



2018年第42期总156期

蔬菜育种专题

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➤ 前沿资讯

1. Researchers unlock secrets of plant development (加拿大: 研究揭示植物发育的秘密)

简介: 加拿大不列颠哥伦比亚大学 (UBC) 的研究人员发现了植物体内的一种内部信息系统, 用于调控植物细胞的生长和分裂。该系统由一种名为CLASP (Cytoplasmic Linker Associated Protein) 的蛋白所驱动。该蛋白存在于植物、动物和真菌中, 通过协调细胞内微管的组装, 在细胞生长和分裂中扮演重要角色。研究成果近日发表在《当代生物学》(Current Biology) 杂志上。

研究人员将拟南芥暴露于高水平油菜素类固醇的环境中发现: 一种被称为油菜素类固醇的植物生长激素会减少CLASP蛋白的产生。这种做法会导致植物发育不良, 其表现与完全缺乏CLASP蛋白质的植物突变体非常相似。进一步的实验最终证明CLASP蛋白的确是油菜素类固醇的直接靶标。研究人员发现CLASP可以防止油菜素类固醇受体的降解。当CLASP缺乏时, 油菜素类固醇的效果会减弱, 这又会导致CLASP水平再次上升。也就是说, CLASP蛋白和油菜素类固醇会相互影响, 形成负反馈循环。

这些研究结果首次表明CLASP蛋白可以通过直接维持激素水平来调节自身表达, 从而掌控自己的命运。下一步研究人员拟利用这种机制培育出能感知环境并调整自身发展的智能植物, 以便在日益恶劣的条件下依然能够保障作物生产。这一新的发现有望帮助农业找到更好应对气候变化的新方法。

来源: AgroPages

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<http://agri.ckcest.cn/ass/8a6db5a9-87b9-491a-9965-3d9f8d11324a.pdf>

➤ 学术文献

1. Genetic investigation and cytological comparison of two genic male sterile lines 9012A and MSL in Brassica napus L. (甘蓝型油菜两个核不育系9012A和MSL的遗传研究及细胞学比较)

简介: Genic male sterility (GMS) is one of the effective pollination control systems in hybrid rapeseed (*Brassica napus* L.) breeding. The recessive GMS lines 9012A and Lembke (MSL) have made a great contribution to the utilization of heterosis in rapeseed. Cytological observation and genetic investigation were employed to reveal anther abortion characters and genetic relationship of 9012A and MSL. Cytological and transmission electron microscopy observation revealed that anther abortion of 9012A and MSL initiated at the microsporocyte stage, both lines showed premature or retarded degradation of tapetum. Some anthers in 9012A developed to the microspore stage since their tapetal cells changed to the secretory type. However, MSL anthers did not progress to the tetrad stage, since the tapetum did not change to the secretory type. Genetic investigation revealed that MSL and 9012A had the same temporary maintainer system, while their cytoplasm types were different. The cytoplasm of MSL was similar to Cam while 9012A was similar to Nap type. The results laid

a solid foundation for utilization of the two male sterile lines in rapeseed hybrid breeding.

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2. Genetic diversity, genetic structure and migration routes of wild *Brassica juncea* in China assessed by SSR markers (中国芥菜型油菜遗传多样性、遗传结构及迁移途径的SSR分析)

简介: The wild *Brassica juncea* (L.) Czern. et Coss., systematically belonging to the genus *Brassica* L. in the Cruciferae family, has become a noxious weed for cropping systems nowadays. Here, simple sequence repeat (SSR) markers were applied to investigate the genetic diversity, genetic structure and migration routes of the wild *B. juncea* populations in China. The results showed that a total of 90 alleles, with extensive allelic diversity, were observed at the 11 SSR loci of the wild *B. juncea*. The STRUCTURE analysis indicated that all the 25 wild populations were best described as belonging to two lineages. High F_{st} value (0.568), together with the partitioning, provided significant evidence for lineage differentiation in wild *B. juncea*. The high differentiation between the two lineages was, perhaps, due to limited gene flow ($N_m = 0.301$) of this species. The analysis of molecular variance with distances among individuals corrected for the dominant nature of SSRs showed that most of the variation (59%) occurred within populations, and the remaining 41% variance was attributed to differences among populations. The distribution of diversity across China was significantly geographically dependent. NJ cluster analysis, based on genetic distance, grouped populations geographically, which further corroborated spatial pattern of two lineages. Based on these results, two routes were proposed for the migration of wild *B. juncea* in China after its origin from northwest China, heading east along the Yellow River or Yangtze River, respectively. We concluded that China, especially the northwest, is one of the primary origins of *B. juncea*.

来源: Genetic Resources and Crop Evolution

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<http://agri.ckcest.cn/ass/58b67205-5bdb-4084-8f45-94a8203f1483.pdf>

3. QTL Mapping of Seed Glucosinolate Content Responsible for Environment in *Brassica napus* (甘蓝型油菜种子硫代葡萄糖苷含量的QTL分析)

简介: Glucosinolates (GSLs) are a major class of secondary metabolites. The content of seed GSL is largely regulated by environments in rapeseed (*Brassica napus*). However, the genetic control of seed GSL content responsible for environment in *B. napus* has been poorly understood. In the current study, a doubled haploid (DH) population from a cross between winter and semi-winter lines of rapeseed was grown in two distinct eco-environments, Germany and China, to evaluate the eco-environment effect and dissect the quantitative trait

loci (QTL) responsible for environment for seed GSL in rapeseed. The deviation value of GSL content between eco-environments (GSLE) was calculated for each line in the DH population and the QTLs for GSLE were detected. GSLE ranged from -46.90 to $36.13\mu\text{mol g}^{-1}$ meal in the DH population, suggesting the prominent eco-environmental effects for seed GSL in rapeseed. Four QTLs for GSLE were identified on chromosomes A04, A06, and A09 explaining 4.70~9.93% of the phenotypic variation. Comparison of QTLs of seed GSL content between different eco-environments found three QTLs for GSL on A02 from 37.6 to 45.4 cM, A04 from 0 to 17.2 cM, and A09 from 67.0 to 98.6 cM exhibited significant difference of QTL effect between the German and Chinese eco-environments ($P < 0.01$), indicating the environment sensibility of these loci on seed GSL content. Moreover, flowering time (FT), an important environment adaptation trait in plant, was also investigated in this study. Comparative QTL analysis among GSLE, GSL, and FT revealed that three regions on chromosomes A02, A04, and A09 not only exhibited significant differences in QTL effect between Germany and China, but also co-located with the QTL intervals of GSLE and FT. Our results revealed that most of the GSL loci can influence GSL accumulation under different eco-environments, whereas the three QTL intervals on A02, A04, and A09 might be sensitive to the eco-environments for seed GSL content.

来源: Frontiers in Plant Science

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4. Genomic methylation and transcriptomic profiling provides insights into heading depression in inbred *Brassica rapa* L. ssp. *pekinensis* (通过基因组甲基化和转录组学分析洞察近交大白菜抽穗衰退)

简介: Inbreeding depression is the reduction in fitness observed in inbred populations. In plants, it leads to disease, weaker resistance to adverse environmental conditions, inhibition of growth, and decrease of yield. To elucidate molecular mechanisms behind inbreeding depression, we compared global DNA methylation and transcriptome profiles of a normal and a highly inbred heading degenerated variety of the Chinese cabbage (*Brassica rapa* L. ssp. *pekinensis*). DNA methylation was reduced in inbred plants, suggesting a change in the epigenetic landscape. Transcriptome analysis by RNA-Seq revealed that genes in auxin-response and synthesis pathways were differentially expressed in the inbreeding depression lines. Interestingly, methylation levels of some of those genes were also changed. Furthermore, endogenous IAA content was decreased in inbred plants, in agreement with expression and methylation data. Chemical inhibition of auxin also replicated the degenerated phenotype in normal plants, while exogenous IAA application had no effect in inbred depression plants, suggesting a more complex mechanism. These data indicate DNA methylation-regulated auxin pathways play a role in establishing inbred depression phenotypes in plants. Our findings reveal new insights into inbreeding depression and leafy head development in Chinese cabbage.

来源: Gene

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