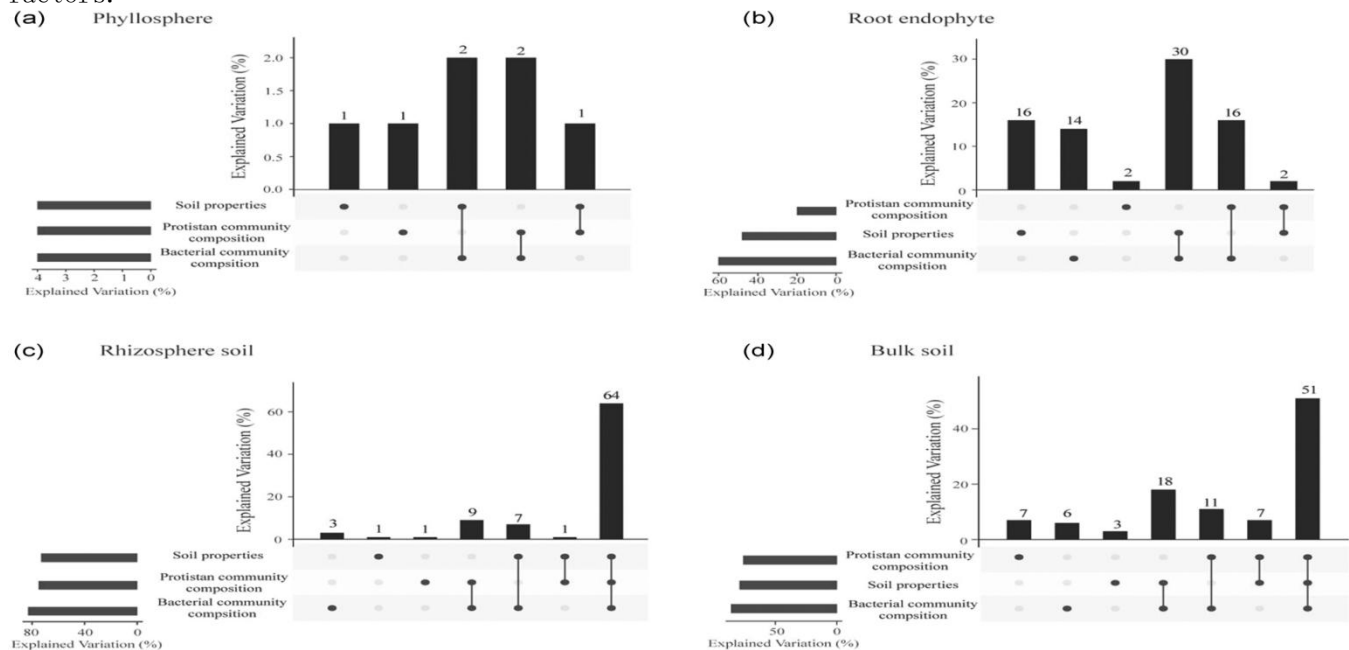


FIGURE 3 (a) The relationship between biotic (including the top 10 bacterial and protistan genera) and abiotic variables and the relative abundance of the top 10 fungal plant diseases in all plant and soil samples. The caption shows that the fill colour correlates to the Spearman's correlation coefficient. Circles (% IncSME) represent the significance of each determinant as determined by the Random Forest model. (b) The correlation between important bacterial and protistan taxa and the relative prevalence of fungal plant diseases. The connections between the primary bacterial and protistan populations and fungal plant diseases are shown by orange lines, which indicate positive associations, and blue lines, which indicate negative relationships. The relative abundance of important bacterial and protistan species as well as fungal plant diseases is correlated with fill colour.

4 DISCUSSION

Although both organic and inorganic fertilisation regimes are often used in agricultural management to increase crop yield, little is known about how they affect fungal plant diseases in different crop plant compartments or the underlying ecological processes. Current agricultural practices, such as monocultures and intense chemical fertilisation, are known to lower soil organic matter content⁴¹ and promote the establishment and spread of novel fungal plant diseases, endangering several major commodity and calorie crops worldwide.⁷ It is crucial to have a thorough knowledge of how plant pathogens react to anthropogenic management methods and how biotic and abiotic variables affect their presence within crop microbiomes in order to build proper disease control strategies under future environmental change scenarios. In this long-term field-based study, we present new evidence that long-term organic fertilisation could successfully lower the proportions of potential fungal plant pathogens in bulk soils and sorghum rhizosphere soils (but not in phyllosphere and root endosphere), potentially by altering soil characteristics and the bacterial and protist community compositions. The fungal plant pathogenic community compositions inside the sorghum-associated microbiomes are shown to be significantly influenced by sorghum-soil compartments (Figure 1b). According to earlier research, microbial community diversity and structure significantly vary across different compartments, from rhizosphere soil to root endosphere,^{42,43} indicating the significance of the unique circumstances of compartments in the processes of microbial community formation. Fungal plant pathogens were found to be much more prevalent in the phyllosphere and root endosphere of sorghum-associated microbiomes than in the rhizosphere and bulk soils (Figure 1c). This result might be explained by the fact that, according to our earlier research utilising the same soil and plant samples, the diversity of microorganisms in the phyllosphere and root endosphere is much lower than in the rhizosphere and bulk soils.¹³ The diversity and composition of the soil microbial population are

thought factors. to be significant disease



suppression,

FIGURE 4 Variation partitioning models indicate the influence of soil characteristics, bacterial communities, and protistan populations on fungal plant diseases in several sorghum-associated compartments. The characteristics of the soil were pH, DOC, TN, TC, C/N, TP, NO₃⁻-N, and NH₄⁺-N. The driving elements of the associated bar are represented by the points or points linked by a line. The barplot on the left shows the overall magnitude of each driving force. As shown by the lower suppressive powers of sterilised soils in comparison to unsterile soils, every potential junction is represented by the bottom plot, and its occurrence (i.e., the numbers above bars) is depicted on the top barplot. The comparatively lower percentage of fungal plant pathogens in rhizosphere and bulk soils may be explained by their comparatively larger microbial diversity. Additionally, we discovered that a large number of the fungal plant diseases identified in this research, including *Alternaria* and *Fusarium*, are worldwide prevalent in soils and probably have an effect on sorghum crop yield. For instance, many pathogenic fungal species, mostly from the genera *Fusarium*, *Curvularia*, and *Alternaria*, produce grain mould, a common sorghum disease. The negative correlations between sorghum yields and protein levels (as measures of grain quality) and the richness of fungal pathogens demonstrate this (Figure 6). However, it should be noted that the occurrence of disease caused by fungal plant pathogens depends on a number of factors (e.g., the interaction of a virulent pathogen with a susceptible host under permissive conditions), and the presence of these fungal pathogens does not always indicate the actual occurrence. A vast variety of bacteria, fungus, and protists are known as plant-associated microorganisms, and their interactions together control plant health and disease. Through trophic predator-prey interactions, protists—the primary predators of microbes—and bacteria—the primary rivals of fungi—may play a significant role in controlling fungal plant diseases in the plant microbiome. Plant pathogens may be directly consumed by some protist species, particularly phagotrophs. *Neoheteromita*, *Sandonidae_X*, *Colpoda*, *Filamoeba*, and *Hartmannella* (Figure 3b) are some common protistan species that represent significant consumer groups that could be able to outcompete fungal diseases. Protists' selective predation on bacteria may also encourage the development of bacteria with the ability to produce secondary compounds that inhibit pathogens. By directly consuming fungal plant pathogens and by altering the functional and taxonomic makeup of bacteria due to predation, these protists may contribute to plant disease. Consequently, it is not unexpected that the protistan community was shown to be a significant factor influencing the

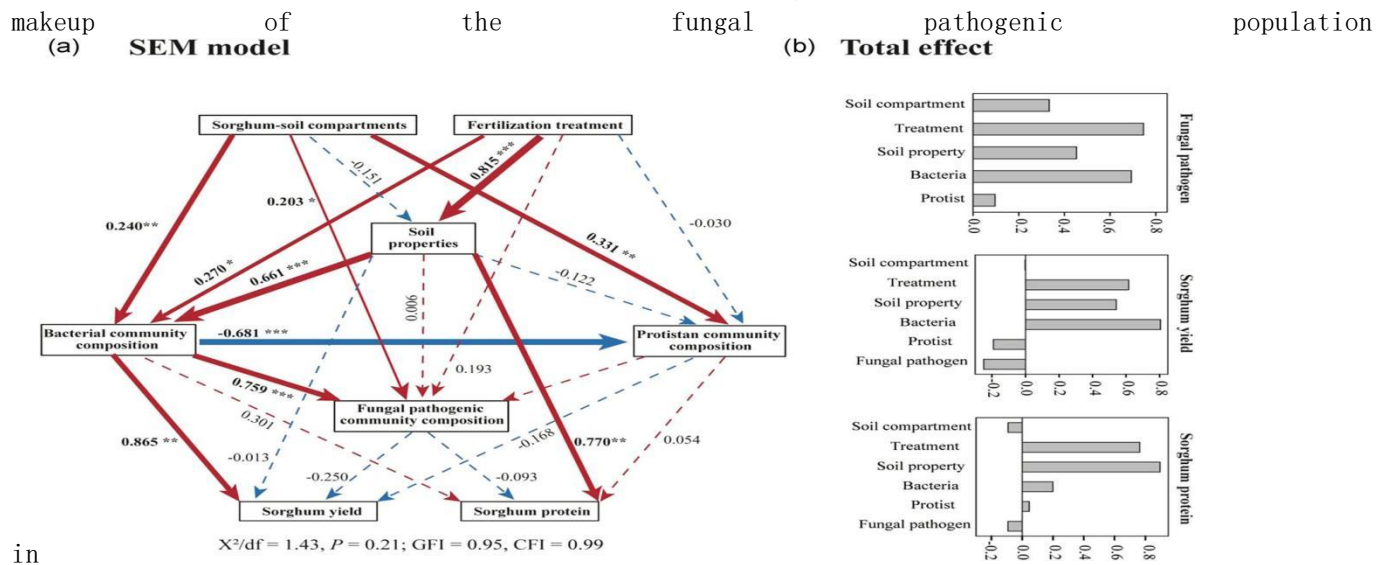
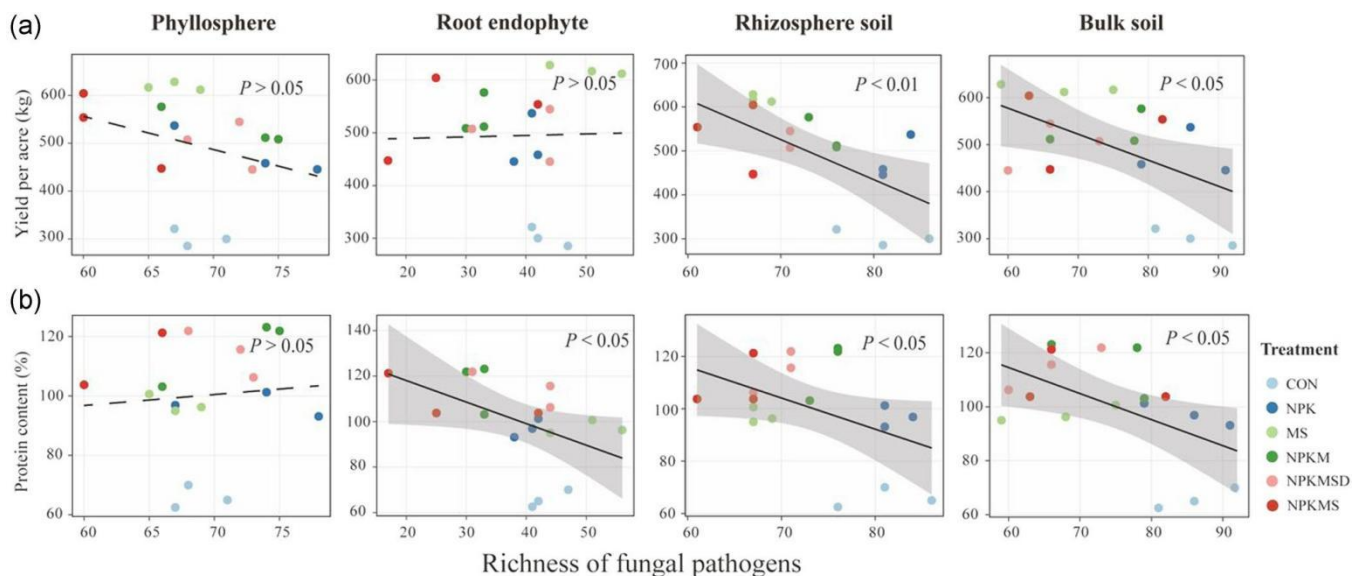


FIGURE 5 The correlations between fertilisation treatments, compartments, soil characteristics, protists, bacteria, fungal plant pathogenic community compositions in rhizosphere and bulk soils, and sorghum yield and protein contents are shown using structural equation modelling (SEM) (a). The significant and nonsignificant correlations are shown by continuous and dashed arrows, respectively. Path coefficients are represented by an adjacent integer in the same direction as the arrow, and the degree of path coefficients is correlated with the arrow's width. * $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$ are used to indicate significance levels. The overall standardised impacts of several parameters on the protein levels, sorghum yield, and fungal plant pathogenic community compositions (b). Comparative fit index (CFI) and goodness-of-fit index (GFI)

FIGURE 6 Relationships between the richness of fungal plant pathogens with sorghum yield (a) and



The ordinary least square regression models of the four sorghum-soil compartments showed the protein contents (b) in each compartment (Figures 4 and 5). In addition to pro-tists, the makeup of the fungal pathogenic population was shown to be significantly influenced by the bacterial

community (Figures 4 and 5). A long-term field research found that changes in bacterial populations in the rhizosphere soils were closely correlated with the dynamics of the take-all disease in wheat (*Triticum aestivum*), which is caused by the pathogenic fungus *Gaeumannomyces graminis* var. *tritici*.⁴⁹ According to other research, plants with a greater diversity of microbial communities are less likely to be infected by pathogens than those with a lower diversity of microbial communities. Possible explanations for this include competition with fungal pathogens for niches, direct antagonism of the pathogens through the production of volatile organic compounds with antifungal functions, or induction of systemic or induced resistance through the production of compounds like salicylic acid.¹⁶ Future research is necessary to better understand how interactions between bacterial and protistan populations impact fungal plant diseases, since interactions among the plant-associated microbiomes are very complex and dynamic. One of the study's main conclusions is that organic fertilisation may effectively lower the percentages of fungal plant pathogens in bulk and rhizosphere soils (Figure 2), most likely by modifying the resident bacterial and protistan populations and altering the characteristics of the soil (Figure 5). Through their effects on the structure and function of the native soil microbiomes, organic fertilisers may reduce the prevalence of fungal plant pathogens.¹⁸ However, the ecological processes behind organic fertilisers' disease-suppressive activities are yet unclear.⁵² Agricultural management techniques were linked to the structure of the soil microbial community and their impact on the suppression of the fungal pathogen *Rhizoctonia solani* AG3 in soils, according to a prior research.²⁵ Here, we show that organic fertilisation may largely alter the diversity and community compositions of bacteria, which in turn affected the protistan communities (because bacteria are crucial protist food sources) (Figure 5). Fungal plant diseases are subsequently suppressed by the resultant alterations in the bacterial and protistan populations as well as the corresponding changes in soil characteristics. Organic fertilisers may have been colonised by certain kinds of hostile microorganisms, or they may have encouraged the development of plant-beneficial microbes, such as protists and bacteria, which may help suppress harmful germs.⁴¹ Through the addition of exogenous organic materials, organic fertilisation may also modify the nutritional status of the soil, which fundamentally changes the interactions between the microbiome and the plant, as well as the interactions between the microbiome and other microbiomes and, crucially, the microbiome-mediated suppression of fungal plant diseases. Together, we suggest that changes in the composition and function of the bacterial and protistan communities brought about by organic fertilisation are probably involved in controlling the growth of fungal plant diseases and, consequently, plant health.

5 | CONCLUSION

All things considered, this long-term field-based study offered fresh proof that organic fertilisation might lower the proportions of fungal plant diseases by modifying the bacterial and protistan populations that live in the soil. We demonstrate that, in addition to bacteria, protists may operate as important factors that control the incidence of fungal plant diseases by a comprehensive microbiome investigation of fungus, protists, and bacteria in different sorghum-plant compartments. According to our research, applying organic fertilizers—whether or not they are mixed with inorganic fertilizers—may have the potential to improve soils' ability to suppress disease and provide resources for managing pathogens. These findings have significant ramifications for the development of more focused microbiome engineering techniques to achieve the desired positive benefits and lessen the negative consequences of fungal diseases on the supply of fibre, food security, and social economics.

REFERENCES

1. Fisher MC, Madoff LC, McCraw SL, Briggs CJ, Brownstein JS, Henk DA, et al. new fungal risks to the health of plants, animals, and ecosystems. *Nature*, 2012, 484:186–94.
2. Fitt BDL, Qi A, and Newbery F. Modelling the effects of climate change on diseases of arable crops: developments, difficulties, and uses. *Curr Opin Plant Biol*. 32:101–9, 2016.
3. Scott PR, Strange RN. Plant diseases pose a risk to the world's food security. *Annu Rev Phytopathol*. 43:83–116, 2005.

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4. Delgado-Baquerizo M, Egidi E, Wang JT, Eisenhauer N, Guerra CA, Cano-Díaz C, et al. Globally, the percentage of soil-borne infections rises as temperatures rise. *National Climate Change*, 2020, 10: 550-4.
5. Chen QL, Hu HW, Yan ZZ, Li CY, Nguyen BAT, Zhu YG, et al. Fungal plant pathogen abundance in the Eucalyptus phyllosphere is increased by precipitation. 2021; 23:7688 - 700; *Environ Microbiol*.
6. Saunders DGO, Corredor-Moreno P. Anticipating the unexpected: elements affecting the development of oomycete and fungal plant diseases. 2020; 225:118 - 25; *New Phytol*.
7. Fones HN, Bebbler DP, Chaloner TM, Kay WT, Steinberg G, Gurr SJ. Emerging fungal and oomycete crop diseases pose a threat to global food security. *Nat Food*, 2020, 1:332 - 42.
8. Tian B, Xie J, Fu Y, Li B, Chen T, Cheng J, et al. Cereal crops are shielded from serious fungal diseases by an endophytic lifestyle adopted by a worldwide fungal pathogen of dicots. *ISME J*. 14:3120 - 35, 2020.
9. Delavaux CS, Bever JD, House GL, Schemanski JL, Tipton AG, and Sikes B. In undisturbed grasslands, root pathogen diversity and composition fluctuate with climate; in anthropogenically damaged grasslands, this is less the case. *ISME J*. 15:304 - 17, 2021.
10. Vorholt JA, Vogel C, Bai Y, Muller DB. Plant microbiota: views and insights at the system level. *Annu Rev Genet*. 50:211 - 34, 2016.
11. Trivedi P, Singh BK, Leach JE, Tringe SG, Sa T. Plant-microbiome interactions: from plant health to community formation. *Nat Rev Microbiol*. 2020; 18:607 - 21.
12. Berendsen RL, Pieterse CM, Bakker PA. Plant health and the rhizosphere microbiota. *Plant Science Trends*, 2012, 17:478 - 86.
13. Sun AQ, Jiao X, Chen Q, Li Z, Li F, Trivedi P, et al. In crop-associated microbiomes, fertilisation modifies parasites and protistan consumers. 2021; 23:2169 - 83; *Environ Microbiol*.
14. Mazzola M. Bacterial populations in the rhizosphere are manipulated to create suppressive soils. *J. Nematol*. 39:213 - 20 (2007).
15. Mendes R, Kruijt M, de Bruijn I, Dekkers E, van der Voort M, Schneider JH, et al. Interpreting the rhizosphere microbiome for microbes that reduce illness. *Science*, 2011, 332:1097 - 100.
16. Havis ND, Ratsep J, Walters DR. Future problems in employing induced resistance to control crop diseases. *J Exp Bot*. 64: 1263 - 80, 2013.
17. Mendes R, Garbeva P, Raaijmakers JM. The rhizosphere microbiome: importance of plant beneficial, plant pathogenic, and human pathogenic bacteria. *FEMS Microbiol Rev*. 37:634 - 63, 2013.
18. Bio-organic fertilisers increase native soil *Pseudomonas* populations to improve plant disease suppression (Tao CY, Li R, Xiong W, Shen Z, Liu S, Wang B, et al. *Microbiome*, 2020, 8:137.
19. Xiong W, Song Y, Yang K, Gu Y, Wei Z, Kowalchuk GA, et al. Plant health is significantly influenced by rhizosphere protists. *microbiome*. 2020, 8:27.
20. Cordovez V, Dini-Andreote F, Carrion VJ, Raaijmakers JM. Plant microbiome ecology and evolution. *Annu Rev Microbiol*. 73:69 - 88, 2019.
21. Sun AQ, Jiao X, Chen QL, Wu AL, Zheng Y, Lin YX, et al. Crop phyllosphere and root endosphere microbial populations are more resistant to fertilisation than soil microbiota. *Soil Biol Biochem*. 153:108113, 2021.
22. Yan ZZ, Chen QL, Li CY, Nguyen BAT, Zhu YG, He JZ, et al. In natural ecosystems, different biogeographic patterns between phyllosphere and soil resistomes are directly driven by biotic and abiotic variables. *ISME Commun*. 2021, 1:13.
23. Chen S, Waghmode TR, Sun R, Kuramae EE, Hu C, Liu B. Wheat root-associated microbiomes under the combined influence of nitrogen fertilisation and plant growth. *microbiome*. 2019, 7:136.
24. Xiong C, He JZ, Singh BK, Zhu YG, Wang JT, Li PP, et al. Rare taxa sustain ecosystem functioning and crop microbiomes. 2021; 23:1907 - 24. *Environ Microbiol*.
25. Garbeva P, van Veen JA, van Elsas JD, Postma J. *Rhizoctonia solani* AG3 suppression and the influence of above-ground plant species on the organization of the soil microbial community. *Environ Microbiol*. 2006; 8:233 - 46.

International Journal of Eco-Agriculture and Sustainable Technologies

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26. Saad MM, Hirt H, Eida AA. A road map for the effective use of plant-associated microbial inoculants in agriculture. *J Exp Bot.* 71:3878–901, 2020.
27. Busby PE, Soman C, Wagner MR, Friesen ML, Kremer J, Bennett A, et al. Priorities for plant microbiome use in sustainable agriculture research. *PLoS Biol.* 15:e2001793, 2017.
28. Pathogen infection affects a unique microbial community composition in sorghum RILs. *Plant Soil.* 2021;463:555–72. Masenya K, Thompson GD, Tekere M, Makhalanyane TP, Pierneef RE, Rees DJG.
29. Nida H, Kee S, Li Y, Mengiste T. Defence regulators and metabolic pathways linked to resistance are revealed by transcriptome analysis of early stages of sorghum grain mould disease. *BMC Genom.* 22:295, 2021.
30. Stoeck T, Breiner H-W, Jones MDM, Bass D, Nebel M, Christen R, and others. In marine anoxic water, a very complex eukaryotic population is shown by multiple marker parallel tag environmental DNA sequencing. *Mol Ecol.* 19:21–31 (2010).
31. Bates ST, Berg-Lyons D, Caporaso JG, Walters WA, Knight R, Fierer N. Investigating the distribution of main soil archaeal populations worldwide. *ISME J.* 5:908–17 (2010).
32. Orgiazzi A, Lumini E, Nilsson RH, Girlanda M, Vizzini A, Bonfante P, et al. Dissecting soil fungus populations from various Mediterranean land-use contexts. *PLoS One*, 7:e34847, 2012.
33. Caporaso JG, Kuczynski J, Stombaugh J, Bittinger K, Bushman FD, Costello EK, et al. QIIME enables high-throughput community sequencing data processing. *Nat Methods.* 2010; 7:335–6.
34. Guillou L, Bittner L, Audic S, Bass D, Bachar D, Berney C, et al. A collection of unicellular eukaryotic small subunit rRNA sequences with carefully chosen taxonomy is called the Protist Ribosomal Reference database (PR2). 2012; 41:597–604; *Nucleic Acids Res.*
35. Pruesse E, Quast C, Knittel K, Fuchs BM, Ludwig W, Peplies J, et al. SILVA: an extensive web-based resource for ARB-compatible ribosomal RNA sequencing data that has been quality-checked and aligned. *Nucl Acids Res.* 35:7188–96, 2007.
36. Nilsson RH, Larsson KH, Taylor AFS, Bengtsson-Palme J, Jeppesen TS, Schigel D, et al. The UNITE database for molecular fungal identification: managing parallel taxonomic classifications and dark taxa. 2019; 47:259–64; *Nucleic Acids Res.*
37. Edgar RC. UPARSE: microbial amplicon readings provide very precise OTU sequences. *Nat Methods.* 2013; 10:996–8.
38. FUNGuild: an open annotation tool for processing fungal community datasets by ecological guild. Nguyen NH, Song Z, Bates ST, Branco S, Tedersoo L, Menke J, et al.
39. Oksanen J, Blanchet FG, Kindt R, Legendre P, O'Hara RB, Simpson G, et al. Package "vegan": community ecology package. *Fungal Ecol.* 20:241–8. R package version 2. 2017; 4.
40. Wiener M, Liaw A. Random Forest classification and regression. *R News*, 2002, 2:18–22.
41. De Corato U. Natural soil suppressiveness against soil-borne plant pathogens is enhanced by disease-suppressive compost: a comprehensive assessment. *Rhizosphere.* 2020, 13:100192.
42. Duran P, Thiergart T, Garrido-Oter R, Agler M, Kemen E, Schulze-Lefert P, et al. Arabidopsis viability is enhanced by microbial interkingdom interactions in roots. *Cell.* 2018;175:973–83.
43. Macia-Vicente JG, Nam B, Thines M. In three naturally occurring Brassicaceae, the composition of root-associated fungus and oomycetes is determined by root filtration rather than host identity or age. 2020; 146:107806; *Soil Biol Biochem.*
44. Bebbler DP, Ramotowski MA, Gurr SJ. In a warmer world, crop pests and diseases migrate poleward.
45. Gao Z, Karlsson I, Geisen S, Kowalchuk G, Jousset A. Protists: puppet masters of the rhizosphere microbiome. *Nat Clim Change.* 2013; 3:985–8. *Plant Science Trends*, 24:165–76, 2019.
46. Chen QL, Yan ZZ, Li CY, He JZ, Hu HW, Nguyen BA. The variety and makeup of protistan consumers and phototrophs in natural soil ecosystems are determined by many causes. 2021; 160:108317; *Soil Biol Biochem.*
47. Geisen S, Bonkowski M, Dumack K, Urich T, Koller R, Kunninghaus M. A review of the soil food chain reveals a large variety of mycophagous soil protists. *Soil Biol Biochem.* 94:10–8, 2016.
48. Mazzola M, de Bruijn I, Cohen MF, Raaijmakers JM. *Pseudomonas fluorescens* uses protozoan-induced control of cyclic lipopeptide production as an efficient predation defence mechanism. 2009; 75:6804–11; *Appl Environ Microbiol.*

International Journal of Eco-Agriculture and Sustainable Technologies

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49. Rhizosphere bacterial populations linked to disease suppressiveness phases of take-all decline in wheat monoculture Sanguin H, Sarniguet A, Gazengel K, Mo'ne-Loccoz Y, Grundmann GL. New Phytol. 184:694-707, 2009.
50. van Elsas JD, Elhottova D, Kristufek V, Chiurazzi M, Mallon CA, Salles JF. The invasion of soil by a bacterial pathogen is determined by microbial diversity. PNAS, 2012, 109:1159-64.
51. Singh A, Lasek-Nesselquist E, Chaturvedi V, Chaturvedi S. Among soil microorganisms, *Trichoderma polysporum* specifically suppresses *Pseudogymnoascus destructans*, the fungal pathogen responsible for white-nose syndrome. Microbiome, 2018, 6:139-49.
52. Vestberg M, Kukkonen S, Rantala S, Prochazka P, Tuohimetsa S, Setälä H, et al. Finnish commercial compost's ability to suppress soil-borne illness. Acta Hort. 891:59-65 (2011).