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蔬菜育种专题

本期导读

▶ 前沿资讯

1. CRISPR新技术可实现单点精确“敲除”基因

▶ 学术文献

1. 油菜春化处理过程中长链非编码RNAs机制的比较转录组学研究和阐释
2. FANCM基因限制油菜的减数分裂交叉
3. 冬季栽培期间干旱胁迫对油菜栽培种质量特征的影响
4. 转录因子WRKY15和WRKY33的相互作用及其在油菜核盘菌感染抗性中的作用

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. New CRISPR technology 'knocks out' yeast genes with single-point precision (CRISPR新技术可实现单点精确“敲除”基因)

简介: 日前, 来自美国伊利诺伊大学的研究人员基因编辑技术以及同源修复技术, 开发出了一种叫做CHANGE的工具, 能够只删除某一DNA序列中的单个碱基。这可以让研究人员分别研究每个基因的作用, 以及该基因与其他基因的共同作用。研究成果发表在《自然》子刊《Nature Biotechnology》上。之前, 研究人员利用CRISPR-Cas9基因编辑技术删除或“敲除”酵母中的一个基因, 来研究每个基因如何促进细胞功能。但是, 因为许多基因相互重叠, 删除一个基因也会删除其他基因的某些部分, 影响到多种功能, 使研究人员难以真正分离出单个基因的影响。利用CHANGE工具精确敲除单个碱基后, 与编辑过的基因重合的基因仍将保持不变且功能正常。研究人员可以在整个染色体上只引入一项碱基变化, 这样对相邻基因功能的干扰将会是最小的, 因此可以研究单个基因的重要性。如此高的精确度是前所未有的, 而且还具有快速、高效和低成本的优点。过去, 敲除酵母中的每个基因需要好几个团队花费数年的时间, 现在通过“CHANGE”技术, 只需一名研究人员就可以在大约一个月的时间里做出酵母整个基因组的突变体。

来源: ScienceDaily

发布日期: 2018-05-07

全文链接:

<https://www.sciencedaily.com/releases/2018/05/180507174020.htm>

➤ 学术文献

1. Comparative transcriptome discovery and elucidation of the mechanism of long noncoding RNAs during vernalization in Brassica rapa (油菜春化处理过程中长链非编码RNAs机制的比较转录组学研究和阐释)

简介: Flowering time is an important agronomic trait in Brassica rapa (*B. rapa*). However, our current understanding of the role of long noncoding RNAs (lncRNAs) in flowering time responded to vernalization is limited. The rapid development of the omics sequencing technology has facilitated the identification of thousands of lncRNAs in various plant species. Here, we used comparative transcriptome analysis between control and vernalized *B. rapa* to identify differentially expressed genes (DEGs) and lncRNAs (DELs). A total of 300 DEGs and 254 DELs were identified. Co-localization networks consisting of 128 DEGs and 127 DELs were established, followed by analyses of hierarchical categories, functional annotations, and correlation from mRNA-to-lncRNA. We found that the BraZF-HD21 (Bra026812) gene which responds to photoperiods and vernalization is correlated with lncRNA TCONS_00035129. The correlated genes that were mapped to the plant hormone signal transduction pathway and increased gibberellin A3 (GA₃) content demonstrated that vernalization influences plant hormone levels. These findings suggest that vernalization alters the process of hormone biosynthesis, which in turn regulates flowering. This study provides

an approach to elucidation of the regulatory mechanism of lncRNAs during vernalization in *B. rapa*.

来源: Plant Growth Regulation

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全文链接:

<http://agri.ckcest.cn/ass/7e023421-e802-4120-afb7-1450b89873ef.pdf>

2. FANCM Limits Meiotic Crossovers in Brassica Crops (FANCM基因限制油菜的减数分裂交叉)

简介: Meiotic crossovers (COs) are essential for proper chromosome segregation and the reshuffling of alleles during meiosis. In WT plants, the number of COs is usually small, which limits the genetic variation that can be captured by plant breeding programs. Part of this limitation is imposed by proteins like FANCM, the inactivation of which results in a 3-fold increase in COs in *Arabidopsis thaliana*. Whether the same holds true in crops needed to be established. In this study, we identified EMS induced mutations in FANCM in two species of economic relevance within the genus Brassica. We showed that CO frequencies were increased in *fancm* mutants in both diploid and tetraploid Brassicas, *Brassica rapa* and *Brassica napus* respectively. In *B. rapa*, we observed a 3-fold increase in the number of COs, equal to the increase observed previously in *Arabidopsis*. In *B. napus* we observed a lesser but consistent increase (1.3-fold) in both euploid (AACC) and allohaploid (AC) plants. Complementation tests in *A. thaliana* suggest that the smaller increase in crossover frequency observed in *B. napus* reflects residual activity of the mutant C copy of FANCM. Altogether our results indicate that the anti-CO activity of FANCM is conserved across the Brassica, opening new avenues to make a wider range of genetic diversity accessible to crop improvement.

来源: Frontiers in Plant Science

发布日期:2018-03-28

全文链接:

<http://agri.ckcest.cn/ass/5c2d921d-8cf3-4073-9bb8-6113f15266d4.pdf>

3. Effect of drought stress on qualitative characteristics of canola cultivars in winter cultivation (冬季栽培期间干旱胁迫对油菜栽培种质量特征的影响)

简介: To determine the appropriate canola cultivars for winter cultivation under late-season drought stress conditions, a factorial split-plot test was conducted in a complete randomized blocks design with three replications for two cultivation years (2014-2016) in Karaj, Iran. In this work, cultivations at two levels included fall cultivation (Oct. 7) and winter cultivation (Feb. 4). The irrigation was conducted at three levels including routine irrigation (control), irrigation interruptions from flowering and pod formation stage in factorial status in main plots and five *Brassica napus* L. cultivars including Sarigol, Delgan, Giacomo, Jerumeh and Hyola 401 in subplots. The interaction effect of cultivation date \times irrigation \times cultivar on the features of palmitic acid, linolenic acid, linoleic acid, oleic acid, erucic acid, glucosinolate

and oil yield was significant at the level of 1%. The results indicated that Delgan cultivar with the highest oil yield (1582 kg/ha) in the winter cultivation date and normal irrigation conditions as well as with standard levels of erucic acid and glucosinolate can be effective in canola cultivation in the new stage of winter cultivation. Moreover, in winter cultivation and in the late-season drought stress conditions, hybrids Hyola 401 with the highest seed yield, and standard oligosaccharide and glucosinolate can also be recommended in late-season drought stress conditions.

来源: Industrial Crops & Products

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全文链接:

<http://agri.ckcest.cn/ass/409eb70c-ae39-40a5-8ad1-6a1221299f1e.pdf>

4. Interactions of WRKY15 and WRKY33 transcription factors and their roles in the resistance of oilseed rape to Sclerotinia infection (转录因子WRKY15和WRKY33的相互作用及其在油菜核盘菌感染抗性中的作用)

简介: WRKY transcription factors are known to participate in the defence responses of higher plants. However, little is known about the roles of such proteins, especially regarding their functions in the resistance of oilseed rape (*Brassica napus*) to *Sclerotinia sclerotiorum*, a necrotrophic fungal pathogen that causes stem rot. In this study, we identified BnWRKY33 as a *S. sclerotiorum*-responsive gene that positively regulates resistance to this pathogen by enhancing the expression of genes involved in camalexin synthesis and genes regulated by salicylic acid (SA) and jasmonic acid (JA). We also identified a *S. sclerotiorum*-responsive region in the promoter of BnWRKY33, which we revealed to be a relatively conserved W-box region in the promoters of homologous genes in different species. Using this *S. sclerotiorum*-responsive region as bait in a yeast onehybrid assay, we identified another WRKY transcription factor, BnWRKY15, and observed that both BnWRKY15 and BnWRKY33 could bind to this region. In addition, BnWRKY15 overexpression simultaneously increased the susceptibility of *B. napus* to *S. sclerotiorum* and down-regulated BnWRKY33 after different durations of infection. Furthermore, BnWRKY15, which contains a transcriptional repression domain, exhibited reduced transactivation ability and could reduce the transactivation ability of BnWRKY33 in *Arabidopsis* protoplast assays. Therefore, we suggest that the increased susceptibility of BnWRKY15-overexpressing plants results from reduced BnWRKY33 expression, which is due to the inhibition of BnWRKY33 transcriptional activation by BnWRKY15.

来源: Plant Biotechnology Journal

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全文链接:

<http://agri.ckcest.cn/ass/de718145-6071-43b8-822c-3c0c04dc74e7.pdf>