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▶ 前沿资讯

1. Scientists engineer shortcut for photosynthetic glitch, boost crop growth 40% (美国：通过设计光呼吸捷径可提高作物生长量40%)

简介：植物通过光合作用将日光转变成能量，但是，一种称作光呼吸的耗费能量的过程极大地抑制了作物产量。美国农业部农业研究局和伊利诺伊大学的研究人员在《科学》杂志上发文称，在现实农业条件下，设计有光呼吸捷径的作物生长量可提高40%。

这一成果来自于一项国际研究项目——增进光合作用效率方法的计划（RIPE）的一部分，该项目希望通过改造作物进行更为有效的光合作用，以可持续地提高全球粮食生产率。

光合作用利用核酮糖-1,5-二磷酸羧化酶/加氧酶（Rubisco）和太阳能将二氧化碳与水转变成糖分，促进作物生长。由于无法准确区分氧气和二氧化碳分子，Rubisco在大约五分之一的时间里抓取的是氧气分子而不是二氧化碳分子，生成了一种对作物有毒的化合物，必须通过光呼吸进行再循环。

一般来说，光呼吸需要穿过植物细胞中三个区室的复杂路径。科学家们设计了三条替代路径改变了原有进程，极大地缩短了距离，节约了大量资源从而使植物产量增加了40%。这是首次经改造的光呼吸补救作物在现实农业环境中进行测试。

为了优化新路径，研究人员利用多套不同启动子和基因设计了基因结构，基本上创建了一套独特的路线图。他们将这些路线图在1,700种植物中进行了测试，筛选出表现最佳的几种。经过两年不断重复的实地研究，研究人员发现这些经过改造的作物长得更快更高，并且生物质提高了约40%，主要表现为茎秆粗壮了一半。

研究团队在烟草上也测试了这一假设，因为作为理想的模式植物，烟草比粮食作物更易改造和测试，而和其他模式植物不同的是，烟草还能长出枝叶冠盖，并能在田野里进行测试。现在，研究团队正在将研究成果转移应用到大豆、豇豆、稻米、马铃薯、番茄、茄子上，以提升产量。

来源：ScienceDaily

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全文链接：

http://agri.ckcest.cn/file1/M00/06/5D/Csgk0FxRYByAFII_AASoykuWKY356.pdf

▶ 学术文献

1. Genome-wide identification of oil biosynthesis-related long non-coding RNAs in allopolyploid Brassica napus (异源多倍体甘蓝型油菜中生物合成相关长链非编码RNA的全基因组鉴定)

简介：Background: Long noncoding RNAs (lncRNAs) are transcripts longer than 200 bp that do not encode proteins but nonetheless have been shown to play important roles in various biological processes in plants. Brassica napus is an important seed oil crop worldwide and the target of many genetic improvement activities. To understand better the function of lncRNAs in regulating plant metabolic activities, we carried out a genome-wide lncRNA identification of lncRNAs in Brassica napus with a focus on lncRNAs involved in lipid

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metabolism. Twenty ribosomal RNA depleted strand specific RNA-seq (ssRNA-seq) datasets were generated using RNAs isolated from *B. napus* seeds at four developmental stages. For comparison we also included 30 publically available RNA-seq datasets generated from poly(A) enriched mRNAs isolated from various *Brassica napus* tissues in our analysis.

Results: A total of 8905 lncRNA loci were identified, including 7100 long intergenic noncoding RNA (lincRNA) loci and 1805 loci generating long noncoding natural antisense transcript (lncNAT). Many lncRNAs were identified only in the ssRNA-seq and poly(A) RNA-seq dataset, suggesting that *B. napus* has a large lncRNA repertoire and it is necessary to use libraries prepared from different tissues and developmental stages as well as different library preparation approaches to capture the whole spectrum of lncRNAs. Analysis of coexpression networks revealed that among the regulatory modules are networks containing lncRNAs and protein-coding genes related to oil biosynthesis indicating a possible role of lncRNAs in the control of lipid metabolism. One such example is that several lncRNAs are potential regulators of BnaC08g11970D that encodes oleosin1, a protein found in oil bodies and involved in seed lipid accumulation. We also observed that the expression levels of *B. napus* lncRNAs is positively correlated with their conservation levels.

Conclusions: We demonstrated that the *B. napus* genome has a large number of lncRNA and that these lncRNAs are expressed broadly across many developmental times and in different tissue types. We also provide evidence indicating that specific lncRNAs appear to be important regulators of lipid biosynthesis forming regulatory networks with transcripts involved in lipid biosynthesis. We also provide evidence that these lncRNAs are conserved in other species of the Brassicaceae family.

来源: BMC Genomics

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<http://agri.ckcest.cn/file1/M00/06/5D/Csgk0FxrT0qA010xAcnKAHHCT7Q015.pdf>

2. Organization of the genome sequence of the polyploid crop species *Brassica juncea* (多倍体芥菜的基因组排序)

简介: A draft genome sequence of *Brassica juncea*, a member of the Brassicaceae and therefore a species benefiting from the functional genomics advances in the 'model' species *Arabidopsis thaliana*, was reported recently by Yang et al.¹. *B. juncea* is a recently formed allotetraploid, whose diploid progenitors were mesohexaploids: *Brassica rapa* (which contributed the A genome) and *Brassica nigra* (which contributed the B genome). In addition to underpinning future trait-oriented work in this important crop species, which includes both vegetable and oil types, the sequences were analyzed for characteristics of genome evolution under crop selection. For both purposes, the genome sequences must represent with high fidelity (though not perfectly in 'draft' form) both the gene complement and gene order of the species. As a model for addressing the challenges of achieving an adequate representation of the latter for allopolyploid crops, the construction methodology employed short shotgun sequence reads, single-molecule long reads, BioNano sequencing and high-resolution genetic mapping.

来源: Nature Genetics

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<http://agri.ckcest.cn/file1/M00/06/5D/Csgk0FxRUJ-AP3t1ACtvod6cG1E997.pdf>

3. Screening of candidate gene responses to cadmium stress by RNA sequencing in oilseed rape (*Brassica napus* L.) (通过油菜籽 (甘蓝型油菜) RNA基因组的排序筛选镉应激反应候选基因)

简介: Cadmium (Cd) stress is one of the most serious threats to agriculture in the world. Oilseed rape (*Brassica napus* L.) is an important oil crop; however, Cd can easily accumulate in rapeseed and thus harm human health through the food chain. In the first experiment, our purpose was to measure the Cd accumulation in mature *B. napus* plants and its influences on fatty acid composition. The results showed that most Cd was accumulated in the root, and the seed fatty acid content was considerably different at different Cd toxicity levels. In the second experiment, 7-day-old *B. napus* seedlings stressed by Cd (1 mM) for 0 h (CK-0h), 24 h (T-24h), or 72 h (T-72h) were submitted to physiological and biological analyses, RNA-Seq and qRT-PCR. In total, 5469 and 6769 differentially expressed genes (DEGs) were identified in the comparisons of “CK-0h vs T-24h” and “CK-0h vs T-72h”, respectively. Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analyses showed that the photosynthetic and glutathione (GSH) pathways were significantly enriched in response to Cd stress. Key factors in the response to Cd stress included BnPCS1, BnGSTU12, BnGSTU5, and BnHMAs. The transcription factors BnWRKY11 (BnaA03g51590D), BnWRKY28 (BnaA03g43640D), BnWRKY33 (BnaA03g17820D), and BnWRKY75 (BnaA03g04160D) were upregulated after Cd exposure. The present study revealed that upregulation of the genes encoding GST and PCS under Cd stress promoted the formation of low-molecular weight complexes (PC-Cd), and upregulation of heavy metal ATPase genes induced PC-Cd transfer to vacuoles. These findings may provide the basis for the molecular mechanism of the response of *B. napus* to Cd.

来源: Environmental Science and Pollution Research

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<http://agri.ckcest.cn/file1/M00/06/5D/Csgk0FxRT3uAQQ5nADRJDi7upqk821.pdf>

4. A Genomic Variation Map Provides Insights into the Genetic Basis of Spring Chinese Cabbage (*Brassica rapa* ssp. *pekinensis*) Selection (基因组变异图为春大白菜选育提供了遗传学基础)

简介: Chinese cabbage is the most consumed leafy crop in East Asian countries. However, premature bolting induced by continuous low temperatures severely decreases the yield and quality of the Chinese cabbage, and therefore restricts its planting season and geographic distribution. In the past 40 years, spring Chinese cabbage with strong winteriness has been selected to meet the market demand. Here, we report a genome variation map of Chinese cabbage generated from the resequencing data of 194 geographically diverse accessions of three ecotypes. In-depth analyses of the selection sweeps and genome-wide patterns revealed

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that spring Chinese cabbage was selected from a specific population of autumn Chinese cabbage around the area of Shandong peninsula in northern China. We identified 23 genomic loci that underwent intensive selection, and further demonstrated by gene expression and haplotype analyses that the incorporation of elite alleles of VERNALISATION INSENSITIVE 3.1 (BrVIN3.1) and FLOWER LOCUS C 1 (BrFLC1) is a determinant genetic source of variation during selection. Moreover, we showed that the quantitative response of BrVIN3.1 to cold due to the sequence variations in the cis elements of the BrVIN3.1 promoter significantly contributes to bolting-time variation in Chinese cabbage. Collectively, our study provides valuable insights into the genetic basis of spring Chinese cabbage selection and will facilitate the breeding of bolting-resistant varieties by molecular-marker-assisted selection, transgenic or gene editing approaches.

来源: Molecular Plant

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