



2018年第45期总159期

蔬菜育种专题

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▶ 前沿资讯

1. EU phases out fungicide thiram (欧盟将逐步停止使用福美双杀菌剂)

简介: 欧盟委员会于2018年10月9日接受了相关法令 (EU) [2018/1500], 决定不再续登活性成分福美双。该项法案于次日发布在了欧盟官方公报上。考虑到鸟类和野生哺乳动物食用经过处理种子后所产生的风险, 销售和使用福美双处理的种子将会被禁止。由于福美双替代品十分有限, 禁令将于2020年1月31日生效, 以便为种子供应链提供足够长的转型期。欧盟成员国要在2019年1月30日以前取消对含有福美双成分植保产品的批准。叶片施用的宽限期将截止到2019年4月30日, 种子处理等其他使用方式将截止到2020年1月30日。然而美国公司Eastman针对此项法案评论道: “科研结果显示, 在恰当的农业操作方式下, 福美双具备安全性, 我们相信这一结果。因此Eastman仍将会向农民供应此类产品。”

来源: AgroPages

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全文链接:

<http://agri.ckcest.cn/ass/d64439fc-370a-49c5-8328-067a4fd1f5ff.pdf>

2. Brassicas species in Brazil: Brief informations (巴西芸薹属蔬菜种植概况)

简介: 芸薹属植物是巴西重要的蔬菜作物, 主要种植区域在巴西东南部和南部地区各州, 包括里约热内卢州、圣保罗州、南里奥格兰德州、巴拉那州、圣卡塔琳娜州、米纳斯州、圣埃斯皮里图州和戈亚斯州, 占全巴西绿菜花、花椰菜和卷心菜产量的92%, 这三个品种也是巴西种植面积最大的芸薹属蔬菜, 其次是羽衣甘蓝, 大白菜的种植规模比较小。巴西绿菜花的种植面积约为15418公顷, 其中抱子甘蓝为6958公顷; 花椰菜的种植面积为11225公顷, 其中夏季品种的种植面积为5675公顷, 冬季品种为5550公顷; 卷心菜的种植面积为30070公顷, 95%为绿包菜。大约20年前, 巴西的绿菜花只有抱子甘蓝, 之后引入了绿菜花, 面积迅速扩大。巴西市场上的卷心菜90%以上是绿叶品种, 紫甘蓝所占份额很小。巴西夏季的花椰菜市场仍然是本地杂交品种占主导地位, 外来杂交种在其他季节里表现出良好的适应性, 但在夏季只有热带杂交种的产量表现良好。巴西三大芸薹属蔬菜中的杂种利用程度很高, 在热带气候条件下, 抗病性是杂交育种的主要目标之一。

来源: AgroPages

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▶ 学术文献

1. Stable, Environmental Specific and Novel QTL Identification as Well as Genetic Dissection of Fatty Acid Metabolism in Brassica napus (甘蓝型油菜稳定的、环境特异性、新颖QTL的识别及脂肪酸代

谢的遗传分析)

简介: Fatty acid (FA) composition is the typical quantitative trait in oil seed crops, of which study is not only closely related to oil content, but is also more critical for the quality improvement of seed oil. The double haploid (DH) population named KN with a high density SNP linkage map was applied for quantitative trait loci (QTL) analysis of FA composition in this study. A total of 406 identified QTL were detected for eight FA components with an average confidence interval (CI) of 2.92 cM, the explained phenotypic variation (PV) value ranged from 1.49 to 45.05%. Totally, 204 consensus and 91 unique QTL were further obtained via meta-analysis method for the purpose of detecting multiple environment expressed and pleiotropic QTL, respectively. Of which, 74 stable expressed and 22 environmental specific QTL were also revealed, respectively. In order to make clear the genetic mechanism of FA metabolism at individual QTL level, conditional QTL analysis was also conducted and more than two thousand conditional QTL which could not be detected under the unconditional mapping were detected, which indicated the complex interrelationship of the QTL controlling FA content in rapeseed. Through comparative genomic analysis and homologous gene annotation, 61 candidates related to acyl lipid metabolism were identified underlying the CI of FA QTL. To further visualize the genetic mechanism of FA metabolism, an intuitive and meticulous network about acyl lipid metabolism was constructed and some closely related candidates were positioned. This study provided a more accurate localization for stable and pleiotropic QTL, and a deeper dissection of the molecular regulatory mechanism of FA metabolism in rapeseed.

来源: Frontiers in Plant Science

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<http://agri.ckcest.cn/ass/fd161852-f215-4d07-b4ae-a9fbb7cd54a6.pdf>

2. Broadening the genetic base of Brassica napus canola by interspecific crosses with different variants of B-oleracea (通过不同甘蓝变种间杂交以拓宽油菜遗传基础)

简介: Broadening the genetic base of the C genome of Brassica napus canola by use of B. oleracea is important. In this study, the prospect of developing B. napus canola lines from B. napus × B. oleracea var. alboglabra, botrytis, italica and capitata crosses and the effect of backcrossing the F₁'s to B. napus were investigated. The efficiency of the production of the F₁'s varied depending on the B. oleracea variant used in the cross. Fertility of the F₁ plants was low—produced, on average, about 0.7 F₂ seeds per self-pollination and similar number of BC₁ seeds on backcrossing to B. napus. The F₃ population showed greater fertility than the BC₁F₂; however, this difference diminished with the advancement of generation. The advanced generation populations, whether derived from F₂ or BC₁, showed similar fertility and produced similar size silique with similar number of seeds per silique. Progeny of all F₁'s and BC₁'s stabilized into B. napus, although B. oleracea plant was expected, especially in the progeny of F₁ (ACC) owing to elimination of the A chromosomes during meiosis. Segregation distortion for erucic acid alleles occurred in both F₂ and BC₁ resulting

significantly fewer zero-erucic plants than expected; however, plants with $\leq 15\%$ erucic acid frequently yielded zero-erucic progeny. No consistent correlation between parent and progeny generation was found for seed glucosinolate content; however, selection for this trait was effective and *B. napus* canola lines were obtained from all crosses. Silique length showed positive correlation with seed set; the advanced generation populations, whether derived from F_2 or BC_1 , were similar for these traits. SSR marker analysis showed that genetically diverse canola lines can be developed by using different variants of *B. oleracea* in *B. napus* \times *B. oleracea* interspecific crosses.

来源: Euphytica

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3. Genotyping-by-sequencing of Brassica oleracea vegetables reveals unique phylogenetic patterns, population structure and domestication footprints (甘蓝型油菜的基因分型揭示其独特的系统发育模式、种群结构和驯化足迹)

简介: *Brassica oleracea* forms a diverse and economically significant crop group. Improvement efforts are often hindered by limited knowledge of diversity contained within available germplasm. Here, we employ genotyping-by-sequencing to investigate a diverse panel of 85 landrace and improved *B. oleracea* broccoli, cauliflower, and Chinese kale entries. Ultimately, 21,680 high-quality SNPs were used to reveal a complex and admixed population structure and clarify phylogenetic relationships among *B. oleracea* groups. Each broccoli landrace contained, on average, 8.4 times as many unique alleles as an improved broccoli and landraces collectively represented 81% of all broccoli-specific alleles. Commercial broccoli hybrids were largely represented by a single subpopulation identified within a complex population structure. Greater allelic diversity in landrace broccoli and 96.1% of SNPs differentiating improved cauliflower from landrace cauliflower were common to the larger pool of broccoli germplasm, supporting a parallel or later development of cauliflower due to introgression events from broccoli. Chinese kale was readily distinguished by principal coordinate analysis. Genotyping was accomplished with and without reliance upon a reference genome producing 141,317 and 20,815 filtered SNPs, respectively, supporting robust SNP discovery methods in neglected or unimproved crop groups that lack a reference genome. This work clarifies the population structure, phylogeny, and domestication footprints of landrace and improved *B. oleracea* broccoli using many genotyping-by-sequencing markers. Additionally, a large pool of genetic diversity contained in broccoli landraces is described which may enhance future breeding efforts.

来源: Horticulture Research

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4 . Sequence diversification and phylogenetic analysis of selfincompatibility specific determinant genes in Brassicaceae(十字花科自交不亲和和特异性决定基因的序列多样化和系统发育分析)

简介: It is a long history of theoretical interest in understanding the genetic causes and consequences of shifts between outcrossing and inbreeding in plant mating systems. Self-incompatibility (SI) systems genetically promote outcrossing, and its transitions to inbreeding potentially changes genetic diversity in the evolution of species. SI in the Brassicaceae family is sporophytically controlled by a single locus (S-locus), which locates the female determinant gene SRK (S-locus receptor kinase) and the male determinant gene SCR (S-locus cysteine rich). Operation of diversifying selection maintains the diversity of SRK and SCR during the evolutionary course of S haplotypes. Here we used deduced amino acid sequences of SRK and/or SCR publicly available from seven species in three genera, Brassica, Arabidopsis and Raphanus, to investigate the sequence diversification and phylogenetic distribution of S haplotypes in the Brassicaceae family. The results reveal that SCR shows higher sequence distance than SRK within or between genera, and also in the interspecific pairs of S haplotypes. Phylogenetic analysis supports the conclusion that SI has a single origin but evolves differently within the Brassicaceae. The genetic mechanisms and consequences of the loss of SI in the Brassicaceae family are discussed.

来源: Indian Journal of Genetics & Plant Breeding

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