

研究报告

荒漠草原盐沼湿地苦豆子土壤细菌群落构建机制及其影响因素

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摘要: 【背景】荒漠草原盐沼湿地是陆地生态系统的重要组成部分, 土壤水分和盐分变化是影响该生态系统土壤细菌群落构建的重要因素。【目的】土壤细菌群落构建是由确定性和随机性主导的连续生态过程, 阐明荒漠草原盐沼湿地土壤细菌群落的构建机制对于加深微生物作为关键生态系统因子重要性的理解具有积极意义。【方法】以宁夏中部典型荒漠草原盐沼苦水湖湿地为研究对象, 对近湖边(near the lake, NL)和远离湖边(far from the lake, FL)苦豆子群落土壤理化特性进行测定并结合土壤细菌高通量测序分析。【结果】NL 和 FL 样地具有明显的水盐梯度变化, NL 样地土壤 pH、含水量和电导率均显著高于 FL 样地; 变形菌门、放线菌门、厚壁菌门、拟杆菌门和黏菌门是研究区域土壤细菌群落的优势菌门, 变形菌门相对丰度随水盐梯度上升而升高, 放线菌门和厚壁菌门相对丰度则随之下降, 门下成员大多与水盐变化具有明显的相关性; 此外, FL 样地土壤细菌网络则具有稳定的网络关系; 随着 NL 样地向 FL 样地的延伸, 土壤细菌群落由随机过程主导, 并且受 pH、电导率和环境变量的影响。【结论】荒漠草原盐沼湿地水分和盐分的变化改变了土壤细菌群落结构; 土壤细菌群落通过生态位占据等策略提高逆境下的生存能力; 细菌群落构建是随机过程和确定性过程组成的连续统一体, 同样受环境变化的影响。本结果揭示了荒漠草原盐沼湿地细菌群落结构和相互关系对环境变化的响应特征, 同时阐明了该区土壤细菌群落的构建机制及影响因素, 也为相关科学研究提供了一定理论参考。

关键词: 盐沼湿地; 苦豆子群落; 土壤细菌; 网络关系; 群落构建

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Factors influencing the bacterial community assembly in the soil of a salt marsh in the desert steppe dominated by *Sophora alopecuroides*

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Abstract: [Background] Salt marshes in desert steppe are an important part of terrestrial ecosystems, and soil moisture and salinity changes are important factors affecting the soil bacterial community assembly in this ecosystem. [Objective] The soil bacterial community assembly is a continuous ecological process dominated by deterministic and stochastic processes. Revealing the assembly mechanism of soil bacterial communities in salt marshes of desert steppe helps to deepen our understanding about the importance of microorganisms as key ecosystem factors. [Methods] The physicochemical properties were measured for the soil samples collected near the Kushuihu lake (NL) and far from the Kushuihu lake (FL), a typical salt marsh area of the desert steppe in central Ningxia. High-throughput sequencing was performed to analyze the bacterial information. [Results] NL and FL sampling sites presented significant water-salt gradients. The NL soil samples had higher pH, water content, and electrical conductivity than the FL soil samples. *Proteobacteria*, *Actinobacteriota*, *Firmicutes*, *Bacteroidota*, and *Myxococcota* were the dominant phyla in the soil samples. As the water-salt gradient increased, the relative abundance of *Proteobacteria* increased, while that of *Actinobacteriota* and *Firmicutes* decreased. Most of the members belong to the phyla had obvious correlations with water-salt changes. In addition, the soil bacterial network in the FL sites had stable network relationship. From the NL to FL sampling sites, the soil bacterial community gradually became being dominated by stochastic factors and was influenced by soil pH, electrical conductivity, and environmental variables. [Conclusion] The changes in soil moisture and salinity in salt marshes of desert steppe altered the soil bacterial community structure. Soil bacterial communities improved the survival under stress by strategies such as niche occupation. The assembly of bacterial communities is a continuum consisting of stochastic and deterministic processes, which are influenced by environmental changes. The results reveal the response characteristics of bacterial community structure and interrelationship to environmental changes in salt marshes of desert steppe and clarify the assembly mechanism and influencing factors of soil bacterial community, providing a theoretical reference for related studies.

Keywords: salt marsh; *Sophora alopecuroides*-dominated community; soil bacteria; network relationship; community assembly

荒漠草原盐沼湿地是陆地生态系统的重要组成部分,地下水入渗和季节性降水是其主要水源^[1-2]。由于荒漠草原盐沼湿地植物群落结构简单、生态环境脆弱,受全球气候变化(干旱、高温频发)的影响,湿地内水分大量散失,土壤盐渍化程度不断加剧^[3-4]。已有研究证明,土壤水分和盐分变化是影响荒漠草原湿地生态系统结构和功能的重要因素^[3-6]。现如今,相关研究已逐步深入至水分和盐分变化对土壤生态系统结构和功能的理解,其中,土壤细菌群落在生物地球化学循环中的重要作用已得到广泛关注^[7-9]。加之,土壤细菌群落间消极(如竞争)或积极(如合作)的复杂联系,它们之间相互作用的强弱在很大程度上决定了微生物群落的稳定性,并进一步影响生态系统的功能^[10-12]。现有学者通过构建细菌共现网络,阐明了森林^[13]、农田^[14]、河流^[15]、荒漠^[16]和湿地^[17]等一系列生态系统下细菌群落相互作用及环境适应机理。由此可见,荒漠草原盐沼湿地土壤细菌群落结构和相互作用的理解还值得深入探讨。

土壤细菌群落的寄主偏好性和环境异质性导致了微生物群落构成的差异^[18-20]。它们的组装模式同时受到随机过程(如扩散限制和均质扩散)和确定性过程(如变量选择和均质选择)的共同影响^[21-23]。学者通过大量实践,基于 OTU 数据构建中性群落模型(neutral community model, NCM),以解析随机过程在塑造微生物群落结构方面的重要作用,如 OTU 出现频率与其相对丰度之间关系越强,则表明随机过程在群落组装中占据主要地位^[24-25]。同时,学者还通过计算 β 最近分类单元指数(beta nearest taxon index, β NTI)加以描述微生物群落系统发育组成的时空变化及影响因素,如 $|\beta$ NTI|<2 时表明随机过程主导群落构建的生态过程,反之则为确定性过程^[26-27]。基于理论实践,微生物群落组装过

程在森林^[28]、草地^[29]、农业^[30]和河流^[31]等生态系统的相关研究中均已得到证实。近期一项研究发现,河口湿地水陆界面向陆地的转变使得土壤细菌群落构建的确定性过程逐渐转为随机过程^[32]。然而,随机过程和确定性过程如何影响荒漠草原盐沼湿地土壤细菌群落的构建机制尚不清楚。

如前所述,荒漠草原盐沼湿地的生态系统极其脆弱,但盐生植物为生态系统的稳定和重建提供了可能^[3,33]。其中,苦豆子(*Sophora alopecuroides*)作为荒漠草原的优势物种,广泛分布于西北干旱荒漠地区^[34-35]。本研究以宁夏中部典型荒漠草原盐沼苦水湖湿地为研究对象,通过土壤理化特性分析和 16S rRNA 基因高通量测序,拟解决以下科学问题:(1) 荒漠草原盐沼湿地水盐变化是否对土壤细菌群落网络关系产生影响;(2) 土壤细菌群落的生态进程对水盐变化如何响应。

1 材料与方法

1.1 研究区域概况及样品采集

研究样地位于宁夏回族自治区灵武市苦水湖湿地(106°78'E, 37°76'N)。该湿地地处宁夏中部,属中温带半干旱气候,年降水量约 200–250 mm。该地区植被类型相对单一,典型植被以苦豆子为主,伴生植物为骆驼蓬(*Peganum harmala*)。取样时间为 2020 年 7 月下旬。根据样地设置(图 1),分别划取 14 个 5 m×5 m 的样方,其中 7 个样方近湖边(near the lake, NL),7 个样方远离湖边(far from the lake, FL),样方间相互间隔 100 m 以上。NL 距湖边 20–30 m,FL 距湖边最小半径大于 200 m。参照 Pan 等^[3]的采样方法,每个样方内通过计数法对苦豆子的数量进行统计(NL=58±15, FL=46±13),同时,通过五点采样法采集土壤样品^[3]。取样时避开植物根系,土

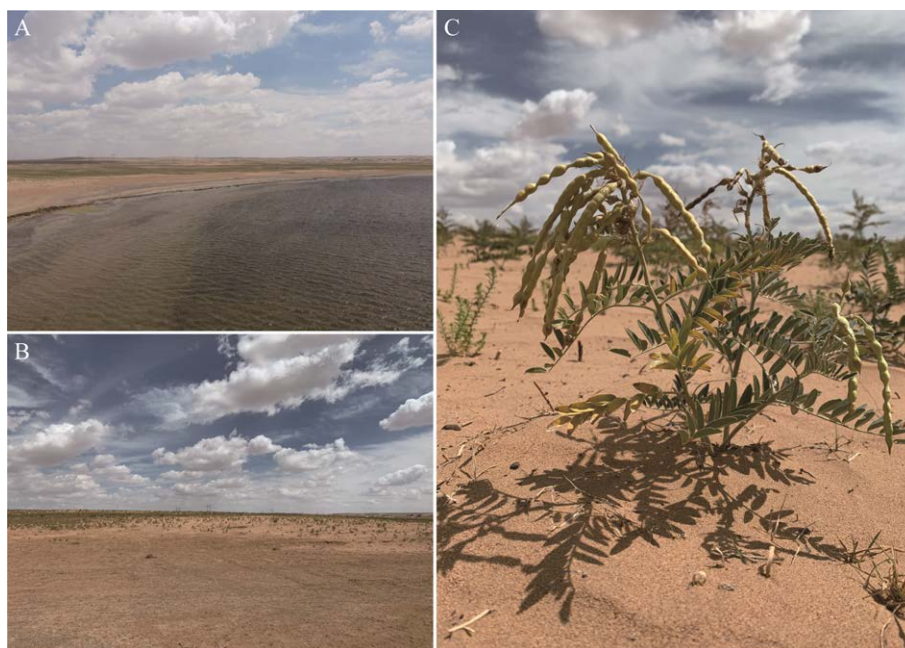


图1 研究样地图 A: 苦水湖湿地. B: 苦豆子群落. C: 苦豆子

Figure 1 Distribution of the plots within the study area. A: Kushuihu wetland. B: *Sophora alopecuroides* plant community. C: *Sophora alopecuroides*.

壤取样深度为 10–20 cm。将 5 个土壤样品混合，定义为一个样方的土壤样品，然后用 2 mm 筛分，分成两部分，一份送北京诺禾致源科技股份有限公司进行土壤细菌 Illumina MiSeq 高通量测序分析；另一份用于测定土壤理化特性。

10×Buffer、dNTPs (2.5 mmol/L)、Phusion DNA 聚合酶和 ddH₂O，默克化工技术(上海)有限公司；重铬酸钾，天津市华盛化学试剂有限公司。多功能酶标仪和高速冷冻离心机，赛默飞世尔科技(中国)有限公司；电子天平，梅特勒-托利多仪器(上海)有限公司；纯水仪，四川优普超纯科技有限公司；水浴锅，上海力辰仪器科技有限公司；pH 测定仪和电导率仪，上海仪电科学仪器股份有限公司。

1.2 土壤理化特性测定

根据土:水质量体积比为 1:5 分别测定 14 个土壤样品的 pH 和电导率(electrical conductivity, EC)；土壤含水量(soil water content, SWC)采用

称重法进行测定(烘箱 105 °C)^[3]。将土壤样品风干后采用原子吸收光谱法测定土壤总氮(total nitrogen, TN)和总磷(total phosphorus, TP)含量；土壤总有机碳(total organic carbon, TOC)通过重铬酸钾氧化-分光光度法进行测定^[36]。土壤理化数据采用 SPSS 25.0 软件进行单因素方差分析(analysis of variance, ANOVA)，邓肯多范围检验在显著性水平($P < 0.05$)上确定平均值之间的显著差异，所有数据均以均数±标准误差表示。

1.3 土壤细菌 DNA 提取和 PCR 扩增

采用十六烷基三甲基溴化铵(cetyltrimethylammonium bromide, CTAB)法对 14 份土壤样品 DNA 进行提取，使用引物 341F (5'-CCTAYGGGRBGCASCAG-3')和 806R (5'-G GACTACNNGGGTATCTAAT-3')对检测合格的样本扩增其细菌 16S rRNA 基因 V3–V4 区域，PCR 反应条件：98 °C 1 min；98 °C 10 s，50 °C 30 s，72 °C 30 s，30 次循环；72 °C 5 min。PCR

反应体系: 10×Buffer 2 μL , dNTPs (2.5 mmol/L) 2 μL , 正、反向引物(10 $\mu\text{mol/L}$)各 0.8 μL , Phusion DNA 聚合酶 0.2 μL , DNA 模板 1 μL , ddH₂O 补足 20 μL ^[37]。之后, 利用 Illumina NovaSeq PE250 平台进行测序, 共获得 1 003 748 高质量细菌 reads, 每个样本归一化后为 21 921 (细菌)。最终获得 609 780 有效细菌 reads (14 个样本), 并根据 97% 的序列相似度阈值分为 5 498 个细菌 OTU。其中, 能够注释到数据库的 OTU 数目为 5 492 (99.89%), 注释到门水平的比例为 75.43%, 纲水平的比例为 69.59%, 目水平的比例为 54.98%, 科水平的比例为 45.02%, 属水平的比例为 28.28%, 种水平的比例为 4.51%。本研究 14 份土壤样品的细菌原始数据存入 NCBI 序列读取档案数据库(PRJNA765898)。

1.4 土壤细菌测序数据分析

获得测序数据后, 使用 QIIME v1.9.1 软件计算 14 个土壤样品细菌 α 多样性指数, 包括 OTU、香农多样性指数(Shannon)和丰富度指数(abundance-based coverage estimator, ACE)^[38-39]。分别使用 R 语言“circlize”包和“ggalluvial”包对 NL 和 FL 样地细菌门和属的相对丰度进行可视化分析^[23,40]。以相对丰度占比前 200 的 OTU 为基础, 构建土壤细菌群落系统发育树, 并结合土壤理化特性进行相关性分析^[41]。之后, 使用“psych”软件包计算了所有样品中 OTU 之间的 Spearman 相关系数($|R|>0.9$), 检出率大于 85.7%, 同时, 利用错误发现率对 P ($P<0.01$) 值多重性检验进行校正, 并使用 Cytoscape 软件(3.7.1)进行可视化分析^[11]。之后, 基于 Bray-Curtis 距离矩阵的非度量多维尺度(non-metric multidimensional scaling, NMDS)进行细菌群落 β 多样性分析^[23]。此外, 使用 R 软件中的“Hmisc”包和“minpack.lm”包构建细菌群落模型^[24]。最后, 利用 R 软件中

的“NST”包计算细菌群落的 β NTI 值和 Raup-Crick 距离 RC 值(Bray-Curtis based Raup-Crick, RC_{bray}), 结合土壤理化特性进行 Spearman 相关性分析^[23,26]。

2 结果与分析

2.1 土壤理化特性差异分析

由图 2 可见, 2 个样地(FL 和 NL)具有较明显的水盐梯度变化, NL 样地的 pH (8.86)、SWC (10.68%)和 EC (1 032.71 $\mu\text{S/cm}$)值均显著高于 FL 样地(pH 7.87, SWC 6.15%, EC 608.57 $\mu\text{S/cm}$), 其中 SWC 较 FL 高出 73.6%, EC 显著高于 FL (69.7%) ($P<0.05$); 虽然 FL 样地 TOC 含量高于 NL 样地, 但并无显著差异; 此外, 2 个样地 TN 和 TP 含量变化也并不显著。

2.2 土壤细菌群落多样性和结构分析

NL 样地土壤细菌 ACE 指数高于 FL, 但无显著差异, OTU 和 Shannon 指数在两个样地间均无显著差异(图 3A)。在门水平上, FL 样地中超过 88.45%的 OTU 被划分为变形菌门(*Proteobacteria*) (32.69%)、放线菌门(*Actinobacteriota*) (34.92%)、未识别细菌菌门(*unidentified Bacteria*) (9.45%)、厚壁菌门(*Firmicutes*) (7.02%)和拟杆菌门(*Bacteroidota*) (4.37%); NL 样地中超过 89.75%的 OTU 被划分为变形菌门(52.49%)、放线菌门(24.39%)、未识别细菌菌门(7.61%)、厚壁菌门(3.86%)和黏菌门(*Myxococcota*) (1.40%) (图 3B)。在属水平上, FL 样地动性球菌属(*Planococcus*) (3.49%)、鞘氨醇单胞菌(*Sphingomonas*) (3.43%)、盐水微菌属(*Salinimicrobium*) (3.39%)、铜绿假单胞菌属(*Pseudomonas*) (2.79%)、土生红色杆形菌属(*Solirubrobacter*) (2.12%)具有较大占比, 而 NL 样地中铜绿假单胞菌属(6.77%)、泛菌属(*Pantoea*) (3.99%)、鞘氨醇单胞菌(3.95%)、节杆菌属(*Arthrobacter*) (3.30%)、贪噬菌属(*Variovorax*)

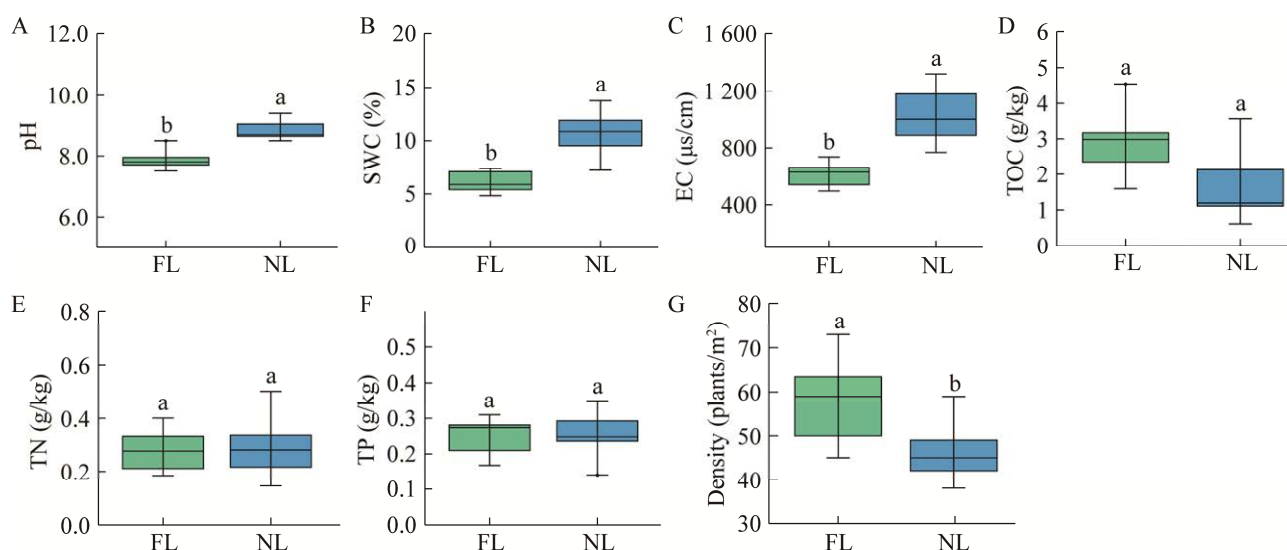


图2 土壤样品理化特性分析 A: 土壤 pH 值. B: 土壤含水量. C: 土壤电导率. D: 土壤有机碳含量. E: 土壤全氮含量. F: 土壤全磷含量. G: 植物密度. 不同小写字母表示差异显著

Figure 2 Analysis on the physicochemical characteristics of soil samples. A: Soil pH. B: Soil water content. C: Soil electrical conductivity. D: Soil total organic carbon. E: Soil total nitrogen. F: Soil total phosphorus. G: Plant density. Different lowercase letters indicate significant difference.

(2.76%)和新根瘤菌属(*Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium*) (2.54%)具有较大占比(图 3C)。此外, 剑菌属(*Ensifer*)、贪噬菌属、假黄色单胞菌属(*Pseudoxanthomonas*)、慢生根瘤菌属(*Bradyrhizobium*)和马赛菌属(*Massilia*)等菌属在 FL 和 NL 样地中差异显著($P<0.05$) (图 3D)。

2.3 土壤细菌群落和理化特性相关性分析

根据土壤细菌群落(前 200 个 OTU)的进化关系, 变形菌门成员最多, 其次是放线菌门和厚壁菌门。环境因子中, pH、SWC 和 EC 与变形菌门成员大多呈正相关, 而与拟杆菌门成员则有较为明显的负相关关系(图 4)。

2.4 土壤细菌共现网络分析

基于显著相关分析, 利用 14 个土壤细菌的数据构建了苦豆子土壤细菌共现网络(图 5)。由图 5 可见, NL 样地苦豆子土壤细菌网络表现出更高的网络连通性和复杂性, 其中 FL 样地苦豆子土壤细菌网络具有 582 个节点, 2 246 个边;

NL 则具有 455 个节点和 3 513 个边, 并且随着土壤含水率和盐分的升高, 细菌共现网络正相关性明显增强。在共现网络中, 变形菌门和放线菌门为主要菌门(表 1)。

2.5 土壤细菌群落组装模式及其影响因素分析

NMDS 分析表明, FL 和 NL 样地苦豆子土壤细菌群落相似性较高($R=0.084\ 5$) (图 6A)。NCM 分析显示, 从 NL 样地($R^2=0.731$)到 FL 样地($R^2=0.819$), 随机过程逐渐主导土壤细菌群落组成(图 6B、6C)。利用 β NTI 和零模型分析表明, 土壤细菌群落的生态过程由确定性过程(80.95%)转变为随机过程(66.67%) (图 6D、6E)。NL 样地中, 生态漂变占主导地位(66.67%) (图 6F), FL 样地中同质选择(76.19%)为主(图 6G)。为了进一步探讨土壤细菌 β NTI 与环境因子的关系, 研究发现土壤细菌 β NTI 与土壤 pH、EC 和环境因子具有显著相关性($P<0.05$) (图 7)。

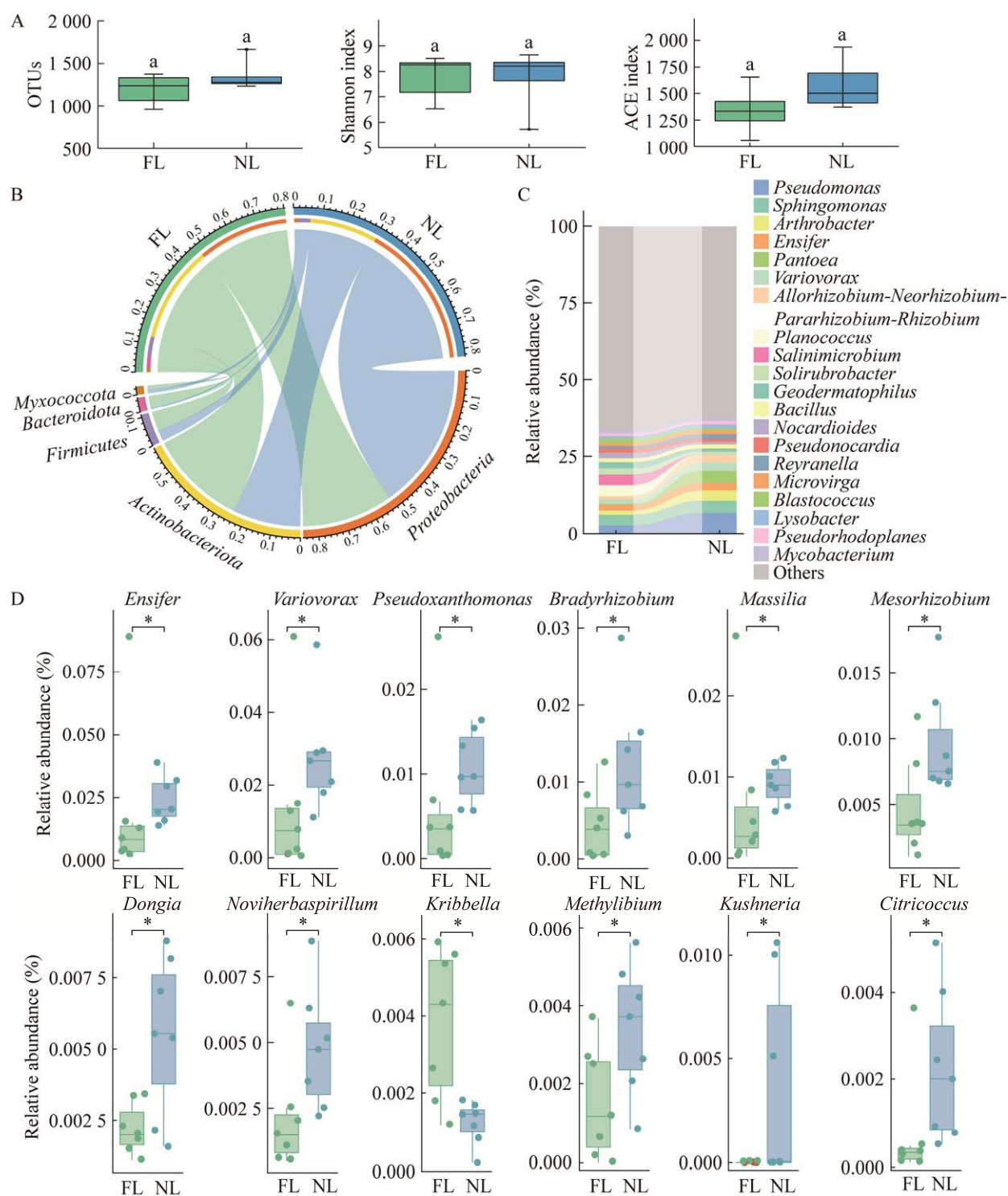


图3 土壤细菌群落多样性和结构分析 A: 土壤细菌 OTU 数量、Shannon 指数和 ACE 指数. B: 土壤细菌门水平上的群落组成. C: 土壤细菌属水平上的群落组成. D: 土壤细菌差异菌属

Figure 3 Analysis on the diversity and structure of soil bacterial community. A: OTU numbers, Shannon index, and ACE index of soil bacteria. B: Community composition at the phylum level of soil bacteria. C: Genus level of soil bacteria. D: Different genus of soil bacteria ($*P < 0.05$).

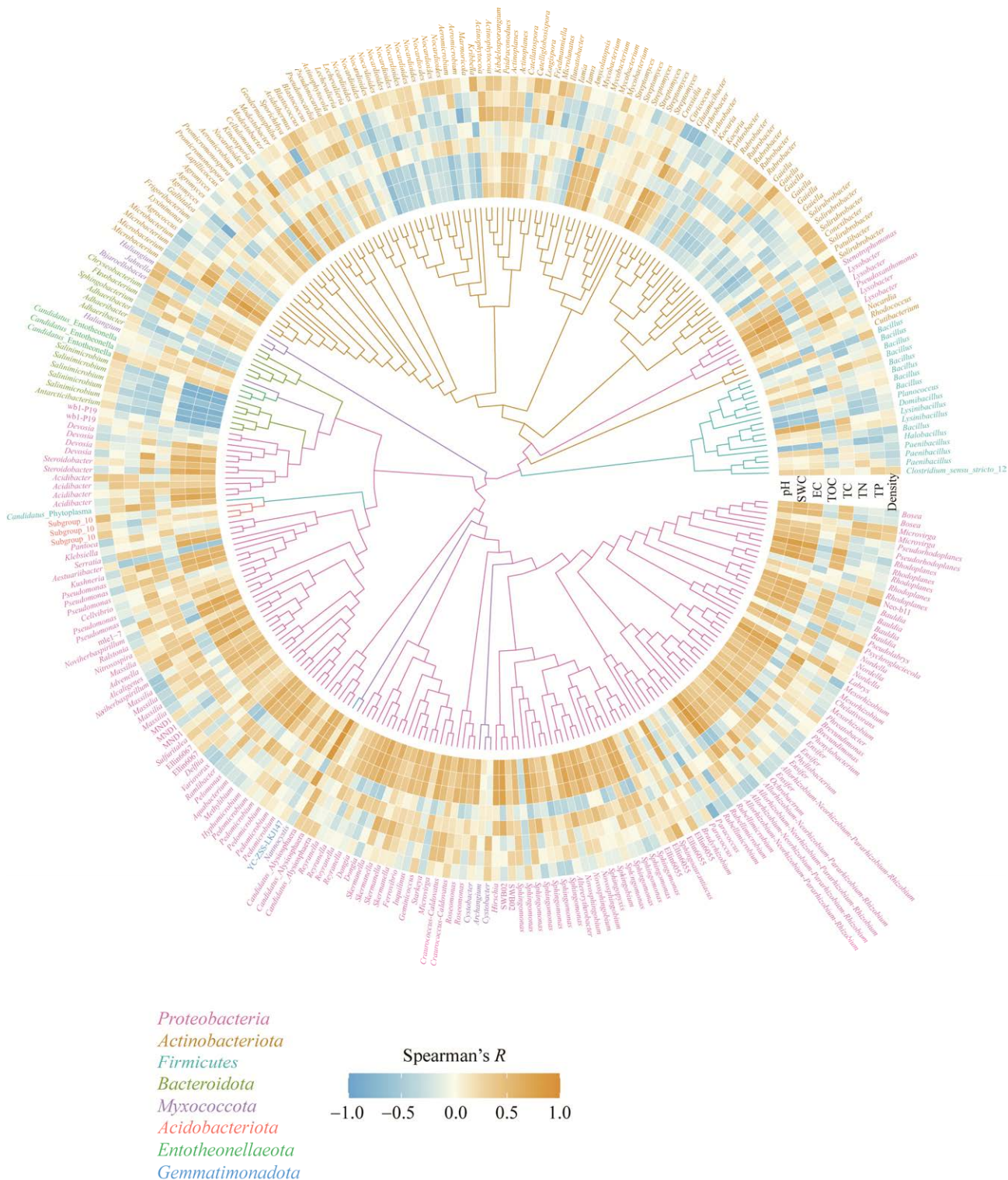


图 4 土壤细菌群落与影响因子相关性分析

Figure 4 Correlation analysis between soil bacterial community and influence factor.

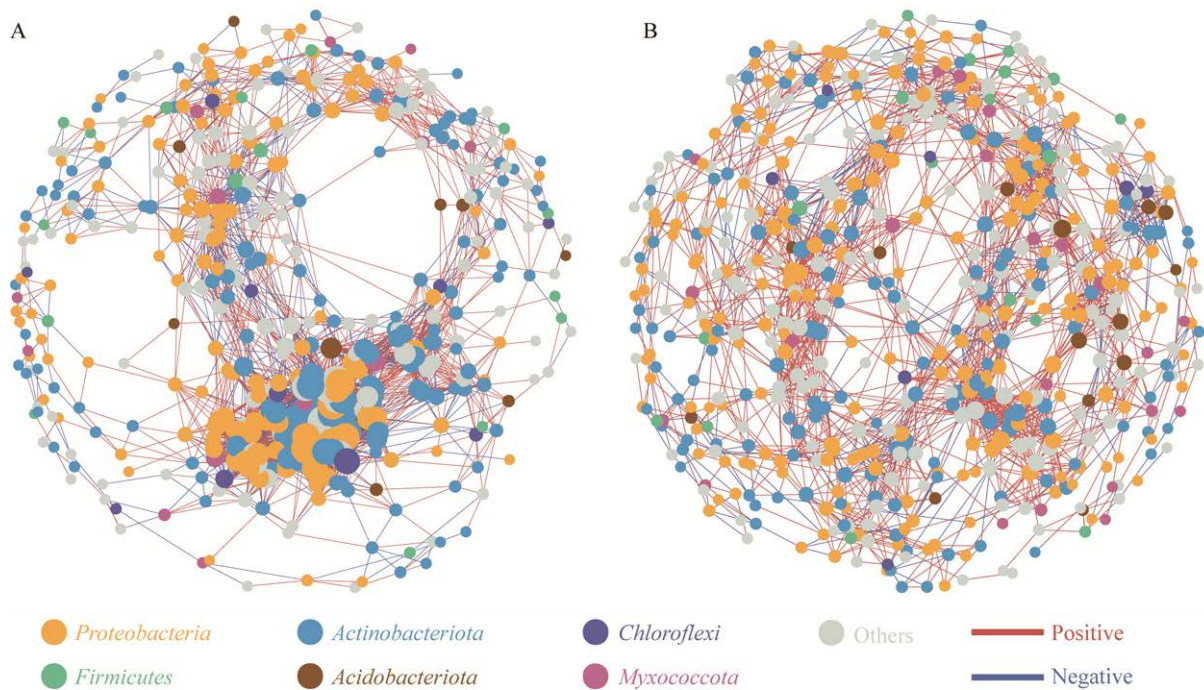


图 5 土壤细菌共现网络分析 A: FL 样地. B: NL 样地

Figure 5 Soil bacterial co-occurrence network analysis based on correlation analysis. A: FL plot. B: NL plot.

表 1 土壤细菌共现网络参数

Table 1 Parameters of soil bacterial co-occurrence network

网络参数 Network parameter	FL	NL
节点数 Nodes	582	455
总边数 Total edges	2 246	3 513
正相关边数 Positive edges	1 874 (84.44%)	2 246 (63.93%)
负相关边数 Negative edges	372 (16.56%)	1 267 (36.07%)
平均度 Average degree	7.72	15.44
模块数量 Number of modules	17	17
平均路径长度 Average path length	5.93	4.95
模块性 Modularity	0.71	0.56
聚类系数 Clustering coefficient	0.48	0.6
图密度 Density	0.013	0.03
网络直径 Diameter	14.93	15.68
介数中心性 Betweenness centralization	0.039	0.058
度中心性 Degree centralization	0.024	0.12

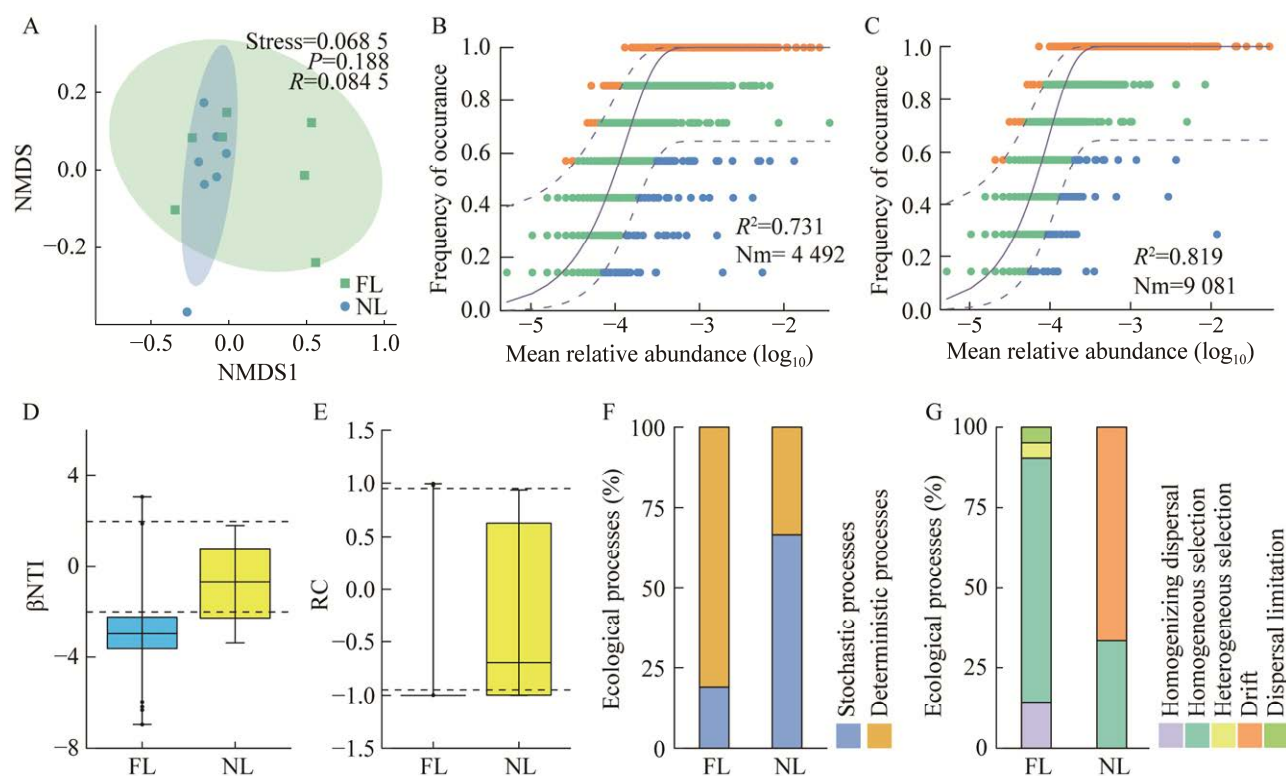


图6 土壤细菌群落 NMDS 分析及群落组成变化的生态过程 A: 土壤细菌群落 NMDS 分析. B: NL 样地土壤细菌群落中性模型分析. C: FL 样地土壤细菌群落中性模型分析. D: 土壤细菌 β NTI 指数. E: 土壤细菌 RC 指数. F: 土壤细菌群落的随机和确定性过程. G: 土壤细菌群落的生态过程. 实线表示最佳拟合趋势, 虚线表示预测模型 95% 置信区间. 橙色代表高于置信区间 OTU, 绿色代表在置信区间内的 OTU, 蓝色代表低于置信区间的 OTU

Figure 6 NMDS analysis and the ecological processes of soil bacterial community. A: NMDS analysis of soil bacterial community. B: NCM analysis of soil bacterial community in FL plot. C: NCM analysis of soil bacterial community in NL plot. D: Analysis of β NTI index. E: Analysis of RC index. F: The stochastic and deterministic processes of soil bacterial community in FL and NL plots. G: The ecological processes of soil bacterial community in FL and NL plots. The solid lines indicate the best fit to the NCM, and the dashed lines represent 95% confidence intervals around the model prediction. The colour of orange represents OTUs above the confidence interval, green represents OTUs within the confidence interval, and blue represents OTUs below the confidence interval.

3 讨论与结论

本研究聚焦于荒漠草原盐沼湿地, 随着 NL 向 FL 的转换, 土壤 pH、SWC 和 EC 显著降低, 这与 Pan 等的研究相一致, 即随着内陆盐沼水盐梯度的降低[SWC 为 19.67%–11.67%; 总盐 (total salinity, TS) 含量为 5.89–0.32 g/kg], pH 值

也随之降低(9.80–7.67)^[3]。与 Pan 等研究不一致的是, FL 和 NL 样地间 TOC 含量并无显著差异, 这可能是样地物种较为单一所致^[3]。研究样地中变形菌门、放线菌门、厚壁菌门、拟杆菌门和黏菌门是土壤细菌群落的优势菌门, 这与前人的研究结果相似^[35,42]。鉴于土壤水分和盐分的变化是影响土壤微生物群落结构的重要因素^[2-3], 研

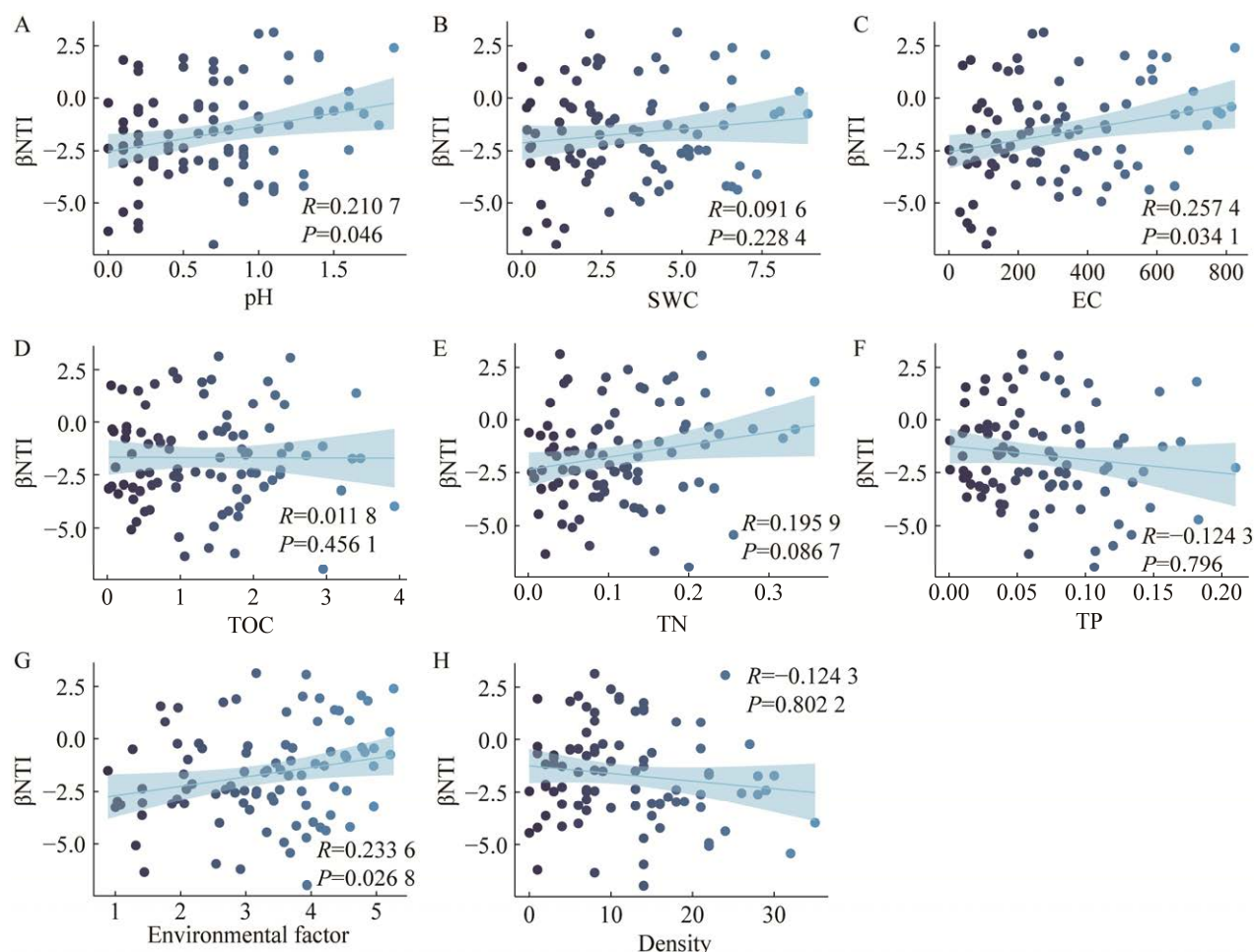


图 7 土壤细菌群落构建的影响因素 A: 土壤 pH 值和 β NTI 的相关性. B: 土壤含水量和 β NTI 的相关性. C: 土壤电导率和 β NTI 的相关性. D: 土壤总有机碳和 β NTI 的相关性. E: 土壤全氮和 β NTI 的相关性. F: 土壤全磷和 β NTI 的相关性. G: 环境因子和 β NTI 的相关性. H: 植物密度和 β NTI 的相关性

Figure 7 Distance-decay relationship for influence factor with soil bacterial community. A: Correlation between soil pH and β NTI. B: Correlation between soil SWC and β NTI. C: Correlation between soil EC and β NTI. D: Correlation between soil TOC and β NTI. E: Correlation between soil TN and β NTI. F: Correlation between soil TP and β NTI. G: Correlation between soil environmental factor and β NTI. H: Correlation between plant density and β NTI.

究发现,变形菌门的相对丰度占比随土壤盐分含量的上升而升高,这是由于变形菌门成员具有较强的异养代谢能力所致^[43-44]。此外,土壤盐分降低了放线菌门的相对丰度,近期一项研究指出,土壤中放线菌门的相对丰度和潜在代谢功能均受盐度增加的影响^[45]。本研究中,土

壤水分含量的降低增加了厚壁菌门的相对丰度,这是由于厚壁菌门成员是具有厚细胞壁的细菌,在水分含量较低的环境下具有更好的适生能力^[46]。值得注意的是,研究样地中土壤以沙土为主,植物生境营养匮乏,这也是厚壁菌门成员聚集的原因之一^[47]。

共现网络分析可以更好地揭示异质环境下微生物对生态位的竞争以及它们之间相互关系的强弱^[23,48]。在本研究中, NL 样地土壤细菌具有更复杂的网络关系(边的数量高于 FL 样地), 这种细菌相互关系的增强或许是微生物在较高 pH 和 EC 环境下竞争有限土壤养分所致^[49]。不同的是, FL 样地土壤细菌网络则具有更多节点和更高边正负比值, 这不仅意味细菌通过竞争和互补争夺有利于自身生长需要的生态位, 同时也表明土壤微生物对环境异质性的响应策略^[50-51]。例如, 草地恢复过程中, 土壤微生物通过生态位竞争避免放牧的侵扰, 以维持土壤生态系统的功能^[52]; 而在另一项研究中, 土壤细菌群落随着整个生长季节的变化, 通过生态位互补策略以此提高对土壤养分资源的获取能力^[53]。同样, 平均路径表示两个节点之间的最短路径, 从生态学角度来看, 节点和路径长度的复杂性则表明微生物类群发挥着更多功能和潜在作用^[54]。本研究中, FL 样地网络平均路径长度高于 NL 样地, 进一步表明水分和盐分对荒漠草原土壤细菌共生网络稳定性的影响^[55]。越来越多的研究表明, 微生物共现网络的属性代表了共存有机体之间的相互作用^[56-58], 这也印证了第一个科学问题, 即荒漠草原盐沼湿地水分和盐分的变化影响了土壤细菌间的相互关系。

环境异质性是影响微生物群落结构地理分布格局的主要因素^[23]。NMDS 分析表明, 两个样地中土壤细菌群落虽然结构相似, 但 NL 样地细菌群落聚集程度更为明显。以往研究指出, 植物类型差异、土壤 pH 值、水分和营养物质等变量, 对土壤微生物群落的构建具有过滤作用^[59-61]。NCM 分析进一步表明, NL 样地向 FL 样地的转变, 使得细菌群落的组装逐渐趋于随机过程。这与人取得了相似的研究结果, 即随着盐沼湿地向陆地的转换, 土壤细菌群落的

构建由随机过程主导^[32]。基于零模型分析发现, 确定性过程在 NL 样地中处于主导地位, 主要以同质选择为主; 随机过程在 FL 样地中处于主导地位, 主要以漂移为主。这不仅证实了荒漠草原盐沼湿地土壤细菌群落构建是确定性和随机过程均存在的一个连续体, 同时也表明土壤细菌群落在沿着稳定的生态系统演替时, 环境过滤减弱了群落组装的随机过程^[62]。更多研究指出, 土壤盐度^[63]、pH 值^[64]、土壤营养物质^[65]均是微生物群落结构的决定因素。在本研究中, 土壤 pH 和 EC 值与土壤细菌群落的聚集密切相关。以往的研究也已证明, 土壤环境对细菌群落随机和确定性生态过程的影响^[23,66]。本研究进一步证实了上述结论, 同时也表明土壤环境对细菌群落构建的影响。

综上所述, 本研究强调了土壤环境变化对荒漠草原盐沼湿地土壤细菌群落组成的影响。随着 NL 样地向 FL 样地的延伸, 土壤 pH、含水量和电导率均显著降低; 变形菌门的相对丰度随水盐梯度的下降而升高, 放线菌门和厚壁菌门的相对丰度则随之下降; 此外, NL 样地土壤细菌网络具有更复杂的网络关系以竞争土壤养分, 而 FL 样地网络则具有更稳定的网络结构以适应水分亏缺环境。NCM 分析进一步解析了土壤细菌群落的构建过程, 确定性过程在 NL 样地中处于主导地位(同质选择), 随机过程在 FL 样地中处于主导地位(漂移), 且土壤细菌群落的生态进程受 pH、EC 和环境变量的影响。本研究进一步表明, 超越多样性分析的分析工具被广泛应用于群落生态学, 这些方法的应用可以有力地促进微生物生态学的相关研究。同时, 揭示了荒漠草原盐沼湿地细菌群落结构和相互关系对环境变化的响应特征, 也阐明了该区土壤细菌群落的构建机制及影响因素, 为相关科学研究提供了一定的理论参考。

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