杂交水稻专题

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前沿资讯

1．研究揭示黑米抗氧化性的代谢机制

简介：近日，中国农业科学院作物科学研究所水稻优异种质资源发掘与创新利用创新团队解析了水稻黑米抗氧化性的代谢机制，在代谢层面揭示了有色糙米与无色糙米、黑米与其他颜色糙米之间代谢产物及代谢通路的差异。8月23日，该成果在线发表于《食品化学（Food Chemistry）》杂志上。据韩龙植研究员介绍，糙米是稻谷脱壳后仍保留种皮和胚的全谷粒米，比精米营养价值高。有色糙米尤其黑米与无色糙米相比，一般含有更多的蛋白质、微量元素、维生素等营养成分，且富含花色苷、酚酸、黄酮类化合物，具有较强的抗氧化特性。至今有关黑米等有色糙米抗氧化性的代谢机制研究鲜有报道。该研究利用本团队创制的黑米、红米、糯米和白米（均为糙米）为试验材料，通过广泛靶向代谢组学分析，系统地解析了有色米和无色米，黑米和非黑米代谢物及代谢通路的差异。共鉴定到732种代谢物，分为12类，包括生物碱（10.25%）、氨基酸及其衍生物（10.25%）、黄酮（16.67%）、脂类（17.62%）、有机酸（10.52%）、酚酸（13.93%）等；分别鉴定到黑米与糯/白米、红米与糯/白米、黑米与红米间的差异代谢物281种、305种、241种、267种和265种。其中，黑米与糯/白米间差异代谢物中次生代谢物占50%以上，红米与糯/白米间差异代谢物中次生代谢物占40%以上。这些次生代谢物包括黄酮、酚酸、生物碱等。黑米与红米间的主要差异代谢物也是黄酮（34.89%）和酚酸（18.30%）。进一步分析黑米特有的117种差异代谢物表明，其中包括黄酮58种（49.57%）和酚酸25种（21.37%），且其主要的显著富集途径为黄酮类化合物的生物合成、花青素的生物合成、黄酮和黄酮醇的生物合成。本研究揭示了不同类型糙米间代谢产物和代谢通路的差异，为功能性水稻育种提供科学依据。

来源：中国农业科学院作物科学研究所

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2．万建民院士团队揭示生长素调控水稻光合产物源库分配的新机制

简介：8月30日，南京农业大学万建民院士团队关于生长素调控水稻光合产物源库分配和生长发育机制的研究成果"Auxin regulates source-sink carbohydrate partitioning and reproductive organ development in rice"在PNAS上发表。光合作用产物在源（叶片）和库（果实和种子）器官间分配与运输将直接影响农作物的产量。作物利用蔗糖转运子（SUTs/SUCs）将光合产物（主要是蔗糖）从源（叶片）经过韧皮部的筛管组织长距离输送到库器官，然后在库中卸载；一方面库中的蔗糖产生膨压将为其他物质（包括营养物质、水和信号分子）长距离运输创造了驱动力，另一方面，运输到库中的蔗糖也是作物籽粒合成淀粉的主要原料。众所周知，植物激素生长素调控作物生长发育的各个方面，然而，目前关于生长素和蔗糖这两大信号分子如何协同调控作物生长发育的分子机制依然不清楚。在前期研究中，该团队筛选获得了一个水稻生长素氧化双加氧酶（Dioxygenase for Auxin Oxidation, DAO）失活的dao突变体（Dev Cell, 2013），该突变体在抽穗开花时期不能将有活性的生长素（IAA）氧化成无活性的OxIAA，破坏了体内IAA的动态平衡，出现颖壳不能正常张开、花药不能正常开裂、籽粒不能正常灌浆和单性结实的表型。本研究发现dao突变体由于生长素水平升高导致植株叶片中

蔗糖含量增加，但花器官（主要是浆片、花药和子房）中的蔗糖含量却显著降低。对野生型和突变体叶片进行[14C]-蔗糖喂养实验，结果显示在dao突变体叶片中显著积累放射性蔗糖，但在花药和子房中放射性蔗糖却显著减少。RNA-Seq分析显示，在dao突变体浆片中生长素转录因子OsARF18表达上调，而OsARF2表达下调。OsARF18的过表达系或OsARF2敲除系能够再现dao突变体的表型。EMSA实验证明OsARF2 通过直接结合OsSUT1启动子中的糖响应元件(SuRE) 调节OsSUT1的表达，而OsARF18 通过直接结合生长素反应元件AuxRE 或SuRE 抑制OsARF2和OsSUT1 的表达，从而调控蔗糖从源到库的运输。而在dao和Osarf2 突变体中过表达OsSUT1基因，能显著提高突变体颖花张开率和小穗结实率。这些研究结果揭示了IAA-OsARF18-OsARF2生长素信号级联反应调控蔗糖转运子OsSUT1表达，调节蔗糖从源（叶片）到库（浆片、花药和子房）的分配，进而影响水稻颖壳张开、花药开裂和籽粒灌浆结实的分子机制，将为如何协调源-库-流提高农作物产量提供理论依据。

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3．发现蛋白GPI修饰调控植物细胞壁力学性能的机制

简介：中国科学院遗传与发育生物学研究所周奕华研究团队长期从事植物细胞壁形成机理研究。近期利用水稻脆秆突变体brittle culm 16 (bc16)，鉴定到植物GPI修饰的脂质重塑关键酶，解析了GPI脂质修饰对蛋白质膜定位及细胞壁形成的重要作用。基因克隆发现BC16 编码GPI脂质重塑中的跨膜O-酰基转移酶，与众多GPI形成基因共表达。BC16定位于内质网及高尔基体，将其导入酵母同源基因突变体gup1能够恢复突变菌株生长受阻表型，并在很大程度上弥补酵母GPI锚定蛋白的脂质结构缺陷。针对水稻GPI锚定蛋白的脂质结构进行质谱分析，发现bc16突变体中饱和磷脂酰肌醇(PI)和磷脂酰神经酰胺(IPC)含量大幅减少，揭示了植物GPI蛋白的主要脂质结构。BC1是已报道的调控水稻次生细胞壁形成的关键GPI锚定蛋白。在bc16中对BC1及多个GPI锚定蛋白开展亚细胞定位分析，证实BC16介导的脂质重塑能够控制BC1质膜定位及靶向质膜特定微区，并发现纤维素合酶CESA4可定位于该微区，为BC16调控细胞壁组装提供了关键证据。原子力显微镜观测和纳米压痕分析发现,bc16中次生细胞壁纤维素纳米纤丝组装与排布与bc1相似,不正常的组装导致细胞壁弹性模量改变、植株机械强度下降，首次从生物力学层面解释了脆性表型。因此，该研究应用多学科研究手段揭示了植物GPI修饰脂质成熟机制，阐释了其调控植物细胞壁力学性能和植株机械强度的机理，为作物支撑力力学性能分子设计改良提供新的理论依据。

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➤ 学术文献

1. **Detection of Rice Spikelet Flowering for Hybrid Rice Seed**

Production Using Hyperspectral Technique and Machine Learning(基于高光谱技术和机器学习的杂交水稻制种小穗开花检测)

简介：Effective detection of rice spikelet flowering is crucial to the determination of optimal pollination timing for hybrid rice seed production. Currently, the detection of rice spikelet flowering status relies on manual observation of farmers, which has low efficiency and large errors. This study attempts to acquire rice spikelet flowering information using a hyperspectral technique and machine learning in order to meet the needs of hybrid rice seed pollination rapidly and automatically. Hyperspectral data of rice male parents with flowering and non-flowering in two experimental sites were collected with an ASD FieldSpec (R) HandHeld (TM) 2 spectrometer. Three traditional classifiers, Random Forest (RF), Support Vector Machine (SVM) and Back Propagation (BP) neural network, and Convolutional Neural Network (CNN), were used to build classification models for rice spikelets flowering detection. Three data processing methods, PCA feature extraction, GA feature selection, and the PCA and GA combination algorithm, were used for data dimensionality reduction. By comparing the precision and recall rate of different algorithms and data processing methods, the algorithms applicable to identify rice spikelet flowering were investigated. Results show that by evaluating different feature reduction methods and classifiers, the optimal model for rice spikelets flowering detection is the BP model with PCA feature extraction. The accuracy of the model reaches up to 96-100%. Hyperspectral technology and machine learning algorithm are capable of effective detection of rice spikelet flowering. This study provides technical reference for accurate judgment of rice flowering and helps to determine the optimal operation time for supplementary pollination of hybrid rice.

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2．Stacking of Pup1 QTL for low soil phosphorus tolerance and bacterial blight resistance genes in the background of APMS6B, the maintainer line of rice hybrid DRRH-3(水稻杂种DRRH-3保持系APMS6B背景下土壤耐低磷和抗白叶枯病基因的Pup1 QTL堆叠)

简介：Phosphorus (P) is one of the macronutrients essential for plant growth and development. Rice (Oryza sativa L.) is sensitive to P starvation and its deficiency influences many key plant functions, resulting in crop yield penalties. Although the hybrid rice segment is well-known for its yield heterosis, P deficiency and bacterial leaf blight diseases are evident limitations. APMS6B, the female parent of DRRH-3 is susceptible to low P and bacterial blight disease. In the present study, the improvement of APMS6B to P starvation and resistance to bacterial leaf blight (BB) was carried out using the marker-assisted backcross breeding approach. Kasalath (+Pup1 QTL) was used as a donor, and a promising IL (ATR 594-1) at BC1F4 generation was identified with 81.15% of recurrent parent genome recovery. Concurrently, this IL was intercrossed with GU-2 (+Xa21 and Xa38). Intercross

F(1)s (ICF1) hybridity was confirmed through foreground selection having maximum RPGR (88.29%) and was selfed to produce ICF2. The resultant progenies were phenotyped for BB using Xoo inoculum (IX-020), simultaneously genotyped with gene-specific functional SSR markers forXa21 and Xa38. The identified BB-resistant plants were subjected to foreground selection for Pup1. Four promising ICF3 plants (BP-10-1, BP-10-3, BP-10-5, and BP-10-15 with Xa21, Xa38, and Pup1) along with parents and checks were screened both in low P plot (< 2 kg P2O5 ha(-1)) as well as in normal plot (> 25 kg P2O5 ha(-1)) during dry and wet seasons 2018. The field evaluation identified four promising intercrossed lines with better root growth in the primary root length of extracted zone and root volume. In addition, fewer reductions in grain yield (39.10%) under P starvation and less susceptibility indices values ($<$ 1) for BB were observed. These lines may be exploited in the CMS conversion and development of climate-resilient, biotic and abiotic stress-tolerant rice hybrids.