



2018年第29期总143期

蔬菜育种专题

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▶ 前沿资讯

1. Gene discovery may yield lettuce that will sprout in hot weather (新发现的基因有助于生菜在高温天气正常萌发)

简介: 加利福尼亚大学戴维斯分校的研究人员发现了一种能在高温天气下影响生菜萌发的基因和相关的酶。这一发现能够让生菜全年发芽, 甚至在高温天气下也能正常萌发。研究结果刊登于《Plant Cell》上。

科研人员观察到, 一种内在的休眠机制可以防止野生生菜种子在过于炎热或干燥的条件下萌发, 但要将其运用于商业生菜品种生产则存在阻碍。为了让生菜这类冬季作物在高温天气下能够开始种子萌发, 农民一般通过喷灌冷却土壤, 或在播种前用冷水浸种再晾干进行催芽, 但这些方法成本高昂, 也并不一定奏效。

在最近的这项研究中, 研究人员在生菜的一种野生祖先内发现了第六号染色体区, 它能够让种子在温暖的条件下萌发。当研究人员将该染色体区导入生菜栽培品种进行杂交时, 这些品种则获得了在温暖条件下萌发的能力。

进一步的基因定位研究集中在一种特定的基因上, 该基因能够控制一种被称为脱落酸的植物激素的产生, 而脱落酸能够抑制种子萌发。当种子处于温暖湿润的条件下, 该基因就会“启动”, 提高脱落酸的含量。而在野生生菜祖先品种中, 这种基因在高温时并不会起作用, 因此脱落酸含量不会升高, 此时种子便可萌发。研究人员指出, 可以“沉默”或改变栽培生菜品种中的发芽抑制基因, 从而使这些品种即使在高温下也能发芽和生长。

来源: AgroPages

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全文链接:

<http://news.agropages.com/News/NewsDetail—26540.htm>

▶ 学术文献

1. Competence of *Xanthomonas campestris* from Cruciferous Weeds and Wallflower (*Erysimum cheiri*) to Induce Black Rot in Cabbage (十字花科杂草和桂竹香中野油菜黄单胞菌诱导甘蓝黑斑病的能力)

简介: In order to verify the role of cruciferous weeds and ornamentals to serve as a source of primary inoculum of *Xanthomonas campestris* pv. *campestris* (Xcc), the causal agent of black rot of Brassicas, *Xanthomonas* isolates from shepherd's purse (*Capsella bursa-pastoris*), fanweed (*Thlaspi arvense*) and wallflower (*Erysimum cheiri*) were characterized by molecular data and by their pathogenicity on kohlrabi and shepherd's purse. These characteristics were compared to those of xanthomonads isolated from infested Brassica crops and contaminated transplants. Only one of 30 *Xanthomonas* isolates from shepherd's purse in boundary ridges and field paths adjacent to Brassica fields, and from plants outside the Brassica growing area, was able to induce black rot (BR) on kohlrabi; nearly all of them (except one) were able to cause black rot like symptoms with black vascular veins (BRL) on

shepherd's purse. Six of ten tested isolates from different asymptomatic weeds growing in BR infested cauliflower fields were able to induce BR on kohlrabi, but all isolates caused BRL on shepherd's purse. All *Xanthomonas* isolates from symptomatic wallflower induced BR on kohlrabi and BRL on shepherd's purse. Inoculations with isolates from BR infested cauliflower, representing the pathovar *campestris* (Xcc), always led to BR on kohlrabi and BRL on shepherd's purse. The isolates from rucola and radish field crops and from Brassica transplants showed typical symptoms of the pathovars *campestris* (Xcc) and *raphani* (Xcr), respectively. In a PCR with the newly designed primer set SP-1, only the isolates which were able to induce BR on kohlrabi could be detected. The sequence analysis of the *gyrB*-gene showed that all *Xanthomonas* isolates which induced BR on kohlrabi clustered in one major clade, while the remaining isolates clustered into several different clades. Based on these results, the authors conclude that *Xanthomonas* isolates from shepherd's purse may not constitute a serious risk to serve as primary inoculum for BR epidemics in Brassicas. By contrast, *Xanthomonas* isolates from wallflower have this potential. Most of the isolates from cruciferous weeds and the wallflower isolates do not fit into the actual classification of *Xanthomonas campestris* pathovars.

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全文链接:

<http://agri.ckcest.cn/ass/a5679304-3214-4a39-be4b-459112083c80.pdf>

2. Cultivation under salt stress conditions influences postharvest quality and glucosinolates content of fresh-cut cauliflower (盐胁迫条件下的耕作影响鲜切花椰菜采后质量和芥子油甙含量)

简介: Quality and chemical composition of two fresh-cut cauliflower cultivars (the white type 'Flamenco' and the green type 'Monteverde'), grown in a soilless system with two electrical conductivities of the nutrient solutions (2.0 and 4.0 dS m⁻¹), were investigated in order to evaluate the effect of salinity on product characteristics and shelf-life during cold storage (14 d at 4°C). Preharvest salinity of 4.0 dS m⁻¹ increased the floret's dry matter and soluble solids content in both genotypes and improved their colour retention during storage. The postharvest CO₂ production was higher in salt-stressed florets compared to control, but after 7 d of storage control florets showed an acceleration in respiratory metabolism, indicating an intensification of senescence processes. Preharvest salt stress increased the concentration of glucosinolates in a genotype-dependent way, improving also the concentration of total polyphenols and ascorbic acid, hence the antioxidant activity of florets. The timecourse of secondary metabolites during storage indicated complex interactions among genotype, preharvest growing conditions and different classes of compounds, whose understanding could help in tailoring specific breeding programmes aimed at improving the postharvest nutraceutical profile of the product. Overall, these results demonstrate that the application of a controlled salt stress, through the use of a soilless system, improves fresh-cut cauliflower characteristics, enhancing also the shelf-life of the product.

来源: Scientia Horticulturae

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全文链接:

<http://agri.ckcest.cn/ass/168829e0-3d95-4a49-b96f-3670d5d2bb13.pdf>

3. Identification of miRNAs that regulate silique development in Brassica napus (调控甘蓝型油菜长角果发育的miRNAs的鉴定)

简介: MicroRNAs (miRNAs) are a class of non-coding small RNAs (sRNAs) that play crucial regulatory roles in various developmental processes. Silique length indirectly influences seed yield in rapeseed (*Brassica napus*); however, the molecular roles of miRNAs in silique length are largely unknown. Here, backcross progenies of rapeseed with long siliques (LS) and short siliques (SS) were used to elucidate these roles. Four small RNA libraries from siliques in an early stage of development were sequenced, and a total of 814 non-redundant miRNA precursors were identified, representing 65 known and 394 novel miRNAs. Expression analyses revealed that 17 miRNAs were differentially expressed in LS and SS lines. Furthermore, through degradome sequencing, we identified 522 cleavage events. Correlation analysis of the differentially expressed miRNAs and their targets suggested that miR159 and miR319 represses cell proliferation and miR160 regulates auxin signal transduction to control silique length. Additionally, the upregulation of miR2111, miR399, miR827, and miR408 reflected restricted silique development due to inorganic phosphate/copper deficiency. More significantly, high expression of miR160 in rapeseed may repress auxin response factors and result in increased silique length, illustrating that silique length might be regulated via an auxin-response pathway.

来源: Plant Science

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全文链接:

<http://agri.ckcest.cn/ass/2688591b-53eb-445b-a7a3-abcbb2b76e10.pdf>

4. Genetic mapping of a lobed-leaf gene associated with salt tolerance in Brassica napus L. (与甘蓝型油菜耐盐性相关的叶缘裂刻基因遗传图谱)

简介: Lobed leaf is a common trait, which is related with photosynthesis and plant stress resistance in crops. In order to fine map and isolate the lobed-leaf gene in *Brassica napus*, an $F_{2:3}$ population derived from 2205 (salt tolerance) and 1423 (salt sensitive) was constructed, and the quantitative trait locus (QTL) technology was adopted to identify the QTLs related to lobed leaf formation. As a result, one major QTL was identified on LG10, and two intron polymorphic (IP) markers and one sequence characterized amplified region (SCAR) marker were successfully developed in QTL region. The lobed-leaf gene was mapped to a region from 15.701 to 15.817 M on A10. In light of annotations of the genes in candidate region, a leaf morphological development related gene, Bra009510, was primary identified as the candidate gene. The full length of the candidate gene was 1390 bp containing three exons and two introns in the two parents. The open reading frame (ORF) was 693 bp and encoded a protein of 229 amino acids. Eight amino acid differences between the two parents in CDS

(coding sequences) region were identified. qRT-PCR analysis showed that the expression of the candidate gene was significantly different between the two parents under salt stress. These results showed that the candidate gene might be related to leaf morphological development and abiotic stresses. Our study will lay a solid foundation for studying lobed leaf mechanism in *B. napus* L.

来源: Plant Science

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全文链接:

<http://agri.ckcest.cn/ass/85234c9f-859e-44b0-a879-edb1f12918a.pdf>