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蔬菜育种专题

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中国农业科学院农业信息研究所

联系人: 王爱玲

联系电话: 010-51503648

邮箱: agri@ckcest.cn

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▶ 前沿资讯

1. Plants grow less in hotter temperatures (植物在较热的温度下生长迟缓)

简介: 植物已经发展出一种强大的系统,可以在异常高温等恶劣环境中停止它们的细胞周期。在这一响应机制中,它们将能量导向生存而不是生长。日本奈良科学与技术研究所(NAIST)的科学家在eLife上发表了一项新的研究成果称,两种转录因子ANAC044和ANAC085对于开花植物拟南芥中的这种反应至关重要。这些发现为调节农作物和其他农产品的生长提供了线索。

在DNA受损时,植物和动物停止细胞分裂并进行DNA修复,这种反应可以防止受损细胞增殖。NAIST的研究人员正在进行这项保护措施背后的分子生物学研究。

研究人员说,SOG1被DNA损伤激活,并调节几乎所有由损伤诱导的基因。该实验室的另一项研究表明,Rep-MYBs在DNA损伤条件下是稳定的,可以抑制细胞分裂。

在实验室的最新研究中显示,ANAC044和ANAC085是SOG1和Rep-MYBs之间的桥梁。

科学家用博来霉素(一种常用来阻止人类癌细胞生长的化合物)处理拟南芥细胞,破坏了细胞中的DNA,正如预期的那样,拟南芥细胞停止了增殖,除非在ANAC044或ANAC085中有突变。

研究人员发现,ANAC044和ANAC085对根生长迟缓和干细胞死亡至关重要,但对DNA修复并不重要。具体地说,ANAC044和ANAC085负责预防从G2期进入有丝分裂的细胞周期的DNA损伤反应。rep-MYBs在细胞周期中引起相同的停滞。在正常细胞中,博来霉素引起Rep-MYBs积累的增加,但在具有ANAC044和ANAC085突变的细胞中则没有。这些发现表明,ANAC044和ANAC085在DNA损伤后细胞周期停止时充当SOG1和Rep-MYBs之间的桥梁。

DNA损伤只是导致细胞周期暂停的一种应激形式。为了研究ANAC044和ANAC085是否对其他形式的外部压力起作用,研究人员将细胞暴露于分别会导致G2和G1发育迟缓的不同温度和渗透压下。在高渗透压下,突变细胞和正常细胞均出现生长停滞,但较高的温度只会导致正常细胞的细胞周期暂停,这表明在非生物应激条件下,ANAC044和ANAC085在细胞周期的G2期阶段起着把关的作用。ANAC044和ANAC085针对不同类型的非生物胁迫反应表明,它们可能是用于调节植物生长的新技术的核心。

这项研究阐明了一种在压力条件下优化器官生长的新机制。科学家可以考虑使用ANAC044和ANAC085提高植物生产力。

来源: ScienceDaily

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/6A/Csgk0Fy-ehmAYQNCAASQYCZ3PzE193.pdf>

▶ 学术文献

1. Fine-mapping of a gene for the lobed leaf, BoL1, in ornamental kale (*Brassica oleracea* L. var. *acephala*) (叶片(BoL1)基因在观赏羽衣甘蓝(*Brassica oleracea* L. var. *acephala*)中的精细定位)

简介: Leaf shape is an important agronomic trait of ornamental kale (*Brassica oleracea* L. var.

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acephala). In this study, we isolated a lobed-leaf DH line by microspore culture of ornamental kale. The genetic analysis indicated that the lobed-leaf trait was quantitatively inherited. By QTL-seq analysis, the candidate region for BoLl (lobed-leaf) was mapped on chromosome 9 (BRAD, Brassica oleracea, chromosome v1.0). The mapping region was confirmed and narrowed by simple sequence repeat (SSR) and insertion-deletion (Indel) markers in the F2 population; BoLl was located between the markers LYIn39 (0.17 cM) and LYIn40 (0.11 cM). According to the B. oleracea genome database (chromosome v1.0), the mapped interval (75.3 kb) contained eight genes, and seven of which were annotated in BRAD and one was not. According to the other B. oleracea genome information on EnsemblPlant, the mapped interval (79.6 kb) contained 11 genes. Two orthologous genes of AtLMI1/ATHB5 related to lobed leaves in Arabidopsis, BoL010029/Bo9g181710 (BRAD/EnsemblPlant) and BoL010030/Bo9g1181720, were identified as possible genes for BoLl, but the sequence analysis revealed no variation in their promoter and coding regions. The expression of BoL010029/Bo9g181710 and BoL010030/Bo9g1181720 was significantly higher in young lobed leaves than in young entire leaves. Among the other genes in the interval, only BoL010025 and BoL010031/Bo9g181730 showed co-dominance in the recombinant individuals, and their expression level was similar in lobed and entire leaves. Three hypotheses were proposed for the formation of lobed leaf. These results lay a foundation for uncovering the molecular mechanism of the lobed-leaf trait in ornamental kale.

来源: Molecular Breeding

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<http://agri.ckcest.cn/file1/M00/06/6A/Csgk0Fy-ecKAWs3oAB4pzDFqHa8172.pdf>

2. Transcriptome analysis of the irregular shape of shoot apical meristem in dt (duo tou) mutant of Brassica napus L. (甘蓝型油菜dt (多头) 突变体茎尖分生组织不规则形态的转录组分析)

简介: Rapeseed (*Brassica napus* L.) is an important oil crop in the world. In order to fulfill the requirement of mechanized harvesting and raised production, it is highly desirable to gain a better understanding of the regulatory networks controlling the main agronomic traits of this crop. In this study, we obtained a natural mutant of rapeseed with more main stems named as dt (duo tou, meaning more main stems in Chinese). The dt mutant exhibits abnormal differentiation of stems, increased leaves, and decreased plant height. Phenotype and tissue section analysis showed that abnormal development of the shoot apical meristem (SAM) led to the dt phenotype. Genes that participated in SAM activity maintenance, cytokinin biosynthesis, and signal transduction displayed greatly variation at transcriptional level, which was associated with the high level of cytokinin in the dt mutant. These results provide desirable material for improving the breeding and production of *Brassica napus*.

来源: Molecular Breeding

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<http://agri.ckcest.cn/file1/M00/06/6A/Csgk0Fy-dzmAWnLhAIbWAUxXjEA106.pdf>

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3. Development of a PCR test for detection of *Xanthomonas campestris* pv. *Raphani* (用于检测黄单胞菌*Xanthomonas campestris* pv. *Raphani*的PCR试验的开发)

简介: Leaf spot of Brassica is an important bacterial seed borne disease caused by *X. campestris* pv. *raphani* (Xcr), one of the three pathovars of *Xanthomonas campestris* species which makes significant economic loss throughout the world. A rapid and reliable detection method will be helpful for early diagnosis of the disease. To do that, we designed Xcr specific sequence-characterized amplified region (SCAR) markers from the Xcr specific genomic fragments, identified by aligning the whole genome sequences of several closely related bacterial pathovars and other bacterial species. Our primer set Xcr_59 produced Xcr specific amplicon of 679 bp in PCR assays. This primer pair was also capable of detecting Xcr strains directly from the artificially infected leaf samples prepared by suspending the diseased leaf area in sterile water without extracting bacterial DNA. This rapid, sensitive and reliable detection technique will be useful for adopting any firsthand plant protection measures against the disease.

来源: Australasian Plant Pathology

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<http://agri.ckcest.cn/file1/M00/06/6A/Csgk0Fy9Y1aAA2CFAAeHZ-ps5SE889.pdf>

4. Chromosome level comparative analysis of Brassica genomes (芸苔属基因组的染色体水平比较分析)

简介: Key message We provided a chromosome-length assembly of *B. nigra* and show the comprehensive chromosome-scale variations among Brassica genomes.

Abstract Chromosome-level assembly of the Brassica species, which include many important crops, is essential for the agricultural and evolutionary studies. While the present *B. nigra* chromosomes was connected with genetic map of *B. juncea*, hindering the comparative analysis of the B chromosomes. Here we present a chromosome-length *B. nigra* assembly constructed with Hi-C connections and its variations on chromosome level compared with other Brassica species. We produced an assembly of 484 Mb annotated with 51,829 genes, of which 393 Mb were anchored onto 8 chromosomes, taking 81.26% of the assembly. Comparison of the B chromosomes shows high concordance of the two *B. nigra* assemblies and reveals comprehensive variations of the B chromosomes after polyploidization and gene loss in syntenic regions. Chromosome blocks with variations have lower gene density and higher TE content. Furthermore, we compared the chromosomes of the three major Brassica diploids, which showed that most of the variations between B and A/C had completed before A/C divergence and there are more variations on C chromosomes after their divergence. In summary, our work presents a chromosome-length assembly of *B. nigra* and comprehensive comparative analysis of the Brassica chromosomes, which provides a useful reference for other studies and comprehensive information of Brassica chromosome evolution.

来源: Plant Molecular Biology

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5. Resistances to downy mildew (*Hyaloperonospora brassicae*) in diverse Brassicaceae offer new disease management opportunities for oilseed and vegetable crucifer industries (不同十字花科植物对霜霉病 (*Hyaloperonospora brassicae*) 的抗性为油料作物和十字花科蔬菜的病害防治提供了新的机遇)

简介: Some 154 Brassicaceae genotypes (78 *Brassica napus*, 38 *B. carinata*, 25 *B. juncea*, three *Raphanus sativus*, two each of *Rapistrum rugosum* and *B. incana* and one each of *Crambe abyssinica*, *B. fruticulosa*, *Hirschfeldia incana*, *B. insularis*, *B. oleracea* and *Sinapis arvensis*), were inoculated with a mixture of seven isolates of *Hyaloperonospora brassicae* to identify effective host resistances. Many highly resistant genotypes were identified, particularly *R. sativus* Krasnodar Market B (%Disease index 6.6) and *Pegletta* (%DI 9.0); *B. carinata* Tamn Rex-sel Green (%DI 7.6), BRA926/18 (%DI 9.7) and PI360884 (%DI 9.7); and *B. juncea*, Ringot1 (%DI 9.7). A further 13 *B. carinata*, seven *B. juncea* and single *R. sativus* (Boss) and *B. incana* (UPM6563) genotypes were also highly resistant (%DI 11.1), as were *B. oleracea* CPI106844 (%DI 14.6) and *Crambe abyssinica* (%DI 17.4). Almost all *B. carinata* and *B. juncea* genotypes showed high resistance (%DI 7.622.2). In contrast, *B. napus* genotypes showed wide ranging responses, from high resistance in SN-8 (%DI 22.2%) to extreme susceptibility in Hyola 450TT and Thunder TT (%DI 83.7, 95.5, respectively). *R. rugosum*, *B. fruticulosa*, *H. incana* and *B. insularis* genotypes ranged from moderately to highly susceptible (%DI 55.2-78.8). This study highlights the ready availability of very high levels of pathotype-independent resistance across diverse Brassicaceae to *H. brassicae*, particularly *R. sativus*, *B. carinata*, *B. juncea*, *B. oleracea* and *C. abyssinica*. Resistances identified can be utilized as sources of resistance in oilseed and vegetable Brassicaceae breeding programs and/or directly deployed as new varieties where downy mildew is prevalent.

来源: European Journal of Plant Pathology

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