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Effects of Different Photovoltaic Installation Modes on Soil Bacterial Community Structure, Diversity, and Assembly Mechanisms in Rocky Desertification Areas

Yunpeng Wu,[1] Yan Wang,[1] Yuanze Hu,[2] Fangjun Liu,[1] Guangxin Che [1] and Yanmei Li[1,*]

Abstract

Soil bacteria regulate nutrient transformation and cycling in the soil, thereby influencing ecosystem functionality and stability. However, the impact pathway and underlying mechanisms of photovoltaic array on soil bacterial community are imperfectly known. This study quantified the impacts of different photovoltaic (PV) installation modes on the structure, diversity, and succession of soil bacterial communities in rocky desertification areas. In contrast to control plot (CP), a two-row PV installation mode (TP) reduced ACE, Chao1, Simpson, and Shannon indices of soil bacterial communities, whereas a flat-top PV installation mode (FP) increased these indices. FP treatment had significantly higher ACE, Chao1, and Shannon indices than TP. PV installations improved the relative abundances of *Myxococcota* and *Bacteroidota*, with FP treatment increasing by 27.9% and 213.4%, respectively, compared to CP treatment, but reduced the relative abundance of *Acidobacteriota*, *Actinobacteriota* and *Gemmatimonadota*, with the largest reduction in *Actinobacteriota* ranging from 36.0% to 32.3%.PV installations indirectly drove changes in bacterial communities by altering the climate and subsequently affecting the soil. Soil physicochemical properties and microclimate were identified as key predictors of bacterial community structure and diversity. Network analysis revealed that different PV installation modes significantly influenced co-occurrence network structure of soil bacterial communities. Compared with the control, both TP and FP enhanced associations among bacterial taxa, with TP showing the strongest network connectivity and FP exhibiting intermediate connectivity between the control and TP. The assembly process of soil bacterial communities was primarily driven by deterministic processes, which dominated in all plots (control, TP, FP). PV installations affected the assembly of soil bacterial communities, in the control, homogeneous selection entirely controlled community assemblages (100%), while in TP, its proportion decreased to 78%,under FP conditions, stochastic processes began to exert influence, with dispersal limitation accounting for 17%. Our data suggested that FP model increased the diversity and richness of soil bacterial community, enhanced stochastic process of community assembly, and had a milder impact on network connectivity in rocky desertification areas compared with TP.

Keywords: Photovoltaic power stations; Installation modes; Bacterial communities; Diversity; Assembly mechanisms.
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1. Introduction

Soil bacteria play key roles in biogeochemical cycles, including those of nitrogen, carbon, and phosphorus.[1] Through processes such as nitrogen fixation, carbon sequestration, and organic matter decomposition, soil bacteria directly regulate nutrient transformation and cycling in the soil, thereby influencing ecosystem functionality and stability.[2] The ecological functions of soil bacteria are closely linked to their assembly processes, which are driven by multiple environmental factors.[3,4] Understanding community assembly mechanisms improves our comprehension of material cycling and energy flow within ecosystems.

With increased global demand for renewable energy, photovoltaic (PV) power stations—a clean energy source—have developed rapidly worldwide.[5] Constructing PV power stations in degraded rocky desertification areas reduces pressure on more arable land.[6] PV power stations can improve local microclimatic conditions, enhancing soil moisture and nutrient retention, thereby contributing to ecosystem

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[1] *College of Soil and Water Conservation, Southwest Forestry University, Kunming, 650224, China*
[2] *Shilin Yundian Investment New Energy Development Co. Ltd., Kunming, 652200, China*
**Email:* kmlymei@126.com (Y. Li)

restoration and stability, preventing further land degradation and rocky desertification.[7-9] Meanwhile, anthropogenic disturbance and ecological restoration activities can significantly affect the assembly mechanisms of soil bacterial communities.[10,11] The photovoltaic power might affect the composition and succession of bacterial communities by influencing environmental factors, microbial community formation and succession are affected by microbial community assembly processes that are typically either deterministic or stochastic.[12,13] Clarifying the relative importance of these processes in shaping microbial community structures and identifying those factors that influence the balance between them is needed to regulate soil microbial communities.[14] However, few studies have explored the long-term impacts of PV power stations on soil bacterial communities, and particularly, the underlying mechanisms of photovoltaic array on soil bacterial community remain poorly understood.

Network analysis can reveal patterns of interaction and complexity within soil bacterial communities, enabling exploration of synergistic interactions and responses to environmental change.[15-17] The stegen null modeling provides a quantitative analysis of community assembly mechanisms by directly quantifying the contributions of deterministic and stochastic processes, pNST further verifies the non randomness of community structure and the existence of specific ecological patterns through a hypothesis testing framework, combining the two methods can help to gain a more comprehensive understanding of the ecological patterns and mechanisms of communities.[18-20] Therefore, we investigated: (a) how different PV installation modes (PVIM) affect the composition and diversity of soil bacterial communities; (b) co-occurrence patterns in bacterial communities under different PVIM; and (c) assembly processes of bacterial communities under varying PVIM. We hypothesized that: (1) different PVIM affect the structure and diversity of soil bacterial communities by altering soil physicochemical properties and microclimatic conditions; and (2) different PVIM change co-occurrence patterns and assembly processes of soil bacterial communities.

2. Materials and methods

2.1 Study area

Surveys were performed in the Shilin Photovoltaic Power Station Demonstration Zone, Shilin Yi Autonomous County, Kunming, Yunnan Province, China (24°50′32″E, 103°24′26″N) (Fig. 1). The power station covers an area of 139.48 hectares and has a total installed capacity of 66 MW. The terrain is characterized by a low northwest and high southeast orientation, and is typical of stone-desertification areas in southwestern China. The power station was constructed in 2015. The region experiences a subtropical plateau monsoon climate, with annual averages for temperature (16.1 °C), precipitation (946.6 mm), evaporation (1909.4 mm), relative humidity (75%), sunshine (2193.1 h), and total solar radiation (>5500 MJ/m^2).

2.2 Experimental design and sampling

Two representative PV array installation modes were selected for study in October 2023:

(a) Two-Row Sloped-Top Bracket (TP): the mode consists of sloped-top bracket PV arrays. Each bracket has a sloped rectangular frame measuring 10.5 m in length (east–west) and 2.96 m in width (north–south). The lower edge of the sloped top is 0.6 m above the ground, and the upper edge is 2.1 m high. Solar panels are arranged in two north–south rows along the short side of the sloped top, inclined at 23°.

(b) FP: the mode features flat-top bracket PV arrays with a rectangular structure measuring 18.9 m in length (east–west), 10.2 m in width (north–south), and 2.2 m in height. Solar panels are arranged in a single east–west row along the long side of the flat top, inclined at 23°.

A control plot (CP) without PV installations was selected. In each experimental area, nine replicate plots of 10×10 m were randomly selected. To minimize the influence of differences in altitude on soil and microbial communities, all plots were within 10 m of elevation of each other. Within each 10×10 m plot, five 1×1 m subplots were established to record information on herbaceous plant species and their abundance. In total, 27 plots were surveyed for plant data. Soil samples were collected using a five-point sampling method. Five soil subsamples from each plot (sampling depth 0–20 cm) were mixed to create a composite soil sample after removing litter, roots, and gravel, a total of 27 soil samples were collected. Soil samples were divided into two portions: one stored at −80 °C for microbial DNA extraction, and the other air-dried, ground, and sieved for soil physicochemical property analysis.

2.3 Environmental factor analysis

In October 2023, meteorological shields (JXBS-3001-BYX, China) were installed directly under the PV arrays and in the control area (unaffected by PV installations) to continuously record temperature, humidity, light intensity, and wind speed at 10-min intervals. Soil total nitrogen, total phosphorus, and total potassium were determined using the Kjeldahl method, molybdenum-antimony anti-spectrophotometry, and atomic absorption spectroscopy, respectively. Available nitrogen, phosphorus, and potassium were measured by alkaline hydrolysis diffusion, sodium bicarbonate extraction, and ammonium acetate extraction, respectively. Soil pH was measured by pH meter with a soil-to-water ratio of 2.5:1; soil organic matter was analyzed by potassium dichromate oxidation, soil moisture content by drying, and soil bulk density by ring knife.[21]

2.4 DNA extraction, amplification, and sequencing

Soil genomic DNA was extracted using the TGuide S96 Magnetic Soil DNA Extraction Kit (DP812, TIANGEN Biotech, Beijing) following instructions of the manufacturer.

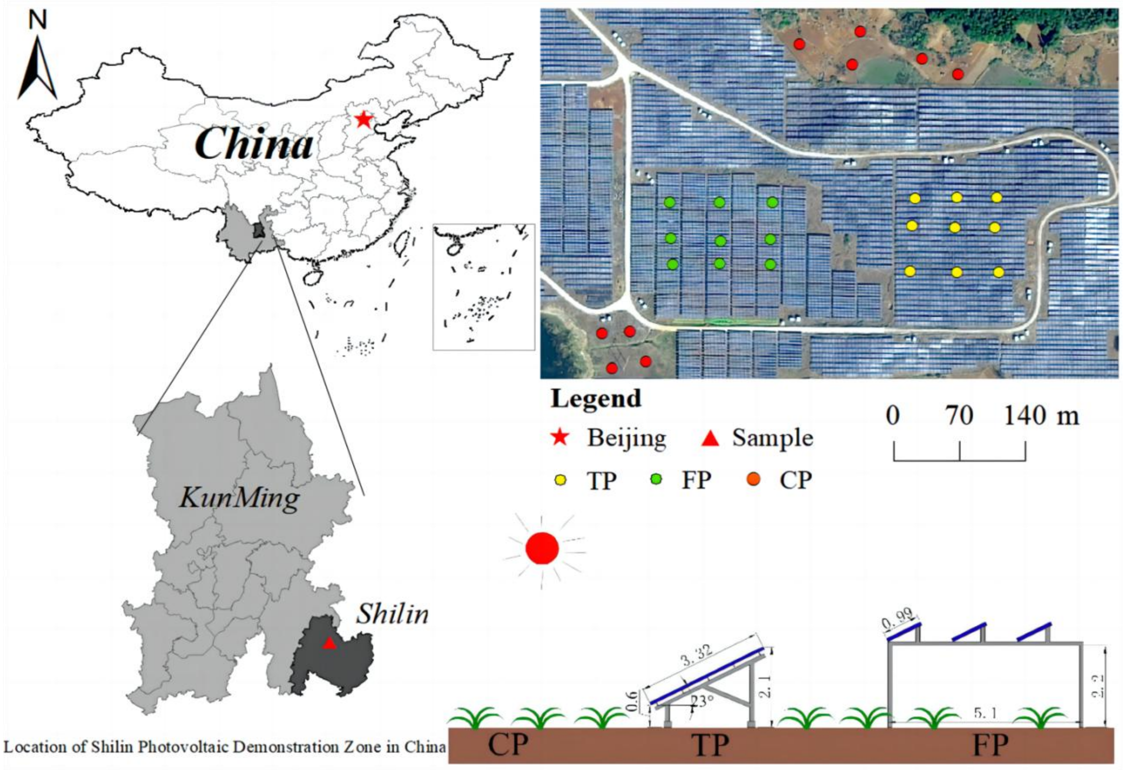

Fig. 1: Location of the research area.

DNA purity (A260/A280) was assessed with a NanoDrop 2.0 spectrophotometer (Thermo Fisher Scientific, USA), and DNA concentration was measured using the Quant-IT Pico Green dsDNA Assay Kit (Invitrogen, USA).[22] The V4 region of the bacterial 16S rRNA gene was amplified using primers 515F (GTGYCAGCMGCCGCGGTAA) and 806R (GGACTACHVGGGTWTCTAAT).[23]

The 20 μL PCR reaction mixture contained 2.5-4 ng of template DNA, 0.3 μL of each primer (10 μM), 5 μL of KOD FX Neo buffer, 2 μL of dNTPs (2 mM each), and 0.2 μL of KOD FX Neo polymerase. The amplification program involved an initial denaturation at 95 °C for 5 min; 25 cycles of 95 °C for 30 s, 50 °C for 30 s, and 72 °C for 40 s, and a final extension at 72 °C for 7 min. PCR products were verified by 1.8% agarose gel electrophoresis and purified using VAHTSTM DNA Clean Beads. Sequencing libraries were constructed and sequenced on an Illumina NovaSeq 6000 platform, producing paired-end reads (2 × 250 bp). Sequencing data were merged using the FLASH program, quality-controlled with QIIME 2 (v2021.11) to retain sequences with Phred scores > Q20, and chimera sequences were removed using USEARCH.[24]

The taxonomic annotation for the sequences was produced from the SILVA database (v138.1) with less than 3% dissimilarity according to recommended standards.[25] The operational taxonomic units (OTUs) at 97% identity were clustered through the Mothur program. OTU richness was determined using Chao1 and ACE indices, while bacterial diversity was estimated by Shannon-Wiener index.[26]

2.5 Co-occurrence network analysis

For network analysis, phyla with an average relative abundance > 1% and OTUs with relative abundances > 0.01% were selected. Spearman correlations ($|r| > 0.6$, $P < 0.05$) were used to calculate associations, and networks were constructed accordingly.[27] Network properties were computed using the "igraph" package in R (v4.4.2). Network visualization was performed via the online tool Chiplot (https://www.chiplot.online/).

2.6 Community assembly process

We first calculated the phylogenetic normalized stochasticity ratio (pNST) to assess the relative contributions of stochastic and deterministic processes to community assembly; pNST values range from 0 to 1. Communities with pNST values predominantly > 0.5 are considered to be stochastically assembled, while values < 0.5 indicate deterministically assembled communities.[28] The pNST was computed using the NST package in R. To further differentiate the contributions of deterministic and stochastic processes, we combined the beta nearest taxon index (βNTI) with the Bray–Curtis-based Raup–Crick metric (RCbray). The βNTI quantifies deviations between observed βMNTD (mean nearest taxon distance) and null-model βMNTD distributions.a Values of $|\beta NTI| < 2$ indicate stochastic dominance, $\beta NTI > 2$ reflects heterogeneous selection, and $\beta NTI < -2$ reflects homogeneous selection.[29,30] For cases where $|\beta NTI| < 2$, RCbray was used to further classify stochastic processes: $RCbray < -0.95$ indicates homogeneous dispersal, $RCbray > 0.95$ indicates dispersal limitation, and |RCbray| < 0.95 represents undominated processes.[1] The neutral theory model was calculated using the Hmisc and minpack.lm packages.

2.7 Statistical analysis

Differences in soil bacterial community diversity and environmental factors were assessed using one-way analysis of variance (ANOVA, stats package Origin), followed by Tukey's HSD test for multiple comparisons. Structural differences in soil bacterial communities were visualized using non-metric multidimensional scaling (NMDS, vegan package R) and tested for significance using the Adonis test. Additionally, to ensure the independence of environmental factors, the variance inflation factor (VIF, car package R) was calculated, and multicollinear variables were excluded.[31] To quantitatively assess the direct and indirect effects of environmental factors on soil bacterial community composition and diversity, structural equation modeling (SEM, lavaan package) was used. Random forest analysis (randomForest package R) was used to determine the relative contributions of environmental factors to bacterial community assembly processes, and linear regression (stats package R) was combined to explore the impact of key environmental factors on bacterial community diversity and functional characteristics. All statistical significance levels were set at $P < 0.05$. All statistical analyses and visualizations were performed using R v4.2.0 software (R Development Core Team, 2022) and Origin 2023 (Origin Lab Corporation, Northampton, Massachusetts, USA).

3. Results

3.1 Effects of PVIM on environmental factors

The photovoltaic arrays significantly increased BD, PS and PR, but reduced N, SOM, AK, AN, T, Li and WS (Table 1, $p < 0.05$). Compared with CP, FP and TP treatments reduced the monthly average wind speed by 84.0% and 88.8%, respectively, and contributed 29.3-32.8% to the variations in plant diversity, while the contribution of plant richness was 6.4–13.8%. In contrast, CP had significantly higher levels of total nitrogen, organic matter, available potassium, available nitrogen, light intensity, and temperature.

For both photovoltaic array modes, there were significant differences in N, K, SOM, RH, AK, AN, PR and Li ($p < 0.05$). FP treatment had higher P, AP, K, T and Li values than TP treatment, and the potassium content of FP is 2.32 times that of TP treatment, and AN is 56.7% of TP treatment. Additionally, compared with TP, FP increases the light intensity by 1.25 times.

3.2 Effects of PVIM on soil bacterial diversity

Compared with the control, PVIM significantly affected the α-diversity of soil microbial communities (Fig. 2a). Microbial richness and diversity indices (ACE, Chao1, and Shannon) in the TP area were significantly lower than those in the control and FP areas ($P < 0.05$). For richness (ACE and Chao1), values were significantly higher in the FP than TP area ($P < 0.05$), with intermediate values for the control, which did not differ significantly from either other group. The Shannon index

Table 1: Environmental factors of different plots.

Parameters	CP	TP	FP
N (g/kg)	1.6±0.14a	1.2±0.13b	0.98±0.06c
P (g/kg)	0.47±0.04a	0.43±0.07a	0.45±0.02a
K (g/kg)	11.06±0.45b	8.61±0.91c	17.97±0.68a
SOM (g/kg)	28.14±2.15a	21.52±1.96b	17.83±0.83c
BD (g/cm^3)	1.47±0.07b	1.63±0.03a	1.58±0.02a
AK (mg/kg)	116.75±18.1a	78.21±6.19b	59.92±5.62c
AP (mg/kg)	138.47±23.37a	129.91±15.82a	140.55±9.96a
AN (mg/kg)	54.66±5.92a	42.52±7.76b	24.09±2.29c
MC (%)	0.18±0.01a	0.19±0.01a	0.18±0.01a
pH	7.96±0.05a	7.78±0.05a	7.76±0.1a
PS	1.16±0.14b	1.5±0.04a	1.54±0.06a
PR	5.55±0.50c	8.22±0.46a	7.56±0.51b
T (℃)	19.24±0.08a	17.93±0.05c	18.83±0.04b
RH (%)	83.12±0.65b	88.54±0.39a	84.39±0.4b
Li (Lux)	29964.02±71.03a	9239.23±57.48c	11516.03±70.84b
WS (m/s)	1.25±0.02a	0.14±0.03b	0.2±0.02b

N: Total Nitrogen, **P**: Total Phosphorus, **K**: Total Potassium, **SOM**: Soil Organic Matter, **BD**: Bulk Density, **AK**: Available Potassium, **AP**: Available Phosphorus, **AN**: Available Nitrogen, **MC**: Moisture Content, **pH**: Potential of Hydrogen, **PS**: Plant Shannon Index, **PR**: Plant Richness Index, **T**: Temperature, **RH**: Relative Humidity, **Li**: Light Intensity, **WS**: Monthly Average Wind Speed. Different lowercase letters indicate significant differences in the average values of environmental factors ($p < 0.05$).

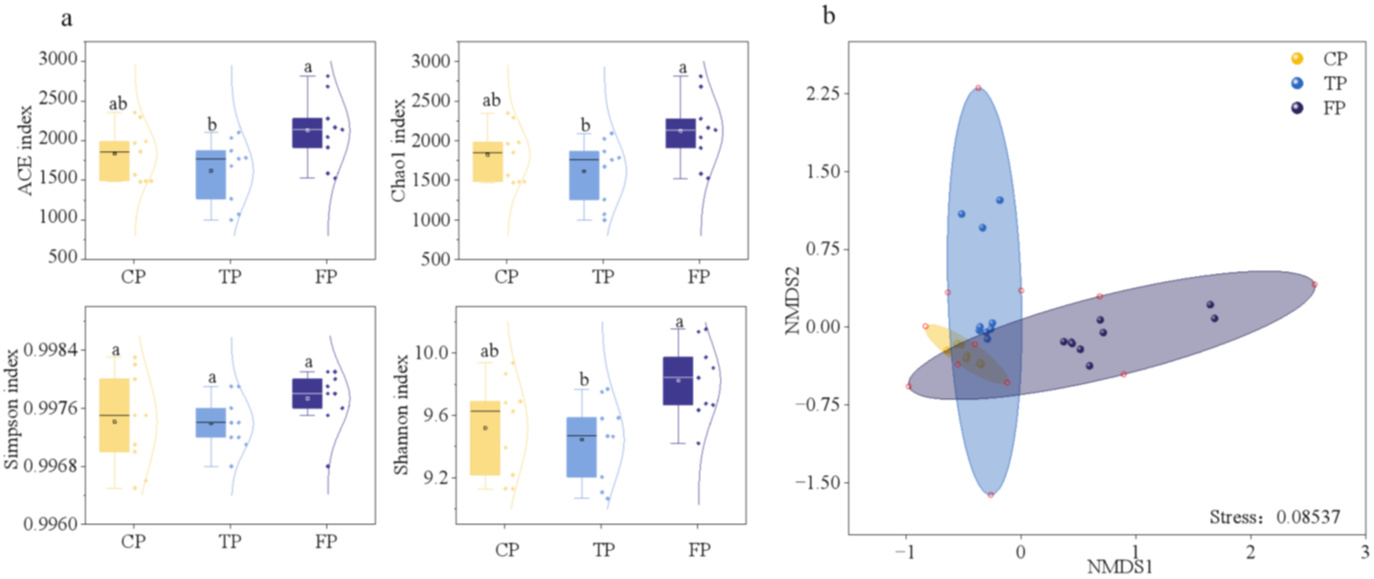

Fig. 2: (a) The soil bacterial diversity and alpha diversity of bacterial communities under different PVIM, (b) Non metric Multidimensional Scaling Analysis (NMDS) of β Diversity.

in the FP area was significantly higher than in the TP area ($P < 0.05$). NMDS analysis revealed that different PVIM significantly influenced the structure of soil microbial communities, with clear differences between the control and experimental areas (Fig. 2b). Specifically, microbial community structures in the FP and TP areas formed distinctclusters, which were significantly differentiated from communities in the control. This indicates that PVIM significantly affects the composition and spatial distribution of soil microbial communities.

3.3 Effects of PVIM on bacterial composition

The top 10 bacterial phyla ranked by relative abundance (Fig. 3) are *Acidobacteriota* (13.92-34.48%), *Proteobacteria* (15.82-32.25%), *Actinobacteriota* (6.09-15.41%), *Methylomirabilota* (2.57-8.29%), *Gemmatimonadota* (1.94-7.75%), *Myxococcota* (2.73-5.45%), *Bacteroidota* (0.51-6.53%), *Planctomycetota* (0.37-2.87%), and *Firmicutes* (0.13-6.36%), which together accounted for 88.81% of all bacterial phyla. Compared with the control, the relative abundances of these top 10 bacterial phyla varied significantly under TP and FP conditions, with PVIM significantly affecting the relative abundances of the main microbial groups ($P < 0.05$). Different PVIMs had selective effects on bacterial dominant phyla. PV installations improved the relative abundances of *Myxococcota* and *Bacteroidota*, with FP treatment increasing by 27.9% and 213.4%, respectively, compared to CP treatment, but reduced the relative abundance of *Acidobacteriota*,

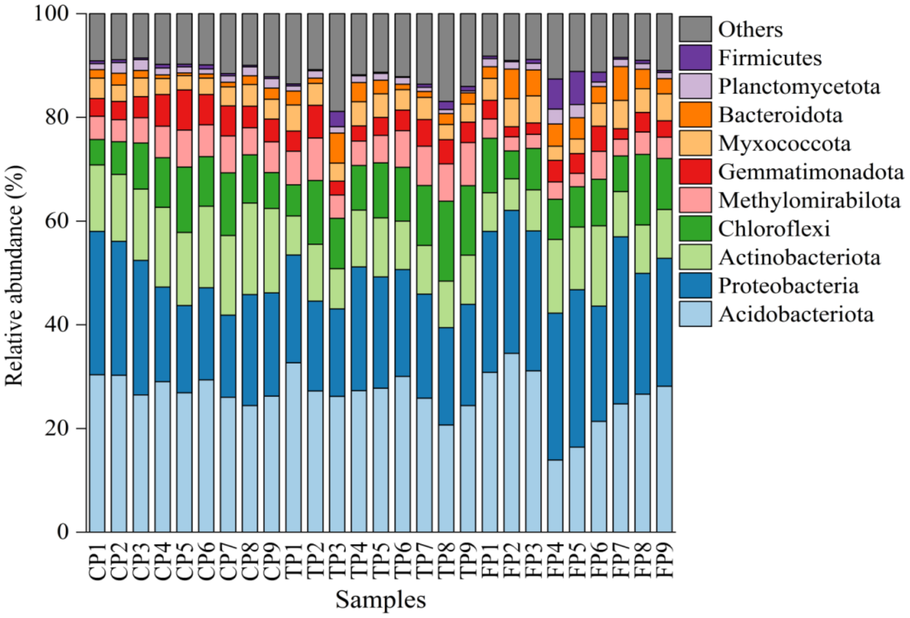

Fig. 3: Bacterial phylum taxa with relative abundance > 1%.

Actinobacteriota and *Gemmatimonadota*, with the largest reduction in *Actinobacteriota* ranging from 36.0% to 32.3%. In FP area, the relative abundance of *Proteobacteria* and *Bacteroidota* was significantly higher than TP area and CP area. In contrast, the abundance of *Actinobacteriota* in CP area was significantly higher than TP area and FP area. Additionally, the abundance of *Methylomirabilota* in CP area and TP area was significantly higher than FP area. Meanwhile, the abundance of *Gemmatimonadota* in CP area was significantly higher than FP area, while the abundance of *Myxococcota* in FP area was significantly higher than CP area.

3.4 Relationships between bacterial communities and environmental factors for different PVIM

SEM was used to evaluate the direct and indirect effects of PVIM on bacterial community composition (Fig. 4a). The model explained 34% of bacterial diversity (represented by the Shannon index) and 84% of community structure (represented by NMDS axis 1). SEM results indicate that: (a) climate significantly influenced soil properties (path coefficient = 0.705, $P < 0.001$) and plant characteristics (path coefficient = 0.473, $P < 0.05$), but that it did not directly, significantly affect bacterial communities or their diversity; and (b) soil had a significant driving effect on bacterial communities (path coefficient = 0.729, $P < 0.001$) and bacterial diversity (path coefficient = 0.637, $P < 0.01$). These findings suggest that PV installations mainly influence bacterial communities indirectly by altering the climate, which then affects soil properties. Random forest analysis (Fig. 4b) revealed that total phosphorus, MC, and RH were the key predictors of soil bacterial communities. These results indicate the importance of soil physicochemical properties and microclimate in shaping bacterial community structure and diversity.

3.5 Co-occurrence patterns of soil bacterial communities for different PVIM

Network analysis was used to investigate interaction patterns in soil bacterial communities beneath the control, TP, and FP installations (Fig. 5 and Table 2). This study observed that different PVIM significantly affect the co-occurrence network structure of soil bacterial communities. TP treatment enhanced the interaction and complexity between soil bacterial groups,in the TP area, the bacterial co-occurrence network exhibited more total links and a higher average degree compared with the control. In contrast, although FP treatment also improved the modularity and clustering coefficient of the network, other network topology properties were lower than TP. In addition, positive correlation links of network analysis dominated in all treatments, especially in TP and FP treatment. Compared with the control, the network modularity of TP and FP treatment improved.

Table 2: Topological characteristics of bacterial networks in different PVIM.

Topological properties	CP	TP	FP
Nodes	485	653	649
Total links	4040	6394	5410
Positive links	3798	6259	5307
Negative links	242	135	103
Average degree	9.889	13.633	12.295
Clustering coefficient	0.747	0.755	0.763
Path.length	6.674	4.972	5.499
Betweenness centralization	0.049	0.021	0.037
Modularity	0.826	0.952	0.924

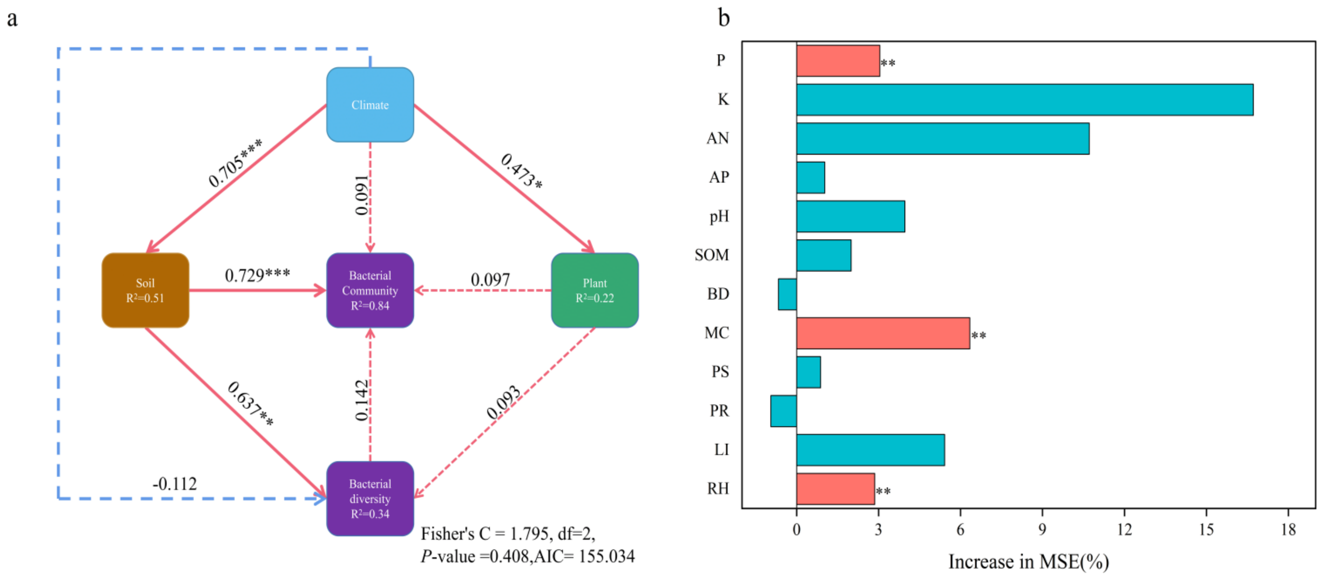

Fig. 4: (a) Structural equation models (SEM) to bacterial community structure. The value in each arrow represents the path coefficient (∗∗∗$p < 0.001$, ∗∗$p < 0.01$, ∗$p < 0.05$). Solid lines indicate significant effects, while dashed lines indicate no significant effects. Red and blue lines represent positive and negative effects, respectively. R^2 values represent the proportion of explained variance. (b) Random forest analysis, the meanings represented by letters are the same as in Table 1.

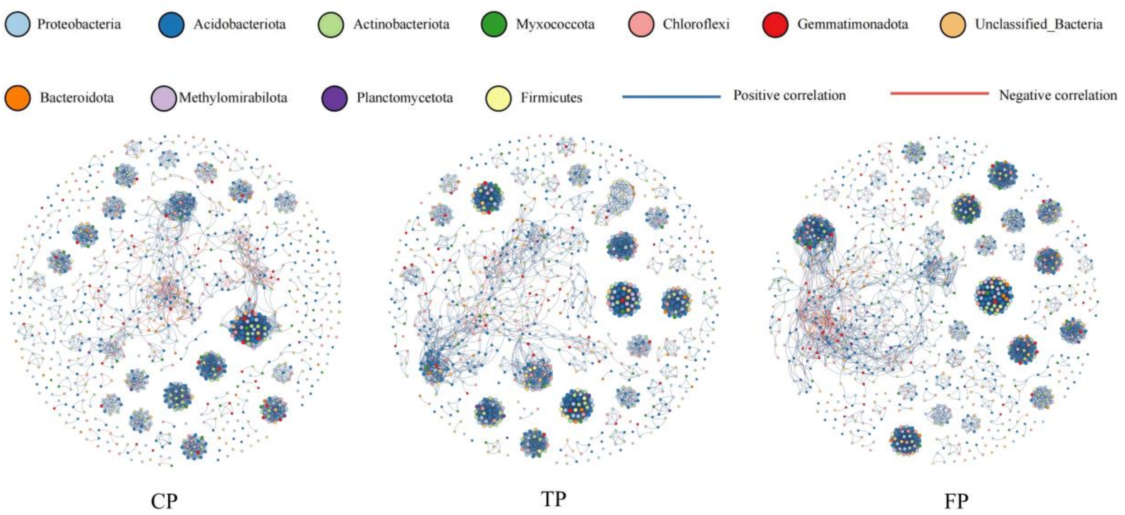

Fig. 5: Network analysis of soil bacterial communities.

3.6 Assembly processes of soil bacterial communities for different PVIM

The phylogenetic normalized stochasticity ratio (pNST) was calculated based on null model analysis (Fig. 6a). Deterministic processes ($pNST < 0.5$) dominated in each area. To further explore the relative contributions of stochastic and deterministic processes, null model analysis based on βNTI and RC revealed that the absolute values of βNTI for each site were > 2, indicating that deterministic processes played a more significant role than stochastic processes in shaping bacterial community assemblages(Fig. 6b). RCbray analysis revealed the relative contributions of deterministic and stochastic processes to community assembly at each site (Fig. 6c) to be: (a) homogeneous selection (a deterministic process) dominated under control and TP conditions. In the control, homogeneous selection entirely controlled community assemblages (100%), while in TP, its proportion decreased to 78%, with heterogeneous selection (22%) also contributing, and (b) Under FP conditions, stochastic processes began to exert influence, with dispersal limitation (a stochastic process) accounting for 17% and homogeneous selection contributing 83%. These results indicate that as environmental conditions change, community assembly mechanisms transition from being solely dominated by environmental selection to being co-influenced by stochastic processes and environmental selection.

A neutral model based on R^2 values was used to analyze community assembly processes ($R^2 = 0.362$ to 0.579), along with the proportion of taxa falling outside of dashed lines of the model (control, 5.2%; TP, 5.4%; FP, 5%). The migration rates (m) estimated by the neutral model, which reflect species dispersal ability, were low across all study areas (control, 0.0078; TP, 0.0058; FP, 0.0067). This suggests that stochastic processes contribute little to microbial community assembly, while deterministic processes dominate, consistent with results of null model analysis (Figs. 6d-f). To further identify those intrinsic factors driving community assembly, unary linear regression was used to examine relationships between βNTI and environmental variables (Fig. 7), βNTI was significantly correlated with AN, SOM, pH, PR, RH and Li.

4. Discussion

PV shading significantly altered soil microbial community composition by affecting microclimatic factors such as soil moisture and precipitation.[32] Differences in shading intensity directly impacted the relative abundances of *Acidobacteriota* and *Proteobacteria*, and significantly increased microbial network complexity.[11] Compared with the control, this study observed that TP treatment reduced microbial richness and diversity index, while FP treatment increased ACE and Chao1 indices. These differences may be attributed to the stronger shading effect of the TP installation, which reduced surface soil temperature and increased soil moisture, reducing soil microbial diversity and certain bacterial groups. In contrast, the FP installation, with its greater height and reduced shading effect, was more conducive to the growth and reproduction of bacterial communities. Microclimatic conditions in PV regions (*e.g.*, soil moisture, electrical conductivity) played dominant roles in regulating soil bacterial diversity and composition.[33] PV panel arrangements significantly enhanced plant diversity and indirectly increased soil microbial community diversity by augmenting water availability.[8] For this study, climate significantly influenced soil properties and plant characteristics, dominant phyla in communities (*e.g.*, *Acidobacteriota*, *Proteobacteria*) differed significantly under PVIM, the relative abundances of these phyla were significantly higher in the FP than TP areas. A possible reason for this may be that the combined effects of microclimatic conditions and soil nutrients under different PVIM significantly influence their survival strategies and ecological adaptability.[34]

SEM analysis revealed PVIM primarily influenced soil physicochemical properties by altering microclimatic conditions, thereby driving changes in bacterial community structure and diversity. Xue *et al*.[35] (2018) reported that shading and microclimatic changes are critical drivers of

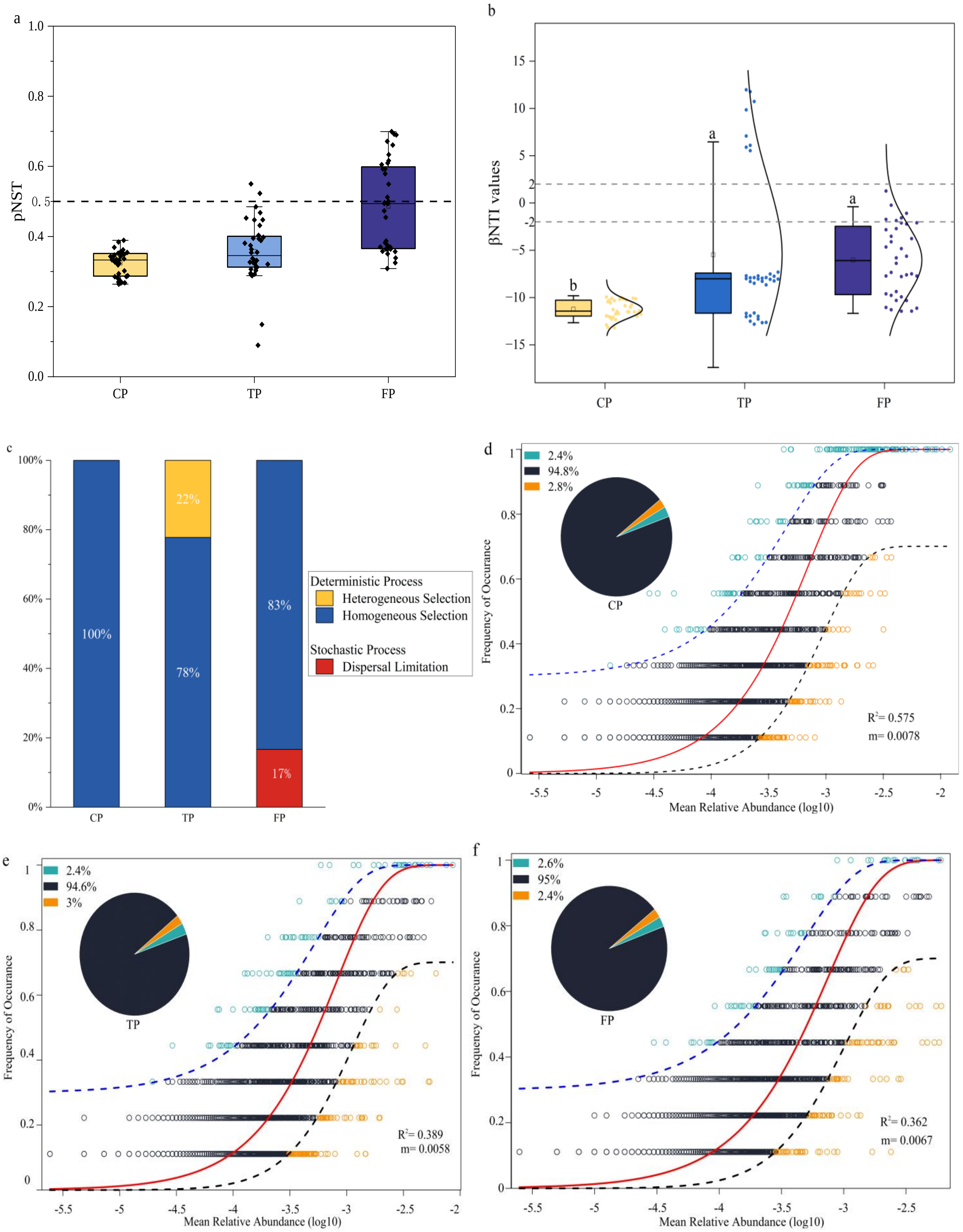

Fig. 6: The construction process of bacterial communities. (a) Normalized stochastic ratio (pNST) of bacterial communities, (b) Variation of βNTI across different plots, (c) The contributions of different ecological processes in assembling the bacterial community, (d-f) Fit of the neutral community model in the CP, TP and FP plots, cyan and orange circles represent ASVs that occurred more and less frequently than predicted, respectively, the solid red line indicates the best fit to the neutral community model, and the dashed line represents the 95% confidence intervals, m is the estimated migration rate, and R² is the fit to the neutral community model.

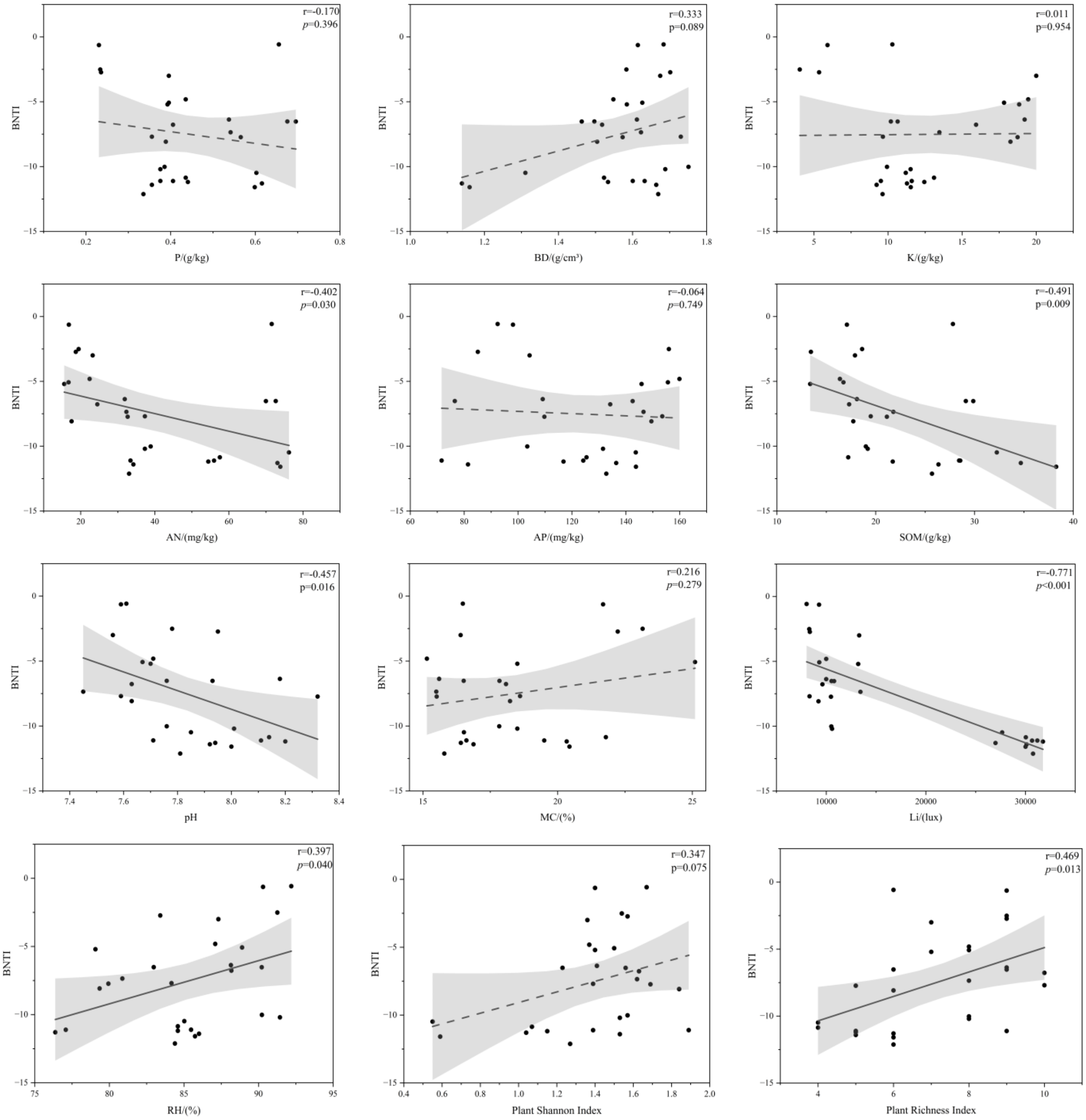

Fig. 7: The linear regression between environmental factors and βNTI. Solid lines indicate significant relationships ($p < 0.05$), while dashed lines indicate non-significant relationships ($p > 0.05$). The gray shaded areas represent the 95% confidence intervals, and the meanings represented by letters are the same as in Table 1.

bacterial community composition and functional shifts. PV installations profoundly affect soil diversity and community structure by regulating soil physicochemical properties and microclimatic conditions.[8,36] Random forest analysis confirmed that soil physicochemical properties and microclimatic factors such as soil moisture and relative humidity were key predictors of bacterial community structure and diversity.

This study further observed that different PVIM significantly influence the co-occurrence network structure of soil bacterial communities. TP installation enhanced interactions and interaction complexity among soil bacterial taxa, this may be because TP treatment created more centralized microenvironmental conditions with optimal variations in temperature and humidity.[37] In contrast, although FP installation increased network modularity and clustering coefficients, other topological properties were lower than those observed in the TP area, a phenomenon that may result from the weaker shading effect of the FP array, which allowed growth of certain bacteria without substantial constraint, reducing interactions within bacterial communities.[32] Additionally, positive correlations dominated both PVIM, suggesting that PV arrays may reduce interspecies competition and enhance cooperation, thereby maintaining the diversity and stability of bacterial communities.[38] The increased modularity observed in the TP and FP networks indicates enhanced niche differentiation within soil bacterial communities, which may improve their adaptability to environmental changes.[39] Previous studies reported that disturbances and changes in soil nutrients can affect network connectivity or complexity.[40] The impact of PV installations may share similarities with such disturbance mechanisms. However, the unique shading effect and microclimate-regulating properties of PV arrays appear to strengthen cooperative relationships among bacteria.[34]

We also found that assembly mechanisms for bacterial communities below PV installations were dominated by deterministic processes (pNST < 0.5), with the absolute value of βNTI being > 2, further supporting the importance of deterministic processes in community assembly. This might have been due to changes in soil environment, as the assembly of soil bacterial communities was significantly influenced by environmental filtering, especially in surface soils where deterministic processes dominate.[14] Different installation modes reduced the contribution of homogeneous selection. Bacterial community assembly mechanisms transition from homogeneous selection to random processes in different soil microenvironments, which may be related to increased environmental heterogeneity.[41] Neutral model analysis revealed that migration rates (m) of all treatments were low (control = 0.0078, TP = 0.0058, FP = 0.0067), further verifying the minimal contribution of random processes to community assembly. Jiao and Lu reported that for agricultural ecosystems, the impact of random processes on community assembly was generally small,[42] with environmental factors such as pH and temperature dominating the bacterial community assembly process. Furthermore, unary linear regression analysis revealed that environmental variables (*e.g.*, AN, SOM, pH, PR, RH, and Li) correlated significantly with βNTI, indicating that these environmental factors played key roles in driving bacterial community assembly. Tripathi *et al*.[43] reported pH to be a key factor influencing the assembly mechanisms of soil bacterial communities, especially in extremely acidic or alkaline conditions, where the impact of deterministic processes was more significant. Therefore, PVIM influences bacterial community assembly mechanisms mainly through deterministic processes by regulating soil physicochemical properties and environmental conditions. In environments with higher plant diversity and more soil nutrients, the impact of deterministic processes is more significant, promoting the stability and functional diversity of bacterial communities. However, the involvement of random processes under FP conditions suggests that in some cases, PVIM may increase community dynamics and adaptability, reflecting the important role of environmental heterogeneity and randomness in community assembly.[44]

5. Conclusion

This study observed that TP installation significantly reduced soil bacterial richness and diversity, while FP treatment increased ACE and Chao1 indices. Network analysis revealed that the TP installation enhances bacterial interactions and network complexity, and the FP installation maintains a certain level of network complexity while reducing interactions among some bacterial groups. Community assembly mechanism analysis proved that although deterministic processes dominated under both installation modes, the proportion of random processes increased under FP conditions, reflecting the importance of environmental heterogeneity and randomness in community construction. Structural equation modeling and random forest analysis further confirmed that soil physicochemical properties and the microclimate were key factors influencing bacterial community structure and diversity. We conclude that different PVIM significantly affect the structure and succession of soil bacterial communities by regulating soil physicochemical properties and microclimate conditions. The TP installation, with its stronger shading effect, caused greater disruption to soil bacterial diversity and community structure, while the FP installation had a more moderate and positive impact on soil bacterial communities. Although construction of PV systems in rocky desertification areas has been justified in terms of more rational land use, we report PV installation modes can affect the direction of bacterial community development.

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Conflict of Interest

There is no conflict of interest.

Supporting Information

Not applicable.

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