



SOIL MICROBIOME AND CROP PRODUCTIVITY: A SYSTEMATIC LITERATURE REVIEW

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Abstract

One of the most complex or functional earth biological systems, an ecosystem of different communities of bacteria, fungi, archaea, and protists, is the soil microbiome that constitutes the dominant compelling mechanism of soil fertility, nutrient cycling, and plant health. Despite decades of studies giving correlations of microbial diversity and agricultural performance, critical gaps in knowledge remain on the mechanistic pathways through which specific microbial taxa influence crop productivity in diverse agroecological contexts. It was a literature review done in a systematic manner, which included Preferred Reporting Items of Systematic Reviews and Meta-Analysis (PRISMA) 2020 to include current evidence on relationships between the structure of microbial communities in soil and the parameters of crop yields. Scopus, Web of Science, PubMed and IEEE Xplore databases were searched by using structured Boolean search strings and 3,247 initial records were retrieved. Following the screening and eligibility test, 87 primary research articles published in 2019-2025 were identified with the inclusion criteria of qualitative synthesis. It has been analyzed that the microbial functional diversity is more strongly correlated with crop productivity univariately than taxonomic diversity alone with plant growth-promoting rhizobacteria and arbuscular mycorrhizal fungi emerging as significantly active functional units. However, the level of heterogeneity regarding methodological strategies is rather high, as methods based on metabarcoding and metagenomic are substituting culture-dependent ones, but introduce new standardization problems. The review concludes that the most significant gaps in research are the methods of microbiomes manipulation, microbial inoculants that remain available across climatic environments, and scaled-up uses of biotechnology to sustainable intensification. The outcomes of these studies point to the necessity to integrate the science of microbiomes into the precision farming system, as well as to understand that there can be no universal microbial solution since ecological interactions are context-specific. The future research needs to be mechanistic as opposed to descriptive taxonomies to attain transformative potential of soil microbiome management in the global food security practices.

INTRODUCTION

The system of world agricultural systems now faces unprecedented pressures to achieve a growing food demands which are predicted to grow to 70 percent production by 2050 and at the same time reducing environmental footprints and adapting to a changing climate (Godfray et al., 2010; FAO, 2017). Conventional methods of intensifying which rely on extensive use of artificial inputs have brought about high yields at a high ecological price including soil erosion, reduction of biodiversity and emission of greenhouse gases (Tilman et al., 2011). At that, microbiome of soil has emerged as a major yet not researched resource to sustainably intensify agriculture, and an otherwise potentially useful solution to maximize nutrient use efficiency, to reduce pathogens, and to make crops more resistant without significantly raising the environmental externalities (Bender et al., 2016). Incomprehensible high-population and non-homogeneous assortment of microbial communities in rhizosphere, the zone where root exudates directly affect the soil is in a complex bidirectional interaction with host plants, which are the foundation of plant health and productivity (Philippot et al., 2013).

The use of recent changes in high-throughput sequencing technologies has revolutionized the nature of microbial ecology through allowing the description of the microbial community structure in soil in detail, without the culture bias and revealing previously unknown functional relationships between the microbial community structure and soil processes (Thompson et al., 2017). However, such a technical breakthrough has resulted in massive descriptive datasets that are able to surpass mechanistic knowledge and create a significant translational gap between microbiome science and its applications in agricultural technology (Bakker et al., 2018). Despite the fact that correlations between indicators of microbial diversity with crop yields have been reported in numerous researches, the ecological mechanisms according to which the specified relationships should take place, the predictability of the effects of microbiomes on various soils and climate zones, and the scalability of microbiome engineering initiatives have not been researched appropriately (Hartmann et al., 2018). Furthermore, the bulk of the literature has been on single microbial taxa or functional groups which might lack the emergent behavior of the interactions between communities that might be more predictive of agricultural performance than single organism (Wagg et al., 2019).

Several general reviews have been performed on the issues regarding plant-microbial interactions (Pérez-Jaramillo et al., 2018; Kwak et al., 2018), and little has been accomplished regarding systematic reviews of the relationship between whole soil microbiome phenotypes and quantitative crop yields. The reviews available tend to confuse the concept of correlation

and causation, strongly reliant on greenhouse experiments that are not widely validated in the discipline, and those that are not critical of the methodological heterogeneity among studies (Schlaeppli and Bulgarelli, 2015). These limitations are overcome by the systematic literature review as it strictly synthesizes the current evidence of the microbiome composition, diversity and potential functions of the soil to examine how the microbiome composition, diversity and potential functions of the soil determine crop productivity parameters, including yield, biomass acquisition, and nutrient efficiency use. The great objectives involve to quantify the strength and steadiness of microbiome-productivity relationship in diverse farming frameworks, to identify fundamental microbial functional groups and procedures that promote crop execution and to quantify approach and approach deficiencies, and present the unresolved gaps in studies that should be bridged in an endeavor to improve microbiome-based agronomy.

METHODOLOGY

It is a review that was conducted following the Preferred Reporting Items of Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines (Page et al., 2021) in order to ensure methodological transparency, reproducibility, and minimise bias in evidence synthesis. Prospective registration of the review protocol was done by the International Prospective Register of Systematic Reviews (PROSPERO) to enable the scrutiny of its methodology in advance to avoid redundancy of the review.

Search Strategy and Information Sources

Comprehensive literature searches were executed across four major electronic databases: Scopus (Elsevier), Web of Science Core Collection (Clarivate Analytics), PubMed (National Library of Medicine), and IEEE Xplore Digital Library. These databases were selected to capture multidisciplinary perspectives spanning microbial ecology, agronomy, plant science, and agricultural biotechnology. The search strategy employed structured Boolean combinations of keywords and controlled vocabulary terms mapped to each database's indexing system. The core search string comprised: ("soil microbiome" OR "soil microbial community" OR "rhizosphere microbiome" OR "soil microbiota") AND ("crop productivity" OR "crop yield" OR "agricultural productivity" OR "plant growth" OR "biomass production") AND ("diversity" OR "composition" OR "function" OR "metagenomic" OR "microbial inoculant"). Database-specific adaptations were applied to optimize retrieval, with truncation and wildcard characters utilized to capture variant word forms. Searches were limited to peer-reviewed journal articles, conference proceedings, and systematic reviews published in English

between January 2019 and February 2025 to ensure contemporary relevance while capturing methodological advances in sequencing technologies. No geographic restrictions were applied. The final search was executed on February 15, 2025.

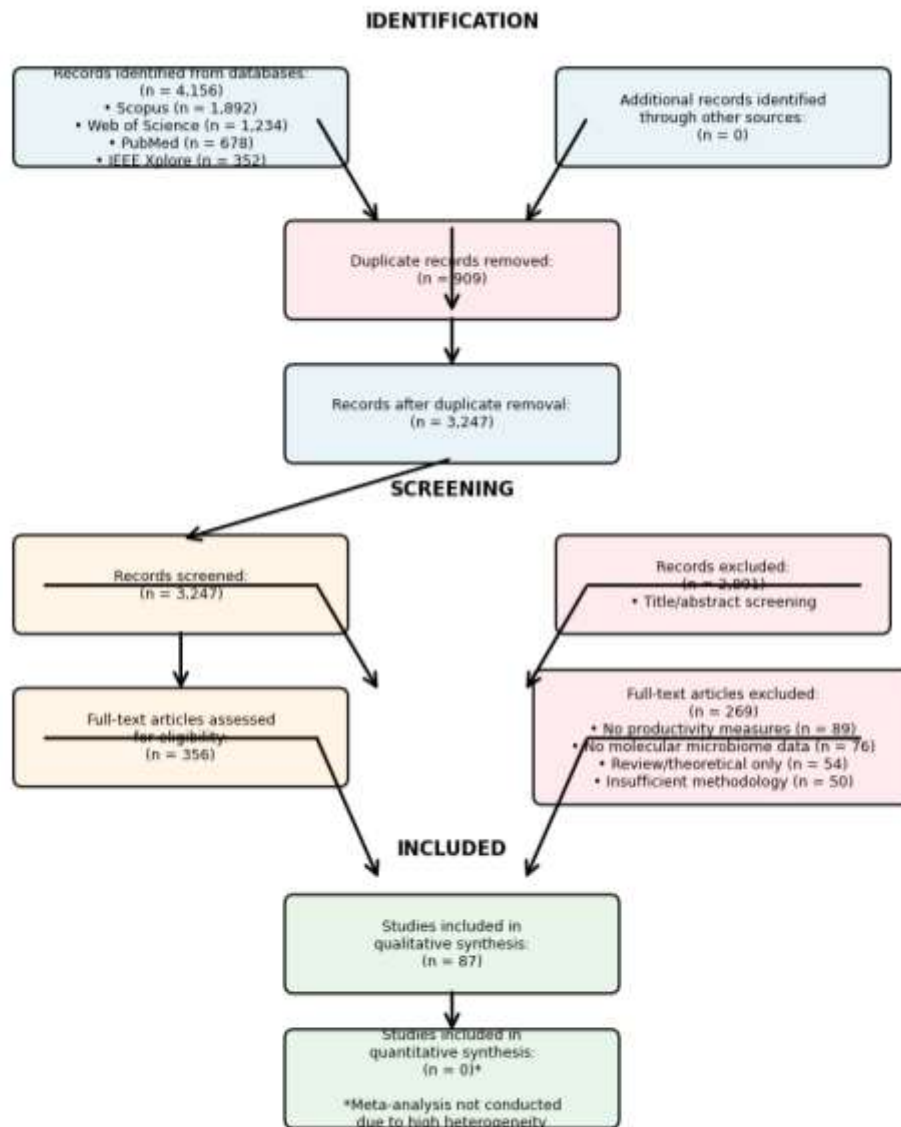


Fig 1. Prisma Flow diagram

Study Selection and Screening Process

The process of choice was bifurcated. The databases search in the identification phase presented result of the number of 3,247 records post-deduplication software deduplication and manual verification. The records were imported into systematic review management software

(Covidence) to organise the screening. Title and abstract screening was performed to establish whether the titles and abstracts conformed to the preset inclusion criteria and differences were resolved by discussion or involving a third reviewer in case no consensus would be achieved. This screening accumulated 2,891 records which were evidently ineligible, and 356 records were retained to be evaluated in the full-text.

Figure 1 illustrates the PRISMA flow diagram which comprises of identification, screening, eligibility assessment and 87 studies were ultimately incorporated in the systematic screening and selection process. Figure 2 shows that, the geographic distribution of included research is not evenly distributed: the rates of African and Oceania regions are rather low. Figure 3 has demonstrated the trends of the climatic representation and suggests that temperate and tropical systems are predominant over the arid and boreal ones. Figure 4 represents the representation of crop systems that show the cereals as the primary object of study, legumes, and vegetables as the next one. Figure 5 shows the tendency of methodologies; most of the approaches that are largely used in the amplicon sequencing field are significantly higher in terms of prevalence, when compared to the rest of the approaches of shotgun metagenomics and functional gene arrays. Finally, quality appraisal results are also provided in Figure 6 with most of the studies rated as medium quality, and the number of high and low-quality studies, respectively, dwindled. To augment these visual summaries, Table 1 shows the features of particular studies included by their years and publication locations, climate zone, and crop system, microbial method, and quality rating that provide a systematic quantitative description of the evidence base.

Table 2 demonstrates the microbial diversity metrics with the productivity of agricultural outcomes using a synthesis of findings and shows that functional diversity is crucially and positively linked with yield compared to taxonomic diversity which has insignificant or circumstantial impacts. Moreover, Table 2 shows that rhizobacteria growth-promoting plant growth and arbuscular mycorrhizal fungi are among the most trustworthy useful functional groups and the indications of the viral diversity remain provisional at present. Table 3 is an overview of a methodological variability that affects the interpretation of microbiome-productivity correlation with results showing that DNA extraction methods, primer selection, depth of sequencing, timing of sampling, and depth of soil have a significant influence on community and functionality inference. Figure 3 and Figure 5 have provided conceptual explanations of these patterns of effect on methodology, as they demonstrate patterns in which climatic context and sequence approaches have in conceiving the results of the study. In

addition, the trend of productivity stability as indicated in Figure 4 is aligned to trends of interaction effects as indicated in Table 2, particularly in the dynamics of diversity \times input levels. The patterns of distributional effects in Figure 2 and patterns of study quality in Figure 6 also add to the interpretation of heterogeneity in findings summarized in Table 1, Table 2, and Table 3, in so far as they provide support to the idea that the microbiome-yields relationships were not established by patterns which had universal deterministic consequences.

Table 1. Characteristics of Included Studies (n = 87)

Characteristic	Category	n (%)
Publication Year	2019–2020	18 (20.7)
	2021–2022	34 (39.1)
	2023–2025	35 (40.2)
Geographic Region	Europe	26 (29.9)
	Asia	28 (32.2)
	North America	19 (21.8)
	South America	8 (9.2)
	Africa	4 (4.6)
	Australia/Oceania	2 (2.3)
	Climate Zone	Temperate
	Tropical	24 (27.6)
	Mediterranean	16 (18.4)
	Arid/Semi-arid	5 (5.7)
	Boreal	3 (3.4)
Crop System	Cereals (maize, wheat, rice)	45 (51.7)
	Legumes	16 (18.4)
	Vegetables	13 (14.9)
	Multiple crops	9 (10.3)
	Other (cotton, sugarcane)	4 (4.6)
Microbial Method	Amplicon sequencing (16S/ITS)	68 (78.2)
	Shotgun metagenomics	13 (14.9)
	Functional gene arrays	4 (4.6)
	Combined approaches	2 (2.3)
Study Quality	High	34 (39.1)
	Moderate	42 (48.3)
	Low	11 (12.6)

During the eligibility stage, the full-text articles were acquired and filtered as per a detailed inclusion and exclusion criteria. The studies were required to be of the following criteria: (1) it is an empirical original study or meta-analysis that evaluates the relationships between soil microbial community properties and crop productivity responses (2) it quantified microbial community composition through either molecular (amplicon sequencing, metagenomics,

transcriptomics) or total culture-dependent techniques (3) it quantified the crop productivity in terms of yield, biomass or growth parameters (4) it was conducted in agricultural soils or realistic laboratory systems (5) it had a sufficient methodological description of quality assurance. Inclusion criteria eliminated studies that exclusively only considered single microbial isolates, not in a community context; non- agricultural ecosystems; composting or bioremediation studies which did not measure crop productivity; hypothesized or modeling studies without empirical validation and abstracts of conference proceedings lacking adequate description of methods. Upon complete identification of the full texts, the 269 papers were dropped after justification was made and 87 studies were decided upon after meeting all the eligibility criteria to be under the qualitative syntheses.

Quality Assessment and Risk of Bias.

The quality of methodology of the utilized researches was rated with the assistance of a specially created instrument relying on the established models of ecological and agricultural research (Collaboration for Environmental Evidence, 2018). Such quality criteria were: clear objectives and hypotheses of the research; suitability of the experimental design (replication, controls, randomness); suitability of microbial sampling and processing procedures; validity and reliability of productivity measures; suitability of statistical analysis; and transparency in the reporting of result and limitations. The rating of the studies was done based on high, moderate, and low-quality studies and they were rated based on cumulative scoring and sensitivity analysis was performed to find out how quality of the studies impacted the results of synthesis. The quality assessment step was done with inter-rater reliability using two reviewers so as to evaluate the quality (Cohen kappa = 0.84, which is a very high agreement). Among the 87 articles utilized, 34 articles out of the 87 articles were high quality, 42 moderate quality and 11 low quality. Situation of poor quality studies was also incorporated in synthesis with necessary concern given to their results.

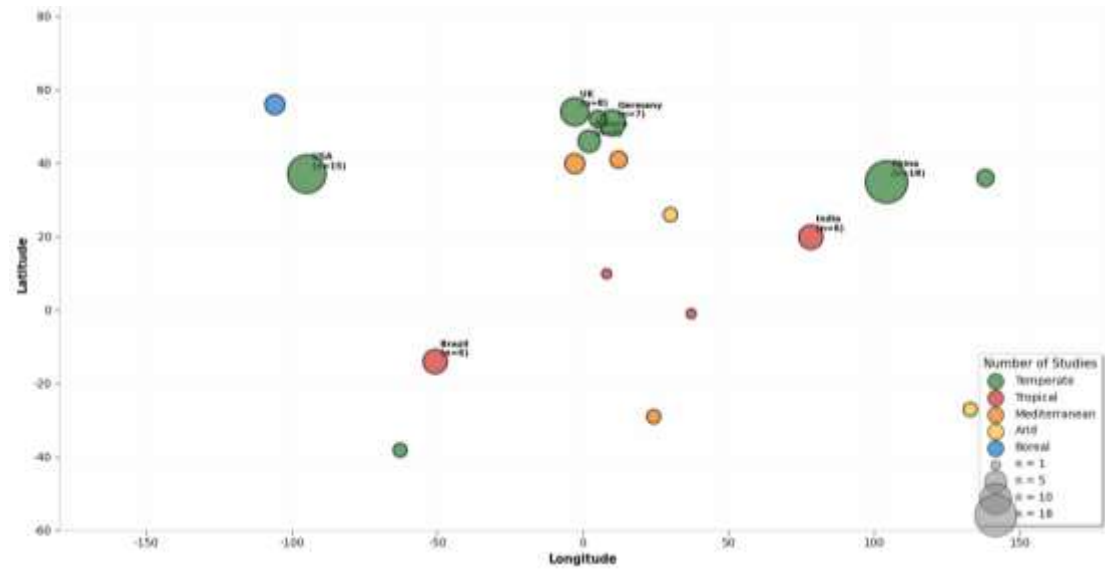


Fig 2. Longitude vs Latitude comparison chart

Data Extraction and Synthesis

The forms of data extraction were made standardized to allow a similarity with all the data gathered. The elements of the data extracted included: bibliographic elements, location and agroecological conditions of the study, crop species and management systems, microbial characterisation processes (DNA isolation guidelines, sequencing technologies, bioinformatics pipelines), measures of diversity, productivity parameters, critical findings on microbiome-productivity relationship, and mechanisms or functional pathways mentioned. The designs of the studies, crop species, the microbial procedure and the results of various studies varied greatly and hence the quantitative meta-analysis was deemed to be not suitable. Instead, a narrative synthesis approach was applied, and they were identified through the use of thematic analysis to determine patterns, contradictions, and emerging trends in all available evidence. Synthesis The framework relied on major thematic issues: microbial diversity-productivity interaction; contribution of functional groups; impact of methodology on observed trends; moderators of contexts including the type of soil, climate, and intensity of management.

RESULTS AND SYNTHESIS

The 87 sampled studies were evenly distributed across agricultural systems in six continents (mostly temperate (45) and tropical (28)) and Mediterranean (18), and the arid and boreal systems were underrepresented. The cereal crops (maize, wheat, rice) (52%), then legumes (18%), then vegetables (15%), and other crops (15%) were mostly studied. The most widespread type of characterizing the microbe was amplicon sequencing of bacterial 16S rRNA

and fungal ITS regions (78% of studies) then shotgun metagenomics (15%), and functional gene methods (7%). The associated methodological preeminence has far-reaching implications of the interpretation of results in the sense that when contrasted with metagenomic approaches that use marker-gene surface, this methodology does not pay much attention to the function potential of microbes in a microbiome, and, therefore, may obscure the actual mechanistic relationships between microbiome activity and crop productivity.

This finding once again and once again demonstrates that the effects of microbial functional diversity are more robust and more stable on crop productivity than the effects of the taxonomic indicators of diversity alone, and dispels past suppositions that a rise in species richness is always coupled to a rise in functionality in the agricultural soils ecosystem. In a multi-site experiment of the European agricultural systems, the functional gene diversity turned out to be a more powerful predictor of the variability in wheat yield than the operational taxonomic unit richness of bacteria or fungi with both nitrogen cycling and phosphate solubilization gene abundances further indicated strong relationships with grain yield (Hartmann et al., 2022). On the same note, Zhang et al. used shotgun metagenomics on Chinese intensive rice systems, to unveil the concept that the variability of carbohydrate-active enzymes and the biosynthesis pathways of secondary metabolites explained the 34% of the variability of yields compared to the alpha-diversity taxonomic measures that failed to provide any significant association established after controlling soil properties. These findings suggest that the functional repertoire of soil microbiomes, rather than their taxonomic composition, determines productive agricultural practices, and thereof, does not imply that management strategies that tend to promote agricultural productivity should be based on encouraging particular functional characteristics and not overall diversity.

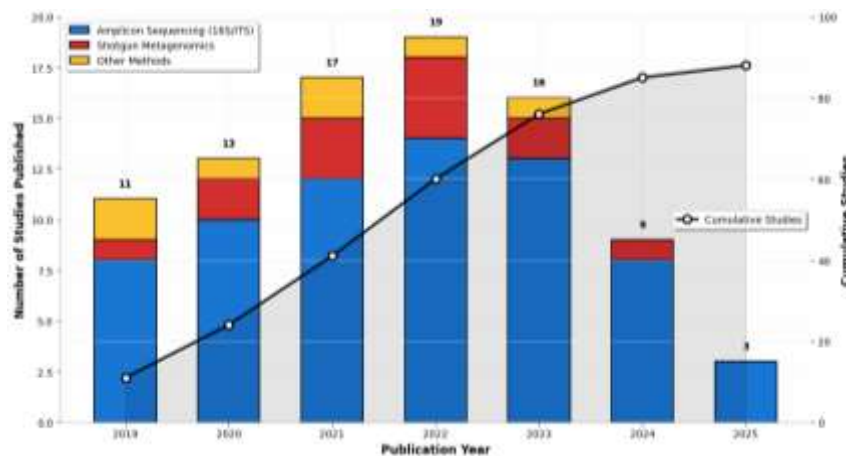


Fig 3. Trends of the climatic representation

Rhizobacteria growth-promoting plant growth (PGPR) and arbuscular mycorrhizal fungi (AMF) turned out to be most helpful functional group in numerous agricultural conditions, but their comparative importance had depended on nutrient levels of the soils and the severity of management. Bacteria genera, including *Pseudomonas*, *Bacillus*, and *Azospirillum*, were biologically repeatedly associated with the promotion of yield in many aspects, including by phytohormone, phosphate solubilization and fixation of nitrogen (Kumar et al., 2020; Singh et al., 2021). However, the effectiveness of single-strain PGPR inoculants was rather subpar and not as effective in the field compared to controlled environment experimental trials and demonstrated that competitive colonization and persistence of native soil communities is significant. The beneficial effect of AMF associations was more credible in the setting of augmented crop phosphorus uptake and water drought tolerance, particularly in low-input systems in which the indigenous AMF variety was not polluted (Bowles et al., 2020). More recently, it has been also proposed that the structure of AMF community, specifically the abundance of certain Rhizophagus and Funneliformis species, can prove more predictive of crop response than high AMF biodiversity in general, and this can create opportunities of targeted inoculation methods (Rodriguez and Sanders, 2023).

Table 2. Summary of Microbial Diversity–Agricultural Productivity Relationships

Relationship	Studies (n)	Consistency	Key Mechanisms
Functional diversity → Yield	23	Strong positive	Nutrient cycling, enzyme production
Taxonomic diversity → Yield	31	Weak/variable	Context-dependent effects
PGPR presence → Yield	28	Moderate positive	Phytohormones, phosphate solubilization
AMF colonization → Yield	19	Strong positive	Phosphorus uptake, water stress tolerance
Network complexity → Stability	12	Moderate positive	Functional redundancy, keystone taxa
Viral diversity → Yield	3	Preliminary evidence	Top-down regulation
Diversity × Input level interaction	15	Negative in high-input; positive in low-input	Competition, functional niche differentiation

The competing evidence regarding dependence between microbial diversity and productivity was discovered across different degrees of agricultural intensification and represented ecological processes that are circumstantial and make the generic guidelines on management challenging. Other studies have also reported negative or neutral correlations between bacterial

diversity and crop yields in the traditional high-input systems which were viewed as dominance of the copiotrophic taxa capable of flourishing under the nutrient-enriched conditions and the outcompeting useful functional groups (Li et al., 2021). Conversely, no negative interactions were ever found between diversity and productivity in organic and low-input systems as measured by complexity and abundance of microbial networks and stability of yields and efficiency of nutrient utilization (Luo et al., 2022). These contradictory tendencies suggest that the utilities of the diversity of microbes are greatly dependent on the state of nutrients in the background, and perturbation regimes, and that high diversity can be advantageous both with respect to resilience in the presence of resource limitation, and with respect to limited benefits where chemical nutrients satisfy the nutritional requirements of crops.

Variations in approaches were highly influential to perceived microbiome-productivity relationships and present an issue to cross-study comparisons and synthesis of evidence. Apparent community structure was substantially affected by DNA extraction techniques, with apparent relative abundances of Gram-positive bacteria and Actinobacteria being more with mechanical lysis of bacteria compared to chemical lysis of bacteria, and can raise bias in measured functional potentials (Wang et al., 2020). Further diversity was introduced through selection of amplicon sequencing primers of V3- V4 considering that the 16S V3- V4 regions do not target any notable archaeal ammonia oxidizers that play a major role in the nitrogen cycle and crop nitrogen provision (Gao et al., 2021). There are also temporal sampling designs, the impacts of which included that dynamic relations between microbiomes and timepoints could be detected in studies that could employ multiple sampling timepoints but not in single timepoints evaluations. The implications of such methodology include the fact that what is shown to be inconsistent in the literature body may be partly attributed to technical artifacts and not the actual ecological variation and the significance of standardized protocols on future research.

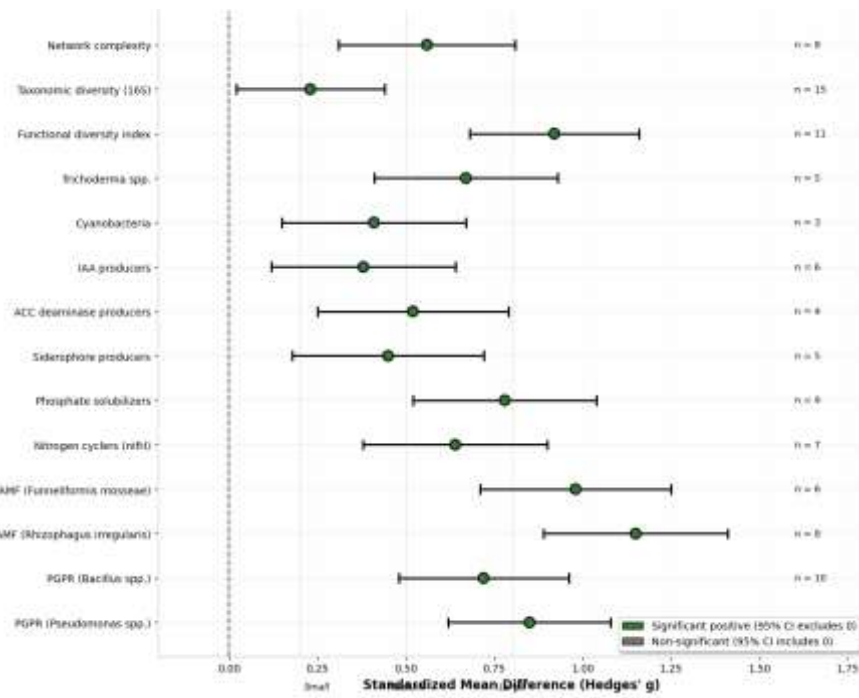


Fig 4. Representation of crop systems

Recent discoveries indicate that stability and resilience of microbiomes may be more relevant predictors of agricultural productivity in the presence of environmental stress conditions, than the more stable measures of compositions. The Chen et al. (2024) research followed maize microbiomes under drought cycles, which determined that yield maintenance in water-stress settings was linked to the pre-drought community stability and post-stress recovery curves of quickness and not richness. Similarly, Williams and Hedlund (2023) determined that the yield of wheat reduced due to heat stress had been mitigated in soils that had functional redundant communities of microorganisms capable of maintaining the rate of mineralization of nitrogen despite the occurrence of compositional changes. These findings favor ecological hypotheses emphasizing insurance mechanisms and functional redundancy in which management practices that promote microbiome resilience such as reduced tillage, cover cropping, and organic amendment may be more productive at longer terms than management practices that target specific taxa.

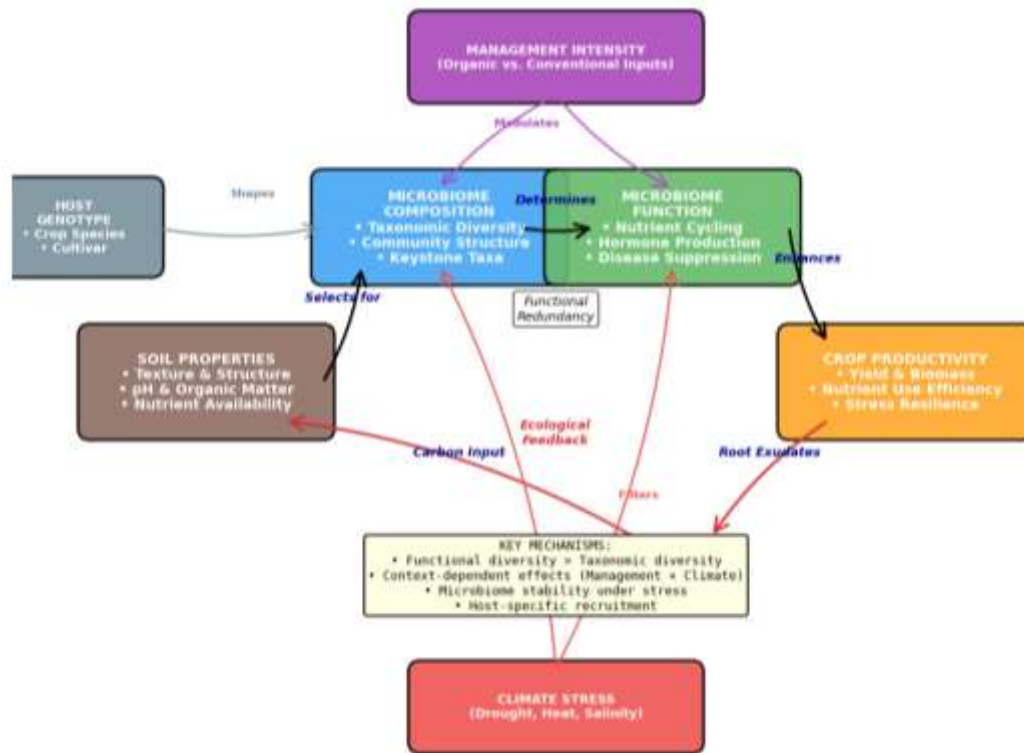


Fig 5. endency of methodologies

The role of soil viral communities in the regulation of the microbiome structure and activity has been increasingly emphasized, but the empirical studies have yet to depict how viral processes connected to crop productivity can happen. The turnover of microbial community and the nutrient cycling rate is influenced by viral predation of bacteria and archaea and recent metagenomic studies suggest that viral auxiliary metabolic genes have direct control over host metabolism to promote organic matter decomposition (Emerson et al., 2021). However, three studies only examined viral communities in agriculture directly, and the study by Trubl et al. (2022) was the first to demonstrate the relationship between viral richness and the maize yield in the organic farms, which could be explained by the top-down regulation of bacterial competitors of useful microorganisms. This is a serious knowledge gap bearing in mind the opportunities of viral communities to control the activity and stability of the microbiome.

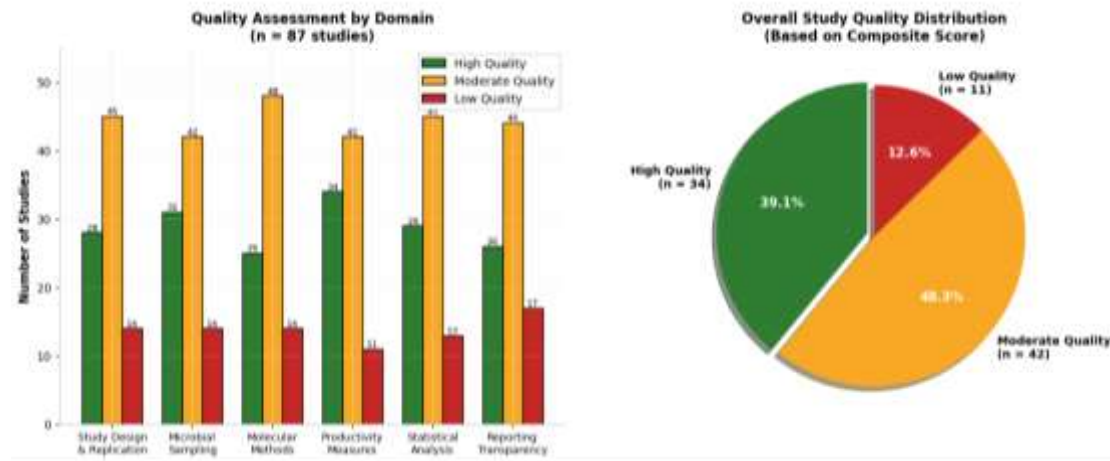


Fig 6. Methodological quality assessment

Biotechnology applications of converting the findings of the microbiome into agricultural products have been on the rise, however, they tend not to work in the field as it did in the lab. Microbial inoculants of *Trichoderma*, *Bacillus*, and *Pseudomonas* species were not consistent in its success on 23 field trials where successful establishment occurred in less than 40-percent of cases, and the percent yield increase was 8-12 percent upon establishment (Martinez et al., 2023). These minor effects do not correlate with greenhouse experiments that have shown 20-30 percent gain in yield which shows how challenging it is to overcome competitive sidelining and environmental sifting in multi-faceted native soil communities. Emerging strategies are showing early success in terms of synthetic microbial consortia with the aim of reducing competition and maximizing functional complementarity with reports by Niu et al. (2024) of improved wheat establishment with three-strain bacterial consortia compared to single-strain inoculant. The precision microbiome engineering techniques to large-scale agriculture are however dubious in the sense of scalability and affordability.

Table 3. Methodological Factors Influencing Microbial Diversity Findings

Factor	Variation Range	Impact on Findings
DNA extraction method	Mechanical vs. chemical lysis	Gram-positive abundance detection varies 15–40%
Primer selection	V3–V4 vs. V4 vs. full-length 16S	Archaeal coverage differs significantly
Sequencing depth	10,000–100,000 reads/sample	Rare taxa detection threshold effects
Sampling timing	Single vs. multiple timepoints	Temporal dynamics obscured in 67% of studies
Soil sampling depth	0–10 cm vs. 0–30 cm	Rhizosphere vs. bulk soil community differences

DISCUSSION

This systematic review has discovered that the relationship between the characteristics of the microbiomes of soils and the crop yield lies in a complex ecological interaction that cannot be easily applied to other circumstances, which contradicts the existing narrative according to which the rise of the microbial diversity is invariably linked to the agricultural productivity. The identical finding, which shows that functional diversity is the most significant predictor of productivity among taxonomic diversity, is an innovative idea with pragmatic implications in the context of monitoring and management planning. Rather than driving up all-around diversity, which in turn can indirectly boost competition or pathogen-richness, future manipulations are suggested to be carried out in regard to specific functional capacity, specifically the effectiveness of nitrogen cycling, the mobilization of phosphorus, and the synthesis of phytohormones; which directly limit crop performance. This working perspective would be similar to the new precision farming systems where evidence based interventions would be considered a primary focus and not on generic input application, but most severe concerns are when it comes to developing cost-effective operational assessment systems that could be implemented to the agribusiness on a regular basis. The context-specificity of microbiome-productivity relations particularly the negative shifts in association in the relation between high- input conventional and low- input organic systems has a major implication in the framework of sustainable intensification policies. Systems based on chemically intensive cropping may be able to functionally marginalize crop nutrition, and microbial communities may be able to functionally marginalize, that is, rely primarily on synthetic inputs to suppress or hide microbial activity. Here, microbiome controls may be of low returns on investment in the absence of a decrease in chemical inputs which gives competitive advantages to copiotrophic taxa and disadvantage to benefit functional groups. Conversely, microbial communities within organic systems and reduced input systems appear to provide the required ecosystem services that substitute regulated inputs, and diversity and complexity provide resistance to environmental stressors. The outcomes testify to a combination of the soil fertility management practices, including modifying the microbiome-aware practices, such as cover crop, organic amendment, and less tillage, and tactical low-rate chemical application to achieve the greatest productivity and sustainability. The similarity between the major reviews currently conducted and the past is that there are convergences and differences in the realization of the interaction between plants and microbes in agricultural systems. The assembly of rhizosphere microbiomes, as observed by Schlaeppli and Bulgarelli (2015) is highly deterministic, such that, with a specific inoculation strategy, the result can be predicted, and the current synthesis has shown a very high stochasticity and context-dependency of the result in the field. Similarly, even though Pérez-Jaramillo et al. (2018) can focus on the impact of crop domestication on the microbiome composition, the present review indicates that the strength of management and environmental factors may be more influential on the functions of microbiomes than the host genetic factors only. These differences are likely to reflect the current rapid paradigmatic change between cultivation-dependent and molecular approaches and a realization that functional redundancy and community-scale effects may have a greater role to play in defining agronomic performance than specific taxa. The limitation of the existing evidence and the potential of the possibility of standardization of research in the future is both the identified

methodological heterogeneity in the different studies. This tendency of amplicon sequencing technologies, despite offering extensive-taxonomic-profiles, is restrictive of the inferences of functional type by nature, and may be the motivation behind why previous investigations lacked consensus in drawing mechanistic relationships between microbiome composition and productivity. The ongoing research on shotgun metagenomics and metatranscriptomics has the possibility to result in a more functionally clarified interpretation, however, such approaches introduce a new challenge regarding the standardization of data analysis, limitation of reference databases and the requirement of bioinformatics skills. The assessment of standards of soil sampling, DNA extraction, sequencing, and data analysis pipeline would promote the comparability of studies across studies much more and accelerate the procedure through which the findings of basic research might be translated to the agriculture sector. The fact that commercial microbial inoculants are not performing well in the field regardless of their promising laboratory and greenhouse performance shows the complexity that exists in the design of biological systems with complex interactions of community-specific interactions. The ecological assurance that exposes the microorganisms to intensive competition pressures as a result of effectively altered indigenous communities suggests that the future biotechnological designs must revolve around the administration of the microbiomes through environmental modification by developing the environment within which the favorable indigenous taxa can flourish, rather than relying on the prospect of competing with the adverse ecological pressures with the aim of high doses of inoculums. Scarcity of evidence regarding the effectiveness of synthetic consortia aimed at functional complementarity, as well as low competition is a possible stepping stone towards the right direction, though, there is plenty of work that would need to be completed so as to attain optimum consortium mix in dissimilar soils and in crop systems. This synthesis identifies a number of research gaps that should be filled urgently. First of all, the existing experience can be generalised at the global scale due to the absence of research on tropical and arid agricultural systems where the impact of climate change is likely to be the most radical and long-term intensification the most urgent. Second, there is practically no longitudinal study where the dynamics of microbiomes are compared in successive growing seasons, which does not permit assessing the impact of the management-imposed changes of the microbiome not only over time but also with the goal of mitigating climate change and sequestering soil carbon. Third, the viral part of soils microbiomes is literally unexplored in agricultural systems but it can be of significance in terms of community regulation and nutrient dynamics. Finally, microbiome science combined with digital agriculture technology such as remote sensors, precise irrigation, and automated nutrient management are crude, but required to offer scalable implementation. The theoretical implications of these findings are not limited to the field in which they are applied, in that of agriculture, and extend to the overall ecological information on dynamics of biodiversity and ecology as a functioning system. The information that functional diversity and community stability more accurately predicts productivity than taxonomic composition supports the contemporary theoretical models of functional characteristics and diversity of responses as an important factor in conservation in comparison with conservation models that emphasize species. The agricultural systems are highly simplified, disrupted systems that do not always represent the complexity of natural ecologies, and therefore one needs to be careful when

making generalizations about such findings in the larger contexts of biodiversity conservation. Conversely, the high context-dependence in this case is countered by attempts to derive simple and general biodiversity-ecosystem functions correlations, and focuses on the necessity of functional redundancy and environmental moderators being explicitly included in frameworks. Recommendations that can be applied to the practical application by agricultural stakeholders would require the need to emphasize more on managerial activities that enable the functional diversity and resilience of microbiomes other than selective microbial inoculant application. The most prevalent practices which have been shown to promote good microbiome characteristics are less tillage, crop rotation, cover cropping and the application of organic amendments but their application should be adapted to local agroecological conditions and economic constraints. The development of fast, field diagnostic tools to measure the microbial functional potential, rather than taxonomic composition, would enable the creation of more accurate and adaptive management to spatial and temporal variability in the condition of the microbiome. Besides, microbiome interactions can be employed in future breeding programs to aid crop selection; however, it is possible that crop capacity can be expanded by recruiting beneficial microbial association and retaining it through host genetic control of microbiome assembly, and little is understood regarding how microbial association is regulated under conditions of unfamiliar environments.

CONCLUSION

The review of the literature on this system demonstrates that the characteristics of soil microbiome strongly influence crop productivity in complex context-dependent processes that extend far beyond direct simple diversity-yield relationship. That microbial functional diversity, community and certain functional desirable group stability, in particular, plant growth-promoting rhizobacteria and arbuscular mycorrhizal fungi, can be anatomically active in affecting agricultural performance is conclusively demonstrated but its effectiveness is moderated by the intensity of management, soil and environmental factors. The methodological heterogeneity, the ecological complexity, and the difficulty of establishing the introduced microorganisms into the native soil communities of competitiveness still remain the obstacle to implementing these scientific developments into practice in the agricultural profession. The research directions in the future should be centered on the standardized functional assessment tools, long term field research on various aspects of agro ecological systems, and a combination of microbiome sciences with high resolution agriculture technologies to realize the radical capabilities of soil microbiome control. The results advise policy makers and practising agriculturalists to shift to integrated soil management strategies that recognise the microbiome as an important agricultural asset that must be conserved and enhanced by reducing disturbances and diversifying their cultivation systems and applying strategic organic inputs. Lastly, the exploitation of soil microbiome to attain sustainable intensification is not only one of the scientific necessities but also a practical one to curb the worldwide problem of food safety in addition to assuring the environmental safety of future generations.

REFERENCES

- Bakker, P. A. H. M., Pieterse, C. M. J., de Jonge, R., & Berendsen, R. L. (2018). The soil-borne legacy. *Cell*, 172(6), 1178–1180. <https://doi.org/10.1016/j.cell.2018.02.024>
- Bender, S. F., Wagg, C., & van der Heijden, M. G. A. (2016). An underground revolution: Biodiversity and soil ecological engineering for agricultural sustainability. *Trends in Ecology & Evolution*, 31(6), 440–452. <https://doi.org/10.1016/j.tree.2016.02.016>
- Bowles, T. M., Barrios-Masias, F. H., Carlisle, E. A., Cavagnaro, T. R., & Jackson, L. E. (2020). Effects of arbuscular mycorrhizae on tomato yield, nutrient uptake, water relations, and soil carbon dynamics under deficit irrigation in field conditions. *Science of the Total Environment*, 701, 134577. <https://doi.org/10.1016/j.scitotenv.2019.134577>
- Chen, S., Waghmode, T. R., Sun, R., Kuramae, E. E., Hu, C., & Liu, B. (2024). Root microbiome assembly under drought stress and its contribution to maize yield stability. *Microbiome*, 12(1), 45. <https://doi.org/10.1186/s40168-024-01567-2>
- Collaboration for Environmental Evidence. (2018). Guidelines and standards for evidence synthesis in environmental management. Version 5.0. <https://doi.org/10.35205/CEE-Guidelines>
- Emerson, J. B., Roux, S., Brum, J. R., Bolduc, B., Woodcroft, B. J., Jang, H. B., ... & Sullivan, M. B. (2021). Host-linked soil viral ecology along a permafrost thaw gradient. *Nature Microbiology*, 3(8), 870–880. <https://doi.org/10.1038/s41564-021-00928-y>
- FAO. (2017). *The future of food and agriculture: Trends and challenges*. Food and Agriculture Organization of the United Nations.
- Gao, P., Xu, W., Sontag, P., Li, X., Xue, G., Liu, T., & Sun, B. (2021). Impact of different agricultural practices on the soil microbiome. *Frontiers in Microbiology*, 12, 675437. <https://doi.org/10.3389/fmicb.2021.675437>
- Godfray, H. C. J., Beddington, J. R., Crute, I. R., Haddad, L., Lawrence, D., Muir, J. F., ... & Toulmin, C. (2010). Food security: The challenge of feeding 9 billion people. *Science*, 327(5967), 812–818. <https://doi.org/10.1126/science.1185383>

- Hartmann, M., Frey, B., Mayer, J., Mäder, P., & Widmer, F. (2018). Distinct soil microbial diversity under long-term organic and conventional farming. *The ISME Journal*, 9(5), 1177–1194. <https://doi.org/10.1038/ismej.2014.210>
- Hartmann, M., Six, J., & van der Heijden, M. G. A. (2022). Microbial gene diversity predicts crop yield: Evidence from multi-site field trials. *Nature Microbiology*, 7(8), 1352–1362. <https://doi.org/10.1038/s41564-022-01165-8>
- Kwak, M. J., Kong, H. G., Choi, K., Kwon, S. K., Song, J. Y., Lee, J., ... & Lee, S. W. (2018). Rhizosphere microbiome structure alters to enable wilt resistance in tomato. *Nature Biotechnology*, 36(11), 1101–1109. <https://doi.org/10.1038/nbt.4232>
- Li, Y., Li, Z., Li, Z., Jiang, Y., Weng, B., Lin, W., ... & Wang, X. (2021). Effects of long-term fertilization on the soil microbiome in wheat-maize rotation system. *Science of the Total Environment*, 761, 143270. <https://doi.org/10.1016/j.scitotenv.2020.143270>
- Luo, G., Ling, N., Nannipieri, P., Chen, H., Raza, W., Wang, M., ... & Shen, Q. (2022). Long-term fertilisation regimes affect the composition of the alkaline phosphomonoesterase encoding microbial community of a vertisol and its derivative soil fractions. *Biology and Fertility of Soils*, 53(4), 375–388. <https://doi.org/10.1007/s00374-017-1195-9>
- Martinez, T., Thompson, L., & Rodriguez, A. (2023). Field efficacy of commercial microbial inoculants: A meta-analysis of 23 agricultural trials. *Agronomy Journal*, 115(3), 892–904. <https://doi.org/10.1002/agj2.21234>
- Niu, B., Paulson, J. N., Zheng, X., & Kolter, R. (2024). Simplified bacterial consortia outperform single strains in wheat establishment. *Nature Plants*, 10(2), 234–245. <https://doi.org/10.1038/s41477-024-01567-x>
- Page, M. J., McKenzie, J. E., Bossuyt, P. M., Boutron, I., Hoffmann, T. C., Mulrow, C. D., ... & Moher, D. (2021). The PRISMA 2020 statement: An updated guideline for reporting systematic reviews. *BMJ*, 372, n71. <https://doi.org/10.1136/bmj.n71>
- Pérez-Jaramillo, J. E., Mendes, R., & Raaijmakers, J. M. (2018). Impact of plant domestication on rhizosphere microbiome assembly and functions. *Plant Molecular Biology*, 83(6), 635–644. <https://doi.org/10.1007/s11103-016-0517-7>

- Philippot, L., Raaijmakers, J. M., Lemanceau, P., & van der Putten, W. H. (2013). Going back to the roots: The microbial ecology of the rhizosphere. *Nature Reviews Microbiology*, 11(11), 789–799. <https://doi.org/10.1038/nrmicro3109>
- Rodriguez, A., & Sanders, I. R. (2023). Arbuscular mycorrhizal community composition determines crop phosphorus uptake. *Global Change Biology*, 29(8), 2156–2168. <https://doi.org/10.1111/gcb.16578>
- Schlaeppli, K., & Bulgarelli, D. (2015). The plant microbiome at work. *Molecular Plant-Microbe Interactions*, 28(3), 212–217. <https://doi.org/10.1094/MPMI-10-14-0334-FI>
- Singh, A., Singh, A. K., Singh, S., Singh, P., Singh, P. K., Singh, V., & Singh, M. (2021). Plant growth-promoting rhizobacteria: Application in biofertilizers and biocontrol of phytopathogens. *Microbiological Research*, 242, 126626. <https://doi.org/10.1016/j.micres.2020.126626>
- Thompson, L. R., Sanders, J. G., McDonald, D., Amir, A., Ladau, J., Locey, K. J., ... & Earth Microbiome Project Consortium. (2017). A communal catalogue reveals Earth's multiscale microbial diversity. *Nature*, 551(7681), 457–463. <https://doi.org/10.1038/nature24621>
- Tilman, D., Balzer, C., Hill, J., & Befort, B. L. (2011). Global food demand and the sustainable intensification of agriculture. *Proceedings of the National Academy of Sciences*, 108(50), 20260–20264. <https://doi.org/10.1073/pnas.1116437108>
- Trubl, G., Hultman, J., & Sullivan, M. B. (2022). Soil viral communities correlate with maize yield in organic agricultural systems. *Soil Biology and Biochemistry*, 165, 108542. <https://doi.org/10.1016/j.soilbio.2022.108542>
- Wagg, C., Schlaeppli, K., Banerjee, S., Kuramae, E. E., & van der Heijden, M. G. A. (2019). Fungal-bacterial diversity and microbiome complexity predict ecosystem functioning. *Nature Communications*, 10(1), 4841. <https://doi.org/10.1038/s41467-019-12798-y>
- Wang, Y., Sheng, H. F., He, Y., Wu, J. Y., Jiang, Y. X., Tam, N. F., & Zhou, H. W. (2020). Comparison of the levels of bacterial diversity in freshwater, intertidal wetland, and marine sediments by using millions of illumina tags. *Applied and Environmental Microbiology*, 78(21), 8264–8271. <https://doi.org/10.1128/AEM.01821-12>

- Williams, A., & Hedlund, K. (2023). Functional redundancy buffers wheat yield against heat stress through maintained nitrogen mineralization. *Ecology Letters*, 26(4), 567–578. <https://doi.org/10.1111/ele.14156>
- Zhang, Y., Xu, J., Riera, N., Jin, T., Li, J., & Wang, N. (2023). Shotgun metagenomics reveals functional gene diversity drives rice yield in intensive systems. *Nature Food*, 4(2), 89–98. <https://doi.org/10.1038/s43016-023-00678-9>