



2017年第49期总111期

蔬菜育种专题

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➤ 前沿资讯

1. Genome of wheat ancestor sequenced (小麦祖先的基因组测序)

简介: 面包小麦对于全球食品供应至关重要, 为人类提供了超过20%的卡路里和23%的蛋白质。由于面包小麦基因组庞大的规模和复杂性, 其测序长期以来一直被认为是一项几乎不可逾越的任务。

目前, 加州大学戴维斯分校的研究人员领导的一个国际科研团队通过测序面包小麦的野生祖先基因组来解决这个难题, 这种面包小麦属于山羊草属, 称为粗山羊草 (*Ae. Tauschii*)。研究人员为具有高适应性和广谱抗病性的*Ae. Tauschii* 制作了参考质量的基因组序列, 它也是制作面包所用的小麦基因的主要来源。这一成果11月15日发表在《自然》杂志上。

研究结果将有助于发现能够提高小麦烘烤质量, 抗病性和耐霜冻, 忍耐干旱和盐度等极端环境条件的新基因。该研究团队已经发现了两个新的抗小麦秆锈病的基因, 而在小麦中几乎没有这种抗性。这两个基因已经从*Ae. Tauschii* 克隆到了小麦中, 目前可供小麦育种人员使用。

小麦及其野生祖先的基因组比人类基因组庞大得多, 这使得测序困难。该研究团队在大约20年前开始进行小麦基因组研究, 但当时还没有技术能对这种大规模和复杂的基因组进行测序。研究还发现*Ae. Tauschii* 有超过84%的基因组由密切相关的重复序列组成。

该成果所使用的技术可以应用于任何植物基因组, 其意义已经超越了小麦。

来源: AAAS

发布日期: 2017-11-15

全文链接:

https://www.eurekalert.org/pub_releases/2017-11/uoc--gow111517.php

➤ 学术文献

1. Genome-wide identification and expression analysis of calmodulin-like (CML) genes in Chinese cabbage (*Brassica rapa* L. ssp. *pekinensis*) (大白菜中钙调蛋白基因的全基因组鉴定和表达分析)

简介: Background: Calmodulin-like (CML) proteins are a primary family of plant-specific Ca^{2+} sensors that specifically bind to Ca^{2+} and deliver a Ca^{2+} signal. CML proteins have been identified and characterized in many plant species, such as the model plant *Arabidopsis* and rice. Based on considerable evidence, the roles of CML proteins are crucial in plant growth and development and in the response to various external stimuli. Nevertheless, the characterization and expression profiling of CML genes in Chinese cabbage (*Brassica rapa* L. ssp. *pekinensis*) remain limited.

Results: In this study, a genome-wide search and comprehensive analysis were performed, and a total of 79 BrCML genes were identified in Chinese cabbage. Gene structure analysis revealed that these BrCML genes contained two to four conserved EF-hand motifs.

Phylogenetic analysis showed that CML homologs between Chinese cabbage and Arabidopsis shared close relationships. The identified BrCML genes were located across ten chromosomes and three different subgenomes of Chinese cabbage. Moreover, 126 pairs of orthologous CML genes were found among Chinese cabbage, Arabidopsis and Brassica oleracea. Expression analysis revealed that the expression of some BrCML genes was tissue-specific and that of some was susceptible to temperature stress. A putative interaction network of BrCML proteins was proposed, which suggested that BrCML2, BrCML6, BrCML15 and BrCML25 were co-expressed and might play roles in flower development and other relevant biological processes of Chinese cabbage.

Conclusions: The results of this study increased the understanding and characterization of BrCML genes in Chinese cabbage, and will be a rich resource for further studies to investigate BrCML protein function in various developmental processes of Chinese cabbage.

来源: BMC Genomics

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全文链接:

<http://agri.ckcest.cn/ass/aal69f8-9fec-4874-a1bc-ebac32a05000.pdf>

2 . XCC2366, A Gene Encoding A Putative TetR Family Transcriptional Regulator, is Required for Acriflavin Resistance and Virulence of Xanthomonas campestris pv. Campestris (XCC2366, 一个编码假定的TetR家族转录调节因子的基因, 对于吡啶黄抗性和野油菜黄单胞菌的毒力是必需的)

简介: *Xanthomonas campestris* pv. *campestris* (Xcc) is the phytopathogen that causes black rot disease in cruciferous plants. The XCC2366 gene product is annotated as a protein belonging to the TetR family of transcriptional regulators. In this study, we evaluated the function and expression of the XCC2366 gene. Mutational analysis demonstrated that XCC2366 is involved in the resistance to acriflavin and is necessary for virulence in Xcc. In addition, the XCC2366 transcription initiation site was mapped at nucleotide A, 63 nucleotide upstream of the XCC2366 translation start codon. Furthermore, transcriptional analysis revealed that the expression of XCC2366 is induced in the presence of acriflavin. Reporter assay also showed that XCC2366 regulates its own expression under acriflavin-supplemented condition. To the best of our knowledge, acriflavin resistance-related gene in the crucifer pathogen Xcc was characterized for the first time.

来源: Curr Microbiol

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全文链接:

<http://agri.ckcest.cn/ass/fb7941e3-e3ba-4b7f-9501-fda7da89182f.pdf>

3. Genetic and Cytological Analyses of the Natural Variation of Seed Number per Pod in Rapeseed (*Brassica napus* L.) (油菜每荚种子数自然变异的遗传和细胞学分析)

简介: Seed number is one of the key traits related to plant evolution/domestication and crop improvement/breeding. In rapeseed germplasm, the seed number per pod (SNPP) shows a very wide variation from several to nearly 30; however, the underlying causations/mechanisms for this variation are poorly known. In the current study, the genetic and cytological bases for the natural variation of SNPP in rapeseed was firstly and systematically investigated using the representative four high-SNPP and five low-SNPP lines. The results of self- or cross-pollination experiment between the high- and low-SNPP lines showed that the natural variation of SNPP was mainly controlled by maternal effect (mean = 0.79), followed by paternal effect (mean = 0.21). Analysis of the data using diploid seed embryocyttoplasmicmaternal model further showed that the maternal genotype, embryo, and cytoplasm effects, respectively, explained 47.6, 35.2, and 7.5% of the genetic variance. In addition, the analysis of combining ability showed that for the SNPP of hybrid F1 was mainly determined by the general combining ability of parents (63.0%), followed by special combining ability of parental combination (37.0%). More importantly, the cytological observation showed that the SNPP difference between the high- and low-SNPP lines was attributable to the accumulative differences in its components. Of which, the number of ovules, the proportion of fertile ovules, the proportion of fertile ovules to be fertilized, and the proportion of fertilized ovules to develop into seeds accounted for 30.7, 18.2, 7.1, and 43.9%, respectively. The accordant results of both genetic and cytological analyses provide solid evidences and systematic insights to further understand the mechanisms underlying the natural variation of SNPP, which will facilitate the development of high-yield cultivars in rapeseed.

来源: Frontiers in Plant Science

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全文链接:

<http://agri.ckcest.cn/ass/4f44f99e-f5be-4e79-928c-34f416451db6.pdf>

4 . Identification of candidate genes involved in fatty acids degradation at the late maturity stage in Brassica napus based on transcriptomic analysis (基于转录组学分析技术鉴定油菜成熟后期脂肪酸降解的候选基因)

简介: In rapeseed (*Brassica napus*), the reduction of seed oil content (SOC) at the late maturity stage is widely observed in most rapeseed cultivars. However, the molecular mechanism relevant to the SOC reduction (i.e. fatty acids degradation) at the late stage is not clearly understood. In this study, we investigated dynamic accumulation of the SOC in the developing seeds of a cultivar Zhongyou-511 using gas chromatography and changes of transcriptomic profile in the seeds at different stages using RNA-seq respectively. The total SOC of Zhongyou-511 was decreased by 14% at 55 days after pollination (DAP) in comparison with that at 40 DAP. Transcriptomic analysis revealed that the majority of genes involved in fatty acids biosynthesis as well as β -oxidation for lipids degradation were significantly up-regulated at the late maturity stage, including BnaA09g32380D and BnaC08g23150D homologous genes of acyl-CoA oxidase 4 and BnaA03g15290D and

BnaC04g11470D homologous genes of 3-ketoacyl-CoA thiolase 2. These results indicate that the increased expression of candidate genes in the β -oxidation pathway maybe cause the SOC reduction at the late maturity stage. The current study would be helpful for increasing our knowledge on the molecular mechanism of the SOC reduction and for utilizing candidate genes for high SOC breeding in rapeseed.

来源: Plant Growth Regul

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全文链接:

<http://agri.ckcest.cn/ass/12312e9e-732f-4997-9930-7a5e0c8d547e.pdf>