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蔬菜育种专题

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▶ 前沿资讯

1. Plant seed research provides basis for sustainable alternatives to chemical fertilizers (植物种子内生菌研究为化肥和农药的可持续替代提供了基础)

简介: 下一代测序技术的最新进展使科学家得以接触和评估以前无法检测到的植物微生物。科学家们早就知道,各种与植物有关的微生物有助于植物的健康和生产力,但由于技术上的限制,无法分析植物种子中的微生物。随着高通量测序方法的不断发展,植物种子微生物群的研究日益增多。

发表在《Phytobiomes Journal》杂志上的一项研究显示, Tomislav Cernava领导的一组科学家利用这项新技术,首次对连续两代番茄植株的种子微生物群进行了评估。研究团队鉴定并表征了番茄不同隔室中的微生物群落。

研究表明,种子内生菌(在种子内部组织中发现的微生物)具有独特的结构,并含有不同的有益细菌。研究团队还发现,植物种子是有益微生物世代传播的重要载体,尤其是植物生长促进细菌的重要媒介。

这个新发现对种子处理的设计产生了影响。研究人员认为,这些发现为进一步探索植物种子如何特异地配置有益的微生物提供了依据,也为农业化肥和农药等化学投入的可持续替代品的研发提供了基础。

来源: AgroPages

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/6A/Csgk0Fy5hPuANIRGAAbtIGCQuwk136.pdf>

▶ 学术文献

1. Development of a Fertility Restorer for inap CMS (*Isatis indigotica*) Brassica napus Through Genetic Introgression of One Alien Addition (以遗传导入一个外源添加来开发inap CMS (*Isatis indigotica*) 甘蓝型油菜育性恢复系)

简介: Novel Brassica napus cytoplasmic male sterility (CMS) with carpelloid stamens (inap CMS) was produced by intertribal somatic hybridization with *Isatis indigotica* (Chinese woad), but its RF (restorer of fertility) gene(s) existed in one particular woad chromosome that was carried by one fertile monosomic alien addition line (MAAL) of rapeseed. Herein, the selfed progenies of this MAAL were extensively selected and analyzed to screen the rapeseed-type plants ($2n = 38$) with good male fertility and to produce their doubled haploid (DH) lines by microspore culture. From the investigation of fertility restoration in the F1 hybrids with inap CMS, one DH line (RF 39) was identified to adequately restore male fertility and likely carried one dominant RF gene. Specifically, this restorer produced brown pollen grains, similar to the woad and the MAAL, suggesting that this trait is closely linked with the RF gene(s) and serves as one phenotypic marker for the restorer. This restorer contained 38 chromosomes of rapeseed and no intact chromosomes of woad, but some DNA

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fragments of woad origin were detected at low frequency. This restorer was much improved for pollen and seed fertility and for low glucosinolate content. The successful breeding of the restorer for inap CMS rendered this new pollination control system feasible for rapeseed hybrid production.

来源: Frontiers in Plant Science

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<http://agri.ckcest.cn/file1/M00/06/6A/Csgk0Fy5giiAdWIgABVQmSy3QtI334.pdf>

2. Abiotic conditions governing the myceliogenic germination of *Sclerotinia sclerotiorum* allowing the basal infection of *Brassica napus* (控制 (导致甘蓝型油菜基础感染的) 菌核病菌菌丝体萌发的非生物条件)

简介: *Sclerotinia sclerotiorum* is the causal pathogen of sclerotinia stem rot (SSR) in canola, causing significant yield losses in this crop globally, when conditions are favourable. The pathogen can cause disease symptoms on canola through ascospore infection from carpogenically germinated sclerotia or by basal infection from myceliogenically germinated sclerotia. While infection through carpogenic germination in canola is the main mode of infection and well-studied, little is known about myceliogenic germination of sclerotia and subsequent basal infection of canola. This review describes the lifecycle of *S. sclerotiorum* on canola and presents an overview of the current knowledge of the factors that influence myceliogenic germination. These include factors such as sclerotium maturity, rind melanisation, temperature and moisture or a combination of these factors. Subsequently, the most likely avenues of *S. sclerotiorum*-based basal infection in canola are discussed and compared to basal infection in other host crops. We conclude that myceliogenic germination can be promoted by incubation of sclerotia at extreme temperatures followed by exposure to moisture. Future research to determine the prevalence of myceliogenic germination and subsequent basal infection of canola in the field is required.

来源: Australasian Plant Pathology

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<http://agri.ckcest.cn/file1/M00/06/6A/Csgk0Fy5gvuA0-s8ACFRYyVBGxE138.pdf>

3. Molecular identification of the magnesium transport gene family in *Brassica napus* (甘蓝型油菜镁转运基因家族的分子鉴定)

简介: Magnesium (Mg^{2+}) is an essential element for plant growth. Its transport and homeostasis in plants is mainly maintained by the MRS2/MGT of Mg^{2+} transporters. Little is known about the MRS2/MGT gene family in *Brassica napus* L. (*B. napus*), one of the most important oil grains. In our present study, we identified 36 putative MRS2/MGT genes (BnMGTs) from *B. napus* and investigated their phylogeny, expression pattern and function. These BnMGT genes were sorted into five distinguished groups by the phylogenetic analysis, and they were clearly homologous with the MRS2/MGT genes in *Arabidopsis* and rice.

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Complementation assays using the *Salmonella typhimurium* mutant MM281 demonstrated that the BnMGT genes were capable of mediating Mg²⁺ uptake and transport, with varied affinities to Mg²⁺. The expression pattern analysis showed that the expression of BnMGTs were tissue-specific and varied in different tissues. This work provides the molecular basis to discover the function of BnMGT gene family in plant growth and development.

来源: Plant Physiology and Biochemistry

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http://agri.ckcest.cn/file1/M00/06/6A/Csgk0Fy5hJKAYWLGAEQ2pX_wMwc561.pdf

4. Analysis of Brassica napus dehydrins and their Co-Expression regulatory networks in relation to cold stress (甘蓝型油菜脱水素及其与冷应激相关的共表达调控网络的分析)

简介: Dehydrins (DHNs) are plant specific cold and drought stress-responsive proteins that belong to late embryogenesis abundant (LEA) protein families. *B. napus* DHNs (BnDHNs) were computationally analyzed to establish gene regulatory- and protein-protein interaction networks. Promoter analyses suggested functionality of phytohormones in BnDHNs gene network. The relative expressions of some BnDHNs were analyzed using qRT-PCR in seedling leaves of both cold-tolerant (Zarfam) and -sensitive (Sari Gul) canola treated/untreated by cold. Our expression data were indicative of the importance of BnDHNs in cold tolerance in Zarfam. BnDHNs were classified into three classes according to the expression pattern. Moreover, expression of three BnDHN types, SK_n (BnLEA10 and BnLEA18), Y_nK_n (BnLEA90) and Y_nSK_n (BnLEA104) were significantly high in the tolerant cultivar at 12 h of cold treatment. Our findings put forward the possibility of considering these genes as screening biomarker to determine cold-tolerant breeding lines; something that needs to be further corroborated. Furthermore, these genes may have some implications in developing such tolerant lines via transgenesis.

来源: Gene Expression Patterns

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<http://agri.ckcest.cn/file1/M00/00/00/Csgk0Vy5f6-AL91DACqhh4btdHc847.pdf>

5. Quantitative resistance to clubroot infection mediated by transgenerational epigenetic variation in Arabidopsis (由拟南芥跨代表观遗传变异调节的对根肿病感染的定量抗性)

简介: Quantitative disease resistance, often influenced by environmental factors, is thought to be the result of DNA sequence variants segregating at multiple loci. However, heritable differences in DNA methylation, so-called transgenerational epigenetic variants, also could contribute to quantitative traits. Here, we tested this possibility using the well-characterized quantitative resistance of *Arabidopsis* to clubroot, a Brassica major disease caused by *Plasmodiophora brassicae*.

For that, we used the epigenetic recombinant inbred lines (epiRIL) derived from the cross

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ddm1-2×Col-0, which show extensive epigenetic variation but limited DNA sequence variation. Quantitative loci under epigenetic control (QTL^{epi}) mapping was carried out on 123 epiRIL infected with *P. brassicae* and using various disease-related traits.

EpiRIL displayed a wide range of continuous phenotypic responses. Twenty QTL^{epi} were detected across the five chromosomes, with a bona fide epigenetic origin for 16 of them. The effect of five QTL^{epi} was dependent on temperature conditions. Six QTL^{epi} co-localized with previously identified clubroot resistance genes and QTL in *Arabidopsis*.

Co-localization of clubroot resistance QTL^{epi} with previously detected DNA-based QTL reveals a complex model in which a combination of allelic and epiallelic variations interacts with the environment to lead to variation in clubroot quantitative resistance.

来源: New Phytologist

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<http://agri.ckcest.cn/file1/M00/06/6A/Csgk0Fy5gT6ACX5kAB01vaAiSp129.pdf>