荒漠草原土壤细菌群落对放牧强度变化的响应

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摘 要:【目的】由于经济发展模式和历史沿革造成的的粗犷式放牧导致我国北方地区草原生态问题突 出,且尚未得到彻底解决。土壤微生物是地下生态系统最重要的结构和功能组份,其群落结构和多样性可 以反映区域生态系统稳定性和土壤质量情况。为了明确不同放牧强度对土壤理化性质与细菌群落的影响。 【方法】在内蒙古自治区荒漠草原开展放牧强度调控试验,设置了封育对照组、轻度放牧、中度放牧和重 度放牧 4 个放牧强度。采用野外调查和 16S rRNA 测序的研究方法比较分析不同放牧强度下土壤细菌群落 结构特征及其与土壤养分因子之间的相关关系。【结果】共获得 4746 个 OTU, 被鉴定为 36 门 95 纲 116 目 206 科 277 属, (1) 轻度放牧组的 Shannon、Simpson 和 Pielou 多样性指数显著高于封育对照组 (P<0.05), 中度和重度放牧组低于封育对照组但差异不显著(P>0.05), 四组的 Chaol 指数无显著差异(P>0.05); (2) 酸杆菌门(Acidobacteria)、放线菌门(Actinobacteria)、变形菌门(Proteobacteria)和绿弯菌门(Chloroflexi)为 研究样地的主要优势菌门;(3)除了土壤有机质和有效钾对土壤细菌的 Shannon 多样性指数具有显著负相 关相关系之外(P<0.05),其余土壤因子与细菌多样性无显著相关性。(4)土壤有机质、全磷、碱解氮、有 效磷和有效钾含量对目前不同放牧强度土壤细菌群落差异性起到主要的贡献。【结论】放牧会改变土壤理 化性质,影响荒漠草原土壤细菌群落组成和结构。轻度放牧能提高土壤细菌群落的多样性,增加土壤速效 养分的输入,而中重度放牧则会有所抑制。从土壤微生物表征作用来看,长时间的封育并非荒漠草原生态 系统恢复的最佳选择,合理安排放牧调控能有效的促进生态系统物质循环、维护生物多样性和提高生态系 统稳定性。

关键词:放牧;土壤细菌;荒漠草原;土壤性质

Responses of soil bacterial communities to grazing regulation in desert steppe

Abstract: [Objective] Due to the characteristic social economy and historical culture, the rough grazing has led to prominent grassland ecological problems in northern China, which have not been completely solved. Soil microorganisms are the most important structural and functional components of underground ecosystems, its community structure and diversity could reflect regional ecosystem stability and soil quality. In order to clarify the effects of different grazing intensity on soil physicochemical properties and bacterial communities. [Method] The grazing intensity regulation experiment was carried out in the desert steppe of Inner Mongolia Autonomous Region, four grazing intensities were set, namely the enclosure control group (CK), light grazing, moderate grazing and heavy grazing. Field investigation and 16S rRNA sequencing were used to compare and analyze soil bacterial community structure characteristics and their correlations with soil nutrient factors under different grazing intensities. [Result] A total of 4746 OTUs were obtained and identified in 36 phyla, 95 classes, 116 orders, 206 families and 277 genera, (1) The Shannon, Simpson and Pielou indices of the light grazing group were significantly higher than the CK (P<0.05), and the moderate and heavy grazing groups were lower than CK, but the difference was not significant (P>0.05), and there was no significant difference in the Chao1 index among them (P>0.05); (2) Acidobacteria, Actinobacteria, Proteobacteria and Chloroflexi were the main dominant bacterial phyla; (3) Except for soil organic matter and available potassium, which had a significant negative correlation with the Shannon index (P < 0.05), other soil factors had no significant correlation with soil bacterial diversity. (4) The contents of soil organic

matter, total phosphorus, alkali-hydrolyzed nitrogen, available phosphorus and available potassium played a major role in the differences of soil bacterial communities with different grazing intensities. 【Conclusion】 Grazing could change the soil physical and chemical properties and affect the soil bacterial community composition and structure in desert steppe. Light grazing could improve the soil bacterial diversity and increase the input of soil available nutrients, while medium and heavy grazing could inhibit it. From the perspective of soil microbial characterization, long-term closure would not be the best choice for ecosystem restoration in desert steppe, and rational grazing control could effectively promote ecosystem material circulation, maintain biodiversity and improve ecosystem stability.

Key words: graze; soil bacteria; desert steppe; soil properties