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蔬菜育种专题

本期导读

前沿资讯

学术文献

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前沿资讯

1. Research identifies mechanism that helps plants fight bacterial infection(美国研究发现能够帮助植物抵抗细菌感染的机制)

简介：日前，美国加州大学河滨分校植物病理研究小组发现，植物中有一种调节性遗传机制有助于抵抗细菌感染。通过这种分子调节机制，研究人员可以诱发作物对细菌性病原体的免疫反应。研究结果刊登于《自然-通讯》杂志。

研究小组以拟南芥为试材研究发现，RNA干扰机制中的主要核心蛋白AGO蛋白质，在细菌感染过程中被一个称为“翻译后修饰”（post-translationalmodification）的过程所控制。这个过程控制着AGO蛋白质及其相关的小RNA的水平，小RNA是通过干扰基因表达来调节生物过程的分子。这在调节RNA干扰机制方面提供了双重安全性。RNA干扰（RNA interference，简称RNAi）是许多生物体用来调节基因表达的重要细胞机制，包括关闭基因，也被称为“基因沉默”。

此前的一项研究发现，拟南芥的10种AGO蛋白质中有一种由细菌感染诱发的蛋白有助于植物免疫——这种蛋白的水平越高，植物的免疫能力就越强。然而，高水平的蛋白质会限制植物的生长。

在正常的植物生长条件下，AGO蛋白及其相关的小RNA被精氨酸甲基化（AGO蛋白的一种翻译后修饰）很好地控制。这可以调节AGO蛋白并防止其积聚到高水平。与AGO蛋白相关的小RNA也被阻止积累到更高的水平，从而使植物为生长节省能量。

然而，在细菌感染过程中，AGO蛋白质的精氨酸甲基化被抑制，从而导致AGO蛋白及其相关的小RNA的积累，这些小RNA有助于植物免疫。这两个变化共同作用，使植物既能生存又能自我保护。

如果在正常条件恢复后，AGO蛋白质和相关的小RNA保持在如此的高水平，将不利于植物生长。但在正常条件下恢复的AGO蛋白质的翻译后修饰降低了AGO蛋白质和小RNA的水平以促进植物生长。

所有植物都具有RNAi机制，以及与植物免疫相关的AGO蛋白质的等效物。RNA沉默在所有哺乳动物、植物和大多数真核生物中都存在。

此这项研究之前，病原体攻击过程中，AGO蛋白是如何被控制的，以及植物的免疫应答是如何被RNAi机制调节的，一直是个谜。该研究首次揭示了翻译后修饰调控植物免疫应答中的RNAi机制。

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学术文献

1. Evaluation and Recommendations for Routine Genotyping Using Skim Whole Genome Re-sequencing in Canola(利用全基因组浅层重测序对油菜（canola）进行常规基因分型的评价与建议)

简介：Whole genome sequencing offers genome wide, unbiased markers, and inexpensive

library preparation. With the cost of sequencing decreasing rapidly, many plant genomes of modest size are amenable to skim whole genome resequencing (skim WGR). The use of skim WGR in diverse sample sets without the use of imputation was evaluated in silico in 149 canola samples representative of global diversity. Fastq files with an average of 10x coverage of the reference genome were used to generate skim samples representing 0.25x, 0.5x, 1x, 2x, 3x, 4x, and 5x sequencing coverage. Applying a predefined list of SNPs versus de novo SNP discovery was evaluated. As skim WGR is expected to result in some degree of insufficient allele sampling, all skim coverage levels were filtered at a range of minimum read depths from a relaxed minimum read depth of 2 to a stringent read depth of 5, resulting in 28 list-based SNP sets. As a broad recommendation, genotyping pre-defined SNPs between 1x and 2x coverage with relatively stringent depth filtering is appropriate for a diverse sample set of canola due to a balance between marker number, sufficient accuracy, and sequencing cost, but depends on the intended application. This was experimentally examined in two sample sets with different genetic backgrounds: 1x coverage of 1,590 individuals from 84 Australian spring type four-parent crosses aimed at maximizing diversity as well as one commercial F1 hybrid, and 2x coverage of 379 doubled haploids (DHs) derived from a subset of the four-parent crosses. To determine optimal coverage in a simpler genetic background, the DH sample sequence coverage was further down sampled in silico. The flexible and cost-effective nature of the protocol makes it highly applicable across a range of species and purposes.

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2. Carotenoid Presence Is Associated with the Or Gene in Domesticated Carrot(栽培胡萝卜中类胡萝卜素的存在与Or基因有关)

简介： Carrots are among the richest sources of provitamin A carotenes in the human diet, but genetic variation in the carotenoid pathway does not fully explain the high levels of carotenoids in carrot roots. Using a diverse collection of modern and historic domesticated varieties, and wild carrot accessions, an association analysis for orange pigmentation revealed a significant genomic region that contains the Or gene, advancing it as a candidate for carotenoid presence in carrot. Analysis of sequence variation at the Or locus revealed a nonsynonymous mutation cosegregating with carotenoid content. This mutation was absent in all wild carrot samples and nearly fixed in all orange domesticated samples. Or has been found to control carotenoid presence in other crops but has not previously been described in carrot. Our analysis also allowed us to more completely characterize the genetic structure of carrot, showing that the Western domesticated carrot largely forms one genetic group, despite dramatic phenotypic differences among market classes. Eastern domesticated and wild accessions form a second group, which reflects the recent cultivation history of carrots in Central Asia. Other wild accessions form distinct geographic groups, particularly on the

Iberian peninsula and in Northern Africa. Using genome-wide F_{st}, nucleotide diversity, and the cross-population composite likelihood ratio, we analyzed the genome for regions putatively under selection during domestication and identified 12 regions that were significant for all three methods of detection, one of which includes the Or gene. The Or domestication allele appears to have been selected after the initial domestication of yellow carrots in the East, near the proposed center of domestication in Central Asia. The rapid fixation of the Or domestication allele in almost all orange and nonorange carrots in the West may explain why it has not been found with less genetically diverse mapping populations.

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3. Molecular cloning, characterization and expression analysis of BcHHP3 under abiotic stress in Pak-choi (Brassica rapa ssp. Chinensis)(小白菜在非生物胁迫下BcHHP3的分子克隆、表征及表达分析)

简介：In this study, BcHHP3 was isolated from Pak-choi; it has an open-reading frame (ORF) of 1044 base pairs, encoding 347 amino acids, a molecular weight of 39.35 kDa, isoelectric point (pI) of 9.08, an instability index of 48.35, and grand average of hydropathicity of 0.382. Multi-alignment and phylogenetic analysis showed that BcHHP3 bears a high similarity to AtHHP2. As predicted by SOMPA and SWISS-MODEL databases, the structure of the BcHHP3 protein is relatively stable and highly conservative. Real-time quantitative polymerase chain reaction (qRT-PCR) analysis showed that BcHHP3 was induced to co-express under cold and abscisic acid (ABA) stresses. The BcHHP3-GFP fusion protein was localized on the cell membrane and nuclear membrane. This work might be useful for future analysis of other HHP-like genes in Pak-choi.

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4. Genetic dissection of the mechanism of flowering time based on an environmentally stable and specific QTL in Brassica napus(基于环境稳定、特定QTL的欧洲油菜开花时间机制的遗传解剖)

简介：Flowering time is an important agronomic trait that is highly influenced by the environment. To elucidate the genetic mechanism of flowering time in rapeseed (Brassica napus L.), a genome-wide QTL analysis was performed in a doubled haploid population grown in winter, semi-winter and spring ecological conditions. Fifty-five consensus QTLs were identified after combining phenotype and genomic data, including 12 environment-stable QTLs and 43 environment-specific QTLs. Importantly, six major QTLs for flowering time were identified, of which two were considered environment-specific QTLs

in spring ecological condition and four were considered environment-stable QTLs in winter and semi-winter ecological conditions. Through QTL comparison, 18 QTLs were colocalized with QTLs from six other published studies. Combining the candidate genes with their functional annotation, in 49 of 55 consensus QTLs, 151 candidate genes in B. napus corresponding to 95 homologous genes in Arabidopsis thaliana related to flowering were identified, including BnaC03g32910D (CO), BnaA02g12130D (FT) and BnaA03g13630D (FLC). Most of the candidate genes were involved in different flowering regulatory pathways. Based on re-sequencing and differences in sequence annotation between the two parents, we found that regions containing some candidate genes have numerous non-frameshift InDels and many non- synonymous mutations, which might directly lead to gene functional variation. Flowering time was negativly correlated with seed yield and thousand seed weight based on a QTL comparison of flowering time and seed yield traits, which has implications in breeding new early-maturing varieties of B. napus. Moreover, a putative flowering regulatory network was constructed, including the photoperiod, circadian clock, vernalization, autonomous and gibberellin pathways. Multiple copies of genes led to functional difference among the different copies of homologous genes, which also increased the complexity of the flowering regulatory networks. Taken together, the present results not only provide new insights into the genetic regulatory network underlying the control of flowering time but also improve our understanding of flowering time regulatory pathways in rapeseed.

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