

Review Article

A REVIEW ON SOIL AND PHYTOMICROBIOME FOR PLANT DISEASE MANAGEMENT

ABSTRACT:

Pests and pathogens significantly reduce crop yields and cost the global economy USD 540 billion annually. The phytomicrobiome is becoming a cornerstone of a comprehensive rethink of agricultural management practices, with microbiome-assisted plant breeding focusing on three principles: minimal soil disturbance, continuous soil cover with crops, cover crops, or a mulch of crop residues, and crop rotation. Plant diseases, phytomicrobiomes, and agricultural practices can all affect plant health. Conservation agricultural practices like minimum tillage and no-tillage have been implemented to reduce anthropogenic activity and preserve microbial diversity. Mulching is a common practice in agriculture to stop moisture loss, maintain soil temperature, control weed growth, and stop soil erosion. Monoculture farming is the practice of cultivating a single crop continuously over several growing seasons on the same field. Intercropping systems encourage the growth of beneficial fungi, such as mycorrhiza, endophytes, saprophytes, decomposers, and bioprotective fungi, and can benefit forest ecosystems by creating disease-suppressive soils. By combining conservation tillage and crop rotation, farmers can reduce disease pressure by disrupting the life cycles of soil-borne pathogens linked to particular crops or genotypes. Composted manure and plant residues can control plant pathogens like *Pythium*, but the effect is thought to be due to microbial competition or plant host resistance. Green manure can control plant diseases brought on by pathogens in *Rhizoctonia*, *Verticillium*, *Sclerotinia*, *Phytophthora*, *Pythium*, *Aphanomyces*, and *Macrophomina*, but manure-derived fertilizers may contain antibiotic resistance genes and mobilomes, which could pose risks to both human and animal health. Climate change impacts crop yields by reducing crop physiology and productivity, increasing pathogen diversity, and affecting pathogen genetic traits and speciation. The state of the environment and the availability of suitable hosts significantly impact the ability of these pathogens to survive and spread. However, PGPRs are unpredictable and soil warming can interfere with their effectiveness. Interdisciplinary collaborations between plant biologists, microbiologists, climatologists, and agronomists are required to create effective strategies to reduce the effects of climate change on plant health, crop production, and ecosystem stability.

Comment [b1]: ?

Keywords: Phytomicrobiome, Soil, pests, fertilizers, pathogens, manures and plant residues

1. INTRODUCTION:

Food security will become a top concern as the world population is expected to increase to 9.7 billion people by 2050 and 10.4 billion by 2100 [1]. Food insecurity is a result of pests and plant-threatening pathogens that reduce crop yields by 20 to 40 percent globally and cost the global economy USD 540 billion annually [2,3]. The phytomicrobiome and its interactions with the environment are becoming a cornerstone of a comprehensive rethink of agricultural management practices as people become more aware of the harm that chemical pesticides cause to human, animal, and environmental health. Research on the microbiome has expanded quickly to include many fields, including medicine, food science, marine science, forestry, aquaculture, and agriculture. The term "microbiome" refers to a broad range of metabolites and structural components found in microorganisms, including proteins and their subunits. The microorganisms connected to any internal or external part of a plant, from the surface to the ground, as well as the outcomes of their activity, is referred to as the phytomicrobiome [4]. In situ manipulations of resident microorganisms through agronomic practices without the need for industrial-scale production are two broad phytomicrobiome-based approaches that may provide alternative strategies for plant disease suppression and management. Direct introduction of microorganisms as inoculants to ecosystems is another. It is based on three principles: (i) minimal soil disturbance or absence of tillage; (ii) continuous soil cover with crops, cover crops, or a mulch of crop residues; and (iii) crop rotation [5]. Conservation agriculture is a prime example of this strategy. While breeding is not a primary focus of conservation agriculture, which places more emphasis on farming

Comment [b2]: ? two approaches

methods, it is important to note that microbiome-assisted plant breeding, which involves choosing plants based on their improved capacity to attract beneficial microorganisms, can be viewed as falling under the second category from a wider perspective [6]. The discovery of the precise genetic loci in charge of these traits has made this significantly more likely [6]. The review will focus on the implications for improving ecosystem resilience as it examines the difficulties and barriers involved with identifying and using the phytomicrobiome for plant disease management. It will also look at possible effects of climate change on phytomicrobiome functioning, including plant pathogens. The research field's applicability spans forestry and landscape management in urban and non-urban settings, among other areas [7].

Comment [b3]: Which areas?

2. Plant diseases, phytomicrobiomes and agricultural practices

The phytomicrobiome, which signals the root and modifies its rhizosphere microbiome, is crucial for supporting soil health, plant health, and disease mitigation [8]. Due to their antagonistic ability and use of management techniques like tillage and crop rotation, suppressive soils serve as the first line of defense against particular nematodes and pathogens [9]. With enrichment in *Pseudomonas* species, suppressiveness can be either general or specific, connected to different diseases. *Flavobacterium*, *Chryseobacterium*, *Burkholderia* and *Streptomyces* are some additional functional guilds accountable for the suppression of soil-specific microbial populations [9, 10]. Following World War II, agricultural practices like the use of pesticides and chemical fertilizers have seriously harmed the microbial life that inhabits arable soils. In order to improve soil fertility and plant pathogen suppression, sustainable agricultural practices modulate the phytomicrobiome for the entire agroecosystem.

2.1 Tillage

Tillage is a common management technique for soil distribution and weed containment. Conventional tillage (CT) can alter the chemical composition of soil and harm soil aggregates, which reduces the diversity and abundance of soil microbiota [11-15]. Extended tillage led to nutrient-poor soils and wind-mediated soil erosion, as seen in the Dust Bowl events in the US and Canada. In order to reduce anthropogenic activity and preserve microbial diversity, conservational agricultural practices like minimum tillage (MT) and no-tillage (NT) have been implemented [16,17]. Positive outcomes from MT and NT include improved arbuscular mycorrhizal colonization, elevated soil carbon levels, and microbial activity. Increased total nitrogen and available nitrogen, as well as an expansion of bacterial communities involved in nitrogen cycling, have all been linked to long-term NT [18,19]. A destructive pathogen that causes Fusarium crown rot or Fusarium head blight, *Fusariumgraminearum*, does not thrive as well in soils under MT because they have more diverse bacterial communities. Our ability to draw firm conclusions about disease management is, however, constrained by the incomplete evaluation of the direct impact on plant disease suppressiveness. In systems like *Pythiummultimum*—*Lepidium sativum* (cress) and *Fusariumgraminearum*-*Triticumaestivum* (wheat), some studies have shown that long-term NT or continuous application of MT can enhance soil suppressiveness [20,21]. Other studies in the Netherlands' arable rotation systems have found little effect of tillage practices on soil suppressiveness against *Rhizoctoniasolani* and *Streptomyces scabies*. When used in conjunction with other conservational agronomic techniques, NT has frequently shown to effectively suppress diseases like take-all brought on by *Gaeumannomycesgraminis* var. *Fusariumpseudograminearum* and Fusarium crown rot are brought on by *F. culmorum* [22].

2.2 Mulching

In order to stop moisture loss, maintain soil temperature, control weed growth, and stop soil erosion, mulching is a common practice in agriculture. However, it has both beneficial and detrimental effects on the health of the soil and plants. Particularly in arid regions, inorganic mulching techniques like plastic film mulching (PFM) are preferred because they have immediate economic advantages like increased crop yield, improved crop quality, reduced water usage, and lower inputs. PFM also encourages soil solarization, increases microbial activity, and reduces soil-borne plant diseases. It has been demonstrated that long-term mulching improves plant root growth, increases Arbuscular Mycorrhizal Fungi (AMF) colonization, and increases bacterial diversity [23,24]. However, it also has drawbacks, including increased carbon/nitrogen metabolism, accelerated biodegradation of soil organic matter (SOM), and the emergence of a new microbial community niche known as the "plastisphere," which may house potential pathogenic organisms [25,26-29]. To address these issues, biodegradable plastic films such as those made of starch-based polymers have been introduced. Mulches made of

organic materials, such as leaves, straw, or wood chips, are an alternative to inorganic plastic mulches. By adding vital elements to the soil, such as carbon, nitrogen, and phosphorus, organic mulching enhances soil physical properties and nutrient uptake by plant roots [30,31-34]. Organic mulches can maintain a favorable soil environment for plant development and growth, which is less conducive to pathogen proliferation and disease establishment [35,36]. In the early stages of decomposition, plant residues in organic mulches readily decompose, enriching the soil with a nutrient pool and encouraging the activity of bacterial communities involved in decomposition, denitrification, and nitrification processes [37,38]. They can control the temperature and moisture of the soil, lessen the arrival of aphids and fungus spores, and perhaps even lessen the prevalence of some diseases. However, depending on the specific type of mulch used, the efficacy of organic mulches may differ. It is essential to use disease-free mulch and to stay away from mulch made from sick plants if you want to stop the introduction or spread of plant pathogens. While mulching can have a number of advantages for enhancing plant and soil health, it's important to understand that other cropping techniques, like crop rotation and soil amendments, can also help prevent disease and promote nutrient-rich soil [35].

2.3 Polyculture vs Monoculture

Monocultural farming is the practice of cultivating a single crop continuously over several growing seasons on the same field. Field farming systems, horticulture, and agroforestry all struggle with this system. Farmers often substitute monocultures of high-value cash crops for intercropping and crop rotation as the world's population rises in an effort to increase yields, profits, and manageable costs [39,40]. But because long-term monocropping disturbs the soil's microecological environment, it has a negative impact on soil health and has led to an increase in plant diseases. A legacy of low Soil Organic Carbon (SOC) and nitrogen, as well as a proliferation of saprotrophic and pathogenic microbes, is left behind by the negative plant-soil feedback over time, ultimately resulting in decreased yields and nutrient-poor soils [41–41]. After a significant disease outbreak, persistent monoculture of susceptible hosts can occasionally paradoxically cause specific suppression against the causative agent. For instance, ongoing barley and wheat monoculture has resulted in a phenomenon known as "take-all decline" (TAD), in which the pathogen *Gaeumannomycesgraminis* var. *tritici*. Due to the enrichment of various fluorescent *Pseudomonas* species, can be specifically suppressed, producing 2,4-diacetylphloroglucinol (DAPG), an antimicrobial. While the crops themselves can recruit and sustain such a symbiotic relationship, the antagonistic microorganism strains that are responsible for this suppressiveness must have a strong affinity for crop roots, facilitating their colonization. The development of diverse fungal taxa with various ecological functions, such as mycorrhiza, endophytes, saprophytes, decomposers, and bioprotective fungi, is facilitated by intercropping systems. For instance, intercropping maize with *Atractylodeslancea* acidified the rhizosphere soil and encouraged the accumulation of advantageous PGPR like *Streptomyces*, *Bradyrhizobium*, *CandidatusSolibacter*, *Gemmatirosa*, and *Pseudolabrys* [45]. Intercropping systems also benefit forest ecosystems by creating disease-suppressive soils when trees are planted in multiple species as opposed to monoculture [46,47]. Similar to intercropping, crop rotation can enhance soil health by fostering a variety of microbiomes and modifying the microbiome of the rhizosphere. Farmers can reduce disease pressure by disrupting the life cycles of soil-borne pathogens linked to particular crops or genotypes by combining conservation tillage and crop rotation. By using this method, the populations of pathogens that may have accumulated in the soil are reduced, lessening their negative effects on subsequent crops. The crops that are included in a rotation can affect how well it works to improve crop productivity and soil health. While grasses help build soil organic matter and improve soil structure, grain legumes can fix atmospheric nitrogen to increase soil fertility. Crop rotations must include non-host plants in order to minimize yield losses brought on by soil-borne diseases. Crop productivity is increased and soil health is optimized when at least three different crops are included in a crop rotation plan [48]. For improving overall soil health, crop rotation with carefully chosen crops that encourage the development of advantageous endophytic and rhizosphere microbial communities is essential. This strategy encourages the development of soils that are more nutrient-rich and have a phytomicrobiome that controls pathogens. To meet crop nutrient needs while maintaining microbial diversity through soil nutrient enrichment, fertilization becomes an additional strategy if monoculture is chosen over polyculture to produce higher yields and profits. To further improve plant defense against phytopathogens, various soil amendment techniques are also used.

Comment [b4]: Rephrase

Comment [b5]: Is this sentence necessary?

2.4 Soil amendments

2.4.1 Fertilization

Traditional tillage methods and intensive monocropping techniques have depleted the soil, leaving it nutrient-poor with low levels of organic carbon and microbial diversity. In order to restore the nitrogen and phosphorus levels in agricultural fields and increase crop yields, fertilization is required. However, using chemical fertilizers continuously has drawbacks, including harming the health of the soil, endangering the lives of animals and people, and increasing air pollution [49,50]. Concerns about eutrophication are made worse by the fact that soil can leach over 50% of nitrogen and 90% of phosphorus into groundwater. The phyllosphere microbiome and root endophytes are not significantly affected by long-term fertilization, whereas the soil microbiome is more sensitive and protists are most affected [33,34]. Long-term fertilization resulted in a 30% reduction in phagotrophic protist diversity, which raises concerns about the potential loss of functionally significant microbial taxa as a result of abiotic changes brought on by fertilization. Copiotrophic bacteria outcompeted oligotrophs in fields that had both mineral and organic fertilizer applied, while organic fertilization increased the overall bacterial community's richness and diversity [51]. To maintain a balance that promotes plant health while lowering the risk of disease development, inorganic/mineral fertilizers should be closely monitored.

To comprehend the precise nutritional circumstances that affect pathogen growth, more study is required. Depending on their trophic modes, plant pathogens react to nitrogen fertilization differently. While facultative parasites exhibit a decrease in infection severity with high nitrogen supply, obligate parasites show an increase in infection severity with increased nitrogen supply. Due to their capacity to improve soil quality by boosting beneficial microbes and nutrient composition, biofertilizers like vermicompost are regarded as sustainable agricultural practices. Biocontrol agents like *Bacillus* spp. are added to biofertilizers made from mature compost. *Trichoderma* species, too, have been found to inhibit the *Fusarium* wilt illness. By directly suppressing pathogens or by altering the local microbial communities, the use of biofertilizers can improve soil health [52, 53, 54]. Organic fertilizers, such as compost, manure, or slaughterhouse waste, provide vital nutrients to plants and enhance soil aggregation, water retention, soil organic carbon, and overall soil health. Additionally, they support microbial diversity, richness, and activity in the soil as well as enzyme activity [13,55-57]. Plant pathogens like *Pythium* can be controlled by composted manure or plant residues, but their effects are thought to be due to microbial competition or plant host resistance. Vineyard pruning waste is one type of composting material that can have an impact on the microbial environment and activities, resulting in suppressive composts with higher relative abundances of Ascomycota and fungi from the genera *Fusarium* and *Zopfiella*. When peat is added to compost, the pH of the soil rises, suppressing pathogens like *Fusarium* that prefer acidic soils. Plant diseases brought on by pathogens in *Rhizoctonia*, *Verticillium*, *Sclerotinia*, *Phytophthora*, *Pythium*, *Aphanomyces*, and *Macrophomina* can be controlled by green manure, particularly from Brassica crops [7]. However, it is crucial to be aware that manure-derived fertilizers may contain antibiotic resistance genes (ARGs) and mobilomes, which could pose risks to both human and animal health, whereas plant residue-based fertilizers frequently contain plant pathogens. Manure is frequently preprocessed before being applied to land in order to reduce the spread of ARGs [58,59]. To address these worries and create plans for the safe and responsible application of organic fertilizers in agriculture, efforts should be made.

2.4.2 Chemical pesticides vs biofungicides

Farmers frequently use pesticides to manage and control pests and plant pathogens that can harm crops. Overuse, however, can result in resistance, decreased fertility, and negative effects on the environment, human health, and soil health. High-risk organisms like *B. cinerea* can arise as a result of overuse [60]. Pesticides can also negatively affect soil diversity, which leads to a loss of biodiversity and a decline in the health and productivity of ecosystems. Additionally, pesticides can harm beneficial microorganisms that are necessary for maintaining soil health and nutrient levels. A combination of sustainable farming methods and prudent pesticide use is crucial to reduce these potential disruptions. The resilience of the agroecosystem is increased by maintaining a diverse rhizosphere microbiome [61–63].

2.4.3 Biochar

A useful tool for soil improvement and carbon sequestration is biochar, a carbon-rich solid created through pyrolysis [64]. It is the perfect substrate for microbial growth due to its high porosity and substantial surface area. By modifying the bacterial and fungal communities in the soil, promoting beneficial bacteria, and suppressing plant pathogens, biochar reduces the negative plant-soil feedback. By adding PGPR and fungi to the root microbiome, it also induces systemic resistance in plants,

lowering their susceptibility to soil- and airborne pathogens [65,66,67-70]. However, given that the mechanisms affecting soil biota health are still not fully understood, worries about long-term safety and implications persist. Predicting biochar's long-term effects is difficult because the chemistry of the material can change depending on the feedstock and production conditions. By promoting long-term carbon sequestration and influencing greenhouse gas fluxes in soil, biochar can also help mitigate climate change by lowering greenhouse gas emissions. As a result, biochar is an effective tool for sustainable agriculture that addresses both environmental and food security concerns [71-73].

2.4.4 Chitin & Derivatives

Arthropod and fungal cell walls are primarily made of chitin, a polymer of N-acetylglucosamine. Its derivatives, such as chitosan and oligosaccharide derivatives are used in a variety of industrial, agricultural, and household applications [74]. Chitosan can trigger defense mechanisms in host plants and has broad-spectrum antimicrobial properties against viruses, bacteria, fungi, oomycetes, and nematodes. Chitosan can prevent the growth and development of post-harvest pathogenic fungi like *Colletotrichum*, *Botrytis cinerea*, and *Rhizopus stolonifer* as well as soil-borne pathogens like *Verticillium dahliae* [74]. Additionally, chitosan increases bacterial chitinase expression and regulates the abundance of Actinobacteria and Oxalobacteraceae members, which enhances the soil's ability to suppress plant pathogens. Potato wart disease, a fungus brought on by *Synchytrium endobioticum*, was shown to be suppressed by the addition of crab shell (23% chitin) to infected soil [75, 76]. In contrast to crop rotations, which showed a decrease in resting spore populations when intercropping potato with rye and sunflower, chitin-mediated management of potato wart disease was less successful.

2.4.5 Bentonite

In arid and semiarid areas, bentonite clay is used to improve the soil. It enhances plant growth and quality by increasing plant available water (PAW) by holding a significant amount of water within its crystals [77]. By creating the ideal moisture environment, bentonite also encourages microbial activity in the soil and the cycling of nutrients. By absorbing heavy metals like cadmium and lead from contaminated agricultural soils, it functions as an important tool for soil detoxification [78,79]. Through improved soil moisture retention and the formation of macroaggregates, bentonite also affects the fungal communities, which results in a decrease in the activity of phytopathogens like *Alternaria*, *Bipolaris*, *Fusarium*, *Leptosphaeria*, and *Microdochium*. This heightened competition from advantageous microorganisms may aid in the control of disease in the soil. To increase the chances of biocontrol agents like *Bacillus subtilis* surviving and functioning against particular plant pathogens like *Rhizoctonia solani*, bentonite has been used in recent biocontrol techniques [80].

2.5 Bio control agents

Biocontrol agents, which are primarily based on microbial inoculants, are a method for reducing pests and diseases through the use of living organisms or their derivatives. Through a variety of mechanisms, including competition with pathogens, antagonistic activity, inducing systemic resistance in plants, and/or direct lysis of the pathogenic organisms' cell walls, these agents aid in the alleviation of plant disease. Numerous microorganisms, including PGPR, endophytes, rhizosphere bacteria, and mycorrhizal fungi, are employed as biocontrol agents. While some biocontrol agents, like PGPR, may be generally advantageous for all plants, others may be host- or pathogen-specific [81, 82, 83]. To aid in the development of a healthy agroecosystem, researchers are investing in the engineering of phytomicrobiome. Selecting potential biocontrol agents may include additional criteria for resilience to climate change. Numerous agronomic techniques, including crop rotation, cover crops, natural selection, and organic mulching, have proven successful in enhancing soil health and disease resistance. The effectiveness of these techniques can, however, differ based on elements like soil types, climatic conditions, and crop genotypes. It is essential to investigate fresh and cutting-edge methods for managing plant diseases if we are to successfully address the issues brought on by climate change. Utilizing phytomicrobiome-based approaches, such as microbial inoculants and practices that take advantage of the complex interactions between plants and their microbial communities to promote disease suppression and improve crop resilience, is one promising area of research. To utilize the full potential of phytomicrobiome-based approaches, however, there are obstacles and pitfalls that must be overcome [84, 85].

3. Phytomicrobiome-Based Approaches- Challenges

Comment [b6]: 'climate change' topic sounds random in this paragraph

Agronomic practices can have an impact on how well an agroecosystem functions, and the phytomicrobiome is essential for plant health. Agronomic adjustments can lessen the impact of plant diseases. Although successful examples demonstrate effectiveness in controlling plant diseases, obstacles such as conceptual, computational, and non-target effects still exist.

3.1 Conceptual Difficulties

A comprehensive comprehension of the interactions between plants and their microbiomes is necessary for the effective application of phytomicrobiome-based approaches. This includes having a thorough understanding of the life cycles, ecology, and etiology of the pathogens that cause plant diseases [86–90]. According to Bass et al., the pathobiome concept refers to the group of organisms associated with the host that have lower health status as a result of interactions between those organisms and the host. The Meloidogyne-based disease complex (MDCs), which causes severe yield loss in important food crops worldwide, is an example of such collaborative work. This complex results from the interaction of phytopathogenic fungi and root-knot nematodes (RKN). The pathobiome concept also covers tree diseases brought on by intricate host, microbiota, and insect interactions [91, 92]. For effective plant disease management strategies, it is essential to comprehend how the phytomicrobiome as a whole contributes to the initiation, promotion, or mitigation of disease development [93–95]. The following issues would need to be resolved in order to develop phytomicrobiome-based strategies for plant disease control: (i) Who are the members of the pathobiome and phytomicrobiome at taxonomic and functional levels? (ii) How do they interact with one another, the plant host, and their surroundings? What is the long-term effect on the development and spread of the disease? Prior to assessing the overall effect on disease incidence and severity, recent studies have concentrated on comparing the microbiota associated with symptomatic versus healthy tissues, suppressive versus conducive soils, and investigating the microbiota shift under various agronomic treatments and/or upon pathogen infection. There is growing interest in investigating the interactions between pathogenic agents and the local microbiota using co-occurrence network analysis based on metabarcoding data [96–98]. Positive correlations between a pathogenic taxon and other taxa may contribute to the development and spread of the disease, according to the widely accepted underlying theory, and can therefore be used to identify pathobiome members. Contrarily, negative correlations between taxa that contain a pathogen may imply antagonistic interactions and aid in the identification of potential biocontrol agents. Alternative biological explanations, such as a prey-predator model or taxon aggregation because of dispersal constraints or related niche requirements, may, however, account for positive or negative correlations [96–99].

Comment [b7]: ?

3.2 Computational Difficulties

By offering more in-depth insights into microbial interactions, metabarcoding has revolutionized microbial interactions. To prevent misunderstandings and draw conclusions with the appropriate level of caution, it is crucial to be aware of the restrictions and limitations associated with this approach. Only genus- or species-level identification is currently possible using metabarcoding techniques like the 16S rRNA gene or Internal Transcribed Spacer (ITS) [100]. Since isolates from the same genus may be phytopathogens, non-pathogenic organisms, or even biocontrol agents, accurate taxonomic identification is essential for identifying pathogenic organisms. For some pathogens, additional barcodes have been created down to the species level, including those for the translated elongation factor (TEF-1), -tubulin, RNA polymerase II second largest subunit (RPB2), and cytochrome c oxidase subunits (COI), but a metabarcoding strategy aimed at these particular barcodes has not yet been created [101–104]. As shown in the study by Belair et al., taxonomic-level resolution can be evaluated by creating a phylogenetic tree based on Bayesian inferences. A multi-affiliation output is offered by the FROGS pipeline to take into account errors in taxonomic assignment. Finding taxa with notable differences in abundance between the treated and control conditions is another common goal. However, metabarcoding restricts the way that data can be expressed, making it compositional [105,106].

Comment [b8]: ?

Since they are lost during sequencing, absolute abundances cannot be inferred from relative abundance. One could estimate the size of the overall population and then infer the population size of each taxon based on its proportion in order to access absolute abundances. It is possible to use traditional microbiological methods that count colony-forming units in Petri dishes, but only populations that are viable and cultivable are taken into account. Traditional qPCR may not be as effective as digital droplet

PCR, which does not require a calibration curve. Because taxa have different numbers of 16SrRNA and ITS gene copies, it still represents a significant bias [107].

Before extracting the DNA from samples, Tkacz et al. suggested a technique that corrects the initial microbial density by adding a synthetic spike. Due to the method's infancy and dependence on microbial eukaryotes, it is not yet widely used. Long-read and single-molecule sequencing methods, like Pacbio or Nanopore SMRT sequencing, may lessen PCR bias and improve taxonomic assignment accuracy. Understanding how microorganisms interact to start or stop pathogenesis and promote or mitigate disease progression is limited by co-occurrence networks. Recent advancements in metagenomics technology, including metagenomics, metatranscriptomics, metabolomic analysis, or metaproteomics, in conjunction with culture-dependent analysis (culturomics), may provide new insight into the underlying mechanisms of microbial interactions in the context of plant diseases. To better understand the underlying functional mechanisms of lesion formation, Broberg et al. compared the metagenome, metatranscriptome, and metaproteome of inner bark tissues in AOD symptomatic versus asymptomatic trees [108]. Using metabarcoding and shotgun metagenomics techniques, Gao et al. also carried out a thorough investigation comparing the taxonomic and functional profiles of microbial communities linked to Fusarium wilt-affected and healthy chili pepper plants.

Comment [b9]: Did the techniques work well? What were the findings?

Finally, although a simplified system lacking the full range of the phytomicrobiota, the use of synthetic communities may present important opportunities to establish causal relationships and advance our knowledge of the individual or collective role of microorganisms and their influence on plant phenotypes [109].

3. Evaluation of Side Effects

Comment [b10]: ?

Plant disease-mitigating inoculants face difficulties adapting to production conditions and establishing a successful colony. Considerations like formulation, dosage adjustments, and strategic positioning of treatments become crucial factors to optimize colonization and disease protection efficacy [110]. While in situ manipulations of resident microorganisms through agronomic practices are unaffected by these issues, approaches involving the introduction of microbial inoculants are most affected.

Another issue is how introducing microorganisms will affect the ecosystem and how they will leave a legacy [111-114]. Numerous studies have demonstrated that the application of microbial inoculants significantly altered soil microbial communities when compared to control treatments, though the demonstration of their beneficial effects was not mentioned [112]. The degree to which these shifts, brought about by the introduction of inoculants, were linked to the agroecosystem's dysfunctional functioning is critical to understanding the risks associated with this type of practice.

Composting or adding manure are known to cause changes in the microbial communities and add a lot of microorganisms to the ecosystem. Except for cyanobacteria blooms, which are partly caused by excess nutrients from fertilizer runoff, particularly from farmers, these practices have never been linked to significant direct microbial invasions. After the introduction of microorganisms, no evidence of microbial invasions has been documented, though it may be challenging to find given how cryptic microbes are [115]. A scientific body of knowledge regarding microorganisms' safety as well as their capacity to produce potentially harmful secondary metabolites is necessary for the development of microbial inoculants. In order to successfully replace aflatoxin producers in maize fields or nut tree orchards, non-aflatoxin producing strains are being used in the US or some African nations. Aflatoxin restoration in non-toxigenic strains through mating has also been raised as a concern regarding the long-term impact of continuous application of biocontrol strains on the native population structure [116, 117, 118]. Information on the mode of action, the potential for related species and strains to produce relevant metabolites or toxins, adverse effects seen in (eco)toxicity tests, and the use of population genomics to examine the impact of biocontrol strains on native populations should all be gathered in order to assess the risk. The most recent consolidated version of European Regulation 1107/2009 calls for a number of protections before product approval, including microorganisms deposited at an internationally renowned culture collection, validated analytical techniques, and proven efficacy in guarding plants against specific pests or pathogens [119].

4. Agro ecosystem Resilience and Adaptation

4.1 Climate Change's Effect on Plant Pathogens

Pests and pathogens have a significant negative impact on crop yields, which causes global food insecurity. This problem is made worse by climate change, which is characterized by global warming and extreme weather. Changes have an immediate impact on crop physiology and productivity while also having an indirect impact on the phytomicrobiome, which includes plant pathogens. Pathogens adapt to climate change by growing, migrating, and evolving; this has an impact on genetic traits and speciation [120].

4.1.1 Multiplication

Important abiotic factors that influence pathogen growth and reproduction include temperature and moisture. A slightly longer season may cause outbreaks by increasing the number of disease propagules [121]. The relative abundance of potential fungal plant pathogens in soils doubles as temperatures rise, having a significant impact on the abundance of soil-borne plant pathogens. *Fusarium* spp. inoculum is expected to rise due to climate change. Due to increased cropping and warmer weather, diseases are more frequently found in soils. Climate has a significant impact on soil-borne pathogenic fungi like *Fusarium*, *Pythium*, *Rhizoctonia*, and *Sclerotinia* throughout their life cycle, but especially during the latency stage of infection. Once conducive conditions for infection are in place, warmer winters with shorter latency periods may cause the emergence of more aggressive pathogens [122].

Since 2015, France's unusually warm summers have helped to lessen the severity of ash dieback brought on by *Hymenoscyphus fraxineus* in French forests [123]. However, there are many different ways that climate change will affect plant pathogens, and not all pathogens will react to temperature changes in the same way. It's crucial to comprehend how each plant pathogen reacts differently to environmental changes in order to create effective crop disease management plans. To accurately estimate the risk of disease epidemics in the future, integrating both disease and crop models is required [124]. This will allow for better predictions and more effective disease management strategies.

4.1.2 Migration

Pathogen populations are significantly impacted by climate change; some may see their ranges shift or expand, while others may see their numbers decline. For instance, over a fifteen-year period, aflatoxin contamination in maize has increased in Northern Italy and Eastern Europe, and since 2015, aflatoxin-positive samples have been rising in France. As the world's temperatures continue to rise, pathogens are also enlarging their foci of infection and migrating toward the poles [125, 126].

Plant pathogens can spread by a number of different channels, including wind, water, rain, insects, and other vectors. The state of the environment and the availability of suitable hosts have a significant impact on the ability of these pathogens to survive and spread. For instance, Hurricane Ivan in September 2004 spread *Phakopsora pachyrhizi*, the fungus that causes Asian soybean rust [127,128]. A Global Rust Reference Center has been established by the Borlaug Global Rust Initiative (BGRI) to track the occurrence and spread of urediniospores from rust fungi, particularly for rusts that infest wheat [129,130]. Due to changes in plant reproduction and distribution patterns, climate change also has an effect on the arthropod vectors used by plant pathogens to disperse their diseases. For instance, the western Canadian mountain pine beetle outbreak and the western corn rootworm outbreak in Europe both showed an expansion pattern as a result of the shorter and milder winters. Another response of plant pathogens to environmental changes is host shifts or jumps. Infamously, the introduction of host plants to non-native regions caused *Phytophthora infestans*, the causative agent of potato late blight [131, 132].

4.1.3 Evolution

The evolution and speciation of organisms, including plant pathogens, are significantly influenced by abiotic factors. A pathogen's lifecycle can be impacted by temperature changes because they shorten their latency times. But these changes can also result in the emergence of novel species or pathotypes that are more tolerant of a wider range of temperatures than their parent species. For instance, grey mold in Allium crops is brought on by *Botrytis sinoallii*, a novel species that was first discovered in China in 2010 [133]. *Puccinia graminis* f. sp. *tritici* Ug99 race East African-born is virulent against Sr31, a common resistant gene in wheat. This race's genetic variations with virulence against additional resistant genes pose a serious threat to global food security. Epidemics of wheat stem rust, which have

been seen in Europe as well as on other continents, are being caused by rising global temperatures [130, 134, 135]. *Puccinia striiformis*, the fungus that causes yellow rust, has seen the emergence of more virulent and aggressive strains that are adapted to warmer climates. In the UK, there have also been reports of a diverse population of wheat yellow rust emerging.

It is difficult to predict how climate change will affect plant-pathogen interactions and disease outcomes because it is dependent on how pathogens, hosts, and the phytomicrobiome will react. Disease surveillance is crucial because it can be difficult to link the emergence, spread, or restriction of current plant diseases to climate change [136]. Genomic epidemiology methods, like those created by Hubbard et al. and Chen et al., have shown to be effective at analyzing migration patterns and forecasting epidemic outbreaks. The detection, monitoring, and forecasting of plant diseases in the fields may also be aided by plant disease sensing based on local and/or remote sensing [137].

5. Impact of Plant Phytomicrobiome on Climate Change

Plant pathogens and the phytomicrobiome have been significantly impacted by climate change, making them more vulnerable to pathogens. The phytomicrobiome, which includes AMF and PGPR, can assist plants in adjusting to and acclimating to climate change by generating substances that shield plants from desiccation, improve water and nutrient uptake, control root morphology, and regulate genes that respond to stress [144]. These advantageous microbes encourage the buildup of plant antioxidants and osmolytes, which aids in plant growth and stress tolerance [138,139]. Many plants growth-promoting microorganisms (PGPM), such as *Pseudomonas fluorescens* and *Bacillus subtilis*, which can fight pathogens like *Fusarium graminearum*, which causes diseases in wheat, have been successfully used for pathogen control. In addition, PGPMs increase plants' induced systemic resistance (ISR), which strengthens their defenses against invading pathogens. Reducing N₂O emissions from agricultural systems can help mitigate climate change [140,141].

However, because of their unpredictable behavior, they can be difficult to use effectively in the field. Since a large portion of PGPR's energy is used to react to high temperatures, soil warming can interfere with how well they work. AMF colonization may be reduced or AMF species with lower carbon requirements may be preferred as a result of warming, which can also alter the flux of photosynthetic material underground [142-143]. To create effective strategies to reduce the effects of climate change on plant health, crop production, and ecosystem stability, interdisciplinary collaborations between plant biologists, microbiologists, climatologists, and agronomists are required. To achieve this, it will be necessary for plant biologists, microbiologists, climatologists, and agronomists to work together interdisciplinary and develop novel crop management and breeding techniques.

6. Conclusions

This review discusses a variety of phytomicrobiome research topics, including difficulties with standardization, translation, and side effects. The effects of climate change on disease outcomes and the operation of the phytomicrobiome are also covered. The phytomicrobiome is essential for the health of ecosystems and soils, and it holds promise for reducing plant diseases and boosting resistance to climate change. It is difficult to identify and use the phytomicrobiome for disease management, and climate change may change how it interacts with plant pathogens, making disease management strategies more difficult. For forestry, agriculture, and urban landscaping, harnessing the phytomicrobiome has significant potential advantages. To comprehend the mechanisms underlying its effects and develop workable management strategies, more research is required.

References

1. UNO. World Population Prospects Report 2022. Available online: <https://population.un.org/wpp/> (accessed on 10 January 2023).
2. Plants, S.o.t.W.s.: London (UK): Royal Botanic Gardens, Kew; 2017. Available online: <https://www.kew.org/about-us/press-media/state-of-the-worlds-plants-2017> (accessed on 8 March 2023).
3. FAO. New Standards to Curb the Global Spread of Plant Pests and Diseases. Available online: <https://www.fao.org/news/story/en/item/1187738/icode/> (accessed on 10 January 2023).
4. Whipps, J.M.; Lewis, K.; Cooke, R.C. Mycoparasitism and plant disease control. In *Fungi in Biological Control Systems*; Burge, M.N., Ed.; Manchester University Press: Manchester, UK, 1988.
5. FAO. Conservation Agriculture. Available online: <https://www.fao.org/conservation->

- agriculture/en/ (accessed on 10 January 2023).
6. Morales-Moreira, Z.P.; Chen, M.Y.; Yanez-Ortuno, D.L.; Haney, C.H. Engineering plant microbiomes by integrating eco-evolutionary principles into current strategies. *Curr. Opin. Plant Biol.* 2023, *71*, 102316.
 7. Chen, W.; Modi, D. and Picot, A. Soil and Phytomicrobiome for Plant Disease Suppression and Management under Climate Change: A Review. *Plants*. *Plants* 2023, *12*, 2736.
 8. Lebeis, S.L.; Paredes, H.; Lundberg, D.S.; Breakfield, N.; Gehring, J.; McDonald, M.; Malfatti, S.; Glavina, T.; Rio, D.; Jones, C.D.; *et al.* Salicylic acid modulates colonization of the root microbiome by specific bacterial taxa. *Sci. New Ser.* 2015, *349*, 860–864.
 9. Schlatter, D.; Kinkel, L.; Thomashow, L.; Weller, D.; Paulitz, T. Disease Suppressive Soils: New Insights from the Soil Microbiome. *Phytopathology* 2017, *107*, 1284–1297.
 10. Weller, D.M.; Raaijmakers, J.M.; Gardener, B.B.M.; Thomashow, L.S. Microbial populations responsible for specific soil suppressiveness to plant pathogens. *Annu. Rev. Phytopathol.* 2002, *40*, 309–348.
 11. Gómez Expósito, R.; De Bruijn, I.; Postma, J.; Raaijmakers, J.M. Current insights into the role of rhizosphere bacteria in disease suppressive soils. *Front. Microbiol.* 2017, *8*, 2529.
 12. Hartman, K.; van der Heijden, M.G.A.; Wittwer, R.A.; Banerjee, S.; Walser, J.C.; Schlaeppi, K. Cropping practices manipulate abundance patterns of root and soil microbiome members paving the way to smart farming. *Microbiome* 2018, *6*, 14.
 13. Kraut-Cohen, J.; Zolti, A.; Shaltiel-Harpaz, L.; Argaman, E.; Rabinovich, R.; Green, S.J.; Minz, D. Effects of tillage practices on soil microbiome and agricultural parameters. *Sci. Total Environ.* 2020, *705*, 135791.
 14. Legrand, F.; Picot, A.; Cobo-Díaz, J.F.; Carof, M.; Chen, W.; Le Floch, G. Effect of tillage and static abiotic soil properties on microbial diversity. *Appl. Soil Ecol.* 2018, *132*, 135–145.
 15. Nikitin, D.A.; Ivanova, E.A.; Zhelezova, A.D.; Semenov, M.V.; Gadzhumarov, R.G.; Tkhakakhova, A.K.; Chernov, T.I.; Ksenofontova, N.A.; Kutovaya, O.V. Assessment of the Impact of No-Till and Conventional Tillage Technologies on the Microbiome of Southern Agrochernozems. *Eurasian Soil Sci.* 2020, *53*, 1782–1793.
 16. Sun, R.; Li, W.; Dong, W.; Tian, Y.; Hu, C.; Liu, B. Tillage changes vertical distribution of soil bacterial and fungal communities. *Front. Microbiol.* 2018, *9*, 699.
 17. Claassen, R. This document is discoverable and free to researchers across the globe due to the work of AgEcon Search. Help ensure our sustainability. *U.S. Dep. Agric. Econ.* 2018, *1*, 1–22.
 18. Hobbs, P.R.; Sayre, K.; Gupta, R. The role of conservation agriculture in sustainable agriculture. *Philos. Trans. R. Soc. B Biol. Sci.* 2008, *363*, 543–555.
 19. Singh, U.; Choudhary, A.K.; Sharma, S. Agricultural practices modulate the bacterial communities, and nitrogen cycling bacterial guild in rhizosphere: Field experiment with soybean. *J. Sci. Food Agric.* 2021, *101*, 2687–2695.
 20. Zhang, H.; Shi, Y.; Dong, Y.; Lapen, D.R.; Liu, J.; Chen, W. Subsoiling and conversion to conservation tillage enriches nitrogen cycling bacterial communities in sandy soils under long-term maize monoculture. *Soil Tillage Res.* 2022, *215*, 105197.
 21. Campos, S.B.; Lisboa, B.B.; Camargo, F.A.; Bayer, C.; Sczyrba, A.; Dirksen, P.; Albersmeier, A.; Kalinowski, J.; Beneduzi, A.; Costa, P.B.; *et al.* Soil suppressiveness and its relations with the microbial community in a Brazilian subtropical agroecosystem under different management systems. *Soil Biol. Biochem.* 2016, *96*, 191–197.
 22. Bongiorno, G.; Postma, J.; Bünemann, E.K.; Brussaard, L.; de Goede, R.G.; Mäder, P.; Tamm, L.; Thuerig, B. Soil suppressiveness to *Pythium ultimum* in ten European long-term field experiments and its relation with soil parameters. *Soil Biol. Biochem.* 2019, *133*, 174–187.
 23. Paulitz, T.C.; Schroeder, K.L.; Schillinger, W.F. Soilborne pathogens of cereals in an irrigated cropping system: Effects of tillage, residue management, and crop rotation. *Plant Dis.* 2010, *94*, 61–68.
 24. Huang, F.; Liu, Z.; Mou, H.; Li, J.; Zhang, P.; Jia, Z. Impact of farmland mulching practices on the soil bacterial community structure in the semi-arid area of the loess plateau in China. *Eur. J. Soil Biol.* 2019, *92*, 8–15.
 25. Wan, P.; Zhang, N.; Li, Y.; Li, S.; Li, F.M.; Cui, Z.; Zhang, F. Reducing plant pathogens could increase crop yields after plastic film mulching. *Sci. Total Environ.* 2022, *861*, 160615.
 26. Steinmetz, Z.; Wollmann, C.; Schaefer, M.; Buchmann, C.; David, J.; Tröger, J.; Muñoz, K.; Frör, O.; Schaumann, G.E. Plastic mulching in agriculture. Trading short-term agronomic benefits for long-term soil degradation? *Sci. Total Environ.* 2016, *550*, 690–705.
 27. Amaral-Zettler, L.A.; Zettler, E.R.; Mincer, T.J. Ecology of the plastisphere. *Nat. Rev. Microbiol.* 2020, *18*, 139–151.
 28. Qi, Y.; Ossowicki, A.; Yergeau, É.; Vigani, G.; Geissen, V.; Garbeva, P. Plastic mulch film residues in agriculture: Impact on soil suppressiveness, plant growth, and microbial communities. *FEMS Microbiol. Ecol.* 2022, *98*, fiac017.
 29. Qi, Y.; Yang, X.; Pelaez, A.M.; Huerta Lwanga, E.; Beriot, N.; Gertsen, H.; Garbeva, P.; Geissen, V. Macro- and micro- plastics in soil-plant system: Effects of plastic mulch film residues on wheat (*Triticum aestivum*) growth. *Sci. Total Environ.* 2018, *645*, 1048–1056.
 30. Gkoutselis, G.; Rohrbach, S.; Harjes, J.; Obst, M.; Brachmann, A.; Horn, M.A.; Rambold, G. Microplastics accumulate fungal pathogens in terrestrial ecosystems. *Sci. Rep.* 2021, *11*, 13214.
 31. Kader, M.A.; Senge, M.; Mojid, M.A.; Ito, K. Recent advances in mulching materials and methods for modifying soil environment. *Soil Tillage Res.* 2017, *168*, 155–166.

32. García-Orenes, F.; Guerrero, C.; Roldán, A.; Mataix-Solera, J.; Cerdà, A.; Campoy, M.; Zornoza, R.; Bárcenas, G.; Caravaca, F. Soil microbial biomass and activity under different agricultural management systems in a semi-arid Mediterranean agroecosystem. *Soil Tillage Res.* 2010, *109*, 110–115.
33. Ai, C.; Liang, G.; Sun, J.; Wang, X.; He, P.; Zhou, W. Different roles of rhizosphere effect and long-term fertilization in the activity and community structure of ammonia oxidizers in a calcareous fluvo-aquic soil. *Soil Biol. Biochem.* 2013, *57*, 30–42.
34. Sun, A.; Jiao, X. Y.; Chen, Q.; Trivedi, P.; Li, Z.; Li, F.; Zheng, Y.; Lin, Y.; Hu, H. W.; He, J. Z. Fertilization alters the structure of soil microbial communities in crop-associated microbiomes. *Environ. Microbiol.* 2021, *23*, 2169–2183.
35. Sun, A.; Jiao, X. Y.; Chen, Q.; Wu, A. L.; Zheng, Y.; Lin, Y. X.; He, J. Z.; Hu, H. W. Microbial communities in the rhizosphere and root endosphere are more resistant than soil microbiota to fertilization. *Soil Biol. Biochem.* 2021, *153*, 108113.
36. Chalker-Scott, L. Impact of Mulches on Landscape Plants and the Environment—A Review. *J. Environ. Hort.* 2007, *25*, 239–249.
37. Summers, C. G.; Mitchell, J. P.; Stapleton, J. J. Management of aphid-borne viruses and *Bemisia argentifolii* (Homoptera: Aleyrodidae) in zucchini squash by using UV reflective plastic and wheat straw mulches. *Environ. Entomol.* 2004, *33*, 1447–1457.
38. Ortiz-Cornejo, N. L.; Romero-Salas, E. A.; Navarro-Noya, Y. E.; González-Zúñiga, J. C.; Ramírez-Villanueva, D. A.; Vázquez-Murrieta, M. S.; Verhulst, N.; Govaerts, B.; Dendooven, L.; Luna-Guido, M. Incorporation of bean plant residue in soil with different agricultural practices and its effect on the soil bacteria. *Appl. Soil Ecol.* 2017, *119*, 417–427.
39. Sun, X.; Ye, Y.; Liao, J.; Tang, Y.; Wang, D.; Guan, Q. Organic mulching alters the composition, but not the diversity, of rhizosphere bacterial and fungal communities. *Appl. Soil Ecol.* 2021, *168*, 104167.
40. Andres, C.; Comoé, H.; Beerli, A.; Schneider, M.; Rist, S.; Jacobi, J. Cocoa in Monoculture and Dynamic Agroforestry. In *Sustainable Agriculture Reviews*; Springer International Publishing: Cham, Switzerland, 2016; pp. 121–153.
41. Loh, S. K.; Asubonteng, K. O.; Adanu, S. K. Effects of Monocropping on Land Cover Transitions in the Wet Evergreen Agro-Ecological Zone of Ghana. *Land* 2022, *11*, 1063.
42. Bai, Y.; Wang, G.; Cheng, Y.; Shi, P.; Yang, C.; Yang, H.; Xu, Z. Soil acidification in continuously cropped potato alters bacterial community structure and diversity via the accumulation of phenolic acids. *Sci. Rep.* 2019, *9*, 12499.
43. Huang, L. F.; Song, L. X.; Xia, X. J.; Mao, W. H.; Shi, K.; Zhou, Y. H.; Yu, J. Q. Plant-Soil Feedbacks and Soil Sickness: From Mechanisms to Application in Agriculture. *J. Chem. Ecol.* 2013, *39*, 232–242.
44. Li, X. G.; Ding, C. F.; Zhang, T. L.; Wang, X. X. Fungal pathogen accumulation at the expense of plant-beneficial fungus as a consequence of consecutive peanut monoculturing. *Soil Biol. Biochem.* 2014, *72*, 11–18.
45. Li, H.; Li, C.; Song, X.; Liu, Y.; Gao, Q.; Zheng, R.; Li, J.; Zhang, P.; Liu, X. Impacts of continuous and rotation cropping practices on soil chemical properties and microbial communities during peanut cultivation. *Sci. Rep.* 2022, *12*, 2758.
46. Peng, Z.; Guo, X.; Xiang, Z.; Liu, D.; Yu, K.; Sun, K.; Yan, B.; Wang, S.; Kang, C.; Xu, Y.; et al. Maize intercropping enriches plant growth-promoting rhizobacteria and promotes both the growth and volatile oil concentration of *Attractylodes lancea*. *Front. Plant Sci.* 2022, *13*, 1029722.
47. Modi, D.; Simard, S.; Bérubé, J.; Lavkulich, L.; Hamelin, R.; Grayston, S. J. Long-term effects of stump removal and tree species composition on the diversity and structure of soil fungal communities. *FEMS Microbiol. Ecol.* 2020, *96*, fiae061.
48. Modi, D.; Simard, S.; Lavkulich, L.; Hamelin, R. C.; Grayston, S. J. Stump removal and tree species composition promote a bacterial microbiome that may be beneficial in the suppression of root disease. *FEMS Microbiol. Ecol.* 2021, *97*, fi aa213.
49. Merz, U.; Falloon, R. E. Review: Powdery Scab of Potato—Increased Knowledge of Pathogen Biology and Disease Epidemiology for Effective Disease Management. *Potato Res.* 2009, *52*, 17–37.
50. Da Costa, P. B.; Beneduzi, A.; de Souza, R.; Schoenfeld, R.; Vargas, L. K.; Passaglia, L. M. P. The effects of different fertilization conditions on bacterial plant growth promoting traits: Guidelines for directed bacterial prospecting and testing. *Plant Soil* 2013, *368*, 267–280.
51. Singh, B. K.; Trivedi, P. Microbiome and the future for food and nutrient security. *Microb. Biotechnol.* 2017, *10*, 50–53.
52. VanderBom, F.; Nunes, I.; Raymond, N. S.; Hansen, V.; Bonnichsen, L.; Magid, J.; Nybroe, O.; Jensen, L. S. Long-term fertilisation form, level and duration affect the diversity, structure and functioning of soil microbial communities in the field. *Soil Biol. Biochem.* 2018, *122*, 91–103.
53. Sun, Y.; Wang, M.; Mur, L. A. J.; Shen, Q.; Guo, S. Unravelling the Roles of Nitrogen Nutrition in Plant Disease Defences. *Int. J. Mol. Sci.* 2020, *21*, 572.
54. Medina-Sauza, R. M.; Álvarez-Jiménez, M.; Delhal, A.; Reverchon, F.; Blouin, M.; Guerrero-Analco, J. A.; Cerdán, C. R.; Guevara, R.; Villain, L.; Barois, I. Earthworms Building Up Soil Microbiota,

- aReview. *Front. Environ. Sci.* 2019, 7, 81.
55. Xiong, W.; Guo, S.; Jousset, A.; Zhao, Q.; Wu, H.; Li, R.; Kowalchuk, G.A.; Shen, Q. Bio-fertilizer application induces soil suppressiveness against Fusarium wilt disease by reshaping the soil microbiome. *Soil Biol. Biochem.* 2017, 114, 238–247.
 56. Bhunia, S.; Bhowmik, A.; Mallick, R.; Mukherjee, J. Agronomic Efficiency of Animal-Derived Organic Fertilizers and Their Effects on Biology and Fertility of Soil: A Review. *Agronomy* 2021, 11, 823.
 57. Liang, Y.; Yang, Y.; Yang, C.; Shen, Q.; Zhou, J.; Yang, L. Soil enzymatic activity and growth of rice and barley as influenced by organic manure in an anthropogenic soil. *Geoderma* 2003, 115, 149–160.
 58. Li, Q.; Zhang, D.; Cheng, H.; Ren, L.; Jin, X.; Fang, W.; Yan, D.; Li, Y.; Wang, Q.; Cao, A. Organic fertilizers activate soil enzyme activities and promote the recovery of soil beneficial microorganisms after dazomet fumigation. *J. Environ. Manag.* 2022, 309, 114666.
 59. Chen, Q.L.; Cui, H.L.; Su, J.Q.; Penuelas, J.; Zhu, Y.G. Antibiotic Resistance in Plant Microbiomes. *Trends Plant Sci.* 2019, 24, 530–541.
 60. Udikovic-Kolic, N.; Wichmann, F.; Broderick, N.A.; Handelsman, J. Bloom of resident antibiotic-resistant bacteria in soil following manure fertilization. *Proc. Natl. Acad. Sci. USA* 2014, 111, 15202–15207.
 61. Hahn, M. The rising threat of fungicide resistance in plant pathogenic fungi: *Botrytis* as a case study. *J. Chem. Biol.* 2014, 7, 133–141.
 62. Markarova, A.E.; Markarova, M.Y.; Razin, O.A.; Nadezhkin, S.M. The microorganisms natural consortia effectiveness in the white cabbage crop cultivation. *IOP Conf. Ser. Earth Environ. Sci.* 2022, 953, 012035.
 63. Noel, Z.A.; Longley, R.; Benucci, G.M.N.; Trail, F.; Chilvers, M.L.; Bonito, G. Non-target impacts of fungicide disturbance on phyllosphere yeasts in conventional and no-till management. *ISME Commun.* 2022, 2, 19.
 64. Pang, G.; Cai, F.; Li, R.; Zhao, Z.; Li, R.; Gu, X.; Shen, Q.; Chen, W. Trichoderma-enriched organic fertilizer can mitigate microbiome degeneration of monocropped soil to maintain better plant growth. *Plant Soil* 2017, 416, 181–192.
 65. Beesley, L.; Moreno-Jiménez, E.; Gomez-Eyles, J.L. Effects of biochar and green waste compost amendments on mobility, bioavailability and toxicity of inorganic and organic contaminants in a multi-element polluted soil. *Environ. Pollut.* 2010, 158, 2282–2287.
 66. Jaiswal, A.K.; Elad, Y.; Paudel, I.; Graber, E.R.; Cytryn, E.; Frenkel, O. Linking the Belowground Microbial Composition, Diversity and Activity to Soilborne Disease Suppression and Growth Promotion of Tomato Amended with Biochar. *Sci. Rep.* 2017, 7, 44382.
 67. Jaiswal, A.K.; Frenkel, O.; Elad, Y.; Lew, B.; Graber, E.R. Non-monotonic influence of biochar dose on bean seedling growth and susceptibility to *Rhizoctonia solani*: The “Shifted Rmax-Effect”. *Plant Soil* 2015, 395, 125–140.
 68. Bakker, P.A.H.M.; Doornbos, R.F.; Zamioudis, C.; Berendsen, R.L.; Pieterse, C.M.J. Induced systemic resistance and the rhizosphere microbiome. *Plant Pathol. J.* 2013, 29, 136–143.
 69. Mehari, Z.H.; Elad, Y.; Rav-David, D.; Graber, E.R.; Meller Harel, Y. Induced systemic resistance in tomato (*Solanum lycopersicum*) against *Botrytis cinerea* by biochar amendment involves jasmonic acid signaling. *Plant Soil* 2015, 395, 31–44.
 70. Samain, E.; Aussenac, T.; Selim, S. The Effect of Plant Genotype, Growth Stage, and *Mycosphaerella graminicola* Strains on the Efficiency and Durability of Wheat-Induced Resistance by *Paenibacillus* sp. Strain B2. *Front. Plant Sci.* 2019, 10, 587.
 71. Samain, E.; van Tuinen, D.; Jeandet, P.; Aussenac, T.; Selim, S. Biological control of septoria leaf blotch and growth promotion in wheat by *Paenibacillus* sp. strain B2 and *Curtobacterium plantarum* strain EDS. *Biol. Control* 2017, 114, 87–96.
 72. Brtnicky, M.; Datta, R.; Holatko, J.; Bielska, L.; Gusiati, Z.M.; Kucerik, J.; Hammerschmied, T.; Danish, S.; Radziemska, M.; Mravcova, L.; et al. A critical review of the possible adverse effects of biochar in the soil environment. *Sci. Total Environ.* 2021, 796, 148756.
 73. Rashid, M.; Hussain, Q.; Khan, K.S.; Al-Wabel, M.I.; Afeng, Z.; Akmal, M.; Ijaz, S.S.; Aziz, R.; Shah, G.A.; Mehdi, S.M.; et al. Prospects of biochar in alkaline soils to mitigate climate change. In *Environment, Climate, Plant and Vegetation Growth*; Springer: Cham, Switzerland, 2020; pp. 133–149.
 74. Brassard, P.; Godbout, S.; Raghavan, V. Soil biochar amendment as a climate change mitigation tool: Key parameters and mechanisms involved. *J. Environ. Manag.* 2016, 181, 484–497.
 75. Chu-hsi, H.; Jui-lien, H.; Rong-huei, C. Wastewater Treatment with Chitosan. 2008. Available online: 5a27 (accessed on 15 February 2023).
 76. Cretoiu, M.S.; Korthals, G.W.; Visser, J.H.M.; van Elsas, J.D. Chitin Amendment Increases Soil Suppressiveness toward Plant Pathogens and Modulates the Actinobacterial and Oxalobacteraceal Communities in an Experimental Agricultural Field. *Appl. Environ. Microbiol.* 2013, 79, 5291–5301.
 77. Chisnall-Hampson, M.; Coombes, J.W. Use of crab shell meal to control potato wart in Newfoundland. *Can. J. Plant Pathol.* 1991, 13, 97–105.
 78. Mi, J.; Gregorich, E.G.; Xu, S.; McLaughlin, N.B.; Liu, J. Effect of bentonite as a soil amendment on field water-holding capacity, and millet photosynthesis and grain quality. *Sci. Rep.* 2020, 10, 18282.
 79. Sun, Y.; Li, Y.; Xu, Y.; Liang, X.; Wang, L. In situ stabilization remediation of cadmium (Cd) and lead (Pb) co-contaminated paddy soil using bentonite. *Appl. Clay Sci.* 2015, 105–106, 200–206.

80. Xu, Y.; Liang, X.; Xu, Y.; Qin, X.; Huang, Q.; Wang, L.; Sun, Y. Remediation of Heavy Metal-Polluted Agricultural Soils Using Clay Minerals: A Review. *Pedosphere* 2017, 27, 193–204.
81. Zhang, H.; Chen, W.; Zhao, B.; Phillips, L.A.; Zhou, Y.; Lapen, D.R.; Liu, J. Sandy soils amended with bentonite induced changes in soil microbiota and fungistasis in maize fields. *Appl. Soil Ecol.* 2020, 146, 103378.
82. CFIA. Import and Release of Biological Control Agents into Canada. (accessed on 19 February 2023).
83. Agriculture, F.M.O. Qu'est-ce que le Biocontrôle? Available online: <https://agriculture.gouv.fr/quest-ce-que-le-biocontrole> (accessed on 22 May 2023).
84. Tymon, L.S.; Morgan, P.; Gundersen, B.; Inglis, D.A. Potential of endophytic fungus collected from *Cucurbita pepo* roots grown under three different agricultural mulches as antagonistic endophytes to *Verticillium dahliae* in western Washington. *Microbiol. Res.* 2020, 240, 126535.
85. Afridi, M.S.; Javed, M.A.; Ali, S.; De Medeiros, F.H.V.; Ali, B.; Salam, A.; Sumaira, M.; R.A.; Alkhalifah, D.H.M.; Selim, S.; *et al.* New opportunities in plant microbiome engineering for increasing agricultural sustainability under stressful conditions. *Front. Plant Sci.* 2022, 13, 899464.
86. Perrone, G.; Ferrara, M.; Medina, A.; Pascale, M.; Magan, N. Toxigenic fungi and mycotoxins in a climate change scenario: Ecology, genomics, distribution, prediction and prevention of the risk. *Microorganisms* 2020, 8, 1496.
87. Vayssier-Taussat, M.; Albina, E.; Citti, C.; Cosson, J.-F.; Jacques, M.A.; Lebrun, M.; Le Loir, Y.; Ogliastrro, M.; Petit, M.A.; Roumagnac, P.; *et al.* Shifting the paradigm from pathogens to pathobiome: New concepts in the light of meta-omics. *Front. Cell. Infect. Microbiol.* 2014, 4, 29.
88. Bass, D.; Stentford, G.; Wang, H.-C.; Koskella, B.; Tyler, C. The Pathobiome in Animal and Plant Diseases. *Trends Ecol. Evol.* 2019, 34, 996–1008.
89. Mannaa, M.; Seo, Y.-S. Plants under the Attack of Allies: Moving towards the Plant Pathobiome Paradigm. *Plants* 2021, 10, 125.
90. Stewart, J.E.; Kim, M.-S.; Lalande, B.; Klopfenstein, N.B. Chapter 15—Pathobiome and microbial communities associated with forest tree root diseases. In *Forest Microbiology*; Asiegbu, F.O., Kovalchuk, A., Eds.; Academic Press: Cambridge, MA, USA, 2021; pp. 277–292.
91. Droby, S.; Zhimo, V.Y.; Wisniewski, M.; Freilich, S. The pathobiome concept applied to postharvest pathology and its implications on biocontrol strategies. *Postharvest Biol. Technol.* 2022, 189, 111911.
92. Lamelas, A.; Desgarennes, D.; López-Lima, D.; Villain, L.; Alonso-Sánchez, A.; Artacho, A.; Latorre, A.; Moya, A.; Carrión, G. The Bacterial Microbiome of Meloidogyne-Based Disease Complex in Coffee and Tomato. *Front. Plant Sci.* 2020, 11, 136.
93. Bruez, E.; Vallance, J.; Gautier, A.; Laval, V.; Compant, S.; Maurer, W.; Sessitsch, A.; Lebrun, M.-H.; Rey, P. Major changes in grapevine wood microbiota are associated with the onset of esca, a devastating trunk disease. *Environ. Microbiol.* 2020, 22, 5189–5206.
94. Haidar, R.; Yacoub, A.; Pinard, A.; Roudet, J.; Fermaud, M.; Rey, P. Synergistic effects of water deficit and wood-inhabiting bacteria on pathogenicity of the grapevine trunk pathogen *Neofusicoccum parvum*. *Phytopathol. Mediterr.* 2021, 59, 473–484.
95. Haidar, R.; Yacoub, A.; Vallance, J.; Compant, S.; Antonielli, L.; Saad, A.; Habenstein, B.; Kauffmann, B.; Grélard, A.; Loquet, A.; *etal.* Bacteria associated with wood tissues of Esca-diseased grapevines: Functional diversity and synergy with Fomitiporia mediterranea to degrade wood components. *Environ. Microbiol.* 2021, 23, 6104–6121.
96. Cobo-Díaz, J.F.; Baroncelli, R.; Le Floch, G.; Picot, A. Combined Metabarcoding and Co-occurrence Network Analysis to Profile the Bacterial, Fungal and Fusarium Communities and Their Interactions in Maize Stalks. *Front. Microbiol.* 2019, 10, 261.
97. Pauvert, C.; Fort, T.; Calonnec, A.; Faivred'Arcier, J.; Chancerel, E.; Massot, M.; Chiquet, J.; Robin, S.; Bohan, D.A.; Vallance, J. Microbial association networks give relevant insights into plant pathobiomes. *BioRxiv* 2020.
98. Qiu, Z.; Verma, J.P.; Liu, H.; Wang, J.; Batista, B.D.; Kaur, S.; de Araujo Pereira, A.P.; Macdonald, C.A.; Trivedi, P.; Weaver, T.; *et al.* Response of the plant core microbiome to Fusarium oxysporum infection and identification of the pathobiome. *Environ. Microbiol.* 2022, 24, 4652–4669.
99. Goberna, M.; Verdú, M. Cautionary notes on the use of co-occurrence networks in soil ecology. *Soil Biol. Biochem.* 2022, 166, 108534.
100. Picot, A.; Doster, M.; Islam, M.-S.; Callicott, K.; Ortega-Beltran, A.; Cotty, P.; Michailides, T. Distribution and incidence of toxigenic *Aspergillus flavus* VCGI tree crop orchards in California: A strategy for identifying potential antagonists, the example of almonds. *Int. J. Food Microbiol.* 2018, 265, 55–64.
101. Chen, W.; Radford, D.; Hambleton, S. Towards improved detection and identification of fruit fungal pathogens in environmental samples using a metabarcoding approach. *Phytopathology* 2022, 112, 535–548.
102. Schoch, C.L.; Seifert, K.A.; Huhndorf, S.; Robert, V.; Spouge, J.L.; Levesque, C.A.; Chen, W.; Bolchacova, E.; Voigt, K.; Crous, P.W.; *etal.* Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. *Proc. Natl. Acad. Sci. USA* 2012, 109, 6241–6246.
103. Chattopadhyay, A.; Tiwari, K.K.; Chaudhary, K.; Pratap, D. Genic molecular markers in fungi: Availability and utility for bioprospection. In *Molecular Markers in Mycology: Diagnostics and Marker Developments*; Springer: Cham, Switzerland, 2017; pp. 151–176.

104. Li, S.; Deng, Y.; Wang, Z.; Zhang, Z.; Kong, X.; Zhou, W.; Yi, Y.; Qu, Y. Exploring the accuracy of amplicon-based internal transcribed spacer markers for a fungal community. *Mol. Ecol. Resour.* 2020, 20, 170–184.
105. Gloor, G.B.; Macklaim, J.M.; Pawlowsky-Glahn, V.; Egozcue, J.J. Microbiome Datasets Are Compositional: And This Is Not Optional. *Front. Microbiol.* 2017, 8, 2224.
106. Fonseca, V.G. Pitfalls in relative abundance estimation using DNA metabarcoding. *Mol. Ecol. Resour.* 2018, 18, 923–926.
107. Tkacz, A.; Hortala, M.; Poole, P.S. Absolute quantitation of microbiota abundance in environmental samples. *Microbiome*. 2018, 6, 110.
108. Gao, M.; Xiong, C.; Gao, C.; Tsui, C.K.; Wang, M.-M.; Zhou, X.; Zhang, A.-M.; Cai, L.J.M. Disease-induced changes in plant microbiome assembly and functional adaptation. *Microbiome* 2021, 9, 187.
109. Vorholt, J.A.; Vogel, C.; Carlström, C.L.; Müller, D.B. Establishing Causality: Opportunities of Synthetic Communities for Plant Microbiome Research. *Cell Host Microbe* 2017, 22, 142–155.
110. Qiu, Z.; Egidi, E.; Liu, H.; Kaur, S.; Singh, B.K. New frontiers in agriculture productivity: Optimised microbial inoculants in situ microbiome engineering. *Biotechnol.* 2019, 37, 107371.
111. Mawarda, P.C.; LeRoux, X.; Dirk van Elsas, J.; Salles, J.F. Deliberate introduction of invisible invaders: A critical appraisal of the impact of microbial inoculants on soil microbial communities. *Soil Biol. Biochem.* 2020, 148, 107874.
112. Jack, C.N.; Petipas, R.H.; Cheeke, T.E.; Rowland, J.L.; Friesen, M.L. Microbial inoculants: Silver bullet or microbial Jurassic Park? *Trends Microbiol.* 2021, 29, 299–308.
113. Liu, X.; Roux, X.; Salles, J. The Legacy of Microbial Inoculants in Agroecosystems and Potential for Tackling Climate Change Challenges. *iScience* 2022, 25, 103821.
114. Moore, J.A.M.; Abraham, P.E.; Michener, J.K.; Muchero, W.; Cregger, M.A. Ecosystem consequences of introducing plant growth promoting rhizobacteria to managed systems and potential legacy effects. *New Phytol.* 2022, 234, 1914–1918.
115. Heimpel, G.E.; Cock, M.J.W. Shifting paradigms in the history of classical biological control. *BioControl*. 2018, 63, 27–37.
116. Ehrlich, K. Non-aflatoxigenic *Aspergillus flavus* to prevent aflatoxin contamination in crops: Advantages and limitations. *Front. Microbiol.* 2014, 5, 50.
117. Olarte, R.A.; Horn, B.W.; Dorner, J.W.; Monacell, J.T.; Singh, R.; Stone, E.A.; Carbone, I. Effect of sexual recombination on population diversity in aflatoxin production by *Aspergillus flavus* and evidence for cryptic heterokaryosis. *Mol. Ecol.* 2012, 21, 1453–1476.
118. Molo, M.S.; White, J.B.; Cornish, V.; Gell, R.M.; Baars, O.; Singh, R.; Carbone, M.A.; Isakeit, T.; Wise, K.A.; Woloshuk, C.P.; et al. Asymmetrical lineage introgression and recombination in populations of *Aspergillus flavus*: Implications for biological control. *PLoS ONE* 2022, 17, e0276556.
119. OECD Guidance to the Environmental Safety Evaluation of Microbial Biocontrol Agents. 2012. Available online: <https://www.oecd.org/env/oecd-guidance-to-the-environmental-safety-evaluation-of-microbial-biocontrol-agents-9789264221659-en.htm> (accessed on 22 May 2023).
120. Raza, M.M.; Bebbler, D.P. Climate change and plant pathogens. *Curr. Opin. Microbiol.* 2022, 70, 102233.
121. Avelino, J.; Cristancho, M.; Georgiou, S.; Imbach, P.; Aguilar, L.; Bornemann, G.; Läderach, P.; Anzueto, F.; Hruska, A.J.; Morales, C. The coffee rust crises in Colombia and Central America (2008–2013): Impacts, plausible causes and proposed solutions. *Food Secur.* 2015, 7, 303–321.
122. West, J.S.; Holdgate, S.; Townsend, J.A.; Edwards, S.G.; Jennings, P.; Fitt, B.D.L. Impacts of changing climate and agronomic factors on fusarium ear blight of wheat in the UK. *Fungal Ecol.* 2012, 5, 53–61.
123. Grosdidier, M.; Ioos, R.; Marçais, B. Do higher summer temperatures restrict the dissemination of *Hymenoscyphus fraxineus* in France? *For. Pathol.* 2018, 48, e12426.
124. Madgwick, J.W.; West, J.S.; White, R.P.; Semenov, M.A.; Townsend, J.A.; Turner, J.A.; Fitt, B.D.L. Impacts of climate change on wheat anthracnose and fusarium ear blight in the UK. *Eur. J. Plant Pathol.* 2011, 130, 117–131.
125. Bailly, S.; El Mahgubi, A.; Carvajal-Campos, A.; Lorber, S.; Puel, O.; Oswald, I.P.; Bailly, J.D.; Orlando, B. Occurrence and identification of *Aspergillus* section *flavi* in the context of the emergence of aflatoxins in french maize. *Toxins* 2018, 10, 525.
126. Bebbler, D.P.; Ramotowski, M.A.T.; Gurr, S.J. Crop pests and pathogens move polewards in a warming world. *Nat. Clim. Change* 2013, 3, 985–988.
127. Rosa, C.R.E.; Spehar, C.R.; Liu, J.Q. Asian Soybean Rust Resistance: An Overview. *J. Plant Pathol. Microbiol.* 2015, 6, 2.
128. Ozkan, H.E.; Zhu, H.; Derksen, R.C.; Guler, H.; Krause, C. Evaluation of various spraying equipment for effective application of fungicide to control Asian soybean rust. *Asp. Appl. Biol.* 2006, 77.
129. McIntosh, R.A.; Pretorius, Z.A. Borlaug Global Rust Initiative provides momentum for wheat rust research. *Euphytica* 2011, 179, 1–2.
130. Hovmøller, M.S.; Thach, T.; Justesen, A.F. Global dispersal and diversity of rust fungi in the context of plant health. *Curr. Opin. Microbiol.* 2023, 71, 102243.
131. Lehmann, P.; Ammouët, T.; Barton, M.; Battisti, A.; Eigenbrode, S.D.; Jepsen, J.U.; Kalinkat, G.;

- Neuvonen, S.; Niemelä, P.; Terblanche, J.S.; *et al.* Complex responses of global insect pests to climate warming. *Front. Ecol. Environ.* 2020, 18, 141–150.
132. Goodwin, S.B.; Cohen, B.A.; Fry, W.E. Panglobal distribution of a single clonal lineage of the Irish potato famine fungus. *Proc. Natl. Acad. Sci. USA* 1994, 91, 11591–11595.
133. Zhang, J.; Zhang, L.; Li, G.-Q.; Yang, L.; Jiang, D.-H.; Zhuang, W.-Y.; Huang, H.-C. Botrytis sinoallii: A new species of the greymould pathogen on Allium crops in China. *Mycoscience* 2010, 51, 421–431.
134. Singh, R.P.; Hodson, D.P.; Huerta-Espino, J.; Jin, Y.; Bhavani, S.; Njau, P.; Herrera-Foessel, S.; Singh, P.K.; Singh, S.; Govindan, V. The emergence of Ug99 races of the stem rust fungus is a threat to world wheat production. *Annu. Rev. Phytopathol.* 2011, 49, 465–481.
135. Hoymøller, M.S.; Walter, S.; Justesen, A.F. Escalating Threat of Wheat Rusts. *Science* 2010, 329, 369.
136. Bezner Kerr, R.; Hasegawa, T.; Lasco, R.; Bhatt, I.; Deryng, D.; Farrell, A.; Gurney-Smith, H.; Ju, H.; Lluch-Cota, S.; Meza, F.; *et al.* Food, Fibre, and Other Ecosystem Products. In *Climate Change 2022: Impacts, Adaptation and Vulnerability. Contribution of Working Group II to the Sixth Assessment Report of the Intergovernmental Panel on Climate Change*; Pörtner, H.-O., Roberts, J., et al., Eds.; Cambridge University Press: Cambridge, 2022; pp. 111–172.
137. Gold, K.M. Plant disease sensing: Studying plant-pathogen interactions at scale. *MSystems* 2021, 6, e01228-21.
138. Vurukonda, S.S.K.P.; Vardharajula, S.; Shrivastava, M.; SkZ, A. Enhancement of drought stress tolerance in crop by plant growth promoting rhizobacteria. *Microbiol. Res.* 2016, 184, 13–24.
139. Jajoo, A.; Mathur, S. Role of arbuscular mycorrhizal fungus as an underground savior for protecting plants from abiotic stresses. *Physiol. Mol. Biol. Plants* 2021, 27, 2589–2603.
140. Itakura, M.; Uchida, Y.; Akiyama, H.; Hoshino, Y.T.; Shimomura, Y.; Morimoto, S.; Tago, K.; Wang, Y.; Hayakawa, C.; Uetake, Y.J.N.C.C. Mitigation of nitrous oxide emissions from soils by *Bradyrhizobium japonicum* inoculation. *Nat. Clim. Change* 2013, 3, 208–212.
141. Jansson, J.K.; Hofmockel, K.S. Soil microbiomes and climate change. *Nat. Rev. Microbiol.* 2020, 18, 35–46.
142. Ma, Z.; Guo, D.; Xu, X.; Lu, M.; Bardgett, R.D.; Eissenstat, D.M.; McCormack, M.L.; Hedin, L.O. Evolutionary history resolves global organization of root functional traits. *Nature* 2018, 555, 94–97.
143. Bergmann, J.; Weigelt, A.; van Der Plas, F.; Laughlin, D.C.; Kuyper, T.W.; Guerrero-Ramirez, N.; Valverde-Barrantes, O.J.; Bruehlheide, H.; Freschet, G.T.; Iversen, C.M.; *et al.* The fungal collaboration gradient dominates the root economics space in plants. *Sci. Adv.* 2020, 6, eaba3756.
144. Qiu, Y.; Guo, L.; Xu, X.; Zhang, L.; Zhang, K.; Chen, M.; Zhao, Y.; Burkey, K.O.; Shew, H.D.; Zobel, R.W.; *et al.* Warming and elevated ozone induce tradeoffs between fine roots and mycorrhizal fungi and stimulate organic carbon decomposition. *Sci. Adv.* 2021, 7, eabe9256.