



2018年第5期总119期

蔬菜育种专题

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▶ 前沿资讯

1. Speed breeding technique sows seeds of new green revolution (澳大利亚研发出快速繁育技术)

简介: 澳大利亚的一个研究团队最近研发了一种快速育种平台，通过强化植物的日间活动，仅用8周就实现了从播种到收获的小麦生产周期。这意味着一年可以种植多达6代的小麦——是目前使用的穿梭育种技术的三倍。这一研究成果日前发表在《自然植物》杂志上。这一突破就影响而言可与绿色革命的穿梭育种技术相提并论。

该技术使用完全可控的生长环境，在玻璃房里利用优化的LED灯强化植物的光合作用，使其光合作用时间长达每天22小时。快速育种作为一个平台可以与其他很多技术结合，比如CRISPR基因编码技术，能够更快获得最终结果。

该研究团队将这一快速育种技术应用于多种重要作物，成功实现了面包小麦、硬质小麦、大麦、豌豆和鹰嘴豆一年6代，芥花籽（一种油菜籽）一年4代的繁殖。研究人员还表示，可以利用这种技术对植物的各种特征，如植物-病菌互作、植物形状和结构，以及花期等进行详细的反复研究。澳大利亚的一家农业企业已经运用这一技术培育出了能够抵抗穗发芽的小麦品种。

来源: AAAS

发布日期: 2018-01-01

全文链接:

https://www.eurekalert.org/pub_releases/2018-01/jic-sbt122817.php

▶ 学术文献

1. Validation of an updated Associative Transcriptomics platform for the polyploid crop species Brassica napus by dissection of the genetic architecture of erucic acid and tocopherol isoform variation in seeds (通过解析种子中的芥酸和生育酚异构体的遗传结构变异来验证多倍体作物油菜的一个更新的联合转录组学平台)

简介: An updated platform was developed to underpin association genetics studies in the polyploid crop species Brassica napus (oilseed rape). Based on 1.92×10^{12} bases of leaf mRNAseq data, functional genotypes, comprising 355 536 single-nucleotide polymorphism markers and transcript abundance were scored across a genetic diversity panel of 383 accessions using a transcriptome reference comprising 116 098 ordered coding DNA sequence (CDS) gene models. The use of the platform for Associative Transcriptomics was first tested by analysing the genetic architecture of variation in seed erucic acid content, as high-erucic rapeseed oil is highly valued for a variety of applications in industry. Known loci were identified, along with a previously undetected minor-effect locus. The platform was then used to analyse variation for the relative proportions of tocopherol (vitamin E) forms in seeds, and the validity of the most significant markers was assessed using a take-one-out approach. Furthermore, the analysis implicated expression variation of the gene Bo2g050970.1, an orthologue of VTE4 (which encodes a γ -tocopherol methyl transferase

converting γ -tocopherol into α -tocopherol) associated with the observed trait variation. The establishment of the first full-scale Associative Transcriptomics platform for *B. napus* enables rapid progress to be made towards an understanding of the genetic architecture of trait variation in this important species, and provides an exemplar for other crops.

来源: The Plant Journal

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全文链接:

<http://agri.ckcest.cn/ass/04d95ad2-cca0-4dfc-809b-08617d10bc2b.pdf>

2. The Role of Non-Coding RNAs in Cytoplasmic Male Sterility in Flowering Plants (非编码RNA在开花植物细胞质雄性不育中的作用)

简介: The interactions between mitochondria and nucleus substantially influence plant development, stress response and morphological features. The prominent example of a mitochondrial-nuclear interaction is cytoplasmic male sterility (CMS), when plants produce aborted anthers or inviable pollen. The genes responsible for CMS are located in mitochondrial genome, but their expression is controlled by nuclear genes, called fertility restorers. Recent explosion of high-throughput sequencing methods enabled to study transcriptomic alterations in the level of non-coding RNAs under CMS biogenesis. We summarize current knowledge of the role of nucleus encoded regulatory non-coding RNAs (long non-coding RNA, microRNA as well as small interfering RNA) in CMS. We also focus on the emerging data of non-coding RNAs encoded by mitochondrial genome and their possible involvement in mitochondrial-nuclear interactions and CMS development.

来源: International Journal of Molecular Sciences

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<http://agri.ckcest.cn/ass/b416ba37-0923-41d1-b3ec-15284135f35e.pdf>

3. Analysis of intergeneric sexual hybridization between transgenic Brassica oleracea and Sinapis alba (转基因甘蓝和白芥的属间有性杂交分析)

简介: *Sinapis alba* possesses a number of desirable traits that can be employed to broaden genetic variability in *Brassica oleracea* or *B. napus*. Using transgenic *B. oleracea* (CC, $2n = 18$) as paternal plants and non-transgenic *S. alba* (SS, $2n = 24$) as maternal plants, 11 hybrid plants were successfully obtained by using a combination of ovary culture and embryo rescue, while 2 seedlings of the reciprocal cross were generated but lost during the propagation. The hybridity of these plants was confirmed by flower color and other agronomic characteristics, chromosome counting, and pollen viability. Most of the intergeneric F1 plants showed only one set each of S and C chromosome (SC, $2n = 21$) and were male sterile, while a few plants were semi-fertile and had one set of S chromosomes but two sets of C chromosomes (CCS, $2n = 30$). PCR, genomic Southern blotting and qRT-PCR for bar gene revealed that among the F1 hybrid plants only 9.1% was bar positive and could be forwarded to F2 and F3 generation. The majority of F3 plants obtained sufficient resistance to *Alternaria brassicae*.

Thus, the generation of disease (*A. brassicae*) and herbicide (Bastar) resistant intergeneric hybrids was of importance for breeding program. The existence of bar gene in these intermediate materials will facilitate the identification of hybridity and transfer of *S. alba* traits into target genetic background.

来源: Euphytica

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全文链接:

<http://agri.ckcest.cn/ass/ea1261b5-4e03-40d6-abb6-c07219311b4e.pdf>

4 . Surviving a Genome Collision: Genomic Signatures of Allopolyploidization in the Recent Crop Species *Brassica napus* (激活基因组互作：在欧洲油菜异源多倍体中进行基因组标记)

简介: Polyploidization has played a major role in crop plant evolution, leading to advantageous traits that have been selected by humans. Here, we describe restructuring patterns in the genome of *Brassica napus* L., a recent allopolyploid species. Widespread segmental deletions, duplications, and homeologous chromosome exchanges were identified in diverse genome sequences from 32 natural and 20 synthetic accessions, indicating that homeologous exchanges are a major driver of postpolyploidization genome diversification. Breakpoints of genomic rearrangements are rich in microsatellite sequences that are known to interact with the meiotic recombination machinery. In both synthetic and natural *B. napus*, a subgenome bias was observed toward exchanges replacing larger chromosome segments from the C-subgenome by their smaller, homeologous A-subgenome segments, driving postpolyploidization genome size reduction. Selection in natural *B. napus* favored segmental deletions involving genes associated with immunity, reproduction, and adaptation. Deletions affecting mismatch repair system genes, which are assumed to control homeologous recombination, were also found to be under selection. Structural exchanges between homeologous subgenomes appear to be a major source of novel genetic diversity in de novo allopolyploids. Documenting the consequences of genomic collision by genomic resequencing gives insights into the adaptive processes accompanying allopolyploidization.

来源: The Plant Genome

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全文链接:

<http://agri.ckcest.cn/ass/992a090e-7cc5-4897-b57f-e6292ed5a607.pdf>