蔬菜育种专题

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前沿资讯

1. No rest for weary canola plants——High nighttime temperatures negatively impact plant production（夜间高温影响油菜产量）

简介：虽然植物不会像人一样睡觉，但有些植物却像人一样在高温下休息不好。夜间温度升高，油菜的产量就会下降。科学家正在试图找寻这一现象背后的原因。

油菜是人类食用植物油的第三大来源。油菜籽粕也是仅次于豆粕的第二大饲料。在美国，大部分的油菜籽粕用于饲喂奶牛，除此之外还用于生产生物柴油。美国的主要油菜种植区在北部平原区和东南各州。在世界范围内，油菜主要在冬季种植，对高温非常敏感，产量会随温度上升而下降。

夜间是油菜进行细胞保养的时间，以保证有足够的能量来产生新细胞，修护旧细胞。夜间的高温胁迫会改变油菜的各种生理过程，最终导致结实率、籽粒数、灌浆持续期、灌浆速率和最终粒重的降低。

研究人员发现，冬油菜在花期和种子形成时期更容易受到夜间高温的影响。科研人员研究了油菜在正常条件和夜间高温条件下的开花时间，以及最终的种子质量。结果表明，20℃-22.8℃（68-73华氏度）的高温对油菜产量有着明显的负面影响。夜间高温会引起油菜早上的开花时间提前。而开花时间的早晚会影响到油菜从受精到最终结实率的各个方面。

研究人员认为，全球气候变暖使得夜间的升温效应更为明显，而夜间高温的影响也会更长远。研究人员正试图培育受夜间高温影响较小的油菜品种，以适应将来的气候变暖。

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学术文献

1. Cloning of the Brcre1 gene involved in cuticular wax production in a glossy mutant of non-heading Chinese cabbage (Brassica rapa L. var. communis)（不结球白菜表皮光泽突变体中参与表皮蜡质产生的Brcre1基因克隆）

简介：Cuticular wax is a complex mixture of very-long-chain fatty acid derivatives. The wax on the surface of plants serves as a protective barrier to reduce non-stomatal water loss and environmental damage. However, the loss of wax may lead to a glossy phenotype, which is an favorable trait in leafy vegetables. The mechanism of glossy mutants in non-heading Chinese cabbage (Brassica rapa L. var. communis) has not been studied yet. In this study, scanning electron microscopy (SEM) showed that the cuticular wax on the leaves and stem of a glossy mutant was dramatically reduced compared with that of the wild-type plant. Transmission electron microscopy (TEM) revealed that the cuticle ultrastructure of glossy mutant leaf and stem were altered when compared with the wild type. A cuticle wax analysis showed the total wax content of leaves, as well as alkanes, ketones and alcohols, was decreased. A genetic analysis indicated that the glossy phenotype was controlled by a single
Based on a homology analysis, the Brcer1 gene was identified as the candidate gene controlling the glossy phenotype. In the glossy mutant, a 39-bp deletion leads to an mRNA disruption and reduces the expression of the BrCER1 gene. Sequence analysis showed that a loss of function mutation in the BrCER1 gene was different from that of Cgl1, which was previously shown to be responsible for the glossy phenotype in B. oleracea, showing typical parallel selection. These findings provide a better understanding of the cuticular wax biosynthesis pathway and offer important information for molecular-assisted breeding of non-heading Chinese cabbage (B. rapa L. var. communis).

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2. GWAS, QTL mapping and gene expression analyses in Brassica napus reveal genetic control of branching morphogenesis

简介：Branch number is an important trait in plant architecture that can influence crop yield and quality in Brassica napus. Here, we detected the QTLs responsible for branch number in a DH population and its reconstructed F2 population over two years. Further, a GWAS research on branch number was performed using a panel of 327 accessions with 33186 genomic SNPs from the 60 K Brassica Illumina® Infinium SNP array. Through combining linkage analysis and association mapping, a new QTL was fine mapped onto C03. Subsequently, we tested the correlations between the SNP polymorphisms and mRNA expression levels of genes in the target interval to identify potential loci or genes that control branch number through expression. The results show that 4 SNP loci are associated with the corresponding gene expression levels, and one locus (BnaC03g63480D) exhibited a significant correlation between the phenotype variation and gene expression levels. Our results provide insights into the genetic basis for branching morphogenesis and may be valuable for optimizing architecture in rapeseed breeding.

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3. Abiotic Stress Responsive miRNA-Target Network and Related Markers (SNP, SSR) in Brassica juncea

简介：Abiotic stress is one of the major factors responsible for huge yield loss in crop plants. MicroRNAs play a key role in adaptive responses of plants under abiotic stress conditions through post-transcriptional gene regulations. In present study, 95 potential miRNAs were
predicted in Brassica juncea using comparative genomics approach. It was noted that these miRNAs, target several transcription factors (TFs), transporter family proteins, signaling related genes, and protease encoding genes. Nineteen distinct miRNA-target regulatory networks were observed with significant involvement in regulation of transcription, response to stimulus, hormone and auxin mediated signaling pathway related gene ontology (GO) term. The sucrose-starch metabolism and pentose-gluconate interconversion pathways were found significantly enriched for these target genes. Molecular markers such as Simple Sequence Repeats (SSR) and Single Nucleotide Polymorphism (SNPs) were identified on miRNAs (miR-SSRs and miR-SNPs) and their target genes in B. juncea. Notably, one of the miR-SNP (C/T) was found at the 5th position on mature region of miR2926. This C/T transition led to the distorted and unstable hairpin structure of miR2926, consequently complete loss of target function. Hence, findings from this study will lay a foundation for marker assisted breeding for abiotic stress tolerant varieties of B. juncea.

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4. Identification of candidate genes involved in fatty acids degradation at the late maturity stage in Brassica napus based on transcriptomic analysis（基于转录组学分析鉴定甘蓝型油菜晚熟期与脂肪酸降解相关的候选基因）

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.

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