



2022年第50期总373期

## 蔬菜育种专题

### 本期导读

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2. 新研究揭示油菜含油量的基因调控网络

#### ▶ 学术文献

1. 油菜 (*Brassica napus*) 中五个核因子Y亚基B基因促进拟南芥开花和根伸长
2. 串联重复序列的进化反映了芸苔属植物多倍体后分支发生的过程

#### ▶ 科技图书

1. 抗生物胁迫蔬菜作物的基因组设计

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2022年12月12日

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## ▶ 前沿资讯

### 1. 作物养分管理团队在油菜氮营养实时遥感估测方法研究上取得新进展

**简介:** 资源与环境学院作物养分管理研究团队在利用遥感技术实时、无损、准确估测油菜氮素营养状况的方法上取得新进展, 相关成果以“Remote estimation of leaf nitrogen concentration in winter oilseed rape across growth stages and seasons by correcting for the canopy structural effect” 题发表在遥感领域期刊Remote Sensing of Environment上。

**来源:** 南湖新闻网

**发布日期:** 2022-11-18

**全文链接:**

<http://agri.ckcest.cn/file1/M00/03/45/Csgk0Yfn-VeARZGUA4awNxSVfc249.pdf>

### 2. 新研究揭示油菜含油量的基因调控网络

**简介:** 11月7日, 华中农业大学油菜团队联合生物信息团队在Genome Biology发表了题为“Comprehensive transcriptional variability analysis reveals gene networks regulating seed oil content of Brassica napus” 的研究论文。该研究全面描述了油菜种子发育过程中转录组变异调控图谱, 并结合机器学习与深度学习算法挖掘了油菜种子含油量调控新基因, 研究结果为多倍体植物的不对称调控提供了借鉴。

**来源:** 南湖新闻网

**发布日期:** 2022-11-09

**全文链接:**

<http://agri.ckcest.cn/file1/M00/10/17/Csgk0GORRdSAWf4PAA7IEaOrjg437.pdf>

## ▶ 学术文献

### 1 . Five NUCLEAR FACTOR-Y subunit B genes in rapeseed (Brassica napus) promote flowering and root elongation in Arabidopsis (油菜 (Brassica napus) 中五个核因子Y亚基B基因促进拟南芥开花和根伸长)

**简介:** The transcriptional regulator NUCLEAR FACTOR-Y (NF-Y) is a heterotrimeric complex composed of NF-YA, NF-YB, and NF-YC proteins and is ubiquitous in yeast, animal, and plant systems. In this study, we found that five NF-YB proteins from rapeseed (Brassica napus), including BnNF-YB2, BnNF-YB3, BnNF-YB4, BnNF-YB5, and BnNF-YB6 (BnNF-YB2/3/4/5/6), all function in photoperiodic flowering and root elongation. Sequence alignment and phylogenetic analysis showed that BnNF-YB2/3 and BnNF-YB4/5/6 were clustered with Arabidopsis AtNF-YB2 and AtNF-YB3, respectively, implying that these NF-YBs are evolutionarily and functionally conserved. In support of this hypothesis, the heterologous expression of individual BnNF-YB2, 3, 4, 5, or 6 in Arabidopsis promoted early flowering

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under a long-day photoperiod. Further analysis suggested that BnNF-YB 2/3/4/5/6 elevated the expression of key downstream flowering time genes including CO, FT, LFY and SOC1. Promoter-GUS fusion analysis showed that the five BnNF-YBs were expressed in a variety of tissues at various developmental stages and GFP fusion analysis revealed that all BnNF-YBs were localized to the nucleus. In addition, we demonstrated that the heterologous expression of individual BnNF-YB2/3/4/5/6 in Arabidopsis promoted root elongation and increased the number of root tips formed under both normal and treatment with simulators of abiotic stress conditions.

来源: Planta

发布日期:2022-11-12

全文链接:

<http://agri.ckcest.cn/file1/M00/03/45/Csgk0Yfn9keASYSKADcECCfHZnA290.pdf>

## **2 . Evolution of tandem repeats is mirroring post-polyploid cladogenesis in Heliophila (Brassicaceae) (串联重复序列的进化反映了芸苔属植物多倍体后分支发生的过程)**

简介: The unigeneric tribe Heliophileae encompassing more than 100 Heliophila species is morphologically the most diverse Brassicaceae lineage. The tribe is endemic to southern Africa, confined chiefly to the southwestern South Africa, home of two biodiversity hotspots (Cape Floristic Region and Succulent Karoo). The monospecific Chamira (*C. circaeoides*), the only crucifer species with persistent cotyledons, is traditionally retrieved as the closest relative of Heliophileae. Our transcriptome analysis revealed a whole-genome duplication (WGD) ~26.15-29.20 million years ago, presumably preceding the Chamira/Heliophila split. The WGD was then followed by genome-wide diploidization, species radiations, and cladogenesis in Heliophila. The expanded phylogeny based on nuclear ribosomal DNA internal transcribed spacer (ITS) uncovered four major infrageneric clades (A-D) in Heliophila and corroborated the sister relationship between Chamira and Heliophila. Herein, we analyzed how the diploidization process impacted the evolution of repetitive sequences through lowcoverage whole-genome sequencing of 15 Heliophila species, representing the four clades, and Chamira. Despite the firmly established infrageneric cladogenesis and different ecological life histories (four perennials vs. 11 annual species), repeatome analysis showed overall comparable evolution of genome sizes (288-484 Mb) and repeat content (25.04-38.90%) across Heliophila species and clades. Among Heliophila species, long terminal repeat (LTR) retrotransposons were the predominant components of the analyzed genomes (11.51-22.42%), whereas tandem repeats had lower abundances (1.03-12.10%). In Chamira, the tandem repeat content (17.92%, 16 diverse tandem repeats) equals the abundance of LTR retrotransposons (16.69%). Among the 108 tandem repeats identified in Heliophila, only 16 repeats were found to be shared among two or more species; no tandem repeats were shared by Chamira and Heliophila genomes. Six “relic” tandem repeats were shared between any two different Heliophila clades by a common descent. Four and six clade-specific repeats shared among clade A and C species, respectively, support the monophyly of these two clades. Three repeats shared by all clade A species corroborate the

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recent diversification of this clade revealed by plastome-based molecular dating. Phylogenetic analysis based on repeat sequence similarities separated the *Heliophila* species to three clades [A, C, and (B+D)], mirroring the post-polyploid cladogenesis in *Heliophila* inferred from rDNA ITS and plastome sequences.

来源: Front Plant Sci

发布日期: 2022-10-25

全文链接:

<http://agri.ckcest.cn/file1/M00/10/17/Csgk0GORQXmAjBxNACnWWn2VXjM605.pdf>

## 科技图书

### **1 . Genomic Designing for Biotic Stress Resistant Vegetable Crops (抗生物胁迫蔬菜作物的基因组设计)**

简介: Biotic stresses cause yield loss of 31-42% in crops in addition to 6-20% during post-harvest stage. Understanding interaction of crop plants to the biotic stresses caused by insects, bacteria, fungi, viruses, and oomycetes, etc. is important to develop resistant crop varieties. Knowledge on the advanced genetic and genomic crop improvement strategies including molecular breeding, transgenics, genomics-assisted breeding and the recently emerging genome editing for developing resistant varieties in vegetable crops is imperative for addressing FPNEE (food, health, nutrition, energy and environment) security. Whole genome sequencing of these crops followed by genotyping-by-sequencing have facilitated precise information about the genes conferring resistance useful for gene discovery, allele mining and shuttle breeding which in turn opened up the scope for 'designing' crop genomes with resistance to biotic stresses.

来源: Springer Nature

发布日期: 2022-11-1

全文链接:

<http://agri.ckcest.cn/file1/M00/10/17/Csgk0GORRDuAVd0wAAXsJb8F3Q435.pdf>