SEL Research
宿主基因型驱动的水稻根系微域细菌群落组装

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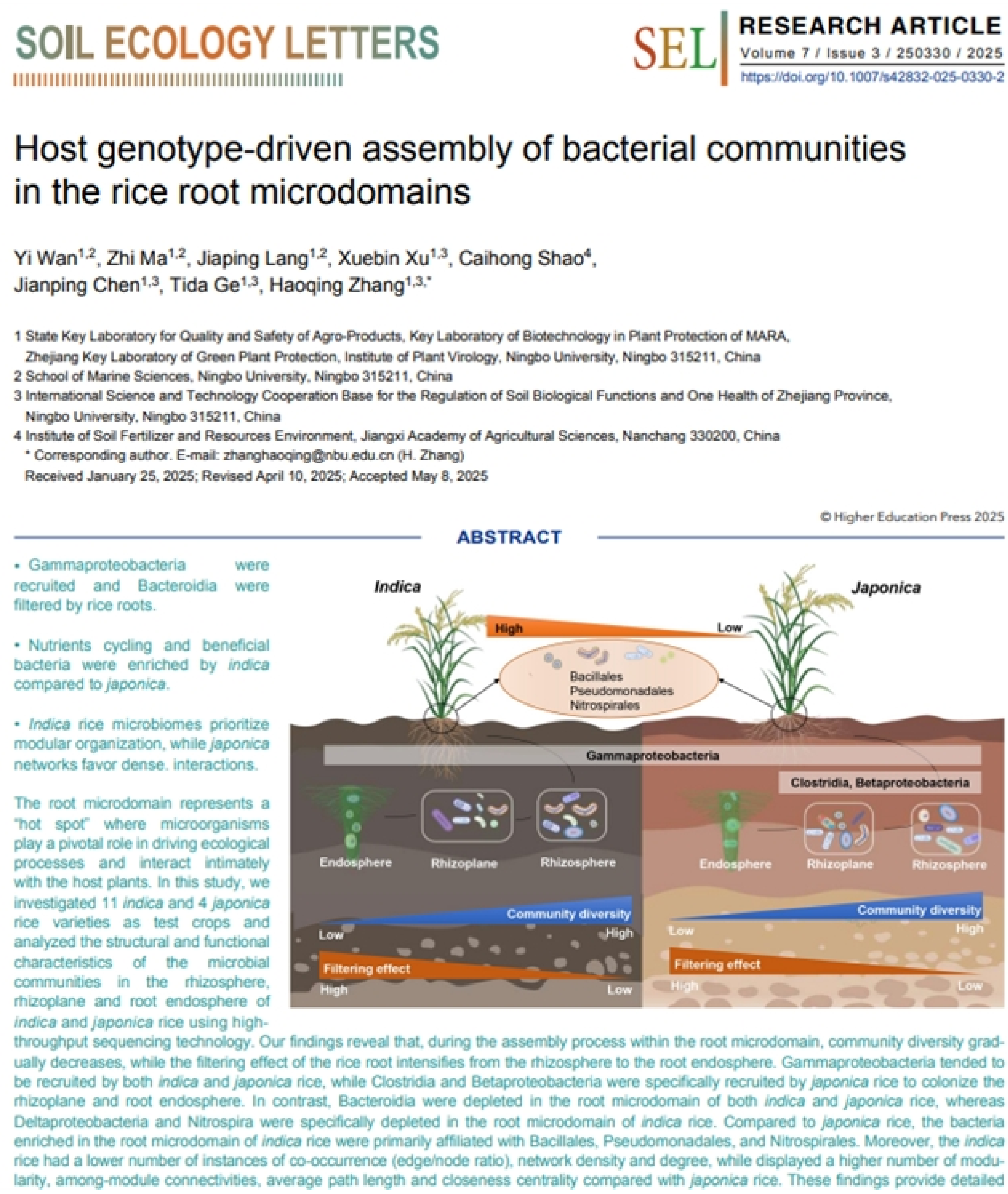

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Host genotype-driven assembly of bacterial communities in the rice root microdomains

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ABSTRACT

- Gammaproteobacteria were recruited and Bacteroidia were filtered by rice roots.
- Nutrients cycling and beneficial bacteria were enriched by *indica* compared to *japonica*.
- *Indica* rice microbiomes prioritize modular organization, while *japonica* networks favor dense. interactions.

The root microdomain represents a "hot spot" where microorganisms play a pivotal role in driving ecological processes and interact intimately with the host plants. In this study, we investigated 11 *indica* and 4 *japonica* rice varieties as test crops and analyzed the structural and functional characteristics of the microbial communities in the rhizosphere, rhizoplane and root endosphere of *indica* and *japonica* rice using high-throughput sequencing technology. Our findings reveal that, during the assembly process within the root microdomain, community diversity gradually decreases, while the filtering effect of the rice root intensifies from the rhizosphere to the root endosphere. Gammaproteobacteria tended to be recruited by both *indica* and *japonica* rice, while Clostridia and Betaproteobacteria were specifically recruited by *japonica* rice to colonize the rhizoplane and root endosphere. In contrast, Bacteroidia were depleted in the root microdomain of both *indica* and *japonica* rice, whereas Deltaproteobacteria and Nitrospira were specifically depleted in the root microdomain of *indica* rice. Compared to *japonica* rice, the bacteria enriched in the root microdomain of *indica* rice were primarily affiliated with Bacillales, Pseudomonadales, and Nitrospirales. Moreover, the *indica* rice had a lower number of instances of co-occurrence (edge/node ratio), network density and degree, while displayed a higher number of modularity, among-module connectivities, average path length and closeness centrality compared with *japonica* rice. These findings provide detailed

本研究选取11个籼稻品种和4个粳稻品种为供试材料，利用高通量测序技术系统解析了籼稻和粳稻的根际、根表以及根内微生物群落特征。结果表明， γ-变形菌纲更易被水稻根系招募，拟杆菌纲则更易被水稻根系过滤。与粳稻相比，籼稻在关键功能菌群富集方面具有优势，其根系微域显著富集更多与养分循环相关的功能菌和促生菌。微生物互作网络分析显示，籼稻根系微域微生物群落趋向于形成特定功能模块的模块化结构，而粳稻根系微域微生物间则构建了更加紧密的协同网络。本研究为阐明籼稻和粳稻根系微域微生物组差异及其生态功能提供了新的见解。

植物的根系微域（根际、根表）作为土壤-植物互作的关键界面，是微生物活动的热点区域。该区域通过根系分泌物介导的化学对话，形成独特的微生物组组装模式：一方面根系分泌物驱动微生物群落的定向选择，另一方面定殖微生物通过代谢反馈调控植物生长与抗逆响应。解析这种根系-微生物互作驱动的微生物组组装机制，对开发基于微生物组的农业增效策略具有重要科学意义。

本研究在中国湖南省浏阳市长期种植水稻试验田，以11个籼稻和4个粳稻品种为研究对象。于秧苗移栽45天后系统采集根际土壤（rhizosphere）、根表（rhizoplane）及根内（endosphere）样品，结合高通量测序与生物信息学分析，揭示籼稻与粳稻根系微域微生物组组装规律。主要发现如下：在根系微域的组装过程中，群落多样性逐渐降低，同时水稻根系的筛选作用从根际到根内逐渐增强。水稻植株能够选择性地招募潜在有益微生物来定殖其根系微域，这些微生物包括γ-变形菌纲、梭菌纲和β-变形菌纲的成员。相反，偏好分解难降解碳的分类群则会被水稻根系筛选掉，比如拟杆菌纲。

进一步对比籼稻与粳稻根系微域微生物组差异，发现与粳稻相比，籼稻根系微域中的微生物组在驱动养分循环、帮助宿主植物抵御病原体以及促进生长方面具有更高的潜力。此外，与粳稻相比，籼稻根际微域微生物互作网络密度和度较低，但模块性、模块间连接性、平均路径长度和接近中心性较高。这意味着籼稻的微生物组更侧重于模块化组织，而粳稻的微生物组网络则更倾向于密集的相互作用。这些结果为深入了解不同水稻品种根系微域中的微生物组组装过程，以及宿主对微生物群落组成的调控提供了详细的见解。

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专题征稿

城市土壤生态与同一健康

Call for papers: Urban Soil Ecology and One Health

Urban landscapes are complex incubators for emerging public health threats, including the persistence and spread of zoonotic pathogens that jeopardize the integrated health of humans, animals, plants, and environments—a nexus addressed by the One Health framework. Within these ecosystems, soil biodiversity is a keystone component that underpins critical ecosystem functions, yet it persists as one of the least understood elements of urban ecosystems.

Aligned with the World Soil Day 2025 theme, "Healthy soils for healthy cities," this special issue calls for research to address this knowledge gap. We seek submissions that illuminate the distribution patterns and functional contributions of urban soil biota, particularly under pressures from human activity and climate change. We are also interested in studies exploring how harnessing urban soil biodiversity can lead to nature-based solutions for mitigating biodiversity loss, adapting to climate change, and reducing the urban burden of disease. We particularly encourage studies proposing frameworks for embedding soil biodiversity into urban governance and policy to directly enhance One Health outcomes.

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