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▶ 前沿资讯

1. Scientists engineer crops to conserve water, resist drought (改变植物基因表达可提高用水效率)

简介：一个“提高光合效率”的国际研究团队近日在《自然通讯》上发表的最新研究成果显示，通过改变一种植物共有基因的表达，首次在保证产量的同时将作物的用水效率提高了25%。该国际团队通过提高光合作用蛋白（PsbS）含量水平，诱导植物关闭部分气孔，从而达到节水的目的。导致气孔开闭的原因有四个：湿度、植株中的二氧化碳水平、光的质量和数量。该研究是首个关于如何根据光的数量来减少气孔反应的研究。PsbS是在植株中负责传递光数量信息的信号通路的关键部分。PsbS水平上升后，植株得到的信号是光能不足，无法进行光合作用，因此气孔就会关闭。该研究是首个关于如何根据光的数量来减少气孔反应的研究。研究表明，增加PsbS和另外两种蛋白质可以增强光合作用，并将植物生产力提高20%。通过平衡这三种蛋白的表达可以提高植物产量和用水效率。研究结果表明，PsbS表达增强使得作物在用水方面更节省，从而帮助植物在整个生长季内更好地分配可用的水资源，并在旱季保持较高的产量。

来源：AAAS

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全文链接：

https://www.eurekalert.org/pub_releases/2018-03/crwi-sec022718.php

▶ 学术文献

1. Inheritance and gene mapping of the white flower trait in *Brassica juncea* (芥菜白花性状的遗传和基因定位)

简介：Despite being a unique marker trait, white flower inheritance in *Brassica juncea* remains poorly understood at the gene level. In this study, we investigated a *B. juncea* landrace with white petal in China. The white petal phenotype possessed defective chromoplasts with less plastoglobuli than the yellow petal phenotype. Genetic analysis confirmed that two independent recessive genes (*Bjpc1* and *Bjpc2*) controlled the white flower trait. We then mapped the *BjPC1* gene in a BC4 population comprising 2295 individuals. We identified seven AFLP (amplified fragment length polymorphism) markers closely linked to the white flower gene. BLAST search revealed the sequence of AFLP fragments were highly homologous with the Scaffold000085 and Scaffold000031 sequences on the A02 chromosome in the *Brassica rapa* genome. Based on this sequence homology, we developed simple sequence repeat (SSR) primer pairs and identified 13 SSRs linked to the *BjPC1* gene, including two that were co-segregated (SSR9 and SSR10). The two closest markers (SSR4 and SSR11) were respectively 0.9 and 0.4 cM on either side of *BjPC1*. BLAST analysis revealed that these marker sequences corresponded highly to A02 in *B. juncea*. They were mapped within a 33 kb genomic region on *B. rapa* A02 (corresponds to a 40 kb genomic region on *B. juncea* A02) that included three genes. Sequence *BjuA008406*, homologous to *AtPES2* in *Arabidopsis thaliana* and *Bra032956* in *B. rapa*, was the most

likely candidate for BjPC1. These results should accelerate BjPC1 cloning and facilitate our understanding of the molecular mechanisms controlling *B. juncea* petal color.

来源: Molecular Breeding

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<http://agri.ckcest.cn/ass/6c232632-72ea-4e9f-a886-d7c0b6fee428.pdf>

2. Genome-Based Prediction of Time to Curd Induction in Cauliflower (基于基因组对花椰菜花球诱导时机的预测)

简介: The development of cauliflower (*Brassica oleracea* var. *botrytis*) is highly dependent on temperature due to vernalization requirements, which often causes delay and unevenness in maturity during months with warm temperatures. Integrating quantitative genetic analyses with phenology modeling was suggested to accelerate breeding strategies toward wide-adaptation cauliflower. The present study aims at establishing a genome-based model simulating the development of doubled haploid (DH) cauliflower lines to predict time to curd induction of DH lines not used for model parameterization and test hybrids derived from the bi-parental cross. Leaf appearance rate and the relation between temperature and thermal time to curd induction were examined in greenhouse trials on 180 DH lines at seven temperatures. Quantitative trait loci (QTL) analyses carried out on model parameters revealed ten QTL for leaf appearance rate (LAR), five for the slope and two for the intercept of linear temperature-response functions. Results of the QTL-based phenology model were compared to a genomic selection (GS) model. Model validation was carried out on data comprising four field trials with 72 independent DH lines, 160 hybrids derived from the parameterization set, and 34 hybrids derived from independent lines of the population. The QTL model resulted in a moderately accurate prediction of time to curd induction ($R^2 = 0.42-0.51$) while the GS model generated slightly better results ($R^2 = 0.52-0.61$). Predictions of time to curd induction of test hybrids from independent DH lines were less precise with $R^2 = 0.40$ for the QTL and $R^2 = 0.48$ for the GS model. Implementation of juvenile-to-adult phase transition is proposed for model improvement.

来源: Frontiers in Plant Science

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<http://agri.ckcest.cn/ass/8bd159a0-cd48-4880-85a9-7c0f9c88b3d0.pdf>

3. Development and Applications of a High Throughput Genotyping Tool for Polyploid Crops: Single Nucleotide Polymorphism (SNP) Array (多倍体作物高通量基因型分型工具的开发与应用: 单核苷酸多态性 (SNP) 微阵列芯片)

简介: Polyploid species play significant roles in agriculture and food production. Many crop species are polyploid, such as potato, wheat, strawberry, and sugarcane. Genotyping has been a daunting task for genetic studies of polyploid crops, which lags far behind the diploid crop species. Single nucleotide polymorphism (SNP) array is considered to be one of,

high-throughput, relatively cost-efficient and automated genotyping approaches. However, there are significant challenges for SNP identification in complex, polyploid genomes, which has seriously slowed SNP discovery and array development in polyploid species. Ploidy is a significant factor impacting SNP qualities and validation rates of SNP markers in SNP arrays, which has been proven to be a very important tool for genetic studies and molecular breeding. In this review, we (1) discussed the pros and cons of SNP array in general for high throughput genotyping, (2) presented the challenges of and solutions to SNP calling in polyploid species, (3) summarized the SNP selection criteria and considerations of SNP array design for polyploid species, (4) illustrated SNP array applications in several different polyploid crop species, then (5) discussed challenges, available software, and their accuracy comparisons for genotype calling based on SNP array data in polyploids, and finally (6) provided a series of SNP array design and genotype calling recommendations. This review presents a complete overview of SNP array development and applications in polyploid crops, which will benefit the research in molecular breeding and genetics of crops with complex genomes.

来源: Frontiers in Plant Science

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全文链接:

<http://agri.ckcest.cn/ass/17c28bc3-9897-46bb-8e0d-9c81616db481.pdf>

4. Association of microRNAs with Types of Leaf Curvature in *Brassica rapa* (microRNA与芸薹叶弯曲类型的关联)

简介: Many vegetable crops of *Brassica rapa* are characterized by their typical types of leaf curvature. Leaf curvature in the right direction and to the proper degree is important for the yield and quality of green vegetable products, when cultivated under stress conditions. Recent research has unveiled some of the roles of miRNAs in Brassica crops such as how they regulate the timing of leafy head initiation and shape of the leafy head. However, the molecular mechanism underlying the variability in leaf curvature in *B. rapa* remains unclear. We tested the hypothesis that the leaf curvature of *B. rapa* is affected by miRNA levels. On the basis of leaf phenotyping, 56 *B. rapa* accessions were classified into five leaf curvature types, some of which were comparable to miRNA mutants of *Arabidopsis thaliana* in phenotype. Higher levels of miR166 and miR319a expression were associated with downward curvature and wavy margins, respectively. Overexpression of the *Brp-MIR166g-1* gene caused rosette leaves to change from flat to downward curving and folding leaves to change from upward curving to flat, leading to the decrease in the number of incurved leaves and size of the leafy head. Our results reveal that miRNAs affect the types of leaf curvature in *B. rapa*. These findings provide insight into the relationship between miRNAs and variation in leaf curvature.

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<http://agri.ckcest.cn/ass/c7cca25f-fb3b-40c8-9672-f2204732a506.pdf>