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## 杂交水稻专题

### 本期导读

#### ▶ 前沿资讯

1. 湖北大学袁文雅课题组揭示水稻分蘖调控新机制
2. 科技创新进展：合作研究揭示水稻抽穗期调控的新机制
3. 专家团队揭示MYBc和E3连接酶协同调控水稻耐盐的机制

#### ▶ 学术文献

1. 长花稻高外交率基因组新区域的QTL定位及水稻不育系的建立
2. 利用水稻核雄性不育性：从分子解剖到育种应用

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## ▶ 前沿资讯

### 1. 湖北大学袁文雅课题组揭示水稻分蘖调控新机制

**简介:** 近日, 湖北大学生命科学学院袁文雅教授团队在The Plant Journal发表了题为OsSPL14 acts upstream of OsPIN1b and PILS6b to modulate axillary bud outgrowth by fine-tuning auxin transport in rice 研究论文, 揭示了水稻分蘖调控新机制。水稻株型决定了水稻的产量、抗倒伏性等重要的农艺性状。培育具备适度分蘖、抗倒伏、营养高效的水稻品种是育种专家们的目标。OsSPL14编码一个典型的含 SBP-box 的转录因子, 是近年来发现的具有理想株型形成潜力的重要控制基因。然而, 其调控水稻株型的分子机理仍有待深入解析。袁文雅教授团队通过分析OsSPL14基因干扰突变体和过表达植株的分蘖表型, 结合侧生分生组织的石蜡切片结果, 证实受 miR529 和 miR156 调控的 OsSPL14 基因可通过抑制水稻分蘖芽的伸长, 从而负调控水稻的分蘖数。体外激素施加实验证实 OsSPL14 受到生长素的诱导, 暗示其可能参与生长素信号相关的调控路径。后续通过酵母单杂交、荧光素酶激活, 凝胶阻滞及染色质免疫共沉淀实验, 共同证实 OsSPL14 可结合在生长素运输基因 OsPIN1b 和 PILS6b 的启动子区域的 GTAC 顺式作用元件上, 激活其表达。研究进一步发现, OsSPL14 基因可通过影响水稻地上部分的生长素极性运输, 从而影响水稻侧生分生组织中的生长素分布, 最终调节水稻分蘖芽的生长。

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### 2. 科技创新进展: 合作研究揭示水稻抽穗期调控的新机制

**简介:** 近日, The Plant Cell在线发表了水稻研究所胡培松院士团队陈颖研究员题为“The tetratricopeptide repeat protein OsTPR075 promotes heading by regulating florigen transport in rice” 的研究论文, 揭示OsTPR075-OsFTIP1/9-RFT1/Hd3a分子模块参与水稻抽穗期的新机制, 对于水稻分子遗传改良具有重要的指导意义。水稻的抽穗期(开花期)是水稻从营养生长转换到生殖生长的重要标志, 是决定水稻繁衍的重要农艺性状, 也是人工选择的主要目标性状之一。水稻抽穗期的调控是一个极其复杂的生命过程, 由基因等内在的遗传因素和光温等外界的环境因素共同决定。抽穗期的早与迟会影响水稻光合作用产物的积累, 进而影响水稻灌浆时期籽粒的充实进程, 最终影响水稻的产量和稻米品质。水稻抽穗期也决定了水稻品种在不同地域的适应能力和产量。因此, 开展水稻抽穗期分子调控机制的研究对分子育种和农业生产具有重要的理论意义和实践意义。在水稻抽穗的过程中, 成花素Hd3a和RFT1扮演着极其重要的角色。Hd3a和RFT1分别作为短日照和长日照的主要成花素, 主要由叶片合成转运到顶端分生组织促进水稻抽穗, 若Hd3a和RFT1缺失后水稻无法抽穗。前期分离鉴定了水稻成花素转运蛋白OsFTIP1, 发现OsFTIP1通过影响RFT1的转运影响长日照下水稻的抽穗期。突变体Osftip1在长日照条件下表现出明显的抽穗变晚的表型, 而在短日照下无无明显表型, 这表明短日照下可能是由其它蛋白负责Hd3a的转运。本研究通过Hd3a的蛋白互作筛选, 分离鉴定到Hd3a互作蛋白OsFTIP9, 通过基因编辑技术, 发现其突变体Osftip9在短日照条件下表现出明显的抽穗变晚的表型, 利用免疫足迹印记和免疫胶体金示踪技术揭示了

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O<sub>s</sub>FTIP9影响Hd3a从叶片到伴胞细胞的转运，进而影响水稻的抽穗期。更有意思的是，研究人员还分离鉴定到了一个功能未知的TPR家族蛋白O<sub>s</sub>TPR075，发现其可以同时与O<sub>s</sub>FTIP1和O<sub>s</sub>FTIP9相互作用，并且影响了O<sub>s</sub>FTIP1-RFT1、O<sub>s</sub>FTIP9-Hd3a之间的互作强度，进而调控成花素的转运。该研究揭示了O<sub>s</sub>TPR075-O<sub>s</sub>FTIP1/9-RFT1/Hd3a分子模块调控水稻在长日照和短日照条件下的成花转变的作用机制。

来源：中国水稻研究所

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### 3. 专家团队揭示MYBc和E3连接酶协同调控水稻耐盐的机制

简介：近日，南京农业大学生命科学学院章文华教授团队在Plant Physiology在线发表了题为“The transcription factor OsMYBc and an E3 ligase regulate expression of a K<sup>+</sup> transporter during salt stress”的研究论文，揭示了RING型E3连接酶OsMSRFP调控转录因子OsMYBc蛋白水平、调节OsHKT1;1转录，参与水稻盐胁迫响应的分子机制。土壤盐渍化是制约农业发展的主要非生物胁迫之一。维持细胞及整株水平的Na<sup>+</sup>/K<sup>+</sup>平衡是植物重要的耐盐机制。高亲和性钾离子转运蛋白HKT (high-affinity K<sup>+</sup> transporter) 具有Na<sup>+</sup>和K<sup>+</sup>转运特性，参与植物Na<sup>+</sup>和K<sup>+</sup>的长距离运输和分配，在植物耐盐性调控中发挥重要作用。HKT基因家族各成员的生理功能在多种植物中已有深入研究，但是关于其转录调控机制知之甚少。该研究团队的前期工作发现OsHKT1;1基因在降低水稻地上部Na<sup>+</sup>积累中发挥重要作用，并且其转录水平受OsMYBc转录因子调控(Wang et al., Plant Physiol. 2015)。在本研究中，他们进一步鉴定了OsHKT1;1基因启动子区域中OsMYBc结合位点；通过表达OsMYBc可以提高OsHKT1;1的表达量并提高植株耐盐性；OsMYBc与OsHKT1;1的组织表达模式基本一致。结果表明OsMYBc通过与OsHKT1;1启动子区的MYB核心元件结合上调其启动子活性，正向调控水稻耐盐性。研究进一步发现，RING型E3连接酶OsMSRFP是OsMYBc的互作蛋白。OsMSRFP泛素化OsMYBc，介导其降解；OsMSRFP与OsMYBc互作减弱了后者对OsHKT1;1的转录调控作用；敲除OsMSRFP基因提高水稻耐盐性，而过表达OsMSRFP基因降低水稻耐盐性。这些结果表明，OsMSRFP与OsMYBc协同调控OsHKT1;1的转录和水稻耐盐性综上所述，该研究揭示了一条精细调节OsHKT1;1基因转录的盐胁迫响应分子机制，并为提高水稻耐盐性的分子育种工作提供了理论依据和基因资源。

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## ➤ 学术文献

### 1. QTL Mapping of a Novel Genomic Region Associated with High Out-Crossing Rate Derived from *Oryza longistaminata* and Development of New CMS Lines in Rice, *O. sativa* L. (长花稻高外交率基因组新区域的QTL定位及水稻不育系的建立)

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**简介:** High seed cost due to poor seed yield severely limits the adoption of hybrid rice by farmers. Increasing the out-crossing rate is one of the key strategies to increase hybrid seed production. Out-crossing rate is highly influenced by the size of female floral traits, which capture pollen grains from male donor plants. In the current study, we identified 14 QTLs derived from the perennial wild rice *Oryza longistaminata* by composite interval mapping for five key floral traits: stigma length (five), style length (three), stigma breadth (two), stigma area (one), and pistil length (three). QTL analysis and correlation studies revealed that these stigma traits were positively correlated and pleiotropic to the stigma length trait. We selected the major-effect QTL qSTGL8.0 conferring long stigma phenotype for further fine mapping and marker-assisted selection. The qSTGL8.0 (~3.9 Mb) was fine mapped using newly developed internal markers and was narrowed down to ~2.9 Mb size (RM7356RM256 markers). Further, the flanking markers were validated in a segregating population and in progenies from different genetic backgrounds. The markers PA08-03 and PA08-18 showed the highest co-segregation with the stigma traits. The qSTGL8.0 was introgressed into two cytoplasmic male sterile (CMS) lines, IR58025A and IR68897A, by foreground, background, and trait selection approaches. The qSTGL8.0 introgression lines in CMS backgrounds showed a significantly higher seed setting rate (2.53-fold) than the original CMS lines in test crosses with their corresponding maintainer lines. The newly identified QTLs especially qSTGL8.0, will be quite useful for increasing out-crossing rate and this will contribute to increase seed production and decrease seed cost.

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## **2. Exploiting Genic Male Sterility in Rice: From Molecular Dissection to Breeding Applications (利用水稻核雄性不育性: 从分子解剖到育种应用)**

**简介:** Rice (*Oryza sativa* L.) occupies a very salient and indispensable status among cereal crops, as its vast production is used to feed nearly half of the world's population. Male sterile plants are the fundamental breeding materials needed for specific propagation in order to meet the elevated current food demands. The development of the rice varieties with desired traits has become the ultimate need of the time. Genic male sterility is a predominant system that is vastly deployed and exploited for crop improvement. Hence, the identification of new genetic elements and the cognizance of the underlying regulatory networks affecting male sterility in rice are crucial to harness heterosis and ensure global food security. Over the years, a variety of genomics studies have uncovered numerous mechanisms regulating male sterility in rice, which provided a deeper and wider understanding on the complex molecular basis of anther and pollen development. The recent advances in genomics and the emergence of multiple biotechnological methods have revolutionized the field of rice breeding. In this review, we have briefly documented the recent evolution, exploration, and exploitation of genic male sterility to the improvement of rice crop production. Furthermore, this review

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describes future perspectives with focus on state-of-the-art developments in the engineering of male sterility to overcome issues associated with male sterility-mediated rice breeding to address the current challenges. Finally, we provide our perspectives on diversified studies regarding the identification and characterization of genic male sterility genes, the development of new biotechnology-based male sterility systems, and their integrated applications for hybrid rice breeding.

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