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蔬菜育种专题

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► 学术文献

1. Integrated genetic mapping and transcriptome analysis reveal the BnaA03.IAA7 protein regulates plant architecture and gibberellin signaling in Brassica napus L. (综合遗传图谱和转录组分析揭示了 Brassica 油菜的 BnaA03. IAA7蛋白调节植物结构和赤霉素信号传导)

简介: Rapeseed (*Brassica napus*) is an excellent and important source for vegetable oil production, but its production is severely affected by lodging. Lodging hinders mechanization and decreases yield, and an ideal solution is semidwarf breeding. Limited by germplasm resources, semidwarf breeding developed slowly in rapeseed. In the current study, a mutant called sdA03 was isolated from EMS-mutagenized lines of Zhongshuang 11 (ZS11). The inheritance analysis showed that phenotypes of sdA03 were controlled by a single semidominant gene. Genetic mapping, RNA-seq and candidate gene analysis identified BnaA03.IAA7 as a candidate gene, and a function test confirmed that the mutated BnaA03.iaa7 regulates plant architecture in a dose-dependent manner. Yeast two-hybrid and transient expression experiments illustrated the P87L substitution in the GWPPV/I degen motif of BnaA03.iaa7 impaired the interaction between BnaA03.IAA7 and TIR1 proteins, and BnaA03.iaa7 prevented ARF from activating the auxin signaling pathway. The gibberellin (GA) content was higher in sdA03 hypocotyls than in those of ZS11. Further expression analysis showed more active gibberellin signaling in hypocotyl and richer expression of GA synthetic genes in root and cotyledon of sdA03 seedlings. Finally, a marker was developed based on the SNP found in BnaA03.iaa7 and used in molecular breeding. The study enriched our understanding of the architectural regulation of rapeseed and provided germplasm resources for breeding.

来源: Theoretical and Applied Genetics

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<http://agri.ckcest.cn/file1/M00/03/3D/Csgk0Ydu6BKANpurACj5LC1n7bQ196.pdf>

2. The chloroplast genome of *Farsetia hamiltonii* Royle, phylogenetic analysis, and comparative study with other members of Clade C of Brassicaceae (Farsetia hamiltonii Royle 叶绿体基因组、系统发育分析以及与十字花科 Clade C 其他成员的比较研究)

简介: *Farsetia hamiltonii* Royle is a medicinally important annual plant from the Cholistan desert that belongs to the tribe Anastaticae and clade C of the Brassicaceae family. We provide the entire chloroplast sequence of *F. hamiltonii*, obtained using the Illumina HiSeq2500 and paired-end sequencing. We compared *F. hamiltonii* to nine other clade C species, including *Farsetia occidentalis*, *Lobularia libyca*, *Notoceras bicornis*, *Parolinia ornata*, *Morettia canescens*, *Cochlearia borzaiana*, *Megacarpaea polyandra*, *Biscutella laevigata*, and *Iberis amara*. We conducted phylogenetic research on the 22 Brassicaceae species, which

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included members from 17 tribes and six clades.

The chloroplast genome sequence of *F.hamiltonii* of 154,802 bp sizes with 36.30% GC content and have a typical structure comprised of a Large Single Copy (LSC) of 83,906 bp, a Small Single Copy (SSC) of 17,988 bp, and two copies of Inverted Repeats (IRs) of 26,454 bp. The genomes of *F. hamiltonii* and *F. occidentalis* show shared amino acid frequencies and codon use, RNA editing sites, simple sequence repeats, and oligonucleotide repeats. The maximum likelihood tree revealed *Farsetia* as a monophyletic genus, closely linked to *Morettia*, with a bootstrap score of 100. The rate of transversion substitutions (Tv) was higher than the rate of transition substitutions (Ts), resulting in Ts/Tv less than one in all comparisons with *F. hamiltonii*, indicating that the species are closely related. The rate of synonymous substitutions (Ks) was greater than non-synonymous substitutions (Ka) in all comparisons with *F. hamiltonii*, with a Ka/Ks ratio smaller than one, indicating that genes underwent purifying selection. Low nucleotide diversity values range from 0.00085 to 0.08516, and IR regions comprise comparable genes on junctions with minimal change, supporting the conserved status of the selected chloroplast genomes of the clade C of the Brassicaceae family. We identified ten polymorphic regions, including *rps8-rpl14*, *rps15-ycf1*, *ndhG-ndhI*, *psbK-psbI*, *ccsA-ndhD*, *rpl36-rps8*, *petA-psbJ*, *ndhF-rpl32*, *psaJ-rpl3*, and *ycf1* that might be exploited to construct genuine and inexpensive to solve taxonomic discrepancy and understand phylogenetic relationship amongst Brassicaceae species.

The entire chloroplast sequencing of *F. hamiltonii* sheds light on the divergence of genic chloroplast sequences among members of the clade C. When other *Farsetia* species are sequenced in the future, the full *F. hamiltonii* chloroplast will be used as a source for comprehensive taxonomical investigations of the genus. The comparison of *F. hamiltonii* and other clade C species adds new information to the phylogenetic data and evolutionary processes of the clade. The results of this study will also provide further molecular uses of clade C chloroplasts for possible plant genetic modifications and will help recognise more Brassicaceae family species.

来源: BMC Plant Biology

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<http://agri.ckcest.cn/file1/M00/10/0F/Csgk0GMYOAmALRgcAFmRbpcm9sw076.pdf>

3. Genome-wide identification and functional analysis of cupin_1 domain-containing members involved in the responses to *Sclerotinia sclerotiorum* and abiotic stress in *Brassica napus* (甘蓝型油菜对菌核病和非生物胁迫响应中cupin_1结构域成员的全基因组鉴定及功能分析)

简介: Cupin_1 domain-containing proteins (CDPs) are ubiquitously present in higher plants, which are known to play essential roles in various biological processes. In this study, we carried out genome-wide characterization and systematic investigation of the CDP genes in *Brassica napus*. A total of 96 BnCDPs, including 71 germin-like proteins (GLPs; proteins with a single cupin_1 domain) and 25 CDP bicupins (proteins with two cupin_1 domains),

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were identified and clustered into six distinct subfamilies (I-VI) based on the phylogenetic analysis, gene structure and motif distribution. Further analysis indicated that whole-genome duplication (WGD) and segmental duplication are main contributors to the species-specific expansion of the BnCDP gene family, and all the duplicated genes subsequently underwent strong purification selection. The promoter region of BnCDPs showed enrichment of cis-regulatory elements associated with development, hormone and stress, as well as transcription factor binding sites, which validates the prediction that BnCDPs are widely involved in plant growth and biotic and abiotic stress responses. The BnCDPs in different subfamilies exhibited obvious differences in expression among 30 developmental tissues/stages of *B. napus*, implying that BnCDPs may be involved in tissue- and stage-specific developmental processes. Similar trends in expression of most BnCDPs were observed under *Sclerotinia sclerotiorum* inoculation and four abiotic stresses (dehydration, cold, ABA and salinity), particularly the BnGLPs in subfamily I and III with single cupin_1 domain, revealing that BnCDPs are of great importance in the environmental adaption of *B. napus*. We then performed a genome-wide association study (GWAS) of 274 *B. napus* core germplasms on *S. sclerotiorum* resistance and identified four significantly associated loci harboring five BnGLPs. The expression levels of two candidate genes, BnGLP1.A08 and BnGLP1.C08, were significantly correlated with *S. sclerotiorum* resistance. Their functional responses to multiple stages of *S. sclerotiorum* inoculation and four abiotic stresses were further examined through qPCR. Overall, this study provides rich resources for research on the function and evolutionary playground of CDP genes.

来源: Front Plant Sci

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<http://agri.ckcest.cn/file1/M00/03/3D/Csgk0Ydu6bWALdn8AIzEmNEzo6E357.pdf>

4. Effect of Melatonin in Broccoli Postharvest and Possible Melatonin Ingestion Level (利用褪黑激素改善西兰花保存能力的研究)

简介: The post-harvest stage of broccoli production requires cold storage to obtain enough days of shelf life. It has been proved that melatonin is useful as a post-harvest agent in fruits and vegetables, including broccoli. In this study, the broccoli heads treated with melatonin have a longer shelf life than the control samples, which was reflected in parameters such as fresh weight, hue angle (expresses color quality), and chlorophyll and carotenoid contents. Treatments with 100 μ M melatonin for 15 or 30 min seem to be the most appropriate, extending the broccoli's shelf life to almost 42 days, when it is normally around 4 weeks. In addition, a study on the possible impact that melatonin treatments in broccoli could have on melatonin intake in humans is presented. The levels of superficial melatonin, called washing or residual melatonin, are measured, showing the possible incidence in estimated blood melatonin levels. Our results suggest that post-harvest treatments with melatonin do not have to be a handicap from a nutritional point of view, but more research is needed.

来源: Plants

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<http://agri.ckcest.cn/file1/M00/10/0F/Csgk0GMYPC-AcndZADGRMwKT4K8864.pdf>

5 . HSP70 Gene Family in Brassica rapa: Genome-Wide Identification, Characterization, and Expression Patterns in Response to Heat and Cold Stress (油菜 HSP70 基因家族: 全基因组鉴定、表征和表达模式对热和冷应激的反应)

简介: Heat shock proteins protect plants from abiotic stress, such as salt, drought, heat, and cold stress. HSP70 is one of the major members of the heat shock protein family. To explore the mechanism of HSP70 in Brassica rapa, we identified 28 putative HSP70 gene family members using state-of-the-art bioinformatics-based tools and methods. Based on chromosomal mapping, HSP70 genes were the most differentially distributed on chromosome A03 and the least distributed on chromosome A05. Ka/Ks analysis revealed that B. rapa evolution was subjected to intense purifying selection of the HSP70 gene family. RNA-sequencing data and expression profiling showed that heat and cold stress induced HSP70 genes. The qRT-PCR results verified that the HSP70 genes in Chinese cabbage (Brassica rapa ssp. pekinensis) are stress-inducible under both cold and heat stress. The upregulated expression pattern of these genes indicated the potential of HSP70 to mitigate environmental stress. These findings further explain the molecular mechanism underlying the responses of HSP70 to heat and cold stress.

来源: Cells

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