



2019年第4期总171期

蔬菜育种专题

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前沿资讯

1. Sunflower pan-genome analysis shows that hybridization altered gene content and disease resistance (向日葵的泛基因组分析)

简介: 驯化的动物和植物通常对于选择的响应有所差异,但人们对其中所隐藏的遗传多样性还了解甚少。栽培种向日葵具有非常高的遗传变异,可能是由于栽培种和近缘野生种的杂交所导致的。为了了解向日葵中的遗传多样性以及向日葵野生近缘种对于栽培种遗传资源的贡献,来自以色列的科学家对287个栽培种品系、17个美国地方种以及代表了11个向日葵野生近缘种的189个个体进行了重测序分析。研究人员将栽培种每个基因型重测序数据未能比对到向日葵参考基因组上的序列进行了从头组装,以获得全部栽培种向日葵的基因库,也就是泛基因组信息。通过对组装的栽培种的基因与野生近缘种的基因进行比较,以确定基因的起源。结果显示,向日葵栽培种泛基因组总共61205个基因,其中27%在不同基因型之间存在变异。大约10%的栽培种泛基因组来自于野生近缘种的渗入,而1.5%的基因来自于基因渗入。基因本体富集分析进一步揭示了在基因渗入区域显著富集了与生物抗性相关的一些基因,这与育种实践中所观察到的现象一致。霜霉病抗性相关的等位基因变异分析作为一个鲜明的例子,说明了基因渗入在提升向日葵对某些日益严重的疾病抗性方面发挥重要作用。

来源: Nature Plants

发布日期: 2018-12-31

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5C/Csgk0Fw79wOASStNABv6MDFajuc588.pdf>

学术文献

1. Mapping of QTLs controlling seed weight and seed-shape traits in *Brassica napus* L. using a high-density SNP map (利用高密度SNP图谱绘制控制甘蓝型油菜种子重量与形态性状的QTL图谱)

简介: Thousand seed weight (TSW) is an important trait in oilseed rape. Seed shape and seed size, which directly affect seed weight, can be characterized by seed length, seed width, length-width ratio, seed cross-section area, seed circumference, seed diameter and seed roundness. In the present study, a high-density SNP map containing 2812 bins (involving 11,458 SNPs) was used for the QTL analysis of the eight traits. As a result, 177 identified QTLs were detected in five environments, 25 for TSW and 152 for seven seed-shape traits. These QTLs were integrated into 149 consensus QTLs by a meta-analysis, including one (TSW, length-width ratio, seed length and seed width), two (seed circumference and seed diameter) and three (seed roundness) QTLs accounted for more than 10.0% of the phenotypic variation (PV). The further integration of these consensus QTLs resulted in 63 unique QTLs, of which 34 controlled at least two different traits. Notably, the unique QTL uqC2-1 affected all eight traits and explained 6.60-7.57% of the PV. Furthermore, 19 pairs of epistatic loci were detected and explained 2.39-19.17% of the PV. These results provide useful information to increase the understanding of the genetic basis of TSW and seed-shape traits.

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<http://agri.ckcest.cn/file1/M00/06/5B/Csgk0Fw766-AV1lnACMS1mgZ1bk523.pdf>

2. Genetic characterization and fine mapping for multi-inflorescence in *Brassica napus* L. (甘蓝型油菜多花序的遗传特征和精细定位)

简介: **Key message** A major QTL for multi-inflorescence was mapped to a 27.18-kb region on A05 in *Brassica napus* by integrating QTL mapping, microarray analysis and whole-genome sequencing.

Multi-inflorescence is a desirable trait for the genetic improvement of rapeseed (*Brassica napus* L.). However, the genetic mechanism underlying the multi-inflorescence trait is not well understood. In the present study, a doubled haploid (DH) population derived from a cross between single- and multi-inflorescence lines was investigated for the penetrance of multi-inflorescence across 3 years and genotyped with 257 simple sequence repeat and sequence-related amplified polymorphism loci. A major quantitative trait locus (QTL) for penetrance of multi-inflorescence was mapped to a 9.31-Mb region on chromosome A05, explaining 45.81% of phenotypic variance on average. Subsequently, 13 single-inflorescence and 15 multi-inflorescence DH lines were genotyped with the *Brassica* microarray, and the QTL interval of multi-inflorescence was narrowed to a 0.74-Mb region with 37 successive single nucleotide polymorphisms between single- and multi-inflorescence groups. A 27.18-kb QTL interval was detected by screening 420 recessive F2 individuals with genome-specific markers. These results will be valuable for gene cloning and molecular breeding of multi-inflorescence in rapeseed.

来源: Theoretical and Applied Genetics

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<http://agri.ckcest.cn/file1/M00/06/5B/Csgk0Fw779qALUyPACWDV4j5Jsg474.pdf>

3. Genome-wide identification, and phylogenetic and expression profiling analyses of CaM and CML genes in *Brassica rapa* and *Brassica oleracea* (甘蓝和芜菁CaM、CML基因的全基因组鉴定、系统发育及表达谱分析)

简介: Calmodulin (CaM) and calmodulin-like (CML) proteins are two kinds of calcium (Ca^{2+})-sensing proteins that are involved in Ca^{2+} -signaling processes. *B. rapa* and *B. oleracea* are two of three diploid *Brassica* species that have undergone recent additional Brassicaceae-lineage-specific whole-genome triplication events. To elucidate the expansion, evolution, expression pattern and interaction network of these Ca^{2+} sensors in *B. rapa* and *B. oleracea*, we conducted a comparative syntenic study on a genome-wide level using *Arabidopsis thaliana*. In total, 80 and 79 CaM/CML genes were identified in *B. rapa* and *B. oleracea*, respectively. The CaM/CML genes have expanded throughout the whole genomes of *B. rapa* and *B. oleracea* by whole-genome and tandem duplication events. The

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CaMs/CMLs of *B. rapa* and *B. oleracea* can be classified into nine subgroups based on their *A. thaliana* orthologs. Expression data from various tissues revealed that a large portion of CaM/CML genes exhibited patterns of differential and tissue-specific expression. The expression levels among duplicated paralogs in different subgenomes demonstrated the expression divergence of these genes in *B. rapa* and *B. oleracea*. The differential expressions of duplicated CaM and CML genes in *B. rapa* indicated that their functional differentiation occurred after polyploidization. The construction of interaction network and GO enrichment analysis of genes in this network revealed Br/BoCaMs/CMLs involving biological processes. This work will promote a better understanding of Ca²⁺ sensors and Ca²⁺-signaling pathways in *B. rapa* and *B. oleracea*.

来源: Gene

发布日期: 2018-07-17

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5B/Csgk0Fw79XqASmrPADqMamNnskM116.pdf>

4. Evaluating multiple resistance to major diseases in a core set of inbred lines of *Brassica rapa* at seedling stage (甘蓝核心自交系苗期多重抗病性评价)

简介: Years of continuous cropping of *Brassica rapa* crops in main producing areas in China lead to the outbreak of some diseases, such as downy mildew (DM), turnip mosaic virus (TuMV), black rot (BR), verticillium wilt (VW), and club root (CR), causing severe loss in yield and quality. Resistance to the aforementioned diseases of 302 inbred lines of *Brassica rapa* to DM, TuMV, BR, VW, and CR were evaluated under controlled conditions at seedling stage. Forty lines were identified to be highly resistant to DM, 13 to TuMV, 0 to BR, 30 to VW, and 24 to CR. Among the 302 lines, 121 exhibited high resistance to two diseases, 70 to three diseases, and eight to four diseases, but none of these lines showed comprehensive resistance to all the five diseases. Chinese cabbage lines XDYFX, 536S, 536Q, DY×T, and CR-C, and Pak choi lines DFAK×SH, NB, and SYHTC showed high resistance to four diseases and therefore represent elite materials in multiple-disease resistance breeding. In addition, different disease resistance tendencies were discovered in diverse Chinese cabbage groups which were classified in different ways, such as the ecotype, heading-type, and geographical origin.

来源: Journal of Plant Pathology

发布日期: 2018-06-06

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5B/Csgk0Fw78LCABWkrABE-aJg-pDQ371.pdf>