



2018年第47期总161期

蔬菜育种专题

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2018年11月19日

▶ 前沿资讯

1. A protein prevents plants from premature flowering (瑞士研究发现一种可阻止植物过早开花的蛋白质)

简介: 环境因素尤其是光照，对植物的开花时间起着调节作用。但是，这些实验通常都在没有UV-B射线（阳光的自然组分之一）的生长箱里进行。近日，日内瓦大学的一支研究团队发现UV-B可以作为一种有效的开花诱导物，但是一种叫做RUP2的蛋白质从中作梗，阻碍植物过早开花。该研究成果刊登于《Genes & Development》。

植物能够对光照进行感知、“分析”，包括光照的强度、色调、持续时间，并视日照时间长短的变化及季节变化来决定开花时间，即所谓的光周期现象。有些植物会在日照时间变长时开花，有些则相反。因此，植物对日照时间长短的感知对于开花和繁殖至关重要。模式植物拟南芥被用来研究开花过程中的各个机制。

研究团队证明了UV-B在全年时间里都能诱导植物开花，但这种诱导作用在短日照时会被一种称为RUP2的蛋白质所阻碍。通过分析在其中起作用的各个分子机制，生物学家们开始理解RUP2的关键作用。研究表明，不管在哪个季节，UV-B都能刺激产生一种开花激素——FT蛋白质，然后迁移到能够使植物生长的分生组织中去，接着对这种蛋白质进行重新编程，使植物进入开花阶段。然而，RUP2会间接阻碍这种激素的产生，最终抑制植物开花。但是，如果日照时间变长，即便有RUP2存在，植物也会开花。即RUP2蛋白质只在短日照时才会抑制开花。

来源: AAAS

发布日期: 2018-09-27

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9C/Csgk0FvhQkWAWhPAA00gFaxCBc826.pdf>

▶ 学术文献

1. Effects of individual and combined effects of salinity and drought on physiological, nutritional and biochemical properties of cabbage (*Brassica oleracea* var. *capitata*) (盐分和干旱对甘蓝生理、营养和生化特性的个体效应和联合效应)

简介: To understand the effects of salt and drought stress factors on the growth, physiological and biochemical responses of cabbage (*Brassica oleracea* var. *capitata*), a greenhouse experiment was conducted with different levels of salinity (S0: tap water, S1: tap water containing extra 75 mM dose of NaCl, and S2: tap water containing extra 150 mM dose of NaCl), irrigation quantity (W0: Full-irrigation, W1: irrigation with 80% of the W0, and W2: irrigation with 60% of the W0), and their combinations. The results showed that antioxidant activity, proline and sucrose contents increased under both salinity and drought stress as well as their combination. Moreover, oxidative damage indicating parameters such as electrical leakage (EL), malondialdehyde (MDA), and hydrogen peroxide (H₂O₂) increased as well. Increased level of salinity and drought stress caused a decrease in chlorophyll content (SPAD), leaf relative water content (LRWC), stomatal conductance (g_s), net photosynthetic

activity (A_n), intercellular CO_2 content (C_i) and transpiration rate (Tr). We observed that proline and sucrose contents could not stimulate the growth of plant under increased levels of salinity and drought stress. Individual drought and salt stress conditions have negatively affected plant growth including the shoot, root fresh and dry weights when applied separately. On the other hand, the combination of drought and salinity enhanced the adverse effects of each stress factor.

来源: Scientia Horticulturae

发布日期:2018-06-15

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9C/Csgk0FvhQeOAYWCrAA2YjuV1ff8744.pdf>

2. Pathotypes and phylogenetic variation determine downy mildew epidemics in Brassica spp. in Australia (致病型与系统发育变异对澳大利亚芸薹属霜霉病流行的影响)

简介: Isolates of *Hyaloperonospora brassicae* inoculated onto cotyledons of 28 diverse Brassicaceae genotypes, 13 from *Brassica napus*, two from *B. juncea*, five from *B. oleracea*, two from *Eruca vesicaria*, and one each from *B. nigra*, *B. carinata*, *B. rapa*, *Crambe abyssinica*, *Raphanus sativus* and *R. raphanistrum*, showed significant effects ($P \leq 0.001$) of isolate, host and their interaction. Host responses ranged from no visible symptom or a hypersensitive response, to systemic spread and abundant pathogen sporulation. Isolates were generally most virulent on their host of origin. Using an octal classification, six host genotypes were identified as suitable host differentials to characterize pathotypes of *H. brassicae* and distinguished eight distinct pathotypes. There were fewer, but more virulent, pathotypes in 2015-2016 isolates than 2006-2008 pathogen populations, probably explaining the increase in severity of canola downy mildew over the past decade. Phylogenetic relationships determined across 20 *H. brassicae* isolates collected in 2006-2008 and 88 isolates collected in 2015-2016 showed seven distinct clades, with 70% of 2006-2008 isolates distributed within clade I (bootstrap value (BVs) of 100%) and the remaining 30% in clade V (BVs 83.3%). This is the first study to define phylogenetic relationships of *H. brassicae* isolates in Australia, setting a benchmark for understanding current and future genetic shifts within pathogen populations; it is also the first to use octal classification to characterize pathotypes of *H. brassicae*, providing a novel basis for standardizing phenotypic characterization and monitoring of pathotypes on *B. napus* and some crucifer species in Australia.

来源: Plant Pathology

发布日期:2018-03-22

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9C/Csgk0FvhPBeAVwtTAAVTtk83i4E247.pdf>

3. Homoeolog expression bias and expression level dominance in resynthesized allopolyploid Brassica napus (人工合成异源多倍体甘蓝型油菜同源基因表达偏差及表达水平优势)

简介: Background: Allopolyploids require rapid genetic and epigenetic modifications to reconcile two or more sets of divergent genomes. To better understand the fate of duplicate genes following genomic mergers and doubling during allopolyploid formation, in this study, we explored the global gene expression patterns in resynthesized allotetraploid *Brassica napus* (AACC) and its diploid parents *B. rapa* (AA) and *B. oleracea* (CC) using RNA sequencing of leaf transcriptomes.

Results: We found that allopolyploid *B. napus* formation was accompanied by extensive changes (approximately one-third of the expressed genes) in the parental gene expression patterns ('transcriptome shock'). Interestingly, the majority (85%) of differentially expressed genes (DEGs) were downregulated in the allotetraploid. Moreover, the homoeolog expression bias (relative contribution of homoeologs to the transcriptome) and expression level dominance (total expression level of both homoeologs) were thoroughly investigated by monitoring the expression of 23,766 *B. oleracea*-*B. rapa* orthologous gene pairs. Approximately 36.5% of the expressed gene pairs displayed expression bias with a slight preference toward the A-genome. In addition, 39.6, 4.9 and 9.0% of the expressed gene pairs exhibited expression level dominance (ELD), additivity expression and transgressive expression, respectively. The genome-wide ELD was also biased toward the A-genome in the resynthesized *B. napus*. To explain the ELD phenomenon, we compared the individual homoeolog expression levels relative to those of the diploid parents and found that ELD in the direction of the higher-expression parent can be explained by the downregulation of homoeologs from the dominant parent or upregulation of homoeologs from the nondominant parent; however, ELD in the direction of the lower-expression parent can be explained only by the downregulation of the nondominant parent or both homoeologs. Furthermore, Gene Ontology (GO) enrichment analysis suggested that the alteration in the gene expression patterns could be a prominent cause of the phenotypic variation between the newly formed *B. napus* and its parental species.

Conclusions: Collectively, our data provide insight into the rapid repatterning of gene expression at the beginning of *Brassica* allopolyploidization and enhance our knowledge of allopolyploidization processes.

来源: BMC Genomics

发布日期:2018-08-06

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9C/Csgk0FvhNnSAUIWiACQapQJWU8Q849.pdf>

4. Molecular characterization, comparison of screening methods, and evaluation of cross-pathogenicity of black rot (*Xanthomonas campestris* pv. *campestris*) strains from cabbage, choy sum, leafy mustard and pak choi from Taiwan (台湾甘蓝、菜心、叶芥菜和小白菜黑腐病的分子特征、筛选方法比较和交叉致病性评估)

简介: Choy sum (*Brassica rapa* var. *parachinensis*), leafy mustard (*Brassica juncea*) and pak choi (*B. rapa* var. *chinensis*) are highly nutritious components of diets in Taiwan and other Asian countries, and bacterial black rot caused by *Xanthomonas campestris* pv. *campestris*

(Xcc) is a major biotic constraint in these crops. As very little was known about the Xcc strains from these crops in these regions, including their cross-pathogenicity and aggressiveness on different hosts, Xcc strains were obtained from cabbage (*Brassica oleracea* var. *capitata*), choy sum, leafy mustard and pak choi crops in Taiwan. Two previously published PCR-based assays reliably distinguished the Xcc strains from other *Xanthomonas* species and subspecies. Phylogenetic analysis based on repetitive sequence-based PCR assays placed the Xcc strains in a clade distinct from other *Xanthomonas* species, and also showed host specificity. Although all of the Xcc strains from the different host species were pathogenic on all five *Brassica* test species in both a detached leaf assay and an intact plant assay, in the intact plant assay they showed differences in virulence or aggression on the different test hosts. The Xcc strains from leafy mustard and pak choi were consistently highly aggressive on all the test host genotypes, but the strains from choy sum and cabbage were less aggressive on leafy mustard and choy sum. The intact plant assay proved more discriminating and reliable than the detached leaf assay for comparing the aggressiveness of Xcc strains on different host genotypes, and so, with the new Xcc strains isolated in this study, will be useful for screening leafy brassica germplasm accessions for resistance to black rot.

来源: Plant Pathology

发布日期:2018-03-15

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9C/Csgk0FvhMzCADzedAAeNiTQ6P6Y146.pdf>