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杂交水稻专题

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前沿资讯

1．专家团队在稻田固碳领域取得重要进展

简介：稻田土中的有机质对于实现作物高产可持续性和缓解气候变化至关重要。该团队依托地处江苏省丹阳市延陵镇南京农业大学实验站的长期稻田定位试验和盆栽试验，首先明确了长期施肥后移（fertilizer postponing，FP）通过提高土壤有机质来提高水稻产量，该部分成果已发表在The Crop Journal上。基于之前的工作，该团队又采用宏基因组测序和13C-PLFA技术从植物残体碳和活根释放碳两个角度探究长期肥料后移提高土壤有机质的固存规律，为长江中下游稻麦轮作区作物高产高效可持续发展提供科学依据和技术支撑。论文Long-term fertilizer postponing promotes soil organic carbon sequestration in paddy soils by accelerating lignin degradation and increasing microbial necromass，该研究表明长期肥料后移主要通过增加根茬生物量提高土壤有机质含量，并影响根残体转化为有机质的过程。一方面，长期肥料后移提高了土壤酚氧化酶和过氧化物酶活性，但不影响β -葡萄糖苷酶活性，表明长期肥料后移加速了木质素降解，而非纤维素降解。宏基因组结果也表明，长期肥料后移通过激活相关微生物的生长显著增加了木质素降解基因的相对丰度。另一方面，肥料后移通过提高微生物生物量显著增加细菌和真菌残体碳含量。并且基于冗余分析、结构方程模型和随机森林回归的结果，该研究得出在较高根残体输入和土壤NH4+-N含量充足的条件下，主要通过加速木质素降解和增加微生物残体含量提高SOM，论文Long-term fertilizer postponing increases soil carbon sequestration by changing microbial composition in paddy soils: A 13CO2labelling and PLFA study，该研究通过对幼穗分化期（panicle initiation stage，PI）和抽穗期（heading stage，HS）的植株进行13CO2脉冲标记，探究在长期肥料后移下，水稻活根释放的碳对土壤有机质的影响。结果表明肥料后移不影响植物在幼穗分化期和抽穗期同化光合碳的能力，但显著降低了幼穗分化期同化光合碳的损失。13C损失量与微生物生物量[13C磷脂衍生脂肪酸（PLFA）含量]和微生物群落组成显著正相关。在幼穗分化期13CO2标记6小时后，肥料后移显著降低了总13C-PLFA含量，这主要是因为肥料后移减少了利用该时期同化13C的优势微生物[即G- （α 15:0和α 17:0）和G+（16:1ω7c）细菌]。而在抽穗期13CO2标记6小时至收获时，肥料后移显著增加了13C-PLFA含量，主要是因为肥料后移增加了利用该时期同化13C的优势微生物（即真菌18:1ω9c和20:1ω9c）。并且冗余分析表明，在幼穗分化期和抽穗期使用13C的微生物分别受到土壤可溶性有机氮和总氮的调节。因此，长期肥料后移通过减少幼穗分化期土壤中G- 和G+细菌的含量降低了同化光合碳的损失，并通过增加抽穗期土壤中真菌的含量提高了土壤中微生物碳源的输入。

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2．在不同种植体系镉污染生物炭修复效果评估方面取得研究进展

简介：近日，华南农业大学资源与环境学院国家环境保护土壤健康诊断与绿色修复重点实验室土壤化学与环境团队，在不同种植体系镉（Cd）污染生物炭修复效果评估方面取得新进展，相关成果发表在Journal of Hazardous Material上。Cd是我国农田土壤的

首要污染物，具有较高的毒性与迁移性，易在水稻、小麦、玉米等主粮的食用部分富集，对人类健康安全构成重大威胁。生物炭因其原位、绿色、可持续性等特征，在降低Cd污染方面极具潜力，被广泛应用于Cd污染土壤的修复治理。然而，生物炭理化性质多变，且应用场景复杂，现有研究对生物炭修复效果的差异性缺乏统一认识。鉴于此，华南农业大学土壤化学与环境团队通过meta分析，量化生物炭在淹水禾谷类、旱地禾谷类、非禾谷类种植体系中对Cd污染土壤修复效果，结合单因素荟萃回归（Single Meta-regressions）和随机森林机器学习（Random Forest），明确了生物炭修复的关键影响因素。研究结果表明，生物炭能显著降低各种植体系土壤、植物根系和可食用部分的Cd含量，下降幅度在24.9%-45.0%之间。生物炭的原料、施用量、pH以及土壤pH和阳离子交换量是影响生物炭Cd修复效果的关键因素。木质纤维素和草本生制备的物炭适用于所有种植体系，而粪便、木材和生物质为前驱物的生物炭在谷类种植体系中的效果有限。通过控制生物炭制备条件并匹配适用场景，可极大提升修复效果并降低环境经济成本，该结论可为实现污染土壤精准高效修复，农业绿色可持续发展提供理论依据和科技支撑。此外，本研究还发现生物炭对水稻土的修复效果比旱地更持久，这可为降低生物炭老化不利影响，近一步优化土壤重金属修复策略提供新思路。

来源：华南农业大学

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学术文献

1. A NAC Transcription Factor from 'Sea Rice 86 ' Enhances Salt Tolerance by Promoting Hydrogen Sulfide Production in Rice Seedlings（‘海水稻86’的NAC转录因子通过促进水稻幼苗中硫化氢的产生提高耐盐性）

简介：Soil salinity severely threatens plant growth and crop performance. Hydrogen sulfide (H2S), a plant signal molecule, has been implicated in the regulation of plant responses to salinity stress. However, it is unclear how the transcriptional network regulates H2S biosynthesis during salt stress response. In this study, we identify a rice NAC (NAM, ATAF and CUC) transcription factor, OsNAC35-like (OsNACL35), from a salt-tolerant cultivar 'Sea Rice 86 ' (SR86) and further show that it may have improved salt tolerance via enhanced H2S production. The expression of OsNACL35 was significantly upregulated by high salinity and hydrogen peroxide (H2O2). The OsNACL35 protein was localized predominantly in the nucleus and was found to have transactivation activity in yeast. The overexpression of OsNACL35 (OsNACL35-OE) in japonica cultivar Nipponbare ramatically increased resistance to salinity stress, whereas its dominant-negative constructs (SUPERMAN repression domain, SRDX) conferred hypersensitivity to salt stress in the transgenic lines at the vegetative stage. Moreover, the quantitative real-time PCR analysis showed that many stress-associated genes were differentially expressed in the OsNACL35-OE and OsNACL35-SRDX lines. Interestingly, the ectopic expression of OsNACL35 triggered a sharp increase in H2S content by upregulating the expression of a

H2S biosynthetic gene, OsDCD1, upon salinity stress. Furthermore, the dual luciferase and yeast one-hybrid assays indicated that OsNACL35 directly upregulated the expression of OsDCD1 by binding to the promoter sequence of OsDCD1. Taken together, our observations illustrate that OsNACL35 acts as a positive regulator that links H2S production to salt stress tolerance, which may hold promising utility in breeding salt-tolerant rice cultivar.

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2. Reconstruction of the High Stigma Exsertion Rate Trait in Rice by Pyramiding Multiple QTLs(多个QTL金字塔化重建水稻高柱头脱落率性状)

简介：Asian cultivated rice is a self-pollinating crop, which has already lost some traits of natural outcrossing in the process of domestication. However, male sterility lines (MSLs) need to have a strong outcrossing ability to produce hybrid seeds by outcrossing with restorer lines of male parents in hybrid rice seed production. Stigma exsertion rate (SER) is a trait related to outcrossing ability. Reconstruction of the high-SER trait is essential in the MSL breeding of rice. In previous studies, we detected eighteen quantitative trait loci (QTLs) for SER from Oryza sativa, Oryza glaberrima, and Oryza glumaepatula using single-segment substitution lines (SSSLs) in the genetic background of Huajingxian 74 (HJX74). In this study, eleven of the QTLs were used to develop pyramiding lines. A total of 29 pyramiding lines with 2-6 QTLs were developed from 10 SSSLs carrying QTLs for SER in the HJX74 genetic background. The results showed that the SER increased with increasing QTLs in the pyramiding lines. The SER in the lines with 5-6 QTLs was as high as wild rice with strong outcrossing ability. The epistasis of additive by additive interaction between QTLs in the pyramiding lines was less-than-additive or negative effect. One QTL, qSER3a-sat, showed minor-effect epistasis and increased higher SER than other QTLs in pyramiding lines. The detection of epistasis of QTLs on SER uncovered the genetic architecture of SER, which provides a basis for using these QTLs to improve SER levels in MSL breeding. The reconstruction of the high-SER trait will help to develop the MSLs with strong outcrossing ability in rice.

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3. Engineering of rice varieties with enhanced resistances to both blast and bacterial blight diseases via CRISPR/Cas9(通过CRISPR/Cas9工程化水稻品种，增强对稻瘟病和白叶枯病的抗性)

简介：Rice blast and bacterial blight represent two of major diseases having devastating impact on the yield of rice in most rice-growing countries. Developments of resistant

cultivars are the most economic and effective strategy to control these diseases. Here, we used CRISPR/Cas9-mediated gene editing to rapidly install mutations in three known broad-spectrum blast-resistant genes, Bsr-d1, Pi21 and ERF922, in an indica thermosensitive genic male sterile (TGMS) rice line Longke638S (LK638S). We obtained transgene-free homozygous single or triple mutants in T-1 generations. While all single and triple mutants showed increased resistance to rice blast compared with wild type, the erf922 mutants displayed the strongest blast resistance similar with triple mutants. Surprisingly, we found that Pi21 or ERF922 single mutants conferred enhanced resistance to most of tested bacterial blight. Both resistances in mutants were attribute to the up-regulation of SA- and JA-pathway associated genes. Moreover, phenotypic analysis of these single mutants in paddy fields revealed that there were no trade-offs between resistances and main agricultural traits. Together, our study provides a rapid and effective way to generate rice varieties with resistance to both rice blast and bacterial blight.
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