



2018年第50期总164期

蔬菜育种专题

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1. 提高作物耐涝性

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▶ 前沿资讯

1. Plant hormone makes space farming a possibility (植物激素研究成果或让太空农业成为可能)

简介: 人们设想有一天能在月球或其他星球上居住, 或者未来进行长期的太空探险, 首先要解决为生活在太空中的人类长期提供食物的难题, 即想办法在太空中种植作物。但是, 月球和其他星球的土壤养分很低, 不适宜种植作物; 而如果要将肥沃的土壤和肥料从地球运到太空, 又会带来高昂的经济和生态成本。不过瑞士苏黎世大学的最新研究发现, 植物激素独脚金内酯或可让这一可能成为现实。这种激素能促进菌根的形成, 即便是处于太空的恶劣环境下, 也能因此而促进植物的生长。

菌根是真菌与植物根部之间的一种共生关系体。在这种共生关系体中, 菌丝为植物根部提供水分、氮、磷以及各种微量元素。作为回报, 菌丝能够获得产自植物的糖分和油脂。独脚金内酯能对这种共生关系起到促进作用, 而大多数植物都会将这种激素分泌在根部周围的土壤中。菌根的形成能够极大地促进植物生长, 由此可持续地提高作物产量, 尤其是低肥力土壤的作物产量。

矮牵牛是茄属作物如西红柿、土豆、茄子等的模式植物。研究人员在模拟太空低重力环境下研究了矮牵牛菌根的形成。实验表明微重力环境会妨碍菌根的形成, 导致茄属作物从土壤中摄取的养分减少。不过独脚金内酯可以抵消这种负面影响。研究发现, 用合成独脚金内酯处理过的真菌和能够大量分泌独脚金内酯的植物一起, 即便是在重力不足的环境下种植于养分稀缺的土壤, 也仍然能够良好生长。这一发现或可实现在太空种植作物。

来源: AAAS

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<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0Fv7ZeWASK5zAAF-5XiSKng763.pdf>

▶ 学术文献

1. Fine Mapping of Lobed-Leaf Genes in Two Brassica napus Lines Using SLAF Sequencing (应用SLAF测序技术对两个甘蓝型油菜品系裂叶基因的精细定位)

简介: Plant ideotypes may be useful for increasing yield in *Brassica napus* L., and leaves play an important role in the development of ideotypes. Previously, we bred two lobed-leaf *B. napus* lines, ll1 and ll2. In the present study, we report the fine mapping of lobed-leaf genes in ll1 and ll2 and annotate their putative functions. We conduct specific-locus amplified fragment sequencing (SLAF-seq) to determine the candidate intervals. Crosses between two lobed-leaf lines ll1 and ll2 and their corresponding wild types e11 and e12 were used to generate two sets of F₁ and F₂ populations. Genome-wide comparison of single-nucleotide polymorphism profiles between lobed- and entire-leaf bulks identified ll1 and ll2 candidate intervals on ChrA10. Lobed-leaf gene ll1 was located in two regions within genomic positions 16,055,155 to 16,158,378 (100 kb in size) and 16,651,387 to 17,120,610 (470 kb in

size), whereas the ll2 gene was located within the genomic region of 16,767,957 to 17,024,885 (260 kb in size), which overlapped with the second region of ll1. These results suggest that the lobed-leaf candidate genes for ll1 and ll2 are alleles. Basic Local Alignment Search Tool (BLAST) analysis identified 139 genes and 49 genes in the associated regions of ll1 and ll2, respectively. Approximately 135 genes in ll1 and 49 genes in ll2 could be functionally annotated, with the majority playing important roles in the regulation of leaf margin and leaf growth. These studies provide useful information for constructing ideotypes and breeding high-yielding *B. napus* hybrids.

来源: Crop Science

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<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0Fv71ViAAhesADwfggoF6EA355.pdf>

2. Quantifying the germination response of spring canola (*Brassica napus* L.) to temperature (春油菜对温度的萌发反应的量化研究)

简介: The models based on thermal time concept have been widely applied to quantify the germination responses of seeds to temperature. The majority of these models assume a Normal distribution for both sub-optimal thermal time $\theta_{T(G)}$ and maximum temperature $T_{c(G)}$ to describe the variation in time to germination. In this study, the response of germination to temperature in six spring canola (*Brassica napus* L.) cultivars was described using the thermal time model. Germination tests were carried out at constant temperatures of 8, 12, 16, 20, 24, 28, 32, 33, 34, 35 and 36 °C. The thermal time model accurately described germination patterns of different cultivars in response to temperature over sub- and supra-optimal. The thermal thresholds for seed germination, base temperature (T_b), suboptimal thermal time needed to achieve 50% germination ($\theta_{T(50)}$), maximum germination temperature for induction of 50% thermoinhibition in seeds ($T_{c(50)}$) and supra-optimal thermal time to complete germination (θ_{Tc}) differed significantly among the canola cultivars studied. The values of T_b , $\theta_{T(50)}$, $T_{c(50)}$ and θ_{Tc} ranged from 4.86 to 7.10 °C, 358.89-407.19 °C h, 33.90-34.42 °C and 27.66-38.26 °C h, respectively. Within each cultivar optimum temperature ($T_{o(G)}$) showed little variation amongst different germination percentiles. The magnitude of $T_{o(50)}$ ranged from 31.86 to 32.25 °C depending on the cultivar. The thermal thresholds for seed germination identified here explained the differences in seed germination found among cultivars. All model parameters may be readily used in crop simulation models.

来源: Industrial Crops & Products

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3. Effect of drought and salinity stresses on morphological and physiological characteristics of canola (干旱和盐分胁迫对油菜形态和生理特性的影响)

简介: Environmental stresses such as salinity and drought are the most important factors

affecting yield reduction and crops productivity. In order to investigate the effects of drought and salinity stresses on morphological and physiological characteristics of canola, an experimental campaign was conducted as a split plot based on a randomized complete block design with three replications at greenhouse of Agriculture Research Center and Natural Resources of East Azarbaijan in 2014. Main plots were including drought stress at four levels (0, -4, -8 and -12 bar polyethylene glycol solution) and subplots including salinity stress at four levels of sodium chloride (0, 75, 150 and 225 mM). The results analysis of variance indicated that the interaction of drought and salinity stresses was significant on leaf area and relative water content of leaf. The most leaf area (383.03 cm^{-2}) was obtained at non-stress treatments. The results showed that drought stress conditions led to significant reduction in relative water content in leaf. The highest proline ($0.08 \mu \text{ m/g}$ fresh weight) and soluble sugars (0.12 mg/g fresh weight) contents were observed at treatments of -12 bar polyethylene glycol. Also, the least proline ($0.04 \mu \text{ m/g}$ fresh weight) and soluble sugar (0.06 mg/g fresh weight) contents were achieved at treatments of drought non-stress.

来源: International Journal of Environmental Science and Technology

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<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0Fv7YDeAWVp0AAutSkJDj1o919.pdf>

4. Improved Brassica rapa reference genome by single-molecule sequencing and chromosome conformation capture technologies (应用单分子测序和染色体构象捕获技术改良甘蓝型油菜参考基因组)

简介: Brassica rapa comprises several important cultivated vegetables and oil crops. Current reference genome assemblies of Brassica rapa are quite fragmented and not highly contiguous, thereby limiting extensive genetic and genomic analyses. Here, we report an improved assembly of the B. rapa genome (v3.0) using single-molecule sequencing, optical mapping, and chromosome conformation capture technologies (Hi-C). Relative to the previous reference genomes, our assembly features a contig N50 size of 1.45 Mb, representing a ~30-fold improvement. We also identified a new event that occurred in the B. rapa genome ~1.2 million years ago, when a long terminal repeat retrotransposon (LTR-RT) expanded. Further analysis refined the relationship of genome blocks and accurately located the centromeres in the B. rapa genome. The B. rapa genome v3.0 will serve as an important community resource for future genetic and genomic studies in B. rapa. This resource will facilitate breeding efforts in B. rapa, as well as comparative genomic analysis with other Brassica species.

来源: Horticulture Research

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科技报告

1. Improving Flooding Tolerance of Crop Plants (提高作物耐涝性)

简介: A major problem of climate change is the increasing duration and frequency of heavy rainfall events. This leads to soil flooding that negatively affects plant growth, eventually leading to death of plants if the flooding persists for several days. Most crop plants are very sensitive to flooding, and dramatic yield losses occur due to flooding each year. This review summarizes recent progress and approaches to enhance crop resistance to flooding. Most experiments have been done on maize, barley, and soybean. Work on other crops such as wheat and rape has only started. The most promising traits that might enhance crop flooding tolerance are anatomical adaptations such as aerenchyma formation, the formation of a barrier against radial oxygen loss, and the growth of adventitious roots. Metabolic adaptations might be able to improve waterlogging tolerance as well, but more studies are needed in this direction. Reasonable approaches for future studies are quantitative trait locus (QTL) analyses or genome-wide association (GWA) studies in combination with specific tolerance traits that can be easily assessed. The usage of flooding-tolerant relatives or ancestral cultivars of the crop of interest in these experiments might enhance the chances of finding useful tolerance traits to be used in breeding.

来源: Agronomy

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