



2019年第24期总191期

## 蔬菜育种专题

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## ▶ 前沿资讯

### 1. How brassinosteroid signaling makes roots grow longer under nitrogen deficiency (在缺氮条件下，油菜素类固醇信号如何使根长得更长)

简介: As sessile organisms, plants rely on their ability to adapt the development and growth of their roots in response to changing nutrient conditions. One such response, known to be displayed by plants grown in low nitrogen conditions, is the elongation of primary and lateral roots to explore the surrounding soil.

来源: ScienceDaily

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/71/Csgk0F0DCc0Afs-8AAQ07Z17osA568.pdf>

### 2. Climate change is already affecting global food production – unequally (气候变化为全球粮食生产带来重要影响)

简介: 世界排名前10大作物有大麦、木薯、玉米、油棕、油菜、水稻、高粱、大豆、甘蔗和小麦，这些作物提供的热量占全球农田可生产总热量的83%。长期以来，由于受气候条件的影响，科学家预测未来气候条件下作物产量会呈现下降趋势。目前新的研究也表明，气候变化已经影响了这些关键能源的生产，一些地区和国家的情况比其他地区和国家更严重。

明尼苏达大学 (University of Minnesota)、牛津大学 (University of Oxford) 和哥本哈根大学 (University of Copenhagen) 的研究人员共同开展了一项研究，利用天气和作物数据来评估观测到的气候变化对作物的潜在影响，研究人员发现：

- 观测到的气候变化对世界排名前10的作物产量均造成了显著的影响，从油棕产量减少13.4%到大豆产量增加3.5%，导致这些前10种作物的可消耗食物热量平均减少约1% ( $-3.5 \times 10^{13}$  千卡/年)；

- 气候变化对全球粮食生产的影响在欧洲、南部非洲和澳大利亚大多是消极的，在拉丁美洲一般是积极的，在亚洲、北非和中美洲则是混合的；

- 半数粮食不安全国家的作物产量正在下降，西欧一些富裕的工业化国家也是如此；

- 相比之下，最近的气候变化增加了美国中西部一些地区某些作物的产量。

明尼苏达大学环境研究所的研究者表示，气候带来的变化，有赢家，也有输家，一些粮食不安全的国家的情况已经恶化。该研究所的高分辨率全球农作物统计数据数据库也被用来帮助识别全球农作物产量随时间的变化。这些研究可以发现哪些地理区域和作物面临的风险最大，使它们被那些致力于实现联合国消除饥饿和限制气候变化影响的可持续发展目标的人员关注。这样的见解会带来新的问题和关键的下一步行动。

明尼苏达大学统计学院的合著者表示，这是一个非常复杂的系统，所以仔细的统计和数据科学建模组件对于理解小变化或大变化的相关性和连锁效应至关重要。

该研究所的《全球景观倡议》(Global Landscape Initiative) 此前已经得出了全球规模的调查结果，联合国、世界银行和布鲁金斯学会等国际组织已将这些调查结果用于评估全球粮食安全和环境挑战。这份报告对主要的食品公司、大宗商品交易商和他们

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经营的国家以及全世界的公民都有影响。

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## 学术文献

### 1. 基于叶球转录组数据比较的甘蓝杂种优势分析

**简介:** 对甘蓝两个杂交组合F1 的杂种优势进行了田间性状统计分析以及叶球转录组测序分析。所调查的9 个园艺学性状中, 单球质量和球主叶柄质量在F1 代及其亲本之间差异显著, 其中单球质量的中亲优势和超亲优势在两个组合F1 中表现突出, 即产量杂种优势较为明显。通过叶球转录组分析, 分别筛选获得了4 组差异表达基因, 在相同标准下, 两个杂交组合中父本与F1 代的差异表达基因明显多于母本与F1 代的差异表达基因, 表明母本的表达谱与F1 更相似, 即母本在F1 叶球杂种优势形成中的贡献较大, 而且上调差异表达基因的差异倍数明显高于下调差异表达基因, 表明上调基因在F1 代甘蓝叶球杂种优势建成中有重要作用。进一步将差异表达基因进行GO (Gene Ontology) 分类、COG (Cluster of Orthologous Groups of proteins) 分类、KEGG (Kyoto Encyclopedia of Genes and Genomes) 通路富集分析以及可变剪接分析, 发现差异表达基因显著富集到生长发育、碳水化合物转运和代谢、信号转导以及氨基酸的合成、转运和代谢等途径。随机选取7 个差异表达基因进行实时荧光定量PCR 验证, 结果与RNA-seq 数据基本一致, 证明转录组数据的可靠性。本研究获得的与甘蓝叶球杂种优势形成相关的差异表达基因, 为后续甘蓝杂种优势分子机制研究提供数据支持。

来源: 园艺学报

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### 2. 油菜不同根肿病抗性材料的室内鉴定及相关生理分析

**简介:** 结合田间种植根肿病抗性表现, 以菌土法和在蘸根法对多个疑似具有抗性的材料进行室内鉴定, 初步筛选出两种对根肿菌4号生理小种具有抗性的油菜材料Kc84-1和OG-13; 用病情统计的方法将Kc84-1与目前已推广种植的抗性材料华双5R和易感材料R-197进行对照验证, 并对三种材料进行抗性生理分析。结果表明: Kc84-1与华双5R具有相同水平的根肿病抗性; 不同材料的防御酶超氧化物歧化酶(SOD)、过氧化物酶(POD)、多酚氧化酶(PPO)、苯丙氨酸解氨酶(PAL)活性以及抗病相关物质丙二醛(MDA)含量的表现各不相同, 两种抗性材料在较高感病等级下的防御酶SOD、POD、PAL活性显著高于感病材料, PPO活性和MDA含量在抗性材料和易感材料之间没有显著差异。通过水培法观测三种材料感病早期的根毛侵染水平, 结果表明, 易感材料R-197的根毛侵染率在侵染第6d到第14d显著高于抗性材料华双5R和Kc84-1。

来源: 四川大学学报(自然科学版)

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### 3. Fine mapping of *lcm1*, a gene conferring chlorophyll-deficient golden leaf in Chinese cabbage (*Brassica rapa* ssp. *pekinensis*) (大白菜(*Brassica rapa* ssp. *pekinensis*) 缺失叶绿素金叶基因*Lcm1*的精细定位)

**简介:** Leaf color mutants are valuable resources for studying regulatory mechanisms of photosynthetic pigment metabolism. In this study, a chlorophyll-deficient golden leaf mutant *lcm1* of Chinese cabbage was identified from its wild-type “FT” by ethyl methanesulfonate (EMS) mutagenesis. The phenotype of the golden leaf mutant *lcm1* was that the leaves remained golden throughout development. Pigment measurements showed that the chlorophyll content of the mutant *lcm1* was less than that of the wild-type “FT”. There were no obvious grana lamellae observed in the chloroplast microstructure of the mutant *lcm1*. Genetic analysis revealed that the mutant *lcm1* phenotype was controlled by a single recessive nuclear gene, *lcm1* (*BrChlH*). The MutMap method and Kompetitive Allele Specific PCR genotyping were used to predict that Bra006208 encoding a Mg-chelatase H subunit, the candidate gene for the mutant *lcm1*. The 4249-bp *lcm1* gene had five exons and a single nucleotide substitution (G to A) in the third exon that resulted in an amino acid substitution (A to V). This SNP2523351 occurred in the highly conserved CobN-Mg\_chel domain of the LCM1 (*BrCHLH*) protein. This study suggests that *lcm1* gene plays an important role in the function of CHLH and provides a solid foundation for further studies on the development of plant leaf color.

**来源:** Molecular Breeding

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<http://agri.ckcest.cn/file1/M00/06/71/Csgk0F0DAwGAb1KfADI6Gqk-yys960.pdf>

### 4. Comparison of physiological and methylational changes in resynthesized *Brassica napus* and diploid progenitors under drought stress (干旱胁迫下人工合成甘蓝型油菜和二倍体祖先的生理和甲基化变化比较)

**简介:** *Brassica napus* is a polyploid of certain research and economical value. Resynthesizing *B. napus* with diploid *B. rapa* and *B. oleracea* is essential for *Brassica* research because of the limited genetic background of *B. napus*. Considering that polyploids possess better agronomic traits and resistance compared with the corresponding diploids, we investigated drought tolerance after polyploidization of *B. napus* and revealed the epigenetic differences between polyploids and diploids. After drought stress, *B. rapa* and first-generation of synthesized hybrids (F1) were more wilted than *B. oleracea* and F2F4 generations. However, the relative water content and water retention in F1 were better than others after drought stress. The increased number of partially opened and closed stomata in F1 was not as significant as that in F2 and F3, but stomata density in F1 was lower than F2, and the

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stomatal size in F1 was significantly reduced than F3. Physiological parameters varied among different generations of *B. napus* and diploid parents, and most of these parameters in hybrids were higher than *B. rapa* and lower than *B. oleracea*. However, the peroxidase activity in F3 and F4 was significantly higher than both parents, and the malondialdehyde content in F3 and F4 was lower than both parents, indicating that F3 and F4 might be more adaptive to oxidative stresses than other generations. DNA methylation level was decreased in F2 and F3 compared with F1, and then increased in F4. Methylation-sensitive amplified polymorphism analysis revealed that DNA methylation and demethylation broadly happened after drought stress. The methylation and demethylation level was F1>F4>*B. oleracea*>F2>F3>*B. rapa* and *B. rapa*>F4>F3>F2>*B. oleracea*>F1, respectively. The epigenetic changes under drought stress might be related to the different stress tolerances during *B. napus* polyploidization.

来源: Acta Physiologiae Plantarum

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<http://agri.ckcest.cn/file1/M00/06/71/Csgk0F0DAeOAEzqHABsJrgyofMw495.pdf>

## 5. Protein interactions of SOC1 with SVP are regulated by a few crucial amino acids in flowering pathways of *Brassica juncea* (SOC1与SVP的蛋白相互作用受芥菜开花途径中几个关键氨基酸的调控)

简介: SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1 (SOC1) is a vital flowering signal integrator to promote flowering, which is inhibited by a MADS-box transcription factor, SHORT VEGETATIVE PHASE (SVP). However, it remains elusive about how SOC1 interacts with SVP in flowering pathways of *Brassica juncea*. Here, *B. juncea* SOC1 (BjuSOC1) gene was cloned and it expressed differently between stem apices and leaves during the low-temperature vernalization and long-day photoperiod pathways. Yeast two-hybrid and BiFC assays indicated that BjuSOC1 directly interacted with BjuSVP in vitro and in vivo. Interestingly, further studies indicated that mutants of BjuSOC1<sup>K108V</sup>, BjuSOC1<sup>R109L</sup>, BjuSOC1<sup>C137K</sup> could no more interact with BjuSVP, and BjuSVP<sup>R137L</sup> also led to loss of the protein interaction. It suggested that the 108th, 109th, and 137th of BjuSOC1 and 137th of BjuSVP regulated the protein interactions between BjuSOC1 and BjuSVP. The results provided valuable information for further study on the control of flowering time in *B. juncea*.

来源: Acta Physiologiae Plantarum

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## 6. Genome-Wide Analysis of Auxin Receptor Family Genes in *Brassica juncea* var. *tumida* (芥菜 (*Brassica juncea* var. *tumida*) 生长素受体家族基因的全基因组分析)

简介: Transport inhibitor response 1/auxin signaling f-box proteins (TIR1/AFBs) play

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important roles in the process of plant growth and development as auxin receptors. To date, no information has been available about the characteristics of the TIR1/AFB gene family in *Brassica juncea* var. *tumida*. In this study, 18 TIR1/AFB genes were identified and could be clustered into six groups. The genes are located in 11 of 18 chromosomes in the genome of *B. juncea* var. *tumida*, and similar gene structures are found for each of those genes. Several cis-elements related to plant response to phytohormones, biotic stresses, and abiotic stresses are found in the promoter of BjuTIR1/AFB genes. The results of qPCR analysis show that most genes have differential patterns of expression among six tissues, with the expression levels of some of the genes repressed by salt stress treatment. Some of the genes are also responsive to pathogen *Plasmodiophora brassicae* treatment. This study provides valuable information for further studies as to the role of BjuTIR1/AFB genes in the regulation of plant growth, development, and response to abiotic stress.

来源: Genes

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## 7. Selection of Salicylic Acid Tolerant Epilines in *Brassica napus* (甘蓝型油菜耐水杨酸突变体的筛选)

简介: Two of the major pathways involved in induced defense of plants against pathogens include the salicylic acid (SA)- and jasmonic acid (JA)-mediated pathways that act mainly against biotrophs and necrotrophs, respectively. However, some necrotrophic pathogens, such as *Botrytis cinerea*, actively induce the SA pathway, resulting in cell death that allows the pathogen to proliferate in the plant. Starting from an isogenic canola (*Brassica napus*) line, epilines were selected with a reduced sensitivity to SA. The genes belonging to the SA pathway had an altered transcription profile in the SA-tolerant lines, when treated with SA. Besides the already known genes of the SA pathway, new SA target genes were identified, creating possibilities to better understand the plant defense mechanism against pathogens. The SA-tolerant line with the lowest SA-induced gene expression is tolerant to *Botrytis cinerea*. When treated with SA, this line has also a reduced histone modification (histone H3 lysine 4 trimethylation) at the genes at the start of the SA pathway.

来源: Agronomy

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<http://agri.ckcest.cn/file1/M00/06/71/Csgk0F0DA9qAEimDACUVrmQfeo0465.pdf>

## 8. The assessment of water stress and delay cropping on quantitative and qualitative traits of rapeseed genotypes (水分胁迫和延迟种植对油菜基因型数量性状和品质性状的影响)

简介: To investigate the effects of water stress and delay cropping on the qualitative and quantitative traits of rapeseed genotypes, a factorial split-plot test was conducted in a complete randomized blocks design with three replications in Karaj, Iran. In this experiment,

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cultivations at two levels included well-timed cultivation (Oct. 7) and delay cropping (Nov. 1). The irrigation was conducted at two levels routine irrigation (control) and the elimination of watering after pod formation stage in factorial status in main plots and five rapeseed genotypes including HW2, HW1, SW102, BAL4, BAL1 and Okapi in subplots. The interaction effect of cultivation date×irrigation on the seed yield and erucic acid traits was significant at 5% level, and on the trait of oil yield was significant at 1% level. The interaction effect of cultivation date×cultivar was significant at 1% level on the traits of stearic acid, oleic acid and seed glucosinolate. The genotypes SW102 and HW1, having the maximum quantity of standard erucic acid, allocated maximum seed yield of 3877 and 3801 kg/ha, respectively. Moreover, these two genotypes, containing maximum amount of oleic acid on average of 64.4 and 63.4% and minimum amount of seed glucosinolate on average of 23.5 and 23.8 $\mu$ mol/g of meal in the delay cropping condition, are recommendable to be cultivated under delay cropping conditions. Therefore, by introducing of suitable varieties for delay cropping as well as by selection of varieties that produce reasonable economical yield and standard qualitative traits, it is possible to increase the under cultivation areas of this plant in the cold and temperate-cold regions with dry and semi-dry climates.

来源: Industrial Crops & Products

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