Soil microbial-mediated sulfur cycle and ecological network under typical desert halophyte shrubs

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Abstract

The sulfur cycle is one of the geochemical element cycles in which microorganisms play a key driving role. The microbial function of soil S cycling in response to desert degradation, however, remains largely unknown. We used metagenomics to analyze the characteristics of microbial communities and their functional genes involved in the S cycles under natural water gradients with three typical halophytes shrubs in the Ebinur Lake Basin Desert, China. Our results showed that the rhizosphere effect, water gradient, and halophyte type played a major role in shaping the S cycle. On the whole, in the rhizosphere type and low water environment, the functional genes involved in the S cycle had high abundance, and the SOX system in *Alhagi sparsifolia* had a high expression level. In the S cycle network structure, as the soil water content decreased, the complexity in S gene networks increased, showing the characteristics of clustering and high connectivity. Indicates the strengthening mode in microbial interactions with the water content. Interestingly, the negative correlation of the network changed with the water gradient. Through the correlation between environmental factors and the network, nitrate (NO $_3$ ⁻) and soil available S (AS) constrained most S gene ecology networks. The key species involved in the S cycle were halophilic microorganisms. These results can enhance the understanding of soil S biogeochemical processes and contribute to the mitigation of desertification by improving soil conservation.

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