



2018年第16期总130期

蔬菜育种专题

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2018年4月16日

➤ 前沿资讯

1. Flood, drought and disease tolerant -- one gene to rule them all (研究发现水稻抗旱耐涝基因)

简介: 日前, 来自哥本哈根大学、名古屋大学和西澳大利亚大学的研究人员在植物生理学方面开展的国际合作取得了突破性进展。他们发现了控制水稻表面特性使叶片具备超疏水性的单一基因。该成果发表在《新植物学家》上。

此次发现的基因名为LGF1, 它控制着叶面的纳米结构。蜡纳米结构保留了一层薄的叶片气体膜(Leaf Gas Film), 使叶面具有超疏水性, 能在淹没期间使气孔发挥功能, 水稻得以存活。研究人员在实验室和大田条件下运用先进的微电极揭示了叶片气体膜在水稻淹没状态下的作用。但同时也观察到, 在淹没几天后, 由LGF1基因编码的叶片超疏水属性消失, 叶片变湿, 植物开始溺水。因此, 研究人员拟将研究重点放在LGF1基因的过度表达上。因为过度表达会为叶片涂上更多的蜡晶, 帮助植物抵御洪水。

LGF1基因同时也赋予了植物耐旱性, 因为微小的蜡晶体也减少了叶面蒸发。这一发现意义巨大。因为全球范围内的气候变化将导致旱涝更加不均, 为维持全球粮食供应, 就迫切需要耐涝性和耐旱性更强的作物。由于植物抗旱抗涝均由一个单一的基因控制, 实现这一目标的可能性就更大了。

来源: AAAS

发布日期: 2018-03-13

全文链接:

https://www.eurekalert.org/pub_releases/2018-03/fos--fda031318.php

➤ 学术文献

1. EMS-induced point mutations in ALCATRAZ homoeologs increase silique shatter resistance of oilseed rape (Brassica napus) (ALCATRAZ同源染色体中EMS诱导的点突变增加甘蓝型油菜长角果落果抗性)

简介: In Arabidopsis (*Arabidopsis thaliana*), the transcription factor ALCATRAZ (ALC) is involved in the control of silique tissue identity, ensuring the establishment of a separation layer that contributes to the fragility of the dry fruit. The silique structure is retained in the related crop species oilseed rape (*Brassica napus*), in which it causes yield losses due to seed shedding. A more robust rapeseed silique through Bnalc loss-of-function mutations was hypothesized. We demonstrated the increased silique shatter resistance of oilseed rape through Cas9-induced targeted Bnalc mutations in a previous work. However, the effect was masked by the high shatter resistance of the transformed cultivar itself. In the present study, we used a rapeseed genotype with low shattering resistance and followed an approach of random mutagenesis. We identified 23 Bnalc mutants by TILLING of an EMS-mutagenized 'Express' population. By measuring tensile forces necessary to disrupt mature siliques, we determined a double mutant with significantly increased shatter resistance. This mutant can readily be introduced into breeding programs.

来源: Euphytica

发布日期: 2018-01-13

全文链接:

<http://agri.ckcest.cn/ass/f2011f28-f1a8-4a34-b8dc-77ca46a1c932.pdf>

2. EMS-induced mutation of an endoplasmic reticulum oleate desaturase gene (FAD2-2) results in elevated oleic acid content in rapeseed (*Brassica napus* L.) (对内质网油酸脱氢酶基因 (FAD2-2) 进行甲基磺酸乙酯 (EMS) 诱变导致甘蓝型油菜油酸含量升高)

简介: The development of rapeseed cultivars (*Brassica napus* L.) with high oleic acid and low linolenic acid is highly desirable for food and industrial applications. In this study, the Korean rapeseed cultivar Tamla was used for ethyl methanesulfonate (EMS)-induced mutagenesis and seed oils were screened up to generation M7 for high oleate mutants. Two mutant populations (M7) with an average of approximately 76% oleic acid content were isolated. Yield components between two mutant populations and untreated Tamla plants were not substantially different, although the mutants in the vegetative stage were slightly smaller in size than Tamla. Genomic analyses of six fatty acid desaturase (four FAD2 and two FAD6) genes revealed that the elevated oleic acid content in the mutants is the result of single gene mutations. Changes in DNA sequence were observed in two genes out of six fatty acid desaturase (four FAD2 and two FAD6). FAD2-2 exhibited a 2-bp deletion in the upstream region of the gene in the two mutants, resulting in a severely truncated polypeptide (57 aa instead of 469 aa), while six point mutations in the other gene did not result in changes in the amino acid sequence. Based on these results, FAD2-2, an endoplasmic reticulum (ER) oleic acid desaturase, is affected in the mutants, resulting in a ~ 7% increase in oleic acid content in comparison to untreated Tamla plants. The induced mutants could be utilized for the development of high oleic oil rapeseed varieties and for regulatory studies of lipid metabolism in seed oils.

来源: Euphytica

发布日期: 2018-01-13

全文链接:

<http://agri.ckcest.cn/ass/84a9b13f-6b37-47ed-b0e0-764a95b61763.pdf>

3. Production and genetic analyses of novel *Brassica rapa* L. introgressions from interspecific crosses with *Brassica juncea* L. landraces native to the Qinghai-Tibet Plateau (与青藏高原土生芥菜种间杂交后形成的芸薹新品种的基因渐渗和遗传分析)

简介: Interspecific hybrids between related species have long been used for transferring desirable genes, broadening genetic diversity and utilizing intersubgenomic heterosis. In this study, we developed a novel *Brassica rapa* type (AA, $2n = 20$) exhibiting certain features derived from interspecific hybridization between natural *B. rapa* and *Brassica juncea* (AABB, $2n = 36$). In pollen mother cells (PMCs) of the novel *B. rapa* type, normal chromosome pairing with 10 bivalents and 10:10 segregation was observed, and the novel *B. rapa* lines

were completely fertile. However, GISH showed that certain B chromosomes or fragments were introgressed into *B. rapa*. Genetic components of the novel *B. rapa* lines were investigated by GISH, AFLP and SSR analyses. GISH analysis of F1, BC1F1, and BC1F2 plants confirmed the identities of three addition lines and seven translocation lines. AFLP and SSR analyses of 60 hybrid progenies from BC1F4 plants, their parents, and some *B. juncea* and *B. rapa* resources indicated that the A and B chromosome(s) or fragment(s) introgressed to the novel *B. rapa*. AFLP revealed that 60 BC1F4 plants contained B chromosomes or fragments, which evidenced introgression into the hybrid progeny. SSR analysis indicated that the A-genome (A1A10) of *B. juncea* was introgressed into the hybrid progeny at 1.0 to 42.7%. Lastly, we obtained some yellow-seed and early-flowering *B. rapa* resources. The novel *B. rapa* lines can be used to genetically improve *B. rapa* in the Qinghai-Tibet Plateau and to study the origin and evolution of the A- and B-genomes.

来源: Euphytica

发布日期: 2018-01-10

全文链接:

<http://agri.ckcest.cn/ass/953f18d0-aa31-4e55-aa34-1f8e81f7ed23.pdf>

4. Characterization of drought and freezing tolerance of three representative cultivars of pak choi (*Brassica rapa* ssp. *chinensis*) (小白菜三种代表性栽培种的抗旱和抗冻性研究)

简介: Pak choi (*Brassica rapa* ssp. *chinensis*) is one of the most important cultivated vegetables in China, and its growth and development are often affected by drought and freezing stresses which often lead to yield reduction. However, the mechanisms by which pak choi responds to drought and freezing stresses are still largely unknown. In this study, we compared the tolerance of three representative Chinese cultivars of pak choi, Suzhouqing (BrL.1), Huangxinwucai (BrL.2) and Heixinwucai (BrL.3), to drought and freezing stresses. We found that BrL.3 showed increased tolerance to both drought and freezing stresses when compared with BrL.1 and BrL.2. Under drought stress, BrL.3 accumulated a higher level of proline, but not soluble sugar, by enhancing the expression of BrP5CS1 and BrP5CS2 genes and thus the activity of P5CS enzyme in proline synthesis pathway. Consistent with this result, exogenous addition of proline can almost diminish the phenotypic difference between BrL.3 and BrL.1/2 under drought stress, suggesting that enhanced drought tolerance in BrL.3 is associated with increased proline accumulation. In addition, under cold stress, there was no significant difference in the contents of proline and soluble sugar among BrL.1, BrL.2 and BrL.3. However, the expression of BrCBF1 gene, which encodes a key transcriptional factor in the cold stress pathway, and its downstream gene BrCOR15a was significantly increased in BrL.3. Further study showed that the heterologous overexpression of BrCBF1 gene in *Arabidopsis* could enhance freezing tolerance, suggesting that enhanced freezing tolerance in BrL.3 might be related to increased expression of the BrCBF1 gene. Taken together, these results indicate that the enhanced tolerance of BrL.3 to drought and freezing stresses is associated with enhanced proline accumulation and increased BrCBF1 expression, respectively.

来源: Molecular Breeding

发布日期: 2018-01-08

全文链接:

<http://agri.ckcest.cn/ass/bf347052-d7cd-4405-9144-0a956296a83d.pdf>