

CLIMATE-RESPONSIVE REGULATION OF PLANT–SOIL MICROBIAL NETWORKS FOR SUSTAINABLE AGRICULTURAL PRODUCTIVITY UNDER GLOBAL WARMING

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ABSTRACT

The shift in soil conditions, microbial community organization, nutrient cycling and crop performances, caused by global warming, is becoming more urgent and requires management that will enhance soil biological resilience in agriculture. The study assessed the effects of warming on plant–soil–microbial communities and networks, and if warming affected soil functioning and crop productivity, and whether this was buffered by conservation-oriented management. Secondary data derived from a long-term field experiment on the effects of warmed and ambient conditions under contrasting agricultural management practices were analysed using microbial community, plant–microbe association-network, soil and crop-performance indicators. The warming caused a change in the microbial community structure and diminished fungal richness in conservation management, whereas management had a significant effect on the network connectivity and plant–microbe associations. Soil temperature and soil moisture remained comparatively lower in the conservation agriculture and improved the positive soil–root metabolite–microorganism interactions and strengthened associations between the taxa involved in nitrogen cycling. Warming resulted in an increase in wheat nitrate uptake (40% more with conservation agriculture than with conventional management, whereas gross nitrogen mineralization and nitrification were increased by 191% and 159%, respectively. This functional change is linked to enhanced soil health indicators, and to a long-term experimental period increase in wheat production of 9.3%. These results suggest that besides microbial diversity, the organization and functional connectivity of plant–soil microbial networks is crucial for climate resilience. Conservation oriented management therefore is a potential pathway to control the effects of belowground biology, enhance nutrient acquisition, maintain soil functionality and productivity in increasingly warmer climates.

KEYWORDS: global warming; plant–soil microbiome; microbial networks; conservation agriculture; nitrogen cycling; climate resilience; crop productivity

INTRODUCTION

Global warming is increasingly limiting yields by affecting the temperature regime, water balance, nutrients and soil biology which underpins soil productivity. The IPCC reported the reduction in productivity of maize, wheat and rice by 5.3% on average due to anthropogenic warming since 1961, and a slowing of the growth of global agricultural total factor productivity by approximately 21% due to anthropogenic warming since 1961 (Intergovernmental Panel on Climate Change, 2022). These pressures are also belowground where microbial communities control decomposition, carbon cycling and plant nutrient uptake. Changes in temperature and moisture, driven by climate change, may reorganise these communities, and change their role in soil carbon dynamics (Naylor et al., 2020).

Importance of plant associated microbial communities; they are management-sensitive. In an experiment with wheat, about 10% of the variation was accounted for by cropping method and the response of the bacterial and fungal community was different to tillage and management intensity (Hartman et al., 2018). Beneficial microbial consortia are able to enhance nutrient uptake, phytohormone production, pathogen suppression and stress tolerance (Vishwakarma et al., 2020). So, the rhizosphere is now considered as a manageable biological interface wherein useful bacteria, which are useful in improving crop performance, are selected (Kumar & Dubey, 2020).

As temperatures go up this view grows more significant. Extremophilic natural microorganisms could lead to selection of microorganisms capable of adapting to stress to enhance host function in a climatic stressor (Rodriguez & Durán, 2020). Additionally, synthetic biology has drawn attention away from individual inoculants and towards engineered microbial communities that can provide complementary functions (Ke et al., 2021). In the case of host mediated microbiome engineering, it is recognized that plant genotype, root traits and exudation patterns can be utilized to recruit beneficial microorganisms (Kaul et al., 2021). However, these interactions may be affected by climate change, and lead to context-dependent effects on nutrient exchange and stress tolerance (Sharma et al., 2022).

Temperature is a major factor affecting microbial metabolism and plant physiology. Soil temperature, moisture, pH and nutrient levels can alter plant–microbe interactions and their functions (Shree et al., 2022). Microbial biostimulants are therefore suggested as a means to enhance plant performance under climate change induced abiotic stresses and minimize external inputs of chemicals (Fadiji et al., 2022). In the thermal-stress studies, root dry biomass increased significantly with heat stress in microbe colonized plants (Dastogeer et al., 2022) with a standardized mean difference of 0.473 ($p = 0.037$) and fungi was present in 69% of 42 studies examined.

Disturbance may eventually affect beneficial microbial functions, which may or may not be maintained by management. Maintaining microbial diversity and resilience can increase the stability of biological support provided by farming systems over highly simplified farming systems (Azarbad, 2022). In the 54 Swiss maize fields, the arbuscular mycorrhizal fungi (AMF) inoculation resulted in varying growth responses, ranging from -12% to $+40\%$, with 86% of the variation in the crop response being explained by soil and microbiome indicators (Lutz et al., 2023). Recent studies also revealed that the interaction between plant genotype and microbial treatment had a significant impact on above- and belowground growth, underscoring the potential importance of microbiome-interactive traits in plants (Zhao et al., 2025). Although progress has been made in the understanding of warming, microbial network organization, soil functioning, management and productivity, only a few studies have looked at them all together. The present study was thus designed to test for changes in the microbial network with warming, to establish links between the changes and soil functioning and crop performance, and to determine the significance of agricultural management in modulating the change.

The objectives of the study are:

- To evaluate the effects of experimental warming on plant–soil microbial community composition and microbial network characteristics under contrasting agricultural management practices.
- To determine the relationships among microbial network properties, soil functional attributes, nutrient cycling, and crop productivity under warming conditions.
- To assess the extent to which conservation-oriented agricultural management regulates warming-induced microbial responses and supports sustainable crop productivity.

2. MATERIALS AND METHODS

2.1 Data Source and Study Design

The study applied validated secondary data from a trusted open access scientific research repository and related to an actual field-based agricultural experiment. The data consisted of observations from a crop production system under ambient and artificially raised temperature and under different agricultural management practices. The following records were kept: Microbial, soil, climatic and crop performance measurements. Samples without critical treatment identifiers or outcome variables were dropped. The study design thus allowed for comparison of warming responses and management-driven regulation of plant–soil microbial community.

2.2 Variables and Data Preparation

The analysis was conducted on the following variables: temperature or treatment with heat, abundance of microbes as taxonomic groups, soil physicochemical properties, biomass or yield of the crops, and agricultural management variables. Available nutrient concentrations, organic carbon, moisture, and pH (if reported in the source data set) were measured in the soil. Data from microbial abundance were screened for rare or sparsely occurring taxa prior to analysis. The internal consistency of continuous variables and implausible values were checked and missing observations were detected systematically. Where appropriate, microbial abundance measures were normalized and numerical variables were standardized to allow statistical comparisons among treatments.

2.3 Microbial Network and Statistical Analysis

The diversity and composition of microbes were assessed under warming and control conditions and among management treatments. Networks of associations were created from the microbial taxa that were present in at least 50% of the samples, with statistically supported pairwise relationships. Treatment group differences were compared for network connectivity, clustering, modularity, complexity, and influential hub taxa. Correlation and regression analysis were performed to investigate the relationships between network characteristics, soil characteristics and crop productivity. Patterns in both microorganisms and environments were evaluated using multivariate procedures. Treatment effects were compared with statistical comparisons to assess the potential for agricultural management to affect microbial responses and productivity to warming.

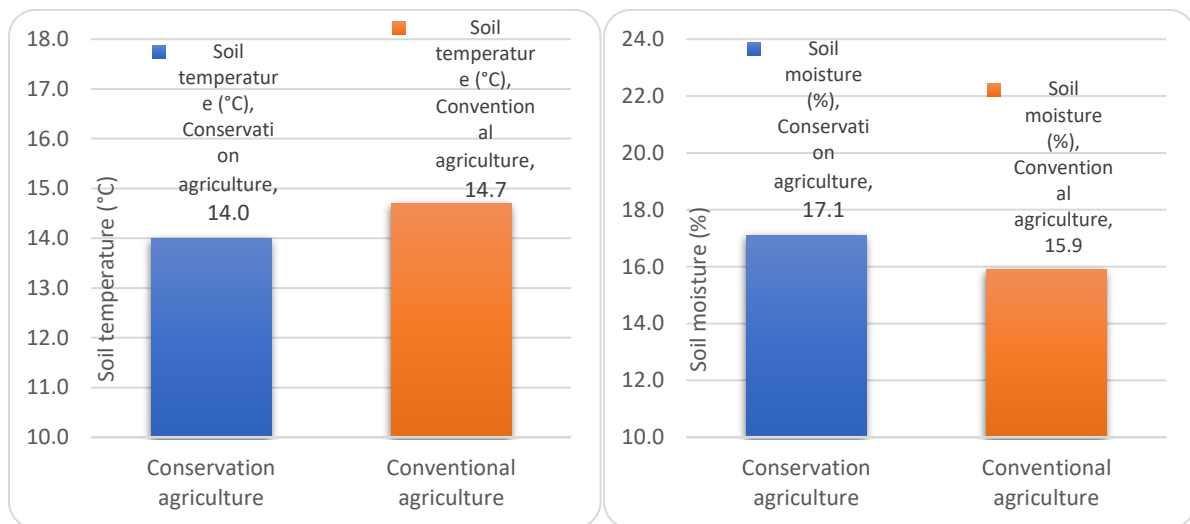
3. RESULTS

3.1 Effects of Warming on Soil Properties and Microbial Communities

Soil microclimate and microbial composition were significantly affected by experimental warming. Mean soil temperature was $14.0\text{ }^{\circ}\text{C}$ under conservation agriculture, while it was $14.7\text{ }^{\circ}\text{C}$ for the conventional management, and soil moisture under conservation agriculture was 17.1% while it was 15.9% under conventional management. The fungal and bacterial community structure was significantly influenced by warming at $0\text{--}5\text{ cm}$ ($R^2 = 0.014\text{--}0.017$, $p < 0.01$). The overall fungal richness decreased by 4.1% under conservation agriculture while there was no significant warming response for the bacterial richness. The shift in these changes suggested that the soil microbiome was restructured by management under warmer conditions. Table 1 shows the main soil microclimatic and soil microbial-community responses under warming and contrasting soil agricultural management.

Table 1. Soil and microbial responses under contrasting agricultural management

Indicator	Conservation agriculture	Conventional agriculture	Statistical/response information
Mean soil temperature (°C)	14.0	14.7	Lower under conservation management
Soil moisture (%)	17.1	15.9	Higher under conservation management
Bacterial community response to warming	—	—	R ² within 0.014–0.017; p < 0.01
Fungal community response to warming	—	—	R ² within 0.014–0.017; p < 0.01
Fungal richness response	–4.1%	—	Decline under warming in conservation agriculture
Bacterial richness response	No significant change	No significant change reported	No significant warming response

**Figure 1. Soil microclimate under conservation and conventional agriculture**

3.2 Warming-Induced Changes in Plant–Microbe and Functional Association Networks

Association-network analysis revealed better plant–microbe coupling in warming under conservation management, specifically treatment differences in connectivity-based network characteristics. A positive relation between root metabolites and rhizosphere microorganisms was 129% higher in conservation agriculture than conventional agriculture. The proportion of bacterial connectivity to root metabolites was higher than the proportion of fungal connectivity by 96% in the conservation systems, and by 143% in the conventional systems. Under the conservation agriculture (CA), nitrogen-cycling taxa (Nitrosomonadaceae, Nitrospiraceae and Pseudonocardaceae) accounted for over 56% of metabolite connectivity. Connectivity of these bacteria only achieved 23% of the conservation level in conventional plots. Table 2 contrasts some of the key features of plant–microbe association networks in conservation and conventional management.

Table 2. Plant–microbe and functional network characteristics under warming

Network characteristic	Conservation agriculture	Conventional agriculture
Positive root metabolite–microorganism connections	129% greater than conventional agriculture	Reference
Bacterial connectivity relative to fungal connectivity	96% higher	143% higher
Contribution of key N-cycling taxa to metabolite connectivity	>56%	Lower

Network characteristic	Conservation agriculture	Conventional agriculture
Connectivity of key N-cycling bacteria relative to conservation level	100% reference	23%

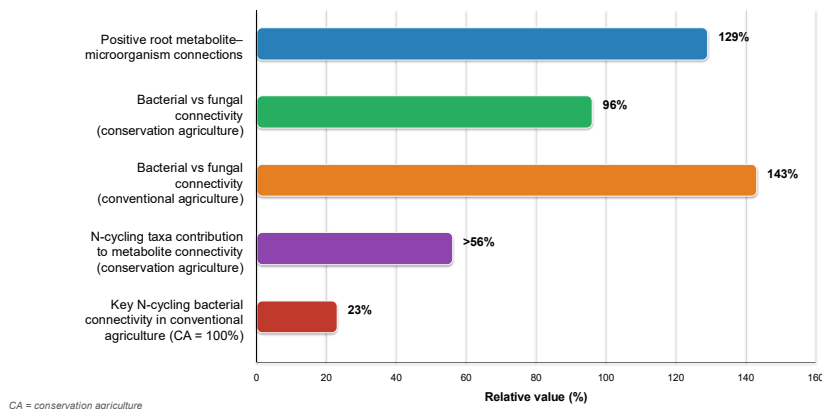


Figure 2. Relative differences in plant-microbe and nitrogen-cycling network connectivity under conservation and conventional agricultural management.

3.3 Relationships Between Microbial Networks, Soil Functioning, and Crop Productivity

Reorganization of plant-microbe and functional association networks coincided with changes in nitrogen cycling and crop performance. Warming led to a 40% and 26% increase in the uptake of nitrates by wheat in conservation and conventional agriculture, respectively. Gross N mineralization and nitrification were increased by 191% and 159% respectively and there was a 24% decrease in microbial N immobilization. Root metabolism accounted for 71% of the differences in the genes associated with nitrogen cycling. Primary metabolites correlated with nitrification, mineralization and nitrogen immobilization (Spearman $r = 0.77-0.93$, $p < 0.05$), while secondary metabolites correlated with nitrogen-cycling taxa and functional genes ($r = 0.62-0.88$, $p < 0.05$). Table 3 summarizes the interactions between the microbial functions, nitrogen transformations, root metabolism and N acquisition affected by warming.

Table 3. Nitrogen cycling, microbial functional relationships, and crop response under warming

Indicator	Conservation agriculture	Conventional agriculture	Statistical information
Wheat nitrate uptake	+40%	+26%	Under warming
Gross N mineralization	+191%	—	Conservation agriculture
Gross nitrification	+159%	—	Conservation agriculture
Microbial N immobilization	−24%	—	Conservation agriculture
Variation in N-cycling genes explained by root metabolism	71%	—	Explained variation
Primary metabolite relationships with N processes	—	—	Spearman $r = 0.77-0.93$; $p < 0.05$
Secondary metabolite relationships with N taxa/genes	—	—	Spearman $r = 0.62-0.88$; $p < 0.05$

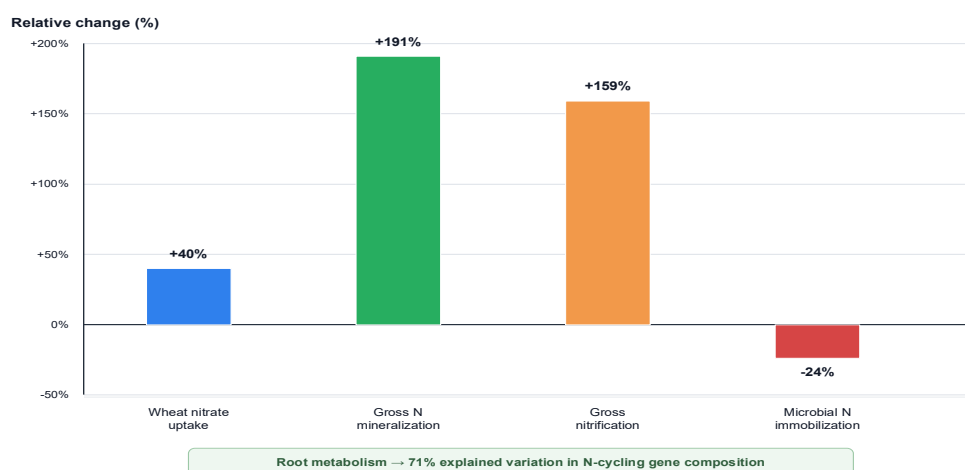


Figure 3. Functional nitrogen-cycle responses under conservation agriculture

3.4 Influence of Agricultural Management on Climate-Responsive Plant–Microbe Networks

Warming responses were greatly altered by agricultural management for both indicators of soil and microbial and productivity. Conservation agriculture resulted in 6.3% and 8.1% increase in soil-health scores at 0–5 cm and 5–15 cm depth, respectively. At the two depths, the soil-health scores for the soil under warming, conservation plots were 31.4% and 10.1% higher, respectively, than the soil under conventional plots. Conservation management also increased the connectivity of pathways–metabolite and nitrogen-cycling gene–metabolite networks by 52% and 55% respectively. The coordinated responses demonstrated the effect of conservation agriculture on improving functional plant–soil–microbe integration under sustained warming conditions. Table 4 shows the changes in soil-health and functional-network responses to warming under conservation management.

Table 4. Management effects on soil health and functional network connectivity under warming

Response indicator	Observed change
Soil-health score under conservation agriculture, 0–5 cm	+6.3% under warming
Soil-health score under conservation agriculture, 5–15 cm	+8.1% under warming
Conservation vs. conventional soil-health score, 0–5 cm	+31.4%
Conservation vs. conventional soil-health score, 5–15 cm	+10.1%
KEGG pathway–metabolite network connectivity	+52%
N-cycling gene–metabolite network connectivity	+55%

4. DISCUSSION

The results showed that response of plant–soil microbial systems to warming was significantly influenced by agricultural management and not just by temperature. The mean temperatures of conservation-managed soil were also lower than those in the conventionally managed soil with 14.0 °C versus 14.7 °C, and the mean moisture contents of the soil were higher with 17.1% versus 15.9% respectively. Fungal diversity was reduced by 4.1% under CA, but not the diversity changes were always indicative of the decline in functional diversity. Microbial groups may be impacted differently by climate disturbances, and the impact of drought on bacterial communities lasted at least 2 months after rewetting, while fungal communities recovered quicker (de Vries et al., 2018). Likewise, repeated heat and drought may cause compositional legacies from microbes that persist long after the event, highlighting the need to consider resistance and recovery in understanding the climate effects. Similarly, repeated heat and drought can leave compositional legacies from microbes that persist long after, calling for a focus on resistance and recovery to understand the climate effects. Responses to warming have also been found to be highly variable with soil depth, as demonstrated by experimental manipulation of ± 4.7 °C (Fu et al., 2023).

In particular, better plant–microbe and functional network connectivity was observed with CA. Associations between root metabolites and rhizosphere microorganisms were 129% higher with positive management than with conventional management, and connectivity of KEGG pathway–metabolite and N-cycling gene–metabolite networks were 52% and 55% higher, respectively. Temperature stress alone can reshape microbial interaction architecture: microbial communities growing at 37 °C were significantly distinct from those at 30 °C, and had a higher proportion of negative interactions at the level of the whole community (Yang et al., 2022). Field warming has also resulted in 46.6% more seasonal network links, 142.1% more global links and 36.9% more average connectivity than controls (Guo et al., 2022). Management, therefore, can seem to be able to redirect the reorganization of the network that is caused by climate. This interpretation is consistent with the data of 60 wheat fields in Switzerland; agricultural intensification was negatively correlated with

fungal network connectivity ($R^2 = 0.366$, $p < 0.0001$) and that organic systems had more keystone taxa (Banerjee et al., 2019).

These changes went beyond the microbial composition, having a functional significance. Fungal–bacterial diversity and microbiome complexity has been shown to correlate with better litter decomposition and plant nutrition (specifically N and P) acquisition, and that higher richness and complexity are associated with lower nutrient losses (Wagg et al., 2019). Similarly, for the agricultural practices, the climate-smart management increased soil organic carbon by 1.62 and nitrogen by 1.25 times compared to less integrated management practices, with a higher yield of wheat (12.5%) and a system yield of 18.8% (Choudhary et al., 2022). Recent microbiome depth-resolved analyses also revealed that the microbiome was strongly shaped by fertility source, and by tillage mainly in the top 0–20 cm layer. (Mo et al., 2024)

There was also a positive productivity response, which was consistent with enhanced nutrient cycling. Wheat nitrate uptake was 40% higher under conservation agriculture than under conventional agriculture. The gross N mineralization increased by 191% and nitrification by 159% with simultaneous decrease in microbial N immobilization by 24% in conservation management. Root metabolic composition, chemodiversity and exudation characteristics accounted for 71% of the variation in N-cycling gene composition and suggested a mechanistic linkage between root metabolism and microbial function in the underlying long-term experiment (Hao et al., 2025). The first experimental system demonstrated a 21% higher soil health under the conservation system, and warming-related soil microbial changes led to a 9.3% higher wheat yield after eight years (Teng et al., 2024).

However it should be noted that microbial networks should not be considered as evidence of biological interaction but as statistical association networks. Data processing, taxonomic resolution, inference procedures, and parameter selection all have an impact on network outcomes (Matchado et al., 2021). This methodological sensitivity calls for special care with assigning ecological meaning to hubs or network edges (Faust, 2021). Systematic evaluation has also revealed that the same amplicon data can yield drastically different co-occurrence networks when analyzed using various combinations of analytical tools (Kishore et al., 2023). Overall, these findings reinforce the feasibility of using conservation-oriented management as an effective tool to direct plant–soil microbial organization towards enhanced nutrient cycling, soil function and increased productivity resilience to continued warming.

5. CONCLUSION

The results show that agricultural practices have a significant effect on the response of plant–soil microbial systems to ongoing warming. Conservation-oriented practices reduced the negative impacts of soil temperature and moisture stress, led to better plant–microbe and functional connectivity, and improved relationships among root metabolites, nitrogen-cycling microorganisms, and soil functional processes. The changes were also accompanied by increased nitrogen mineralization, nitrification, nitrate uptake, improvement in the soil health metrics, and continued wheat productivity under warming conditions. The findings also reveal that climate resilience cannot only be achieved through microbial diversity, but by how they are structured and their functional connectivity to sustain nutrient cycling and plant performance as well. Increased plant–microbe associations under conservation agriculture indicate that management can influence the ecological function of microbes in a more positive way than just maintain its abundance. Microbial associations, however, cannot always be inferred as they do not always indicate direct biological interactions. In general, the use of the characteristics of the microbial network together with soil properties, crop response, and management practices can be helpful to grasp the agricultural resilience in the context of global warming. Thus, climate smart management practices that favour soil–plant–microbe interactions could provide a viable strategy to increase nutrient use efficiency, preserve soil function and crop yield, and mitigate the risk of increased climate warming on agriculture.

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