侵蚀-沉积作用对黄土高原林地土壤中固碳细菌群落分布特征的影响

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摘　要：针对黄土高原土壤固碳细菌对侵蚀-沉积的响应规律尚不清晰这一科学问题，在甘肃省罗峪沟流域的主要分支—桥子沟流域选择包括未开垦坡面的侵蚀点和沉积点、刺槐坡面的侵蚀点和沉积点等 4 个具有代表性的采样点，以土壤样品中有固碳功能基因 cbbL 的自养细菌为研究对象，采用高通量测序技术研究固碳细菌群落的多样性、分布特征和结构差异。结果显示：刺槐坡面固碳细菌多样性和丰富度明显低于未开垦坡面（$P<0.01$）。测序数据鉴定出 21 个拥有 cbbL 固碳功能基因的自养细菌属，这些属隶属于 3 个细菌门，包括芽单胞菌门、变形菌门和放线菌门。主坐标分析和聚类分析表明同一坡面下侵蚀点和沉积点的自养固碳细菌群落构成相似。相关分析表明土壤总钾、全氮和 pH 值与细菌群落组成的变化有很高的相关性。研究发现，土壤总氮通过影响有机碳和 pH 值的有效性在一定程度上影响土壤微生物群落，进而影响土壤生物量。cbbL 基因主要存在于粉粒和粘粒中，而在不同管理的农业土壤中，沙土中几乎没有 cbbL 基因。以上研究结果表明，植被覆盖和土壤处理都会影响土壤细菌群落，因为土壤性质控制着生物地球化学过程和生态系统功能。

Effects of Erosion-Sedimentation on Distribution Characteristics of Carbon Fixing Bacteria Community in Woodland Soil of Loess Plateau

Abstract: In view of the scientific problem that the response law of soil carbon-fixing bacteria to erosion-deposition in the Loess Plateau is unclear, four representative sampling points, including erosion points and deposition points on uncultivated slopes and erosion points and deposition points on Robinia pseudoacacia slopes, were selected in Qiaozigou watershed, Gansu Province. Autotrophic bacteria with carbon-fixing function gene cbbL in soil samples were taken as the research object, and the diversity, distribution characteristics and structural differences of carbon-fixing bacteria communities were studied by high-throughput sequencing technology. The results showed that the diversity and richness of carbon-fixing bacteria on Robinia pseudoacacia slope were significantly lower than those on uncultivated slope ($P< 0.01$). Twenty-one autotrophic bacteria genera with cbbL carbon fixation function genes were identified by sequencing data. These genera belong to three bacterial phyla, including Blastomycetes, Proteobacteria and Actinomycetes. Principal coordinate analysis and cluster analysis show that the composition of autotrophic carbon-fixing bacteria communities in erosion sites and deposition sites under the same slope is similar. Correlation analysis showed that soil total potassium, total nitrogen and pH value were highly correlated with the changes of bacterial community composition. It is found that soil total nitrogen affects soil microbial community to some extent by affecting the availability of organic carbon and pH value, and then affects soil biomass. CbbL gene mainly exists in silt and clay, but there is almost no cbbL gene in sandy soil under different management. The above results show that both vegetation cover and soil treatment will affect soil bacterial community, because soil properties control biogeochemical processes and ecosystem functions.