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科技报告

1. 国际蔬菜育种：大规模发展的战略

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前沿资讯

1. Structural changes in the seed industry(种子产业的结构变化)

简介：背景

种子产业通过推出新品种来创造附加值。每个新品种的总投资约为1.36亿美元，根据育种方法的不同，需要8到10年的时间来开发。由于开发新品种的成本很高，种子公司往往投资于广泛种植的作物，以及大规模的农业体系，比如美国的玉米和巴西的大豆。然而，如此高度集中的产品组合可能存在风险。例如，禁止使用草甘膦影响了145个玉米品种、23个大豆品种、22个棉花品种和15个油菜品种的销售。因此，种子产业成功的关键是知道如何准确地提供满足农民/消费者需求的新品种。

种子公司的未来育种：定制化育种

想象农民像订购MacBook那样在线订购他们的种子：马铃薯的颜色、大豆的脂肪酸比例、病虫害抗性等。性状可根据其需要进行调整。此外，这也允许预测产量。在这种情况下，种子公司根据订单来制定生产计划。没有库存压力，研究资源没有浪费。消费者可以通过与农民沟通需求来选择他们的食物。

改变游戏规则的技术，基因编辑工具:CRISPR/Cas

我们如何从当前的系统转移到这样一个未来的场景?一切都始于基因编辑工具CRISPR/Cas。简单地说，这个工具允许我们在任何地方编辑基因组，使用两个主要组件:CRISPR和Cas。CAS是指进行DNA切割的蛋白质。CRISPR是指将Cas引导至用于切割的基因组的期望位置的DNA序列，其最初由细菌用于其免疫系统，并于1987年在大肠杆菌基因组中首次发现。自2012年以来，CRISPR/Cas系统已经表明其可以被编程用于靶向DNA切割，并且已经被应用于诸如人类疾病治疗、动物育种以及植物育种的领域。

该系统可用于在三个步骤中编辑基因：

1.在基因组（DNA序列）中寻找相应的位置进行编辑

2.切割DNA

3.用所需的DNA去除/替换不需要的DNA。

基因编辑就像纠正微软Word中的错误：寻找错别字（找到要编辑的基因），删除错别字（剪切DNA），替换为正确的单词（粘贴新DNA）。

Corteva正在使用CRISPR/Cas作为玉米品种的育种工具，这将育种周期从8年缩短到5年。

不同于常规的转基因方法，CRISPR/Cas需要基因组中特定位置的精确顺序来进行基因编辑。这需要关于基因组的更多信息，只有少数作物为此积累了足够的知识(例如，玉米、大豆和大米）。

在基因编辑方面的一些问题

在短期内，种子公司可以编辑具有已知基因功能的作物，但许多基因功能仍然缺乏，例如耐旱性。

为了加快作物基因功能的研究，植物科学家一直在使用最先进的技术。其中包括利用无人机收集图像，利用信息技术揭示新的监管网络，以及通过深度学习训练计算机进行高通量表型分析。大量的数据输入促进了产量预测模型的开发。结合最新的测序技术和良好的预测模型，通过作物基因组序列准确预测产量将是可行的。这将在育种上节省大量的时间和金钱，并降低风险。

传感器和无人机技术等允许在给定的时间和空间内收集更多的数据，这意味着可以用于了解作物性能的更多细节。然而，为了从成百上千的图像中提取信息，需要(生物)

信息学领域的研究人员。然而，这样的专家很难找到，因为在农业部门，工资往往没有吸引力，这意味着可能没有足够的人来处理大量的数据。

机遇：数据、建模、基因编辑

总之，实现定制育种的关键是数据（包括表型和基因组）、建模和基因编辑。首先，利用表型和基因组数据建立了基因与其功能之间的关系。其次，通过建模我们预测给定基因型的性能。最后，通过基因编辑，可以尽快创建所需的基因型。

结论

育种对种子公司来说是一项长期而昂贵的任务，但这将随着新技术的出现而改变。有三种技术（基因编辑、表型分析和深度学习）可以缩短育种周期并降低成本。基因编辑允许我们在不丢失高产背景的情况下精确地编辑作物的基因组，从而节省时间。使用无人机进行表型分析提高了数据收集的效率，而深度学习提高了数据处理的效率。随着信息和通信技术驱动的数字化在农业实践和生物技术中的融合，种子行业将转向预测和客户需求驱动的育种策略。

来源：AgroPages

发布日期:2019-07-05

全文链接:

http://agri.ckcest.cn/file1/M00/06/88/CsgkOFOj9wWAVsP9AAw8rS5mDFI097.pdf

学术文献

1. Effects of brassinolide on microspore embryogenesis and plantlet regeneration in pakchoi (Brassica rapa var. multiceps)(油菜素内酯对小白菜(Brassica rapa var. multiceps)小孢子胚胎发生和植株再生的影响)

简介：Hybrids are often superior to conventional varieties because of their high yield and strong stress resistance. The production of homozygous inbred lines is an important prerequisite for hybrid seed production; however, they may require more than six years by traditional breeding methods. Microspore culture is an attractive approach to obtain homozygous doubled haploids (DHs) in a short period. However, low embryogenesis frequency and high rates of embryo callus or mortality remain the main problems of this method in pakchoi. In this study, four different concentrations (0.01, 0.02, 0.04, 0.08 mg L^{-1}) of brassinolide (BR) were added into NLN liquid medium and used to examine the effect of microspore embryogenesis frequency and plant regeneration rate in three genotypes of pakchoi. The results showed that 0.01 mg L^{-1} BR was the optimum concentration for genotype ‘XM2’, significantly increasing the frequency of embryogenesis induction and plant regeneration by 2.05-fold and 1.25-fold, respectively, compared with those in the control treatment; there was also an observed 0.56-fold decrease in the rate of callus formation. For both ‘XM1’ and ‘XM3’, 0.02 mg L^{-1} BR was the most optimum concentration, resulting in a 3.41-fold and 6.39-fold increase in embryogenesis frequency compared with that in the control treatment; the frequency of plant regeneration was more than 74%. Meanwhile the rate of callus formation decreased 0.28-fold and 0.59-fold, respectively. The average spontaneous doubling rate of the three genotypes was 68.50%, whereas the lowest

spontaneous doubling rate of the genotype ‘XM2’ was 65.8%. For ‘XM1’, ‘XM2’ and ‘XM3’, we obtained 202, 144 and 85 DHs, respectively. Excellent horticultural traits were identified in DH lines from XM2, including increased leaf number and bright leaf color. All DH lines derived in this study were self-incompatible lines and showed high stability and consistency, which will effectively accelerate the application of microspore technology in hybrid breeding.

来源： Scientia Horticulturae

发布日期: 2019-04-10

全文链接:

http://agri.ckcest.cn/file1/M00/06/88/CsgkOFOj8MiAGjw4AIOlt_kfMTc544.pdf

2. A missense mutation of STERILE APETALA leads to female sterility in Chinese cabbage (Brassica campestris ssp. pekinensis)(STERILE APETALA基因的错义突变导致大白菜（Brassica campestris ssp.pekinensis）的雌性不育)

简介： Flower development is essential for the sexual reproduction and crop yield of plants. Thus, a better understanding of plant sterility from the perspective of morphological and molecular genetics is imperative. In our previous study, a recessive female-sterile Chinese cabbage mutant fsm was obtained from a doubled haploid line ‘FT’ via an isolated microspore culture combined with EMS mutagenesis. Pistil aniline blue staining and stigma scanning observation showed that the growth of the stigma papillar cells and pollen tubes of the mutant fsm were normal. Therefore, the female sterility was due to abnormal development of the ovules. To map the mutant fsm, 3108 F2 individuals were selected for linkage analysis. Two closely linked markers, Indel-I2 and Indel-I7, were localized on the flanking region of fsm at distances of 0.05 cM and 0.06 cM, respectively. The physical distance between Indel-I2 and Indel-I7 was ~1376 kb, with 107 genes remaining in the target region. This region was located on the chromosome A04 centromere, on which low recombination rates and a high frequency of repetitive sequences were present. Whole-genome re-sequencing detected a single-nucleotide (C-to-A) transition (TCG/TAG) on the exon of BraA04001030, resulting in a premature stop codon. Genotyping revealed that the female-sterile phenotype was fully cosegregated with this SNP. BraA04001030 encodes a homologue of STERILE APETALA (SAP) transcriptional regulator, which plays vital roles in floral development. The results of the present study suggest that BraA04001030 is a strong candidate gene for fsm and provide the basis for exploring the molecular mechanism underlying female sterility in Chinese cabbage.

来源： Plant Reproduction

发布日期: 2019-02-26

全文链接:

http://agri.ckcest.cn/file1/M00/00/00/CsgkOVOj7GCAGzZEABi8p7-micU687.pdf

3. Transgenic Wucai (Brassica campestris L.) produced via Agrobacterium-mediated anther transformation in planta(农杆菌介

导植物花药转化产生的转基因乌菜(Brassica campestris L.))

简介：Key message We developed a novel Agrobacterium-mediated anther transformation for Wucai in planta, and in this procedure, the male germ line was the predominant target.

Abstract Wucai (Brassica campestris L.), a variant of non-heading Chinese cabbage, is widely cultured in China and only improved by classic breeding methods. Here, a novel and efficient in planta Agrobacterium-mediated anther transformation method is developed based on the optimization of several factors that affect anther transformation. After optimization, transformation with the manual pollination application led to increased transient GUS expression in anthers (reaching 91.59%) and the transformation efficacies in planta (0.59-1.56% for four commercial cultivars). The stable integration and inheritance of the transgenes were further examined by molecular and genetic analyses. Three T2 transgenic lines presented a segregation ratio of 3:1, which was consistent with the Mendelian feature of a single dominant gene. In addition, the GUS histochemical assay and genetic crossing analysis revealed that the male germ line was the predominant target in this transformation. This optimized transformation system could provide a useful tool for both the improvement of cultivar qualities and investigation of functional genes in Wucai.

来源： Plant Cell Reports
发布日期:2019-02-13
全文链接:
http://agri.ckcest.cn/file1/M00/06/88/CsgkOF0j7bOABLeiADQSDmPMS7U455.pdf

4. Resolving the backbone of the Brassicaceae phylogeny for investigating trait diversity(解析十字花科系统发育的主干以研究性状多样性)

简介： The Brassicaceae family comprises c. 4000 species including economically important crops and the model plant Arabidopsis thaliana. Despite their importance, the relationships among major lineages in the family remain unresolved, hampering comparative research.

Here, we inferred a Brassicaceae phylogeny using newly generated targeted enrichment sequence data of 1827 exons (> 940 000 bases) representing 63 species, as well as sequenced genome data of 16 species, together representing 50 of the 52 currently recognized Brassicaceae tribes. A third of the samples were derived from herbarium material, facilitating broad taxonomic coverage of the family.

Six major clades formed successive sister groups to the rest of Brassicaceae. We also recovered strong support for novel relationships among tribes, and resolved the position of 16 taxa previously not assigned to a tribe. The broad utility of these phylogenetic results is illustrated through a comparative investigation of genome‐wide expression signatures that distinguish simple from complex leaves in Brassicaceae.

Our study provides an easily extendable dataset for further advances in Brassicaceae systematics and a timely higher‐level phylogenetic framework for a wide range of comparative studies of multiple traits in an intensively investigated group of plants.

来源： New Phytologist
发布日期:2019-02-08

全文链接:
http://agri.ckcest.cn/file1/M00/00/00/CsgkOVOj7xaAA7mgABToliuH16U611.pdf

5．Abnormal tapetum development and energy metabolism associated with sterility in SaNa-1A CMS of Brassica napus L.(甘蓝型油菜SANA-1A不育系绒毡层发育及能量代谢异常与不育性的关系)

简介：**Key message** Abnormal tapetum degradation and anther development in cytoplasmic male sterility SaNa-1A are the main reasons for the anther abortion.

Abstract SaNa-1A is a novel cytoplasmic male sterility (CMS) line of Brassica napus derived from somatic hybrids of B. napus-Sinapis alba, and SaNa-1B is the corresponding maintainer line. Ultrastructural comparison between developing anthers of sterile and maintainer lines revealed abnormal subcellular structure of pollen mother cells (PMCs) in the CMS line. The PMC volume and size of nucleus and nucleolus in the CMS line were smaller than those in the maintainer line. The abnormal tapetum cell development and delayed tapetum degradation inhibited microspore development. Finally, anther abortion in the CMS line occurred. Physiological and biochemical analyses of developing anthers and mitochondria revealed that over-accumulation of reactive oxygen species (ROS) in the SaNa-1A and deficiency in antioxidant enzyme system aggravated the oxidization of membrane lipids, resulting in malondialdehyde (MDA) accumulation in anthers. High MDA content in the CMS line was toxic to the cells. ROS accumulation in SaNa-1A also affected anther development. Abnormal structure and function of terminal oxidase, which participates in the electron transport chain of mitochondrial membrane, were observed and affected the activity of cytochrome c oxidase and F1F0-ATPase, which inhibited ATP biosynthesis. Proline deficiency in SaNa-1A also affected anther development. Few hybridization signals of programmed cell death (PCD) in tetrads of SaNa-1A were identified using TdT-mediated dUTP Nick-End Labeling assay. PCD was not obvious in tapetum cells of SaNa-1A until the unicellular stage. These results validated the cytological differences mentioned above, and proved that abnormal tapetum degradation and anther development in SaNa-1A were the main reasons for the anther abortion.

来源：Plant Cell Reports
发布日期:2019-01-31
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http://agri.ckcest.cn/file1/M00/06/88/CsgkOFOj7SmAdG6SACyN9N8CIbY596.pdf

6．Proteomic analysis provides integrated insight into mechanisms of Turnip mosaic virus long distance movement in Brassica rapa(蛋白质组学分析为深入研究芜菁花叶病毒在芸薹属植物中的长距离运动机制提供了综合依据)

简介：In non-heading Chinese cabbage, the yield relies mostly on the health of leaves, which can be heavily impacted by turnip mosaic virus (TuMV). The virions or viral ribonucleoprotein complexes are transported through the phloem and xylem. Plasmodesmata

are indispensable because they traverse cell walls and connect companion cells, allowing virus particles long distance movement. However, which complexes and genes participate in this process is still unknown. Plants can activate defense mechanisms and apply disease resistance genes to respond to pathogen attacks. In this study, we collected the stems and petioles infected by TuMV for 7 d (TuMV-7), 14 d (TuMV-14), and 21 d (TuMV-21). Using isobaric tags for relative and absolute quantification-based proteomic technology, 6 043 distinct proteins were identified and 323, 240, 285, 203, 253, and 363 differentially expressed proteins were found in the comparable pairs of TuMV-7/control, TuMV-14/TuMV-7, TuMV-14/control, TuMV-21/TuMV-7, TuMV-21/TuMV-14, and TuMV-21/control, respectively. We performed a functional annotation analysis of all identified proteins and a functional enrichment analysis of all differentially expressed proteins. The results indicated that the long distance movement of TuMV involved many complex regulatory pathways. The respective proteins were related to those occurring in plasmodesmata and to Ca2+ transporters. Further, we also found proteins related to heat shock proteins, pathogenesis-related proteins, and proteins scavenging reactive oxygen species.

来源：Biologia Plantarum

发布日期:2019-01-19

全文链接:

http://agri.ckcest.cn/file1/M00/06/88/CsgkOFOj8B2AKarIACVTVOwOrlY931.pdf

科技报告

1．International vegetable breeding: A strategy to create development impact at scale（国际蔬菜育种：大规模发展的战略）

简介：This document reflects the current thinking within the World Vegetable Center on how our breeding research can contribute to realizing the potential of vegetables for healthier lives and more resilient livelihoods.

来源：World Vegetable Center

发布日期:2019-07-01

全文链接:

http://agri.ckcest.cn/file1/M00/00/00/CsgkOVOj866AF9aOAJKkHk_2VNs459.pdf