



2018年第2期总116期

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## ▶ 前沿资讯

### 1. Tracing a plant's steps: Following seed dispersal using chloroplast DNA (利用叶绿体DNA追踪种子传播)

**简介:** 对植物物种来说, 建立新种群的能力对于拓展自己的领地至关重要。植物一般通过种子传播来开拓新领地, 但如何追踪植物足迹, 对于生物学家来说一直是个难题。目前, 美国的科研人员开发出一种新技术, 可以同时数百株植物进行叶绿体DNA测序, 从而更好地了解植物种群的足迹。

数十年来, 生物学家一直在研究种子传播的过程, 但由于难以区分基因差异是来自花粉(雄性基因)传播还是种子(雌雄DNA均有)传播, 对植物种群的基因研究一直受到阻碍。叶绿体通常只通过雌株遗传, 因而其遗传变异可以用来追踪种子的传播而排除花粉干扰。叶绿体的进化十分缓慢, 因此研究人员可以通过新一代测序技术来寻找叶绿体基因组的细微差别, 从而确定不同种群的两株植物之间的关系。为降低此类研究的成本, 美国科研人员开发了新的测序工具“CallHap”, 可以同时大量植物进行基因测序。

在使用CallHap之前, 研究人员必须首先获取目标物种的参考基因组序列, 要么通过查阅已发表的论文, 要么通过对单个植株进行基因测序。接着要对几株植物的叶绿体进行基因测序, 并校正结果以匹配参考基因组序列, 从而生成研究需要的基础数据库。然后就可以使用CallHap来对数百株植物同时进行基因测序。这一方法可以为大量植株提供叶绿体基因组的基因序列数据, 从而生成对种子传播稳健估计所需的大量样本。

研究人员先将CallHap运用到人工基因网络当中, 用它来研究美国俄勒冈州南部一种叫California goldfields(又称Lasthenia californica)的雏菊种子传播率, 而后又将该方法运用在其他四种植物上。结果显示, CallHap可以同时多达200株植物的叶绿体进行基因测序, 并能准确将每株植物的叶绿体基因序列单独列出, 从而显著降低研究这些种群基因的成本。

除种子传播研究外, CallHap还可以用于研究单株亲本遗传下来的包括线粒体在内的其他类型基因组之间的关系, 也可以用于细菌与病毒的传播研究。

来源: AAAS

发布日期: 2017-12-14

全文链接:

[https://www.eurekalert.org/pub\\_releases/2017-12/bsoa-tap121317.php](https://www.eurekalert.org/pub_releases/2017-12/bsoa-tap121317.php)

## ▶ 学术文献

### 1. Sit4-Associated Protein is Required for Pathogenicity of Leptosphaeria maculans on Brassica napus (Sit4相关蛋白参与甘蓝型油菜的茎基溃疡病菌病原致病过程)

**简介:** An insertional mutant with reduced pathogenicity on Brassica napus was identified in the plant pathogenic fungus Leptosphaeria maculans. The transfer-DNA molecule from Agrobacterium tumefaciens inserted into a gene encoding a protein with similarity to Sit4-associated proteins (SAPs). In contrast to Saccharomyces cerevisiae which has four

members of the SAP family, there is a single copy of the gene in *L. maculans*. The mutant had normal spore production and spore germination, but altered hyphal branching, suggesting that nutrient signaling is impaired in the strain. This is the first time that a SAP gene has been mutated in a filamentous fungus and links the function of SAP proteins to plant pathogenesis and hyphal branching.

来源: Current Microbiology

发布日期: 2017-08-24

全文链接:

<http://agri.ckcest.cn/ass/bbc225b8-1165-4cd9-b7b1-8980602b0393.pdf>

## **2. Development of Brassica oleracea-nigra monosomic alien addition lines: genotypic, cytological and morphological analyses (甘蓝黑芥单体异源附加系的研究进展: 遗传学, 细胞学和形态学分析)**

简介: **Key message** We report the development and characterization of *Brassica oleracea-nigra* monosomic alien addition lines (MAALs) to dissect the Brassica B genome.

**Abstract** *Brassica nigra* ( $2n = 16$ , BB) represents the diploid Brassica B genome which carries many useful genes and traits for breeding but received limited studies. To dissect the B genome from *B. nigra*, the triploid F1 hybrid ( $2n = 26$ , CCB) obtained previously from the cross *B. oleracea* var. *alboglabra* ( $2n = 18$ , CC)  $\times$  *B. nigra* was used as the maternal parent and backcrossed successively to parental *B. oleracea*. The progenies in BC1 to BC3 generations were analyzed by the methods of FISH and SSR markers to screen the monosomic alien addition lines (MAALs) with each of eight different B-genome chromosomes added to C genome ( $2n = 19$ , CC + 1B1-8), and seven different MAALs were established, except for the one with chromosome B2 which existed in one triple addition. Most of these MAALs were distinguishable morphologically from each other, as they expressed the characters from *B. nigra* differently and at variable extents. The alien chromosome remained unpaired as a univalent in 86.24% pollen mother cells at diakinesis or metaphase I, and formed a trivalent with two C-genome chromosomes in 13.76% cells. Transmission frequency of all the added chromosomes was far higher through the ovules (averagely 14.40%) than the pollen (2.64%). The B1, B4 and B5 chromosomes were transmitted by female at much higher rates (22.38-30.00%) than the other four (B3, B6, B7, B8) (5.04-8.42%). The MAALs should be valuable for exploiting the genome structure and evolution of *B. nigra*.

来源: Theoretical and Applied Genetics

发布日期: 2017-09-07

全文链接:

<http://agri.ckcest.cn/ass/f05aea6a-2c9a-4d69-a72a-a21df609c46d.pdf>

## **3. Omics Meets Phytonutrients in Vegetable Brassicas: for Nutritional Quality Breeding (组学分析芸薹属蔬菜中的营养元素差异: 用于营养品质方面的育种)**

简介: Consumers understand the health benefits of eating vegetables nowadays and thus

there is currently a high demand for phytonutrient products. Recent advances in genomics, transcriptomics, proteomics and metabolomics have allowed the investigation of the genetic mechanism involved in Brassica phytonutrient metabolism. We discuss the application and opportunity of an omics approach to reveal the underlying genetics of the accumulation and regulation of various phytonutrients, such as well-known glucosinolates, carotenoids, anthocyanin and vitamins, which may assist in molecular breeding and metabolic engineering designed for nutritional quality enhancement of vegetable Brassica crops.

来源: Horticultural Plant Journal

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全文链接:

<http://agri.ckcest.cn/ass/dlad0a36-0578-422d-a54d-33ea2fb2ef25.pdf>

#### **4. Genome-Wide Identification and Structural Analysis of bZIP Transcription Factor Genes in Brassica napus (甘蓝型油菜bZIP转录因子基因的基因组结构分析和鉴定)**

简介: The basic region/leucine zipper motif (bZIP) transcription factor family is one of the largest families of transcriptional regulators in plants. bZIP genes have been systematically characterized in some plants, but not in rapeseed (*Brassica napus*). In this study, we identified 247 BnbZIP genes in the rapeseed genome, which we classified into 10 subfamilies based on phylogenetic analysis of their deduced protein sequences. The BnbZIP genes were grouped into functional clades with *Arabidopsis* genes with similar putative functions, indicating functional conservation. Genome mapping analysis revealed that the BnbZIPs are distributed unevenly across all 19 chromosomes, and that some of these genes arose through whole-genome duplication and dispersed duplication events. All expression profiles of 247 bZIP genes were extracted from RNA-sequencing data obtained from 17 different *B. napus* ZS11 tissues with 42 various developmental stages. These genes exhibited different expression patterns in various tissues, revealing that these genes are differentially regulated. Our results provide a valuable foundation for functional dissection of the different BnbZIP homologs in *B. napus* and its parental lines and for molecular breeding studies of bZIP genes in *B. napus*.

来源: Genes

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全文链接:

<http://agri.ckcest.cn/ass/6521cb8e-b3be-430b-adc4-42cc135f0872.pdf>