Organic amendments enhance soil microbial diversity, microbial functionality and crop yields: A meta-analysis

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HIGHLIGHTS

- Organic amendments enhanced microbial diversity relative to mineral fertilization.
- Organic amendments also increased microbial functionality and crop yields.
- Microbial diversity was positively correlated with functionality and yield.
- Microbial diversity driven crop yields via boosting microbial functionality.

GRAPHICAL ABSTRACT
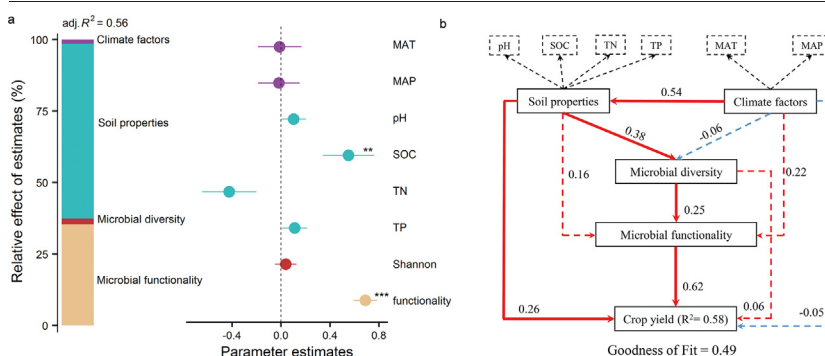
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ABSTRACT

Fertilization plays an important role in changing soil microbial diversity, which is essential for determining crop yields. Yet, the influence of organic amendments on microbial diversity remains uncertain, and few studies have addressed the relative importance of microbial diversity versus other drivers of crop yields. Here, we synthesize 219 studies worldwide and found that organic amendments significantly increased microbial diversity components (i.e., Shannon, richness, and phylogenetic diversity) and shifted microbial community structure compared to mineral-only fertilization. The performance of microbial alpha diversity varied substantially with organic amendment types, microbial groups and changes in soil pH. Both microbial diversity and community structure exhibited significantly positive relationships with microbial functionality and crop yields. In addition, soil abiotic properties and microbial functionality had a much stronger impact on crop yields than microbial diversity and climate factors. Partial least squares path modeling showed that soil microbial diversity was an important underlying factor driving crop yields via boosting soil microbial functionality. Overall, our findings provide robust evidence for the positive diversity-functions relationships, emphasizing that substituting mineral fertilizers with organic amendments is a promising way to conserve microbial diversity and promote soil microbial functions and crop yields.

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1. Introduction

Soil microbial communities makeup to a substantial portion of earth's biodiversity and involve in a variety of ecosystem processes, such as organic matter decomposition, nutrient cycling, and plant productivity (Bender et al., 2016; Crowther et al., 2019; Saleem et al., 2019; Xia et al., 2020). Over the past half-century, excessive application of mineral fertilizers has resulted in the loss of microbial diversity in agricultural soils at an unpredictable rate (Xu et al., 2020a, 2020b; Zhou et al., 2020). As a substitute for chemical fertilizers, organic amendments (e.g., livestock manure, crop residue, compost, green manure, and their combination) are considered as a sustainable agronomic practice because they cannot only improve crop productivity and soil fertility but also enhance microbial biomass and associated activities (Gravuer et al., 2019; Li et al., 2021a, 2021b; Xia et al., 2017; Young et al., 2021). However, there are still knowledge gaps about the response of soil microbial diversity to the substitution of chemical fertilizers by organic amendments. Previous studies have shown that organic amendments may increase or decrease soil microbial diversity compared to mineral fertilization (Ahn et al., 2012; Feng et al., 2018; Hu et al., 2018a, 2018b; Xu et al., 2020a, 2020b; Yang et al., 2020). Meanwhile, the response of microbial diversity to organic amendments was affected by microbial groups (Chen et al., 2016; Fan et al., 2021; Feng et al., 2018; Guo et al., 2018; Pan et al., 2020), organic amendment types (Chen et al., 2021; Sun et al., 2015; Ye et al., 2019), experimental conditions (Li et al., 2021a, 2021b; Yang et al., 2019), and initial soil properties (Meng et al., 2021; Ning et al., 2020). We urgently need to understand the generalizable patterns and regulating factors of the substitution mineral fertilizers by organic amendments effect on soil microbial diversity, because this knowledge will have important implications for conserving soil biodiversity and improving agricultural management practices.

Among the multiple ecosystem functions and services of agricultural ecosystems, crop yields is the most critical for supporting human well-being (Garland et al., 2021; Ray et al., 2012; Renard and Tilman, 2019). Understanding the major factors mediating crop yields under a changing environment is critical to preserve and manage agroecosystems. A growing body of experimental and observational studies provide evidence that soil microbial diversity plays an important role in mediating soil multiple functions and plant productivity in natural and managed ecosystems (Bastida et al., 2016; Delgado-Baquerizo et al., 2016; Semchenko et al., 2018; van der Heijden et al., 2008). The role and contribution of microbial diversity for crop yields in agricultural soils are mediated by multiple abiotic factors, which depend on agricultural management practices and climate factors (M. Li et al., 2021). Recent studies provide evidence that organic amendments can promote crop yields in agroecosystems in a wide variety of ways, such as altering soil abiotic factors (Li et al., 2021a, 2021b; Xia et al., 2017), improving soil microbial activities (Luo et al., 2018a), and changing microbial diversity and composition (Kumar et al., 2018; Liu et al., 2021a, 2021b; Ning et al., 2020; Xiang et al., 2020). However, few studies have addressed the relative importance of soil microbial diversity versus other drivers of crop yields under organic amendments, such as soil abiotic properties, climate, and soil microbial functionality. This knowledge gap limits our understanding of the linkages between microbial diversity, crop yields and agricultural management practices and thus hampers our ability to enhance crop yields through targeted agricultural management practices.

Here we conducted a comprehensive meta-analysis by compiling 219 studies (687 observations) to investigate the effects of organic amendments (herein referred to as both organic-only amendments and organic amendments plus mineral fertilizers) on microbial diversity, microbial functionality and crop yields compared to mineral fertilizers (Dataset1). The objectives of this study are: 1) to investigate the impact of substituting mineral fertilizers with organic amendments on microbial diversity and community structure; 2) to identify the potential factors of microbial diversity and community structure responses; 3) to determine the relationship between microbial diversity, microbial functionality and crop yields; and 4) to assess the relative importance of microbial diversity in determining crop yields under the substitution of mineral fertilizers by organic amendments.

2. Materials and methods

2.1. Data collection

An extensive literature survey was conducted through Google Scholar, Web of Science and China National Knowledge Infrastructure databases until March 2021 with no restriction on publication year. We searched the literature using keywords (fertiliz* OR fertilis* OR organic amendment OR manure OR straw OR compost OR waste OR plant residue) AND (OTU OR DNA OR microb*) AND (soil). The following criteria were used to select eligible studies: 1) only field studies were selected; 2) at least one microbial variable was documented, including microbial diversity (i.e. Shannon-Wiener index, richness, and phylogenetic diversity) and community structure; 3) the duration of experiments was at least one years; 4) if one paper reports a variety of independent experiments, each of them was considered as an individual study and incorporated into our dataset as an independent observation; and 5) if one paper contains results from various sampling dates and soil depths, we only used the data from the latest sampling time-point and the uppermost layer of soil. Our dataset collected location (latitude and longitude), climate factor (mean annual temperature (MAT) and mean annual precipitation (MAP)), initial soil pH and soil clay content, land use types, organic types, experimental duration, soil abiotic properties (i.e., pH, organic carbon (C), soil total nitrogen (N), total phosphorus (P)), and crop yields from the papers or their cited papers or the papers from the same experiments. The missing climatic information (i.e. MAT and MAP) extract from www.worldclim.com with the site information. In total, 219 peer-reviewed publications (687 observations) were included in the meta-analysis (Fig. 1). Majority of the studies were conducted in the temperate regions in North Hemisphere, whereas no studies were found in the continents in South Hemisphere.

2.2. Quantification of microbial functionality

Soil enzymes are good proxies of processes driving soil C, N, P cycling, and are often used to calculate the functionality of microbial communities (Chen et al., 2020; Han et al., 2021; Luo et al., 2018b; Zhou et al., 2020). In this study, the soil enzymes related to soil C, N and P cycling were collected including hydrolytic C-degrading enzymes (i.e. α-1,4-glucosidase (AG), β-1,4-glucosidase (BG), β-D-cellobiosidase (CBH), and β-1, 4-xylosidase (XYL)), oxidative C-degrading enzymes (catalase (CAT), peroxidase (PER), and phenol oxidase (PhOx)), N-cycle enzymes (urease (URE), protease (BBA), leucine aminopeptidase (LAP), and β-1,4-N-acetylglucosaminidase (NAG)), and P-cycle enzymes (phosphatase (Pho)). If one paper reported one or more types of hydrolytic C-degrading enzymes, oxidative C-degrading enzymes, and N-cycle enzymes, their mean values were considered as the overall hydrolytic C-degrading enzymes, oxidative C-degrading enzymes, N-cycle enzymes (Luo et al., 2018b; Zhou et al., 2020). The soil microbial functionality was represented by the mean value of all of enzymes. Notably, microbial functionality can only reflect part of microbial functions due to data limitation. The random-effect model was used to evaluate response ratios of hydrolytic C-degrading enzymes, oxidative C-degrading enzymes, N-cycle enzymes and P-cycle enzymes, and microbial functionality for each observation (Zhou et al., 2020).

2.3. Data analysis

The natural log of response ratio (RR) was used to evaluate the response of target variables to substituting mineral fertilizers by organic amendments. The RR was calculated according to the following equation:

$$RR = \ln X_t - \ln X_c \tag{1}$$

where X_t and X_c denote the mean value of organic amendments and mineral fertilizers treatment, respectively. Notably, we use Δ pH (i.e., pH (organic) − pH (mineral)) to indicate the effects of substituting mineral fertilizers by
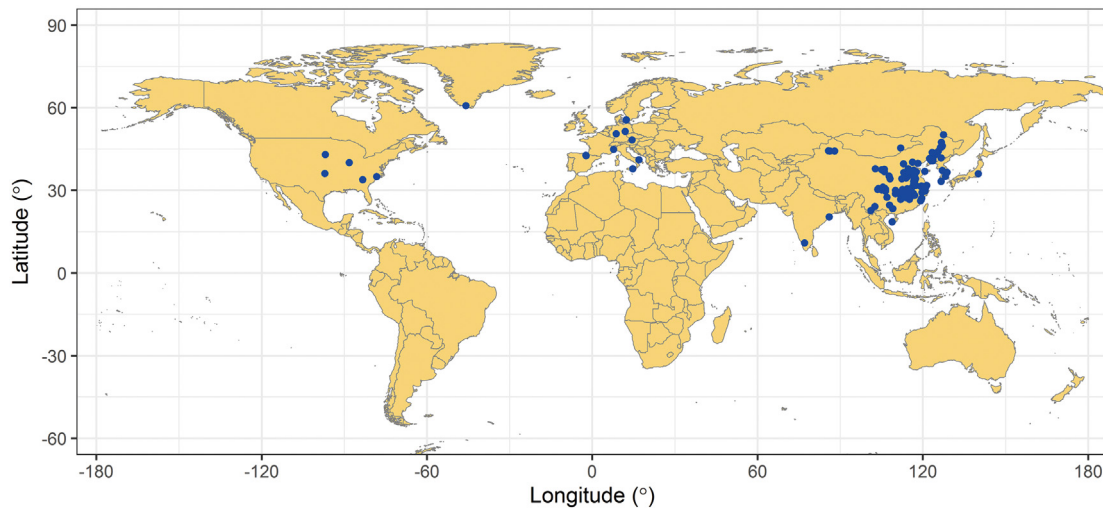
Fig. 1. Distribution of study site in the meta-analysis. Source data are provided as a Source Data file.

organic amendments on soil pH because the soil pH is calculated as the negative value of logarithmic H^+ concentration (Zhou et al., 2020).

The ordination analysis is an important method for analyzing microbial community. The ordination plots are considered to show the community structure differences among treatments (Paliy and Shankar, 2016; Zhou et al., 2020). In this study, the influence of substituting mineral fertilizers with organic amendments on microbial community structure is considered if the distance between mineral fertilizers and organic treatment is significantly greater than the distance within the group. Firstly, we extracted the positions of samples on the first two ordination axes. Second, Euclidean distances among different samples were calculated with the R packages of 'vegan', including the distance within mineral fertilizers treatment (Dc), that within organic amendments (Dt), and that between mineral and organic amendments (Db). Third, we calculated the means, standard deviations (SD), and sample sizes of Dc, Dt, Db, and overall Dc and Dc (Dc + Dc), respectively. Finally, the natural log of response ratio (RR) of microbial community structure was calculated according to the following equation:

$$RR_{structure} = \ln \overline{D_b} - \ln \overline{D_t + D_c} \tag{2}$$

where $\overline{D}t$, $\overline{D}c$, $\overline{D}b$ and $\overline{D_t + D_c}$ denote the average values of the Dt, Dc, Db, and Dc + Dc, respectively.

Observation's variances (ν) was calculated according to the following equation:

$$\nu = \frac{S_t^2}{N_t X_t^2} + \frac{S_c^2}{N_c X_c^2} \tag{3}$$

where N_t and N_c denote the sample size of organic amendments and mineral fertilizers treatment, respectively; S_t and S_c denote the standard deviations (SD) of organic amendments and mineral fertilizers treatment, respectively.

2.4. Statistical analysis

The random-effect model computed the overall natural log of response ratio and corresponding 95% confidence intervals of target variables. Omnibus test (Q_M) was used to compare the natural log of response ratio of target variables to organic amendments among microbial groups, organic types, land use types, experimental duration and soil properties. In the subgroup analysis, the groups with less than five sample sizes were excluded. The microbial groups include fungi, bacteria, and nine specialized microbes (i.e. diazotroph, phosphorus mineralizer, denitrifier, nitrifier, anammox bacteria, nitrite

oxidizer, methanotroph, methanogen, and CO_2-fixing bacteria). The organic types include livestock manure, plant residue, green manure, compost, waste, and their combinations. Land use types were grouped into three categories: upland, upland-paddy and paddy. Initial soil pH was grouped into three categories: acidic soils (≤ 6), neutral soils (6–8) and alkaline soils (≥ 8). Soil textures were classified into four categories: clay, loam, sandy, and clay loam. The experimental duration was categorized into according to short-term (≤ 10 years), medium-term (10–30 years) and long-term (≥ 30 years) duration. Substitution ratios (SR) was classified into two categories: partial (0 < SR < 100%) and full (SR = 100%) substitution based on the data availability.

Model selection was based on the Akaike's information criterion (AIC) corrected (Chen et al., 2018; Terrer et al., 2019). The relative importance value for a particular predictor was equivalent to the sum of the Akaike weights of the models in which the predictor appears. A cutoff of 0.8 is set to differentiate between important and nonessential predictors. Five types of candidate predictors were included in our model selection analysis, i.e., 1) experimental conditions, including organic types and experimental duration; 2) climate factors, including MAT and MAP; 3) microbial groups; 4) land use types; and 5) changes in edaphic variables, including changes in soil pH, the log of response ratio of soil organic carbon, and total nitrogen. For microbial community structure, the absolute values of changes in soil pH, the log of response ratio of soil organic carbon, and the total nitrogen were used in the model selection analysis.

In addition, we evaluated the relative importance of the predictors under consideration as drivers of crop yields using multiple regression models (Gross et al., 2017; Sirami et al., 2019). The model includes the following variables: climate factors (MAT and MAP), soil properties (changes in pH, SOC, TN, and TP), microbial diversity (microbial Shannon index), and microbial functionality. We calculated the relative effect of the parameter estimates for each of the predictors compared with the effect of all parameter estimates in the model. Notably, all predictors and response variables were standardized before analyses using the Z-core to interpret parameter estimates on a comparable scale. A partial least squares path modeling (PLS-PM) was used to explore the direct, indirect, and interactive relationships between various variables for the response ratio (RR) of crop yields. The net influence of one variable on another was computed by synthesizing all direct and indirect pathways between the two variables. The model is assessed using the Goodness of Fit statistics. The estimates of path coefficients and the coefficients of determination (R^2) were calculated with the R packages of 'plspm'. All data analysis was performed in R 4.0.2.

3. Results and discussion

3.1. Organic amendments pose positive effect on microbial diversity

Based on the quantitative synthesis of 219 studies, we conducted a comprehensive response pattern of soil microbial diversity and community structure to organic amendments. We found that the microbial Shannon, richness, and phylogenetic diversity were significantly increased by 3.0%, 10.2% and 6.7%, respectively, under organic amendments than in the mineral-only fertilization ($P < 0.05$) (Fig. 2a, b and c). This result suggested that organic amendments show a promising potential as an alternative to

mineral fertilizers to preserve soil microbial diversity in agricultural ecosystems. The natural log of response ratios (RRs) of community structure were greater than zero, indicating that organic amendments could significantly shape soil microbial community structure (Fig. 2d).

3.2. Factors regulating responses of microbial diversity to organic amendments

The subgroup analysis indicated that the performance of microbial diversity varied substantially depending on organic amendment types ($P < 0.05$) (Fig. 2a, b). Indeed, there is large heterogeneity in the characteristics of different organic amendments, which makes the
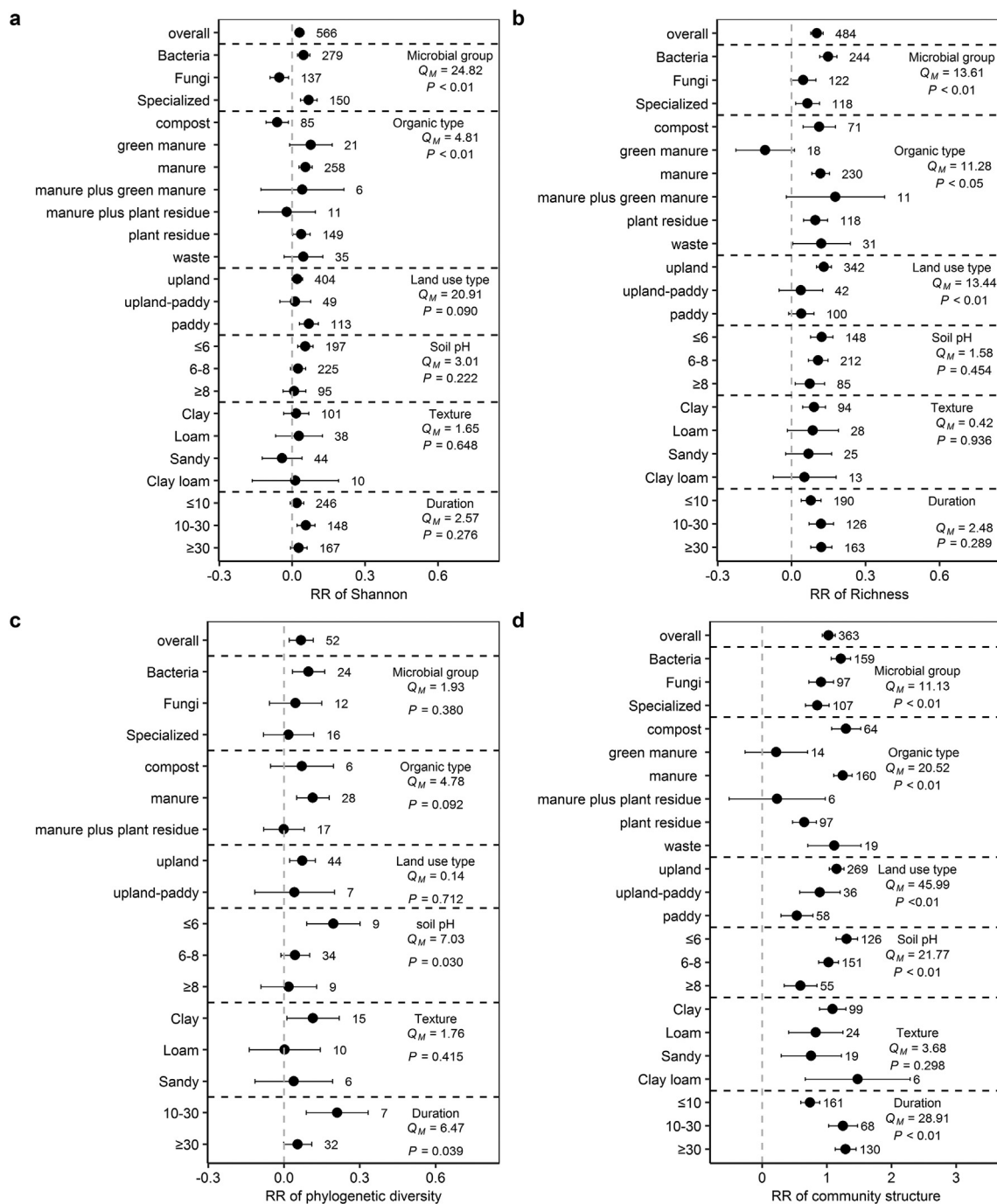

Fig. 2. The effect of organic amendments and mineral-only fertilization on microbial diversity and community structure across microbial groups, organic types, land use types, initial soil properties, and experimental duration. (a) Microbial Shannon index. (b) Microbial richness index. (c) Microbial phylogenetic diversity. (d) Microbial community structure. Weighted means and their 95% confidence intervals of response ratio are given. The numbers at the right side of the confidence intervals represent the sample sizes. The significances of microbial groups, organic types, land use types, initial soil properties, and experimental duration are tested by the omnibus test (Q_M).

application of these amendments have various effects on the living environment of soil microorganisms (Bao et al., 2020; Xu et al., 2017a, 2017b; Ye et al., 2019). Compared to mineral-only fertilization, organic amendments increased the alpha diversity of soil bacteria and specialized microbe, but had no significant effect on fungal richness (Fig. 2a, b). We further split the data by organic amendment types, finding that the aforementioned patterns of organic amendments' effects on the diversity of different microbial groups are largely maintained (Fig. S1a, b). These results were consistent with recent meta-analysis, indicating that soil bacteria are more sensitive to soil environment changes caused by agricultural practices than fungi (Bebber and Richards, 2020; Li et al., 2020). An interesting finding was that compost application significantly decreased the fungal Shannon index (Fig. S1a). However, this may not represent a negative result. In fact, previous studies have shown that compost application significantly reduces soil fungal

diversity mainly due to its ability to suppress the growth of animal and plant pathogens or enhance competition between fungal species (Vida et al., 2020; Yang et al., 2020).

The model selection analysis indicated that the soil pH changed by organic amendments was the most important predictor for microbial richness, phylogenetic diversity and community structure among the potential factors examined, such as organic amendment types, climates, experimental duration, and soil C and N contents (Fig. 3b, c and d) (Dai et al., 2019; Meng et al., 2021). Meanwhile, the changes in pH also significantly explained variation in the response of microbial Shannon to organic amendments (Fig. 3a). The predominant role of soil pH in our meta-synthesis was consistent with previous studies at local sites and large spatial regions (Bahram et al., 2018; Delgado-Baquerizo et al., 2018; Karimi et al., 2018; Zheng et al., 2019). Moreover, we found that both RRs of bacterial diversity and specialized microbial diversity were significantly and positively
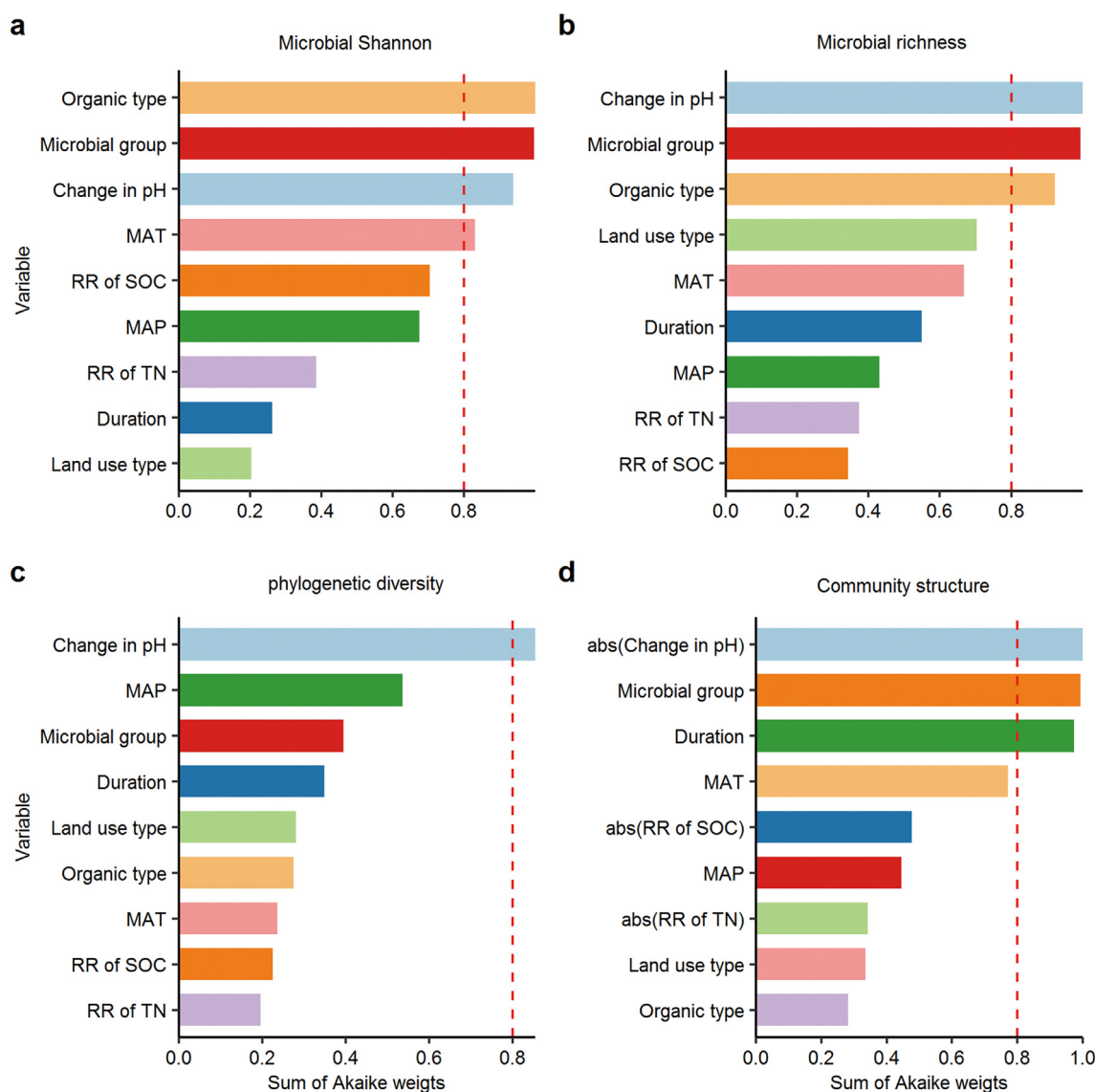

Fig. 3. Contributors to response of microbial diversity and community structure to organic amendments. (a) Model-averaged importance of the predictors for response ratios (RRs) of Shannon index. (b) Model-averaged importance of the predictors for response ratios (RRs) of richness. (c) Model-averaged importance of the predictors for response ratios (RRs) of phylogenetic diversity. (d) Model-averaged importance of the predictors for response ratios (RRs) of community structure. The importance is based on the sum of Akaike weights derived from the model selection using Akaike's information criteria (AIC) corrected for small samples. A cutoff of 0.8 (the red dashed line) is set to differentiate between important and on-essential predictors. RR: response ratio, Abs: absolute value, SOC: soil organic carbon, TN: total nitrogen, Duration: experimental duration, MAT: mean annual temperature, MAP: mean annual precipitation.
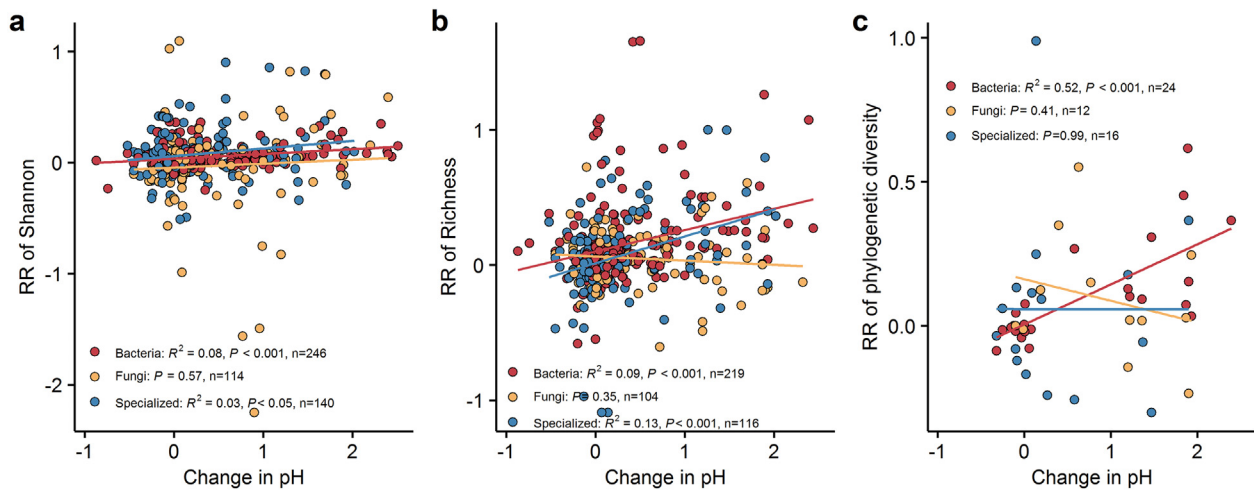
Fig. 4. Coordinated changes between soil pH and microbial diversity. (a) Linear relationships between changes in soil pH and RR of Shannon index. (b) Linear relationships between changes in soil pH and response ratio (RR) of richness. (c) Linear relationships between changes in soil pH and response ratio (RR) of phylogenetic diversity.

correlated with changes in pH, whereas RRs of fungal alpha diversity were insignificantly correlated with changes in pH (Fig. 4a, b). This result might be due to relatively narrow optimal pH range for bacterial/specialized microbial growth but wide pH ranges for fungal growth (Rousk et al., 2010). Notably, we observed that RRs of fungal Shannon were negatively correlated to RRs of SOC (Figs. S2 and S3). This result may be due to the following two reasons. One is that carbon enrichment under organic amendments may disturb the adaptation of some fungal taxa with host plants and reduce the below-ground C allocation and thus reduce fungal diversity (Vida et al., 2020). With regard to the second reason, the accumulation of SOC under organic amendments may promote changes in the biological properties of soils, causing the competition among fungal species (Pec et al., 2021; Sun et al., 2020). This, in turn, may lead to a loss of some fungal species and dominance of certain fungal species.

Mean annual temperature (MAT) was an important environmental factor in affecting the response ratio of microbial Shannon index to organic amendments (Fig. S2). RRs of microbial Shannon index were positively correlated with MAT (Fig. S3), which might be attributed to the fact that high mean annual temperature can increase the availability of nutrients for microbial growth via accelerating the decomposition of organic materials, and consequently enhancing the microbial diversity (Guo et al., 2019; C. Liu et al., 2021).

The substation ratio was an important factor that affects the response of soil properties and crop yields to organic amendments (Xia et al., 2017). In this study, we found that the response of microbial Shannon index to organic amendments was not statistically different between the full substitution and partial substitution ratio ($P > 0.05$) (Fig. S4). However, RRs of microbial richness and community structure at full substitution were significantly higher than at partial substitution ($P < 0.05$). One possible explanation was that full substitution of mineral fertilizer by organic amendments can more effectively alleviate chemical fertilization-induced soil acidification relative to the partial substitution (Bebber and Richards, 2020; Liu et al., 2021a, 2021b).

Furthermore, the responses of soil microbial Shannon index, phylogenetic diversity, and bacterial and specialized microbial Shannon index to organic amendments significantly varied with initial soil pH (Figs. 2a, c and S5a, c). The mean response ratio of these indicators was higher in acidic soil, possibly due to the liming effects of organic amendments that can decrease the physiological constraint on soil microbial communities (Chen et al., 2019). In addition, organic amendments showed a positive effect on bacterial alpha diversity in clay texture soils (Fig. S5a, d), which might be contributed to high clay content favoring microbial growth through larger aggregates, greater water holding capacity, and enhanced nutrient retention (Stefan et al., 2021).

3.3. Positive relationships between microbial diversity and microbial functionality

Compared to mineral-only fertilization, Organic amendments significantly increased overall microbial functionality (Fig. S6b). Importantly, RRs of microbial diversity were positively correlated with RRs of microbial functionality, MBC and most individual functions ($P < 0.05$) (Figs. 5, S7 and S8). These results were consistent with previous studies, finding that higher microbial diversity can promote greater performance in soil microbial functions due to the potentially high functional redundancy of soil microbial communities (Delgado-Baquerizo et al., 2017; Maron et al., 2018; Wagg et al., 2019). Meanwhile, we observed that RRs of community structure also positively correlated with RRs of microbial functionality ($P < 0.05$) (Fig. 5d). The interpretation was that organic amendments might enhance the abundance of some specific microbial taxa which have strong effect on soil microbial functions (Chen et al., 2020; Fan et al., 2021). For different microbial groups, we found a stronger positive relationship between microbial functionality and the diversity and community structure of bacteria than that of fungi (Fig. 5). The possible interpretation was that bacteria had a faster growth and turnover rate than fungi, and thus bacterial diversity may have a predominant effect on soil microbial functionality under organic amendments (Ai et al., 2018; Guo et al., 2018).

3.4. Microbial diversity determine crop yields via boosting functionality

Current consensus accepts that soil microbes play critical roles in mediating plant productivity and quality in agroecosystems (Garland et al., 2021). In this study, organic amendments significantly increased crop yields relative to mineral-only fertilization (Fig. S6a). Meanwhile, RRs of crop yields were positively correlated to RRs of microbial diversity and RRs of community structure (Fig. 5e, f, g and h). This result can be explained by the following mechanism. On the one hand, soils with high microbial diversity may accelerate the turnover rate of nutrients, as supported by our findings of direct and positive correlations between microbial diversity and microbial functionality, which implied that microbial diversity facilitated more nutrients for plant growth and that there was less competition from microbes (Fan et al., 2021). On the other hand, high microbial diversity may confer protection against soil-borne diseases, and ultimately increased plant productivity (Vida et al., 2020; Yang et al., 2020). Apart from microbial diversity, soil microbial community structure may also play a critical role in mediating crop yields, corroborating the strong correlations between RRs of
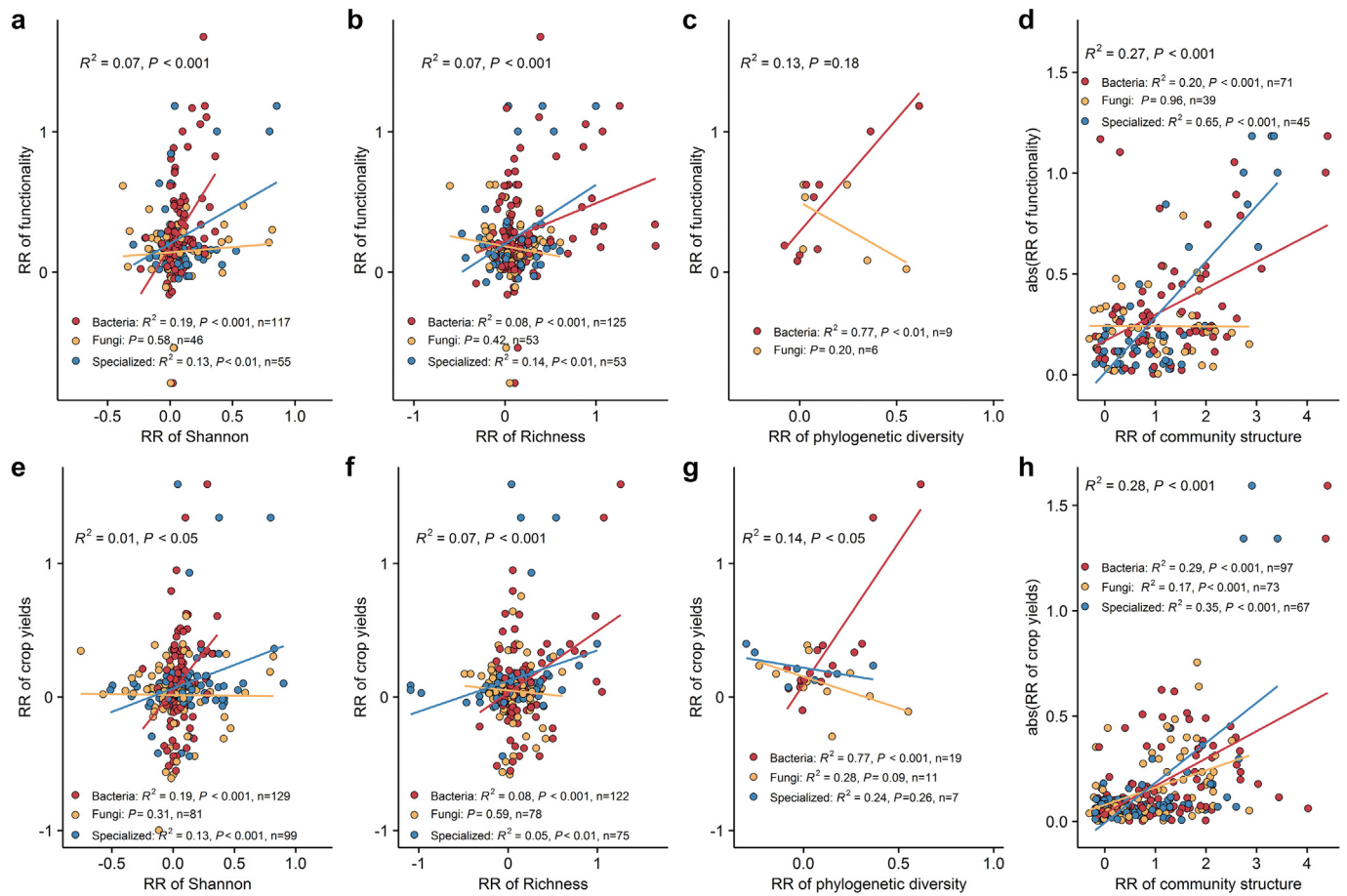
Fig. 5. Coordinated changes between microbial traits and microbial functionality and crop yields under organic amendments. (a–d) Linear relationships between response ratio (RR) of functionality and RR of microbial diversity and community structure. (e–h) Linear relationships between response ratio (RR) of crop yields and response ratio (RR) of microbial diversity and community structure. The absolute value is used because we assume that great change in microbial community structure would result in great change (both increase or decrease) in functionality and the community structure cannot be quantified as increasing or decreasing.
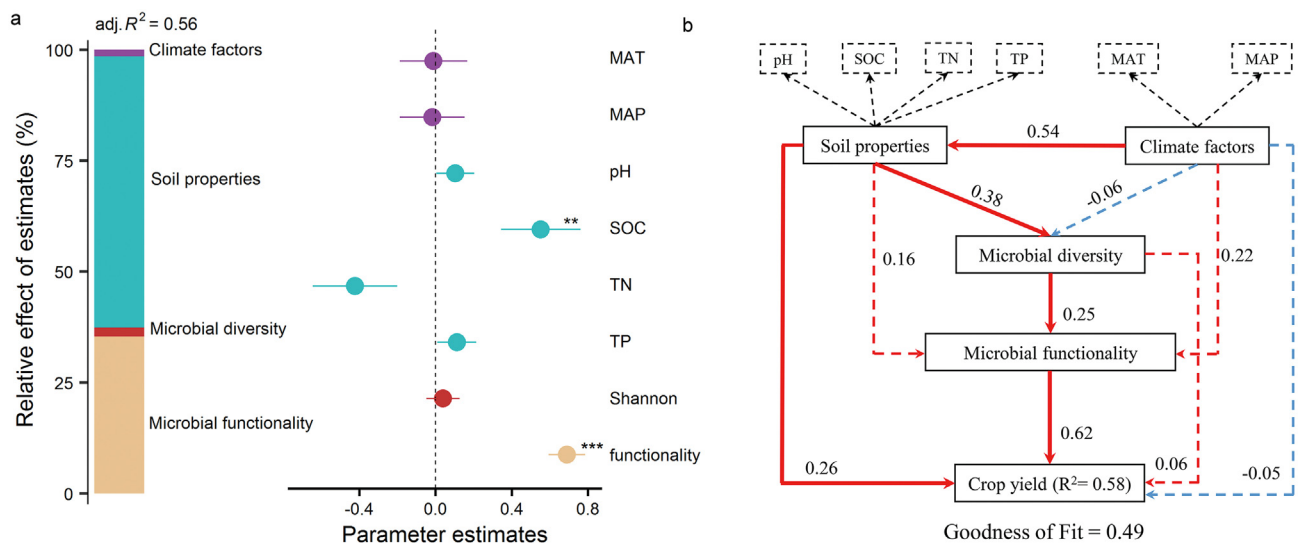

Fig. 6. Effect of biotic and abiotic factors on crop yields under organic amendments. (a) Average parameter estimates (standard regression coefficients) of model predictors, associated 95% confidence intervals and relative effect of each factor, expressed as the percentage of explained variance. The adjusted (adj.) R^2 of the averaged model and the P value of each predictor are given as: * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$. (b) PLS-PM for crop yields. Each box represents an observed variable or latent variable. The loading for soil properties and climate factors that create the latent variables are shown in the dashed rectangle. Path coefficients and coefficients of determination (R^2) are calculated after 999 bootstraps. Path coefficients reflected in the width of the arrow, with red and blue indicating positive and negative effects, respectively. Dashed arrows show that coefficients did not differ significantly from 0 ($P < 0.05$).

bacterial/fungal/specialized microbial community structure and RRs of crop yields observed here. The interpretation was that organic amendments may lead to a higher relative abundance and diversity of keystone species such as nitrogen fixers and growth-promoting microbes (Fig. S9). These beneficial microorganisms can enhance plant defense and nutrient uptake capacity, and finally promote food productivity (Fan et al., 2021).

We conducted multiple regression model and PLS-PM analysis to determine the role and relative importance of soil microbial diversity versus other drivers of crop yields. Multiple regression modeling indicated that soil properties, microbial functionality, microbial diversity and climate metrics were responsible for 61.2%, 35.4%, 2.0% and 1.4% of the explained variance in crop yields, respectively (Fig. 6a). Meanwhile, PLS-PM analysis showed that both microbial functionality ($\lambda = 0.26$, $P < 0.05$) and soil properties ($\lambda = 0.62$, $P < 0.05$) had a positive effect on crop yields (Fig. 6b). This result could be partly due to supply of available nutrient and energy that can be used by plant growth (Luo et al., 2018a). We found that microbial diversity had direct and indirect positive effect on crop yields via microbial functionality. Indeed, a recent study revealed that crop yields under fertilization are mainly directly regulated by the diversity of key-stone taxa, rather than the overall microbial diversity (Fan et al., 2021). Overall, these findings suggested that soil fertility, soil microbial diversity, and microbial functionality jointly mediated the positive response of crop yields to substituting mineral fertilizers by organic amendments.

3.5. Limitations and look forward

In this study, our results provide evidence that substituting mineral fertilizers by organic amendments had positive effects on soil microbial diversity and crop yields. Yet, it is worth noting that some organic amendments (e.g. manure, sewage sludge, and solid waste) can induce the distribution and spread of antibiotic resistance genes and the accumulation of heavy metals in soils (Tang et al., 2015; Wan et al., 2020; Xia et al., 2017). In the future, how to control these negative effects caused by the application of organic amendments still needs further investigation. In addition, most sampling sites of our meta-analysis are located in Asia and Europe, while few studies are available in other regions such as Africa and South America. In this case, bias is expected to be eliminated by conducting more future research in those missing areas, which are the mosaics that build an increasingly obvious picture of the response of microbial diversity to substituting mineral fertilizers with organic amendments from a global perspective.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgements

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.scitotenv.2022.154627.

References

Ahn, J.-H., Song, J., Kim, B.-Y., Kim, M.-S., Joa, J.-H., Weon, H.-Y., 2012. Characterization of the bacterial and archaeal communities in rice field soils subjected to long-term fertilization practices. J. Microbiol. 50, 754–765. https://doi.org/10.1007/s12275-012-2409-6.

Ai, C., Zhang, S., Zhang, X., Guo, D., Zhou, W., Huang, S., 2018. Distinct responses of soil bacterial and fungal communities to changes in fertilization regime and crop rotation. Geoderma 319, 156–166. https://doi.org/10.1016/j.geoderma.2018.01.010.

Bahram, M., Hildebrand, F., Forslund, S.K., Anderson, J.L., Soudzilovskaia, N.A., Bodegom, P.M., Bengtsson-Palme, J., Anslan, S., Coelho, L.P., Harend, H., Huerta-Cepas, J., Medema, M.H., Maltz, M.R., Mundra, S., Olsson, P.A., Pent, M., Põlme, S., Sunagawa, S., Ryberg, M., Tedersoo, L., Bork, P., 2018. Structure and function of the global topsoil microbiome. Nature 560, 233–237. https://doi.org/10.1038/s41586-018-0386-6.

Bao, Y., Feng, Y., Stegen, J.C., Wu, M., Chen, R., Liu, W., Zhang, J., Li, Z., Lin, X., 2020. Straw chemistry links the assembly of bacterial communities to decomposition in paddy soils. Soil Biol. Biochem. 148, 107866. https://doi.org/10.1016/j.soilbio.2020.107866.

Bastida, F., Torres, I.F., Moreno, J.L., Baldrian, P., Ondoño, S., Ruiz-Navarro, A., Hernández, T., Richnow, H.H., Starke, R., García, C., Jehmlich, N., 2016. The active microbial diversity drives ecosystem multifunctionality and is physiologically related to carbon availability in mediterranean semi-arid soils. Mol. Ecol. 25, 4660–4673. https://doi.org/10.1111/mec.13783.

Bebber, D.P., Richards, V.R., 2020. A meta-analysis of the effect of organic and mineral fertilizers on soil microbial diversity. Ecology https://doi.org/10.1101/2020.10.04.325373.

Bender, S.F., Wagg, C., van der Heijden, M.G.A., 2016. An underground revolution: biodiversity and soil ecological engineering for agricultural sustainability. Trends Ecol. Evol. 31, 440–452. https://doi.org/10.1016/j.tree.2016.02.016.

Chen, C., Zhang, J., Lu, M., Qin, C., Chen, Y., Yang, L., Huang, Q., Wang, J., Shen, Z., Shen, Q., 2016. Microbial communities of an arable soil treated for 8 years with organic and inorganic fertilizers. Biol. Fertil. Soils 52, 455–467. https://doi.org/10.1007/s00374-016-1089-5.

Chen, J., Luo, Y., van Groenigen, K.J., Hungate, B.A., Cao, J., Zhou, X., Wang, R., 2018. A keystone microbial enzyme for nitrogen control of soil carbon storage. Sci. Adv. 4, eaaq1689. https://doi.org/10.1126/sciadv.aaq1689.

Chen, L., Jiang, Y., Liang, C., Luo, Y., Xu, Q., Han, C., Zhao, Q., Sun, B., 2019. Competitive interaction with keystone taxa induced negative priming under biochar amendments. Microbiome 7, 77. https://doi.org/10.1186/s40168-019-0693-7.

Chen, Q.-L., Ding, J., Zhu, D., Hu, H.-W., Delgado-Baquerizo, M., Ma, Y.-B., He, J.-Z., Zhu, Y.-G., 2020. Rare microbial taxa as the major drivers of ecosystem multifunctionality in long-term fertilized soils. Soil Biol. Biochem. 141, 107686. https://doi.org/10.1016/j.soilbio.2019.107686.

Chen, H., Zheng, C., Qiao, Y., Du, S., Li, W., Zhang, X., Zhao, Z., Cao, C., Zhang, W., 2021. Long-term organic and inorganic fertilization alters the diazotrophic abundance, community structure, and co-occurrence patterns in a vertisol. Sci. Total Environ. 766, 142441. https://doi.org/10.1016/j.scitotenv.2020.142441.

Crowther, T.W., van den Hoogen, J., Wan, J., Mayes, M.A., Keiser, A.D., Mo, L., Averill, C., Maynard, D.S., 2019. The global soil community and its influence on biogeochemistry. Science 365, eaav0550. https://doi.org/10.1126/science.aav0550.

Dai, X., Zhou, W., Liu, G., Liang, G., He, P., Liu, Z., 2019. Soil C/N and pH together as a comprehensive indicator for evaluating the effects of organic substitution management in subtropical paddy fields after application of high-quality amendments. Geoderma 337, 1116–1125. https://doi.org/10.1016/j.geoderma.2018.11.023.

Delgado-Baquerizo, M., Maestre, F.T., Reich, P.B., Jeffries, T.C., Gaitan, J.J., Encinar, D., Berdugo, M., Campbell, C.D., Singh, B.K., 2016. Microbial diversity drives multifunctionality in terrestrial ecosystems. Nat. Commun. 7, 10541. https://doi.org/10.1038/ncomms10541.

Delgado-Baquerizo, M., Eldridge, D.J., Ochoa, V., Gozalo, B., Singh, B.K., Maestre, F.T., 2017. Soil microbial communities drive the resistance of ecosystem multifunctionality to global change in drylands across the globe. Ecol. Lett. 20, 1295–1305. https://doi.org/10.1111/ele.12826.

Delgado-Baquerizo, M., Oliverio, A.M., Brewer, T.E., Benavent-González, A., Eldridge, D.J., Bardgett, R.D., Maestre, F.T., Singh, B.K., Fierer, N., 2018. A Global Atlas of the Dominant Bacteria Found in Soil, p. 7.

Fan, K., Delgado-Baquerizo, M., Guo, X., Wang, D., Zhu, Y., Chu, H., 2021. Biodiversity of keystone phylotypes determines crop production in a 4-decade fertilization experiment. ISME J. 15, 550–561. https://doi.org/10.1038/s41396-020-00796-8.

Feng, M., Adams, J.M., Fan, K., Shi, Y., Sun, R., Wang, D., Guo, X., Chu, H., 2018. Long-term fertilization influences community assembly processes of soil diazotrophs. Soil Biol. Biochem. 126, 151–158. https://doi.org/10.1016/j.soilbio.2018.08.021.

Garland, G., Edlinger, A., Banerjee, S., Degrune, F., García-Palacios, P., Pescador, D.S., Herzog, C., Romdhane, S., Saghai, A., Spor, A., Wagg, C., Hallin, S., Maestre, F.T., Philippot, L., Rillig, M.C., van der Heijden, M.G.A., 2021. Crop cover is more important than rotational diversity for soil multifunctionality and cereal yields in european cropping systems. Nat. Food 2, 28–37. https://doi.org/10.1038/s43016-020-00210-8.

Gravuer, K., Gennet, S., Throop, H.L., 2019. Organic amendment additions to rangelands: a meta-analysis of multiple ecosystem outcomes. Glob. Chang. Biol. 25, 1152–1170. https://doi.org/10.1111/gcb.14535.

Gross, N., Bagousse-Pinguet, Y.L., Liancourt, P., Berdugo, M., Gotelli, N.J., Maestre, F.T., 2017. Functional trait diversity maximizes ecosystem multifunctionality. Nat. Ecol. Evol. 1, 0132. https://doi.org/10.1038/s41559-017-0132.

Guo, J., Liu, W., Zhu, C., Luo, G., Kong, Y., Ling, N., Wang, M., Dai, J., Shen, Q., Guo, S., 2018. Bacterial rather than fungal community composition is associated with microbial activities and nutrient-use efficiencies in a paddy soil with short-term organic amendments. Plant Soil 424, 335–349. https://doi.org/10.1007/s11104-017-3547-8.

Guo, X., Zhou, X., Hale, L., Yuan, M., Ning, D., Feng, J., Shi, Z., Li, Z., Feng, B., Gao, Q., Wu, Linwei, Shi, W., Zhou, A., Fu, Y., Wu, Liyou, He, Z., Van Nostrand, J.D., Qiu, G., Liu, X., Luo, Y., Tiedje, J.M., Yang, Y., Zhou, J., 2019. Climate warming accelerates temporal scaling of grassland soil microbial biodiversity. Nat. Ecol. Evol. 3, 612–619. https://doi.org/10.1038/s41559-019-0848-8.

Han, S., Delgado-Baquerizo, M., Luo, X., Liu, Y., Van Nostrand, J.D., Chen, W., Zhou, J., Huang, Q., 2021. Soil aggregate size-dependent relationships between microbial functional diversity and multifunctionality. Soil Biol. Biochem. 154, 108143. https://doi.org/10.1016/j.soilbio.2021.108143.

Hu, X., Liu, J., Wei, D., Zhu, P., Cui, X., Zhou, B., Chen, X., Jin, J., Liu, X., Wang, G., 2018a. Soil bacterial communities under different long-term fertilization regimes in three

locations across the black soil region of Northeast China. Pedosphere 28, 751–763. https://doi.org/10.1016/S1002-0160(18)60040-2.

Hu, X., Liu, J., Zhu, P., Wei, D., Jin, J., Liu, X., Wang, G., 2018b. Long-term manure addition reduces diversity and changes community structure of diazotrophs in a neutral black soil of Northeast China. J. Soils Sediments 18, 2053–2062. https://doi.org/10.1007/s11368-018-1975-6.

Karimi, B., Terrat, S., Dequiedt, S., Saby, N.P.A., Horrigue, W., Lelièvre, M., Nowak, V., Jolivet, C., Arrouays, D., Wincker, P., Cruaud, C., Bispo, A., Maron, P.-A., Bouré, N.C.P., Ranjard, L., 2018. Biogeography of soil bacteria and archaea across France. Sci. Adv. 4, eaat1808. https://doi.org/10.1126/sciadv.aat1808.

Kumar, U., Kumar Nayak, A., Shahid, M., Gupta, V.V.S.R., Panneerselvam, P., Mohanty, S., Kaviraj, M., Kumar, A., Chatterjee, D., Lal, B., Gautam, P., Tripathi, R., Panda, B.B., 2018. Continuous application of inorganic and organic fertilizers over 47 years in paddy soil alters the bacterial community structure and its influence on rice production. Agric. Ecosyst. Environ. 262, 65–75. https://doi.org/10.1016/j.agee.2018.04.016.

Li, Y., Song, D., Liang, S., Dang, P., Qin, X., Liao, Y., Siddique, K.H.M., 2020. Effect of no-tillage on soil bacterial and fungal community diversity: a meta-analysis. Soil Tillage Res. 204, 104721. https://doi.org/10.1016/j.still.2020.104721.

Li, M., Guo, J., Ren, T., Luo, G., Shen, Q., Lu, J., Guo, S., Ling, N., 2021. Crop rotation history constrains soil biodiversity and multifunctionality relationships. Agric. Ecosyst. Environ. 319, 107550. https://doi.org/10.1016/j.agee.2021.107550.

Li, P., Li, Y., Xu, L., Zhang, H., Shen, X., Xu, H., Jiao, J., Li, H., Hu, F., 2021. Crop yield-soil quality balance in double cropping in China's upland by organic amendments: a meta-analysis. Geoderma 403, 115197. https://doi.org/10.1016/j.geoderma.2021.115197.

Liu, C., Wang, S., Yan, J., Huang, Q., Li, R., Shen, B., Shen, Q., 2021. Soil fungal community affected by regional climate played an important role in the decomposition of organic compost. Environ. Res. 197, 111076. https://doi.org/10.1016/j.envres.2021.111076.

Liu, J., Shu, A., Song, W., Shi, W., Li, M., Zhang, W., Li, Z., Liu, G., Yuan, F., Zhang, S., Liu, Z., Gao, Z., 2021. Long-term organic fertilizer substitution increases rice yield by improving soil properties and regulating soil bacteria. Geoderma 404, 115287. https://doi.org/10.1016/j.geoderma.2021.115287.

Luo, G., Li, L., Friman, V.-P., Guo, J., Guo, S., Shen, Q., Ling, N., 2018a. Organic amendments increase crop yields by improving microbe-mediated soil functioning of agroecosystems: a meta-analysis. Soil Biol. Biochem. 124, 105–115. https://doi.org/10.1016/j.soilbio.2018.06.002.

Luo, G., Li, L., Friman, V.-P., Guo, J., Guo, S., Shen, Q., Ling, N., 2018b. Organic amendments increase crop yields by improving microbe-mediated soil functioning of agroecosystems: a meta-analysis. Soil Biol. Biochem. 124, 105–115. https://doi.org/10.1016/j.soilbio.2018.06.002.

Maron, P.-A., Sarr, A., Kaisermann, A., Lévêque, J., Mathieu, O., Guigue, J., Karimi, B., Bernard, L., Dequiedt, S., Terrat, S., Chabbi, A., Ranjard, L., 2018. High microbial diversity promotes soil ecosystem functioning. Appl. Environ. Microbiol. 84. https://doi.org/10.1128/AEM.02738-17.

Meng, X., Liao, H., Fan, H., Zhang, X., Li, Y., Yao, H., Razavi, B.S., 2021. The geographical scale dependence of diazotroph assembly and activity: effect of a decade fertilization. Geoderma 386, 114923. https://doi.org/10.1016/j.geoderma.2020.114923.

Ning, Q., Chen, L., Jia, Z., Zhang, C., Ma, D., Li, F., Zhang, J., Li, D., Han, X., Cai, Z., Huang, S., Liu, W., Zhu, B., Li, Y., 2020. Multiple long-term observations reveal a strategy for soil pH-dependent fertilization and fungal communities in support of agricultural production. Agric. Ecosyst. Environ. 293, 106837. https://doi.org/10.1016/j.agee.2020.106837.

Paliy, O., Shankar, V., 2016. Application of multivariate statistical techniques in microbial ecology. Mol. Ecol. 25, 1032–1057. https://doi.org/10.1111/mec.13536.

Pan, H., Chen, M., Feng, H., Wei, M., Song, F., Lou, Y., Cui, X., Wang, H., Zhuge, Y., 2020. Organic and inorganic fertilizers respectively drive bacterial and fungal community compositions in a fluvo-aquic soil in northern China. Soil Tillage Res. 198, 104540. https://doi.org/10.1016/j.still.2019.104540.

Pec, G.J., Diepen, L.T.A., Knorr, M., Grandy, A.S., Melillo, J.M., DeAngelis, K.M., Blanchard, J.L., Frey, S.D., 2021. Fungal community response to long-term soil warming with potential implications for soil carbon dynamics. Ecosphere 12. https://doi.org/10.1002/ecs2.3460.

Ray, D.K., Ramankutty, N., Mueller, N.D., West, P.C., Foley, J.A., 2012. Recent patterns of crop yield growth and stagnation. Nat. Commun. 3, 1293. https://doi.org/10.1038/ncomms2296.

Renard, D., Tilman, D., 2019. National food production stabilized by crop diversity. Nature 571, 257–260. https://doi.org/10.1038/s41586-019-1316-y.

Rousk, J., Bååth, E., Brookes, P.C., Lauber, C.L., Lozupone, C., Caporaso, J.G., Knight, R., Fierer, N., 2010. Soil bacterial and fungal communities across a pH gradient in an arable soil. ISME J. 4, 1340–1351. https://doi.org/10.1038/ismej.2010.58.

Saleem, M., Hu, J., Jousset, A., 2019. More than the sum of its parts: microbiome biodiversity as a driver of plant growth and soil health. Annu. Rev. Ecol. Evol. Syst. 50, 145–168. https://doi.org/10.1146/annurev-ecolsys-110617-062605.

Semchenko, M., Leff, J.W., Lozano, Y.M., Saar, S., Davison, J., Wilkinson, A., Jackson, B.G., Pritchard, W.J., De Long, J.R., Oakley, S., Mason, K.E., Ostle, N.J., Baggs, E.M., Johnson, D., Fierer, N., Bardgett, R.D., 2018. Fungal diversity regulates plant-soil feedbacks in temperate grassland. Sci. Adv. 4, eaau4578. https://doi.org/10.1126/sciadv.aau4578.

Sirami, C., Gross, N., Baillod, A.B., Bertrand, C., Carrié, R., Hass, A., Henckel, L., Miguet, P., Vuillot, C., Alignier, A., Girard, J., Batáry, P., Clough, Y., Violle, C., Giralt, D., Bota, G., Badenhausser, I., Lefebvre, G., Gauffre, B., Vialatte, A., Calatayud, F., Gil-Tena, A., Tischendorf, L., Mitchell, S., Lindsay, K., Georges, R., Hilaire, S., Recasens, J., Solé-Senan, X.O., Robleño, I., Bosch, J., Barrientos, J.A., Ricarte, A., Marcos-Garcia, M.Á., Miñano, J., Mathevet, R., Gibon, A., Baudry, J., Balent, G., Poulin, B., Burel, F., Tscharntke, T., Bretagnolle, V., Siriwardena, G., Ouin, A., Brotons, L., Martin, J.-L., Fahrig, L., 2019. Increasing crop heterogeneity enhances multitrophic diversity across

agricultural regions. Proc. Natl. Acad. Sci. 116, 16442–16447. https://doi.org/10.1073/pnas.1906419116.

Stefan, L., Hartmann, M., Engbersen, N., Six, J., Schöb, C., 2021. Positive effects of crop diversity on productivity driven by changes in soil microbial composition. Front. Microbiol. 12, 660749. https://doi.org/10.3389/fmicb.2021.660749.

Sun, R., Zhang, X.-X., Guo, X., Wang, D., Chu, H., 2015. Bacterial diversity in soils subjected to long-term chemical fertilization can be more stably maintained with the addition of livestock manure than wheat straw. Soil Biol. Biochem. 88, 9–18. https://doi.org/10.1016/j.soilbio.2015.05.007.

Sun, R., Chen, Y., Han, W., Dong, W., Zhang, Y., Hu, C., Liu, B., Wang, F., 2020. Different contribution of species sorting and exogenous species immigration from manure to soil fungal diversity and community assemblage under long-term fertilization. Soil Biol. Biochem. 151, 108049. https://doi.org/10.1016/j.soilbio.2020.108049.

Tang, X., Lou, C., Wang, S., Lu, Y., Liu, M., Hashmi, M.Z., Liang, X., Li, Z., Liao, Y., Qin, W., Fan, F., Xu, J., Brookes, P.C., 2015. Effects of long-term manure applications on the occurrence of antibiotics and antibiotic resistance genes (ARGs) in paddy soils: evidence from four field experiments in south of China. Soil Biol. Biochem. 90, 179–187. https://doi.org/10.1016/j.soilbio.2015.07.027.

Terrer, C., Jackson, R.B., Prentice, I.C., Keenan, T.F., Kaiser, C., Vicca, S., Fisher, J.B., Reich, P.B., Stocker, B.D., Hungate, B.A., Peñuelas, J., McCallum, I., Soudzilovskaia, N.A., Cernusak, L.A., Talhelm, A.F., Van Sundert, K., Piao, S., Newton, P.C.D., Hovenden, M.J., Blumenthal, D.M., Liu, Y.Y., Müller, C., Winter, K., Field, C.B., Viechtbauer, W., Van Lissa, C.J., Hoosbeek, M.R., Watanabe, M., Koike, T., Leshyk, V.O., Polley, H.W., Franklin, O., 2019. Nitrogen and phosphorus constrain the CO2 fertilization of global plant biomass. Nat. Clim. Chang. 9, 684–689. https://doi.org/10.1038/s41558-019-0545-2.

van der Heijden, M.G.A., Bardgett, R.D., van Straalen, N.M., 2008. The unseen majority: soil microbes as drivers of plant diversity and productivity in terrestrial ecosystems. Ecol. Lett. 11, 296–310. https://doi.org/10.1111/j.1461-0248.2007.01139.x.

Vida, C., de Vicente, A., Cazorla, F.M., 2020. The role of organic amendments to soil for crop protection: induction of suppression of soilborne pathogens. Ann. Appl. Biol. 176, 1–15. https://doi.org/10.1111/aab.12555.

Wagg, C., Schlaeppi, K., Banerjee, S., Kuramae, E.E., van der Heijden, M.G.A., 2019. Fungal-bacterial diversity and microbiome complexity predict ecosystem functioning. Nat. Commun. 10, 4841. https://doi.org/10.1038/s41467-019-12798-y.

Wan, Y., Huang, Q., Wang, Q., Yu, Y., Su, D., Qiao, Y., Li, H., 2020. Accumulation and bio-availability of heavy metals in an acid soil and their uptake by paddy rice under continuous application of chicken and swine manure. J. Hazard. Mater. 384, 121293. https://doi.org/10.1016/j.jhazmat.2019.121293.

Xia, L., Lam, S.K., Yan, X., Chen, D., 2017. How does recycling of livestock manure in agroecosystems affect crop productivity, reactive nitrogen losses and soil carbon balance? Environ. Sci. Technol. 13, 7450–7457.

Xia, Q., Rufty, T., Shi, W., 2020. Soil microbial diversity and composition: links to soil texture and associated properties. Soil Biol. Biochem. 149, 107953. https://doi.org/10.1016/j.soilbio.2020.107953.

Xiang, X., Liu, J., Zhang, J., Li, D., Xu, C., Kuzyakov, Y., 2020. Divergence in fungal abundance and community structure between soils under long-term mineral and organic fertilization. Soil Tillage Res. 196, 104491. https://doi.org/10.1016/j.still.2019.104491.

Xu, Y., Chen, Z., Ding, W., Fan, J., 2017a. Responses of manure decomposition to nitrogen addition: role of chemical composition. Sci. Total Environ. 587–588, 11–21. https://doi.org/10.1016/j.scitotenv.2017.02.033.

Xu, Y., Chen, Z., Fontaine, S., Wang, W., Luo, J., Fan, J., Ding, W., 2017b. Dominant effects of organic carbon chemistry on decomposition dynamics of crop residues in a mollisol. Soil Biol. Biochem. 115, 221–232. https://doi.org/10.1016/j.soilbio.2017.08.029.

Xu, P., Liu, Y., Zhu, J., Shi, L., Fu, Q., Chen, J., Hu, H., Huang, Q., 2020. Influence mechanisms of long-term fertilizations on the mineralization of organic matter in ultisol. Soil Tillage Res. 201, 104594. https://doi.org/10.1016/j.still.2020.104594.

Xu, Q., Ling, N., Chen, H., Duan, Y., Wang, S., Shen, Q., Vandenkoornhuyse, P., 2020. Long-term chemical-only fertilization induces a diversity decline and deep selection on the soil bacteria. mSystems 5, e00337-20. https://doi.org/10.1128/mSystems.00337-20 / msystems/5/4/msys.00337-20.atom.

Yang, L., Bai, J., Zeng, N., Zhou, X., Liao, Y., Lu, Y., Rees, R.M., Nie, J., Cao, W., 2019. Diazotroph abundance and community structure are reshaped by straw return and mineral fertilizer in rice-rice-green manure rotation. Appl. Soil Ecol. 136, 11–20. https://doi.org/10.1016/j.apsoil.2018.12.015.

Yang, Y., Li, X., Liu, J., Zhou, Z., Zhang, T., Wang, X., 2020. Fungal community structure in relation to manure rate in red soil in southern China. Appl. Soil Ecol. 147, 103442. https://doi.org/10.1016/j.apsoil.2019.103442.

Ye, G., Lin, Y., Liu, D., Chen, Z., Luo, J., Bolan, N., Fan, J., Ding, W., 2019. Long-term application of manure over plant residues mitigates acidification, builds soil organic carbon and shifts prokaryotic diversity in acidic ultisols. Appl. Soil Ecol. 133, 24–33. https://doi.org/10.1016/j.apsoil.2018.09.008.

Young, M.D., Ros, G.H., de Vries, W., 2021. Impacts of agronomic measures on crop, soil, and environmental indicators: a review and synthesis of meta-analysis. Agric. Ecosyst. Environ. 319, 107551. https://doi.org/10.1016/j.agee.2021.107551.

Zheng, Q., Hu, Y., Zhang, S., Noll, L., Böckle, T., Dietrich, M., Herbold, C.W., Eichorst, S.A., Woebken, D., Richter, A., Wanek, W., 2019. Soil multifunctionality is affected by the soil environment and by microbial community composition and diversity. Soil Biol. Biochem. 136, 107521. https://doi.org/10.1016/j.soilbio.2019.107521.

Zhou, Z., Wang, C., Luo, Y., 2020. Meta-analysis of the impacts of global change factors on soil microbial diversity and functionality. Nat. Commun. 11, 3072. https://doi.org/10.1038/s41467-020-16881-7.