nature communications

Article

https://doi.org/10.1038/s41467-024-47159-x

Legume rhizodeposition promotes nitrogen fixation by soil microbiota under crop diversification

Received: 6 April 2023

Accepted: 22 March 2024

Published online: 04 April 2024

Check for updates

Mengjie Qiao[1,2,10], Ruibo Sun[3,10], Zixuan Wang[1,4], Kenneth Dumack[5], Xingguang Xie[6], Chuanchao Dai[7], Ertao Wang[6], Jizhong Zhou[8], Bo Sun[1,11], Xinhua Peng, Michael Bonkowski[5,9] & Yan Chen[1]

Biological nitrogen fixation by free-living bacteria and rhizobial symbiosis with legumes plays a key role in sustainable crop production. Here, we study how different crop combinations influence the interaction between peanut plants and their rhizosphere microbiota via metabolite deposition and functional responses of free-living and symbiotic nitrogen-fixing bacteria. Based on a long-term (8 year) diversified cropping field experiment, we find that peanut co-cultured with maize and oilseed rape lead to specific changes in peanut rhizosphere metabolite profiles and bacterial functions and nodulation. Flavonoids and coumarins accumulate due to the activation of phenylpropanoid biosynthesis pathways in peanuts. These changes enhance the growth and nitrogen fixation activity of free-living bacterial isolates, and root nodulation by symbiotic *Bradyrhizobium* isolates. Peanut plant root metabolites interact with *Bradyrhizobium* isolates contributing to initiate nodulation. Our findings demonstrate that tailored intercropping could be used to improve soil nitrogen availability through changes in the rhizosphere microbiome and its functions.

Chemical signaling between plants and soil microbiota plays a critical role in microbial symbioses and rhizosphere microbiome assembly[1,2]. The secondary metabolites exuded by plant roots are believed to attract and filter species-specific microbial taxa[3,4], including microbiota that complement their host's functional repertoire with traits not encoded in the plant genome[5], such as biological nitrogen fixation and phosphorus uptake[6,7]. In turn, compounds released by rhizosphere microbes trigger plant responses that further adjust microbiome specificity and composition[8,9]. This continuous chemical dialog is reflected in the metabolic deposition of the host plant rhizosphere, also known as rhizodeposition[10–12].

Although great mechanistic insights have been obtained on rhizosphere chemical signaling and rhizomicrobiome assembly of individual plant species[1,13,14], much less is known about how these processes are influenced by interspecific interactions between coexisting plant species. Various studies have found that interspecific neighbor-driven species recognition can induce a metabolic response in the neighbor and change the chemical composition of its

[1]State Key Laboratory of Soil and Sustainable Agriculture, Institute of Soil Science, Chinese Academy of Sciences, Nanjing 210008, China. [2]University of Chinese Academy of Sciences, Beijing 100049, China. [3]Anhui Province Key Lab of Farmland Ecological Conservation and Nutrient Utilization, College of Resources and Environment, Anhui Agricultural University, Hefei 230036, China. [4]College of Land Resource and Environment, Jiangxi Agricultural University, Nanchang 330045, China. [5]Terrestrial Ecology, Institute of Zoology, University of Cologne, Zülpicher Str 47b, Cologne 50674, Germany. [6]National Key Laboratory of Plant Molecular Genetics, Center for Excellence in Molecular Plant Sciences, Institute of Plant Physiology and Ecology, Chinese Academy of Sciences, Shanghai 200032, China. [7]College of Life Sciences, Nanjing Normal University, Nanjing 210023, China. [8]Institute for Environmental Genomics and Department of Microbiology and Plant Biology, University of Oklahoma, Norman 73019, USA. [9]Cluster of Excellence on Plant Sciences (CEPLAS), University of Cologne, Cologne 50674, Germany. [10]These authors contributed equally: Mengjie Qiao, Ruibo Sun. [11]Deceased: Bo Sun. e-mail: chenyan@issas.ac.cn