



2018年第40期总154期

蔬菜育种专题

本期导读

▶ 前沿资讯

1. 澳英科学家成功克隆三个抗条锈病基因

▶ 学术文献

1. 剖析三种种子质量性状的遗传结构及对甘蓝型油菜育种的影响
2. 拟南芥和甘蓝中J-蛋白的系统发育优势分类
3. 全基因组鉴定甘蓝型油菜的己糖激酶基因家族：结构、系统发育分析、表达和功能表征
4. 甘蓝生物钟相关基因（BoCCA1）等位变异与抗冻性有关

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

2018年10月1日

▶ 前沿资讯

1. Australian, UK scientists solve 30-year wheat rust genetics puzzle (澳英科学家成功克隆三个抗条锈病基因)

简介：锈病是小麦波及面最广、最具破坏性的病害之一，其中条锈病因能适应不同气候和环境而最难防控。现有小麦品种中能对抗条锈病的基因寥寥无几。澳大利亚和英国的研究人员日前首次成功分离了抗条锈病的主要基因。

世界小麦锈病研究的带头人悉尼大学罗伯特·帕克（Robert Park）教授及其谷类锈病研究团队于2015年培养出突变种群并识别出每个基因的突变体。同期，英国研究人员也在研究其中两个基因。两国科学家在2017年了解到了彼此的研究工作并开始合作。

研究人员克隆了三个抗条锈病的相关基因，即Yr7、Yr5、YrSP。这一研究发现将有助于准确监测这三个重要基因，并将其整合到育种项目中，对抗能致死约70%小麦作物的条锈病多变病原体。在此之前，克隆一个小麦抗性基因需时多年。但随着变异基因组学、测序、克隆技术的进步，克隆出全部三个基因的时间大大缩短。

研究人员表示，这一研究大大加深了对小麦抗性基因免疫受体蛋白的了解：尽管基因结构非常类似，但每个基因都具备对条锈病病原体的特异性识别。这一发现揭示了三个基因间的关系，回答了一个30年来悬而未决的难题。这一研究也是首次真正实现条锈病主要抗病基因的分子分离。

相关诊断标记业已开发完成，这三个基因很快就能够应用到全球小麦育种当中。这一突破还能帮助实现对锈病病原体无效基因的编辑，重新恢复其抗病效用，以减少杀菌剂的使用。

来源：AAAS

发布日期：2018-08-27

全文链接：

<http://agri.ckcest.cn/ass/3a1eddb1-7b36-4ba8-a816-d120b691f4a0.pdf>

▶ 学术文献

1. Dissection of the genetic architecture of three seed-quality traits and consequences for breeding in Brassica napus (剖析三种种子质量性状的遗传结构及对甘蓝型油菜育种的影响)

简介：Genome-wide association studies (GWASs) combining high-throughput genome resequencing and phenotyping can accelerate the dissection of genetic architecture and identification of genes for plant complex traits. In this study, we developed a rapeseed genomic variation map consisting of 4 542 011 SNPs and 628 666 INDELS. GWAS was performed for three seed-quality traits, including erucic acid content (EAC), glucosinolate content (GSC) and seed oil content (SOC) using 3.82 million polymorphisms in an association panel. Six, 49 and 17 loci were detected to be associated with EAC, GSC and SOC in multiple environments, respectively. The mean total contribution of these loci in each environment was 94.1% for EAC and 87.9% for GSC, notably higher than that for SOC (40.1%). A high correlation was observed between phenotypic variance and number of

favourable alleles for associated loci, which will contribute to breeding improvement by pyramiding these loci. Furthermore, candidate genes were detected underlying associated loci, based on functional polymorphisms in gene regions where sequence variation was found to correlate with phenotypic variation. Our approach was validated by detection of well-characterized FAE1 genes at each of two major loci for EAC on chromosomes A8 and C3, along with MYB28 genes at each of three major loci for GSC on chromosomes A9, C2 and C9. Four novel candidate genes were detected by correlation between GSC and SOC and observed sequence variation, respectively. This study provides insights into the genetic architecture of three seed-quality traits, which would be useful for genetic improvement of *B. napus*.

来源: Plant Biotechnology Journal

发布日期:2017-12-19

全文链接:

<http://agri.ckcest.cn/ass/9663a930-c0e3-4172-9c91-b4bcf1f9c59e.pdf>

2. Phylogeny-dominant classification of J-proteins in *Arabidopsis thaliana* and *Brassica oleracea* (拟南芥和甘蓝中J-蛋白的系统发育优势分类)

简介: Hsp40s or DnaJ/J-proteins are evolutionarily conserved in all organisms as co-chaperones of molecular chaperone HSP70s that mainly participate in maintaining cellular protein homeostasis, such as protein folding, assembly, stabilization, and translocation under normal conditions as well as refolding and degradation under environmental stresses. It has been reported that *Arabidopsis* J-proteins are classified into four classes (types AD) according to domain organization, but their phylogenetic relationships are unknown. Here, we identified 129 J-proteins in the world-wide popular vegetable *Brassica oleracea*, a close relative of the model plant *Arabidopsis*, and also revised the information of *Arabidopsis* J-proteins based on the latest online bioresources. According to phylogenetic analysis with domain organization and gene structure as references, the J-proteins from *Arabidopsis* and *B. oleracea* were classified into 15 main clades (I-XV) separated by a number of undefined small branches with remote relationship. Based on the number of members, they respectively belong to multigene clades, oligo-gene clades, and mono-gene clades. The J-protein genes from different clades may function together or separately to constitute a complicated regulatory network. This study provides a constructive viewpoint for J-protein classification and an informative platform for further functional dissection and resistant genes discovery related to genetic improvement of crop plants.

来源: Genome

发布日期:2018-04-05

全文链接:

<http://agri.ckcest.cn/ass/eb6be61b-cc56-4e6a-9618-835ab28fe5d5.pdf>

3. Genome-wide identification of hexokinase gene family in *Brassica napus*: structure, phylogenetic analysis, expression, and functional

characterization (全基因组鉴定甘蓝型油菜的己糖激酶基因家族：结构、系统发育分析、表达和功能表征)

简介： Main conclusion Genome-wide identification, expression analysis, and functional characterization of previously uncharacterized hexokinase family of oil crop, Brassica napus, underscore the importance of this gene family in plant growth and development.

In plants, the multi-gene family of dual-function hexokinases (HXKs) plays important roles in sugar metabolism and sensing that affect growth and development. Rapeseed (*Brassica napus* L.) is an important oil crop; however, little is known about the *B. napus* HXK gene family. We identified 19 putative HXKs in *B. napus* genome. *B. rapa* and *B. oleracea*, the two diploid progenitors of *B. napus*, contributed almost equally to the BnHXK genes. Phylogenetic analysis divided the 19 BnHXKs into four groups. The exon-intron structures of BnHXKs share high similarity to those of HXKs in *Arabidopsis* and rice. The group III and IV BnHXKs are highly expressed in roots, whereas group I members preferentially express in leaves. Analysis of seed transcriptomes at different developmental stages showed that most of group I and IV HXKs are highly expressed 2-weeks after pollination (2WAP), compared to 4WAP for group III. BnHXKs are differentially expressed in susceptible and tolerant *B. napus* cultivars after fungal infection, suggesting the possible involvement in defense response. We generated rapeseed RNAi lines for BnHXK9, a member of relatively less characterized group IV, by pollen-mediated gene transformation. The seedlings of BnHXK9-RNAi lines showed delayed growth compared to the wild type. The RNAi plants were dwarf with curly leaves, suggesting the involvement of BnHXK9 in plant development. Collectively, our findings provides a comprehensive account of BnHXK gene family in an important crop and a starting point for further elucidation of their roles in sugar metabolism and sensing, as well as plant growth and development.

来源: Planta

发布日期:2018-04-11

全文链接:

<http://agri.ckcest.cn/ass/07650146-0488-43a2-9ee4-96d959dfea2b.pdf>

4. Allelic variation in Brassica oleracea CIRCADIAN CLOCK ASSOCIATED 1 (BoCCA1) is associated with freezing tolerance (甘蓝生物钟相关基因 (BoCCA1) 等位变异与抗冻性有关)

简介：Freezing tolerance is an important horticultural trait in cabbage (*Brassica oleracea*). Molecular markers for freezing tolerance are needed for marker-assisted breeding of freezing-tolerant cabbage plants. To develop gene-based molecular markers for freezing-tolerance in cabbage, we focused on CIRCADIAN CLOCK ASSOCIATED 1 (CCA1), a core circadian clock component that affects metabolic pathways and confers cold tolerance by upregulating C-repeat binding factor (CBF) pathway genes. We cloned and analyzed CCA1 genes (BoCCA1s) from seven inbred lines and one cultivar of *B. oleracea* ssp. *capitata*. Two types of BoCCA1 alleles were detected: BN106-type (freezing-tolerant; BoCCA1-1) and BN107-type (freezing-susceptible; BoCCA1-2). Numerous insertions/deletions (InDels), simple sequence repeats, and single nucleotide polymorphisms

(SNPs) were found in the exons and introns of BoCCA1s from the ATG start codon at the second exon to the TGA stop codon at the eighth exon. Using InDels and SNPs, we designed PCR primer pairs to distinguish the freezing-tolerant lines, and validated these markers using 102 cabbage lines and cultivars. The inbred lines possessed either the BN106-type or BN107-type allele, but most cultivars had both alleles. Freezing-tolerant cabbage plants had BN106-type InDels and/or BN106-type SNPs regardless of the presence of BN107-type InDels and SNPs, and BN106-type SNPs were more widely detected in the freezing-tolerant cabbage plants than BN106-type InDels. The expression patterns of BoCCA1-1 and BoCCA1-2 were similar under normal versus temperature-stressed conditions (low and high temperatures), suggesting a functional difference at the post-transcriptional level. Cabbage breeders should use several markers derived from different genes and independently established inbred lines from different seed companies.

来源: Horticulture, Environment, and Biotechnology

发布日期: 2018-04-20

全文链接:

<http://agri.ckcest.cn/ass/941f4264-f304-4604-b2fe-c12e6380e9dc.pdf>