Community assembly of rice paddy soil methanogens

Dong Li
Haowei Ni
Shuo Jiao
Yahai Lu
Jizhong Zhou
Bo Sun
Yuting Liang

Video Byte

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Abstract

Methane (CH_4) is regarded as an important greenhouse gas, with a global warming potential 25 times higher than CO_2 . Soil methanogens – organisms that generate CH_4 in the soil – participate in complex interactions, which determine the community structures and functions. Better understanding patterns in these interactions will help to address issues surrounding methane emissions. A recent study evaluated methane emissions and methanogenic archaeal communities. Beginning in rice paddies across Asia, a major source of CH_4 emissions, researchers measured archaea from 429 soil samples in 13 different regions in China. They found that network topological properties – which were correlated with mean annual temperature – were the chief predictor of CH_4 emissions. Methanogenic groups involved in commonly occurring links in the co-occurrence networks contributed the highest proportion of CH_4 . Potential keystone taxa, including *Methanobacterium*, *Methanocella*, *Methanotherix*, and *Methanosarcina* were highly linked to functional methane-generation genes such as *mcrA*, *fwdB*, *mtbA*, and *mtbC*. These results suggest that coexistence patterns of microbes are closely tied to their functional significance implying a critical role for complex interaction networks in determining soil function.