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蔬菜育种专题

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▶ 前沿资讯

1. New CRISPR-based technology developed to control pests with precision-guided genetics (基于CRISPR的精确遗传控制害虫新技术)

简介: 加利福尼亚大学的科研人员利用CRISPR基因编辑工具,设计了一种改变控制昆虫性别和繁殖能力关键基因的方法——“精确引导不育昆虫技术”。研究人员将经精确引导不育昆虫技术处理的卵子植入目标昆虫群体后,仅形成了成年雄性不育昆虫,因而获得了一种环境友好型、且成本相对低廉的新方法来控制害虫种群数量。未来这一技术可安全应用于生物领域,帮助抑制、甚至是根除目标物种,从而彻底改革昆虫的管理和控制方式。

与之前使用的辐射方法不同,科研人员通过果蝇实验研发了一种新的精确引导不育昆虫技术,利用CRISPR技术同时扰乱昆虫种群中控制雌性生育能力和雄性繁殖力的关键基因。研究人员表示,精确引导不育昆虫技术能形成雄性不育后代。由于大量具有代表性的昆虫都拥有一样的目标基因,因此研究人员相信该技术可以应用于许多昆虫。

研究人员设想能够大批量更改目标昆虫群体的卵子基因并生成新的卵子,然后运至世界各地的虫害地点,新出生的不育雄性无法让大自然中的雌性孕育后代,从而减少种群数量。

这项新技术有别于传统技术不断自我繁殖的“基因驱动”系统,新技术由于不育的雄性昆虫能有效关闭生产后代的大门。这种昆虫不育技术被证实是一种环境友好型技术,其目标是开发出一种新的、安全可控的、非侵入性CRISPR基因技术,可以应用于全世界各个物种,短期内减少野生种群的数量。

来源: ScienceDaily

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/5C/Csgk0FxFW7qANJBFAARezSJ2yrQ802.pdf>

▶ 学术文献

1. Molecular and phenotypic identification of B-genome introgression linked to *Leptosphaeria maculans* resistant gene Rlm6 in *Brassica napus* × *B. juncea* interspecific hybrids (欧洲油菜与芥菜型油菜异种杂交茎基溃疡病菌抗性基因Rlm6的分子与表型鉴定)

简介: Blackleg is a devastating disease in canola worldwide, except in China, caused by the fungal pathogen *Leptosphaeria maculans*. The B-genome Brassica species were reported to have a strong resistance to the blackleg pathogen *L. maculans*. Backcross (BC) generations, BC1F1 to BC4F1, were derived from a cross *B. napus* × *B. juncea*. Phenotype of *L. maculans* isolate J20 showed that 49% of BC1F1, 27% of BC2F1, 15% of BC3F1, and 10% of BC4F1 plants were resistant to the isolate J20. Offspring from the interspecific hybridization were also analysed for the presence of dominant type SCAR markers detecting loci linked to the *B. juncea* genome. The plants with *B. juncea* introgression had a decrease in the presence of SCAR markers ranging from 47% in BC1F1 to 30% in BC2F1 and further down to 18% in

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BC3F1 and 11% in BC4F1 with respect to the marker B5Rlm6_1. A similar trend of loci reduction was also observed for the marker B5-1520. In contrast, the progression of the *B. napus* genome correlated with an incremental increase in the presence of the two markers with the advancement of the generations. However, segregation of SCAR markers and phenotypes for the blackleg resistance in BC1F1 plants had an acceptable fit to a Mendelian ratio of resistant versus susceptible, supporting the assumption that the genetic control of resistance is governed by a single dominant gene. The BC generations developed in this study, which show introgression of the *B. juncea* genome linked to the *L. maculans* resistance gene Rlm6, would facilitate breeding a *B. napus* variety resistant to blackleg in the future.

来源: Euphytica

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<http://agri.ckcest.cn/file1/M00/06/5C/Csgk0FxFJS2AQdjAAAzJt7E-SHA216.pdf>

2. Overexpression of Soybean Transcription Factors GmDof4 and GmDof11 Significantly Increase the Oleic Acid Content in Seed of *Brassica napus* L. (大豆转录因子GmDof4和GmDof11显著增加甘蓝型油菜籽的油酸含量)

简介: Rapeseed (*Brassica napus* L.) with substantial lipid and oleic acid content is of great interest to rapeseed breeders. Overexpression of Glycine max transcription factors Dof4 and Dof11 increased lipid accumulation in *Arabidopsis* and microalgae, in addition to modifying the quantity of certain fatty acid components. Here, we report the involvement of GmDof4 and GmDof11 in regulating fatty acid composition in rapeseeds. Overexpression of GmDof4 and GmDof11 in rapeseed increased oleic acid content and reduced linoleic acid and linolenic acid. Both qPCR and the yeast one-hybrid assay indicated that GmDof4 activated the expression of FAB2 by directly binding to the cis-DNA element on its promoters, while GmDof11 directly inhibited the expression of FAD2. Thus, GmDof4 and GmDof11 might modify the oleic acid content in rapeseed by directly regulating the genes that are associated with fatty acid biosynthesis.

来源: Agronomy

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/5C/Csgk0FxFJHCAKFT8ACEwEppnP78385.pdf>

3. Characterization of the Leaf Color Mutant hy and Identification of the Mutated Gene in Chinese Cabbage (大白菜叶色突变体hy的特性及突变基因的鉴定)

简介: Leaf color mutants play an important role in our understanding of chlorophyll biosynthesis and catabolism. In this study, we obtained a yellow-green leaf mutant hy in an ethyl methanesulfonate mutagenized population of chinese cabbage (*Brassica rapa* ssp. *pekinensis*). The hy phenotype was controlled by a recessive allele at a single locus. The intrinsic photochemical activity of photosystem II (PSII) is impaired in hy, suggesting that

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absorbed light energy is not efficiently transferred from the light-harvesting complexes antenna to the PSII reaction centers and dissipated as heat or fluorescence. We measured chlorophyll content and chlorophyll precursors and analyzed the expression of key genes in the chlorophyll synthetic pathway in hy and wild type. The mutation phenotype was consistent with inhibited expression of chlorophyll a oxygenase (CAO) gene in the chlorophyll synthetic pathway. In mutant hy, CAO cDNA was cloned so that a C to T mutation at 1099 bp caused a conserved proline (Pro) to serine (Ser) mutation at the 367th amino acid in C-domain, which changed the secondary structure of CAO protein. We speculate that the mutation amino acid changed in the C-domain may affect the catalytic function in mutant CAO.

来源: Journal of the American Society for Horticultural Science

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<http://agri.ckcest.cn/file1/M00/06/5C/Csgk0FxF03GAESEuAEBI1k6EIQY989.pdf>

4. Genome re-sequencing, SNP analysis, and genetic mapping of the parental lines of a commercial F1 hybrid cultivar of Chinese cabbage (大白菜商用杂交F1亲本系的基因组重测序、单核苷酸多态性分析和遗传图谱)

简介: The genome-wide characterization of single nucleotide polymorphism (SNP) between cultivars or between inbred lines contributes to the creation of genetic markers that are important for plant breeding. Functional markers derived from polymorphisms within genes that affect phenotypic variation are especially valuable in plant breeding. Here, we report on the genome re-sequencing and analysis of the two parental inbred lines of the commercial F1 hybrid Chinese cabbage cultivar “W77”. Through the genome-wide identification and classification of the SNPs and indels present in each parental line, we identified about 1,500 putative nonfunctional genes in each parent. We designed cleaved amplified polymorphic sequence (CAPS) markers using specific mutations found at Eco RI restriction sites in the parental lines and confirmed their Mendelian segregation by constructing a linkage map using 96 F2 plants derived from the F1 hybrid cultivar, “W77”. Our results and data will be a useful genomic resource for future studies of gene function and metagenomic studies in Chinese cabbage.

来源: Breeding Science

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/5C/Csgk0FxFW2qAEa7YACWcxVMbAlg989.pdf>