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蔬菜育种专题

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中国农业科学院农业信息研究所

联系人：王爱玲

联系电话：010-51503648

邮箱：agri@ckcest.cn

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▶ 前沿资讯

1. Breakthrough in fighting plant disease (英国科学家在植物病害防御机理研究上实现突破)

简介: 在英国谢菲尔德大学(University of Sheffield)的领导下, 研究小组首次确定了植物染色体内的特定位置(基因座), 该位置通过对病原菌攻击的反应进行可逆的生化修饰(称为DNA甲基化), 将抗病性传递给后代。这些发现可能会带来预防农作物疾病的新方法。

发表在《eLife》杂志上的这项研究确定了四个控制植物霜霉病病原体抗病性的DNA基因座。重要的是, 这种抗性与生长的任何负面影响或对其它环境应力的抗性无关。

拉筹伯大学研究人员说, 当植物被病原体反复攻击时, 它们会产生这种遭遇的“记忆”(在植物中被称为启动), 使它们在再次受到攻击时能够有效地抵御。通过种子将这种“记忆”转移到下一代的机制之一是DNA甲基化, 这是一种表观遗传现象——意味着DNA序列没有变化。

研究人员介绍说, 这一重大发现不仅能为重要作物的疾病预防带来新的途径, 还能帮助农民减少对杀虫剂的依赖。这项研究的发现为进一步研究表观遗传学如何帮助提高粮食作物的抗病性铺平了道路。

研究人员希望在这项研究的基础上进行深入研究, 以了解这些表观遗传位点如何控制这么多不同的防御基因, 同时开展更多的转化研究, 以发现表观遗传学是否能提高对全球粮食供应至关重要的作物的抗病性。

该项目由英国谢菲尔德大学牵头, 联合拉筹伯大学、巴黎PSL大学和德国慕尼黑技术大学共同开展合作研究。

来源: AgroPages

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▶ 学术文献

1. Response of stigma receptivity in CMS and male fertile line of Indian mustard (*B. juncea*) under variable thermal conditions (多种热状态下印度芥菜 (*B. juncea*) CMS和雄性可育系柱头可授性响应)

简介: Field experiments were conducted for 2 years to examine the response of stigma in two different pollination systems, viz., CMS line (MJA5) and open-pollinated variety (Pusa Bold) of Indian mustard (*Brassica juncea*), to varying weather conditions created by different sowing dates. The CMS line MJA5 (female) with its male line in 8:2 (A:R) row ratio, and Pusa Bold in an isolated field were sown on 21st of October, 30th of October, and 18th of November in 2 consecutive years in North Indian condition. Temporal differences in sowing provided differed weather conditions during flowering, which resulted in variations in the duration to attain the peak flowering stage. Stigma was receptive for longer duration (8 days from the day of anthesis) in CMS line which needs an external pollen source for fertilization

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to happen, whereas it was only 4 days in open-pollinated variety, assessed in terms of siliqua set and number of seeds/siliqua. Substantial effect of sowing date on stigma receptivity was observed; it was longer in plants sown during October in comparison to those of November in both years. The energy requirement parameters, viz., growing degree days and photo-thermal unit, confirmed that plants sown later failed to accumulate sufficient energy for satisfactory phenological growth and for good seed development.

来源: International Journal of Biometeorology

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2. Transcriptional profiling identifies critical steps of cell cycle reprogramming necessary for Plasmodiophora brassicae - driven gall formation in Arabidopsis (转录谱分析确定拟南芥中芸苔根肿菌驱动的瘿形成所必需的细胞周期重编程的关键步骤)

简介: Plasmodiophora brassicae is a soil-borne biotroph whose life cycle involves reprogramming host developmental processes leading to the formation of galls on its underground parts. Formation of such structures involves modification of the host cell cycle leading initially to hyperplasia, increasing the number of cells to be invaded, followed by overgrowth of cells colonised by the pathogen. Here we show that P. brassicae infection stimulates formation of the E2Fa/RBR1 complex and upregulation of MYB3R1, MYB3R4 and A- and B-type cyclin expression. These factors were previously described as important regulators of the G2-M cell cycle checkpoint. As a consequence of this manipulation, a large population of host hypocotyl cells are delayed in cell cycle exit and maintained in the proliferative state. We also report that, during further maturation of galls, enlargement of host cells invaded by the pathogen involves endoreduplication leading to increased ploidy levels. This study characterises two aspects of the cell cycle reprogramming efforts of P. brassicae: systemic, related to the disturbance of host hypocotyl developmental programs by preventing cell cycle exit; and local, related to the stimulation of cell enlargement via increased endocycle activity.

来源: The Plant Journal

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<http://agri.ckcest.cn/file1/M00/06/68/Csgk0FyhbVuA0xtbACyXzrMV6YY720.pdf>

3. Adaptive significance of functional germination traits in crop wild relatives of Brassica (芸苔属作物野生近缘种功能性发芽性状的适应性意义)

简介: Functional germination traits contribute to both niche competitiveness and crop yield outcomes. However, there is little understanding of the adaptive significance of the germination thermal- and hydro-parameters in crop wild relatives (CWRs), yet these species

are anticipated to be the source of adaptive traits for future agriculture. Seeds of 10 seed lots of Brassica species, sub-species and inbred lines from across Europe, North Africa and the Middle East were subjected to a range of temperature and water potential conditions. The germination progress curves recorded were analysed using repeated probit analysis and the functional trait parameters (thermal- and hydro thresholds and times) determined. Relationships between these seed parameters (and the physical trait, seed mass) and the seed source environment were investigated.

The Brassica genus was found to have diverse seed germination phenotypes, with thermal (θ_T) and hydro times (θ_H) differing by 3 to 7-fold, base temperatures (T_b) by c. 9 °C and base water potentials (ψ_b) by -1.5 MPa. Crop seed lots of Brassica oleracea had shorter θ_H for germination and higher values of ψ_b , but longer θ_T for germination than their CWR. For the CWRs, the mean monthly precipitation and the precipitation of the predicted month of germination of the seed collection site, was linearly correlated with T_b , θ_T , and ψ_b . This increases the predictability of identifying valuable brassica germplasm for crop development through regeneration trait screening.

In conclusion, the selection of the crop B. oleracea for fastest germination under irrigated conditions likely limits the capacity of the current gene pool to cope with erratic periods of drought predicted in future European climates.

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<http://agri.ckcest.cn/file1/M00/06/68/Csgk0FyhaGSALshWABYUzMWH4Z4745.pdf>

4. Identification and characterization of two ammonium transporter genes in flowering Chinese cabbage (*Brassica campestris*) (大白菜中两种铵离子转运蛋白基因的识别与特征描述)

简介: Ammonium transporters (AMTs), which include AMT1 and AMT2 subfamilies, have been identified and partially characterized in many plants. In this study, two AMT2-type genes from *Brassica campestris*, namely BcAMT2 and BcAMT2like, were identified and characterized. BcAMT2 and BcAMT2like are 2666 bp and 2952 bp, encode proteins of 490 and 489 amino acids, respectively, and contain five exons and four introns. Transient expression of these proteins labelled with green fluorescence protein in onion epidermal cells indicated that both are located on the plasma membrane. When expressing BcAMT2 or BcAMT2like, the mutant yeast strain 31019b could grow on medium containing 2mM ammonium as the only nitrogen source when expressing BcAMT2 or BcAMT2like, indicating that both are functional AMT genes. Quantitative PCR results showed that BcAMT2 and BcAMT2like were expressed in all tissues, but they displayed different expression patterns in the reproductive stages. BcAMT2s transcript levels in leaves were positively correlated with ammonium concentration and external pH. Moreover, the expression BcAMT2s responded to diurnal change. Furthermore, the uncharged form of ammonium, i.e., ammonia, might also be transported by BcAMT2s. These results provide new insights into the molecular mechanisms underlying ammonium absorption and

transportation by the AMT2 subfamily in *B. campestris*.

来源: Plant Biotechnology

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<http://agri.ckcest.cn/file1/M00/06/68/Csgk0FyhaW-AKo8LAB6gYC62eJs902.pdf>