·热点评·

根际微生物促进水稻氮利用的机制

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摘要 根际微生物影响植物的生长及环境适应性。不同种属、不同种群的植物影响其环境微生物群落; 反之, 根际微生物也影响宿主植物生长发育与生态适应性。植物与根际微生物的互作现象及其机制, 是生命科学研究关注的热点, 也是农业微生物利用的关键问题。近期, 中国科学家在该领域取得了突破性进展。通过对不同籼稻(*Oryza sativa* subsp. *indica*)和粳稻(*O. sativa* subsp. *japonica*)品种的根际微生物组进行研究, 发现籼稻根际比粳稻根际富集更多参与氮代谢的微生物群落, 且该现象与硝酸盐转运蛋白基因*NRT1.1B*在籼粳之间的自然变异相关联。通过对粳稻接种籼稻根际特异富集的微生物群体可以提高前者对有机氮的利用, 促进其生长。该研究揭示了籼稻和粳稻根际微生物分化的分子基础, 展示了利用根际微生物提高水稻营养高效吸收的应用前景。

关键词 水稻, *NRT1.1B*, 根际微生物, 氮素利用

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在土壤中, 植物根系与微生物互作。根际微生物可以促进植物在自然界的生存, 其作用机制主要包括: (1) 促进植物从环境中获取营养, 例如, 菌根真菌溶磷和根瘤菌固氮(Oldroyd et al., 2011; Mbodj et al., 2018); (2) 通过激素合成或降解调控植物的生长和环境适应性(Duan et al., 2014); (3) 通过与致病菌的作用或诱导植物产生抗性而调控免疫反应(Bulgarelli et al., 2013; Santhanam et al., 2015)。此外, 根际微生物也可以与宿主植物竞争土壤中的营养物质, 或作为致病菌攻击植物(Berendsen et al., 2012)。研究表明, 植物根系选择性地招募特定的土壤微生物, 主要包括变形杆菌(*Proteobacteria*)、拟杆菌(*Bacteroidetes*)、放线菌(*Actinobacteria*)和厚壁菌(*Firmicutes*)等, 而微生物特异富集主要取决于植物的根际区系、土壤类型、营养状况和发育阶段等因素(Bulgarelli et al., 2012; Edwards et al., 2015; Walters et al., 2018)。然而, 同一物种的不同植物群体间根际微生物的组成变化及遗传调控机理却鲜有报道。

亚洲栽培稻(*Oryza sativa*)主要分为籼稻(*Indica*)和粳稻(*Japonica*)。籼稻通常比粳稻具有更高的氮利用效率, 其中一个主要因素与其从土壤中吸收氮的效率相关(Hu et al., 2015)。最近, 中国科学院遗传与发育生物学研究所白洋课题组与储成才课题组合作, 揭示了土壤微生物群落调控籼稻和粳稻的氮利用效率差异的重要机制。通过对68份籼稻材料和27份粳稻材料的根际微生物进行研究, 他们发现籼稻根系特异富集的微生物类群分布在δ-变形菌纲(*Deltaproteobacteria*)、放线菌门(*Actinobacteria*)、酸酐菌门(*Acidobacteria*)和拟杆菌门(*Bacteroidetes*)等, 而粳稻根系富集的微生物主要集中在α-变形菌纲(*Alphaproteobacteria*)。对籼稻根系特异富集的微生物功能进行预测分析, 发现参与氮代谢的通路被富集, 包括氨化信号通路(nitrate ammonification and nitrite ammonification pathway)和氮呼吸信号通路(nitrate respiration, nitrite respiration and nitrogen respiration pathway) (Zhang et al., 2019)。上述结果暗示根际微生物群落的变化可能与籼粳之间氮素利用效率相关。

储成才研究团队前期对水稻氮肥利用效率的研究显示, 硝酸盐转运蛋白NRT1.1B的单个氨基酸变异是决定籼稻氮利用效率高于粳稻的主要因素之一

(Hu et al., 2015)。近期, 通过比较野生型中花11与*nrt1.1b*突变体的根际微生物, 他们发现*NRT1.1B*的缺失改变了籼稻中49.6%的根际微生物群属, 表明NRT1.1B在籼稻招募特异的根际微生物中扮演着重要角色(Zhang et al., 2019)。

作者通过分离粳稻和籼稻特异富集的微生物, 进一步构建人工微生物群落(SynCom), 验证其在水稻生长及营养吸收中的作用。通过分别接种粳稻和籼稻特异富集的人工微生物群落, 在硝态氮或氨态氮充足条件下, 人工微生物群落会抑制水稻的生长; 但在以有机氮作为唯一氮源的条件下, 籼稻特异富集的人工微生物群落能促进水稻的生长, 表明水稻可以通过招募特异的根际微生物提高对有机氮源的利用效率(Zhang et al., 2019) (图1)。该研究结果为解析微生物群落调控植物氮营养, 特别是籼稻与粳稻氮利用效率的分子机制提供了重要线索。
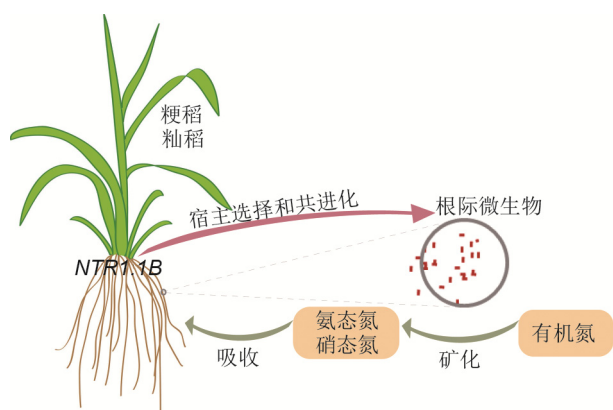
图1 水稻通过*NRT1.1B*基因协同根系微生物利用土壤氮元素
籼稻比粳稻富集更多参与氮代谢的根系微生物。这些微生物将有机氮转化为氨态氮, 提高水稻氮元素利用效率。籼稻和粳稻特异富集的根系微生物与*NRT1.1B*基因相关联。

Figure 1 Rice plants coordinate root microbiota to utilize soil nitrogen by *NRT1.1B*
Indica and *japonica* rice varieties recruit distinct root microbiota. The biological progresses related to nitrogen metabolism are specifically enriched in *indica*-enriched bacteria. These bacteria transform organic nitrogen to ammonium, facilitating the nitrogen utilization in rice. *NRT1.1B* is associated with the recruitments of *indica* and *japonica*-specific bacterial taxa.

在全球生态系统退化和气候变化的背景下, 强化微生物在农业生态系统中的功能可能是未来农业可持续发展的重要方向之一(Toju et al., 2018)。然而, 如何利用微生物群落提高作物生长和环境适应性仍然面临挑战(Bender et al., 2016; Toju et al., 2018)。植物可以选择根内和根际微生物群落(Bulgarelli et al., 2013), 这一特性为通过选择特定土壤微生物促进作物营养吸收提供借鉴(Toju et al., 2018)。前人的研究表明, 对植物进行遗传修饰、改造根际微生物群落, 可提高作物的营养吸收效率, 有利于降低农业化肥污染(Chaparro et al., 2012; Beckers et al., 2016)。该研究揭示了水稻不同群体的遗传特性与根际微生物差异之间的调控机制, 为通过根际微生物管理提高作物营养吸收提供了理论支撑。

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NRT1.1B Connects Root Microbiota and Nitrogen Use in Rice

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Abstract   Root-associated microbial communities in the soil play fundamental roles in plant nutrition uptake and fitness. However, how plants shape root microbial communities and how the microbes affect the fitness of their hosts remain elusive. Recently, Chinese scientists have made a breakthrough discovery that the nitrogen-use efficiency between *indica* and *japonica* rice varieties is associated with different root microbiota in rice. Nitrogen metabolism is greatly enriched in *indica*-enriched bacteria as compared with *japonica*-enriched bacteria. Rice NRT1.1B, a nitrogen sensor contributing to nitrogen use divergence between rice subspecies, is associated with the recruitment of these bacterial taxa. Inoculation of the *japonica* variety with *indica*-enriched bacteria can improve rice growth in organic nitrogen conditions in the SynCom experimental system. This work highlights the links between root microbiota and nitrogen use in rice and could be exploited to modulate the root microbiota that increase crop productivity and sustainability.

Key words   rice, *NRT1.1B*, root microbiota, nitrogen use

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