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小麦遗传育种专题

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2019年07月01日

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▶ 前沿资讯

1. Effects of ten years organic and conventional farming on early seedling traits of evolving winter wheat composite cross populations (10年有机耕作和常规耕作对冬小麦复合群体早期育苗性状的影响)

简介: 以高产 (Y)、优质 (Q) 和高产*优质 (Y*Q) 品种杂交组合为基础, 对小麦杂交组合 (CCPs) 的早期活力性状进行了水培试验研究。为了消除贮藏和年份效应, 在同一块田中对冷冻F6、F10、F11和F15种子进行繁殖, 产生了各自的F_x. 1代。这消除了F6. 1、F10. 1和F15. 1的世代和生长系统对种子大小的影响。由于严冬影响F11, 世代效应持续存在, 导致F11. 1种子较大, 幼苗性状与F10. 1和F15. 1明显不同。平行群体间幼苗性状相似。在F11. 1之前, 两个系统的茎长和茎重都有所增加, 此后保持不变。随着时间的推移, 有机CCPs的种子根长和根重明显增加, 总根长和比根长显著低于传统CCPs。有机条件下的生根模式表明, 获得深层土壤养分的能力更强。在这两个系统中, Q和YQ CCPs都比Y CCPs更强, 证实了种群间的遗传差异。总体而言, 有机体系中的异质群体表现出更强的可塑性和选择压力。

来源: Nature

发布日期: 2019-06-21

全文链接:

<http://agri.ckcest.cn/file1/M00/06/80/Csgk0FORkVmAGjXZACB4KwYiyKI607.pdf>

▶ 学术文献

1. Map-based cloning of QFhb.mgb-2A identifies a WAK2 gene responsible for Fusarium Head Blight resistance in wheat (基于QFhb.mgb-2A克隆图像鉴定小麦抗镰刀菌头枯萎病的WAK2基因)

简介: *Fusarium graminearum* is one of the most threatening pathogen of wheat, responsible for Fusarium head blight (FHB) which annually leads to yield losses, grain quality decay and accumulation of harmful mycotoxins in kernels. Host resistance represents the most effective approach to limit disease damages; however, only a limited number of resistant loci have currently been detected in durum genotypes. In this work we report the map-based cloning of a FHB-QTL on 2A chromosome of durum wheat, introgressed from a resistant line derived from the Chinese wheat cv. Sumai-3. A marker enrichment of the QTL region was carried out leading to the inclusion of 27 new SNPs respect to the previous map. A wall-associated receptor-like kinase (WAK2) gene was identified in the region and sequenced, in the resistant parent (RP) one gene was predicted accounting for a genomic sequence of 5,613 structured into 6 exons, whereas two adjacent genes were predicted on the same DNA plus strand of the susceptible parent (SP). The involvement of WAK2 gene in FHB resistance mechanism was assessed by gene expression comparison between resistant and susceptible wheat lines, and disease symptoms evaluation in 3 TILLING mutants for WAK protein function.

来源: Nature

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发布日期:2019-05-06

全文链接:

<http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0RuvWAEqYQADHwBRlenHc626.pdf>

2. Diversity of Puroindoline genes and their association with kernel hardness in Chinese wheat cultivars and landraces (中国小麦品种和地方品种中嘌呤基因的多样性及其与籽粒硬度的关系)

简介: 籽粒硬度是影响普通小麦碾磨和烘烤品质的一个重要性状。籽粒硬度主要受Pina和Pinb基因的控制。在这里,我们研究了107个中国小麦品种和地方品种中Pina和Pinb等位基因的多样性。在两个田间季节(2016/2017和2017/2018)测定了这些研究材料的籽粒硬度值,2年的数值具有很强的相关性,硬度指标为5.4~91.8。检测到5个已知的Pina-D1等位基因和4个已知的Pinb-D1等位基因。特别是,我们鉴定出一种新的Pinb无效等位基因(被称为Pinb-D1z),其3382-bp的缺失可以被新的分子标记Pina-N5检测到。我们还鉴定出一个含有29-kb缺失的Pina/Pinb双空等位基因,它们是改善籽粒结构的有用基因型。这些群体中最常见的基因型是Pina-D1a/Pinb-D1a和Pina-D1a/Pinb-D1b(分别为39.3%和34.6%),其次是Pina-D1a/Pinb-D1p(13.2%)。本研究与以往研究的基因型比较表明,中国小麦地方品种在Pina基因上的等位基因变异比较多。对小麦籽粒硬度的相关性分析表明,15个Pina-D1等位基因和6个Pinb-D1等位基因可能与普通小麦的硬粒表型有关。值得注意的是,这项研究表明,中国的地方品种是一个宝贵的资源,遗传变异的Puroindoline基因,为研究Puroindoline基因的基因型与表型之间的关系提供了更深入的理解。

来源: Springer

发布日期:2019-04-01

全文链接:

<http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0RwY-AMOurABfj55oa3cc375.pdf>

3. Wheat powdery mildew resistance gene Pm64 derived from wild emmer (*Triticum turgidum* var. *dicoccoides*) is tightly linked in repulsion with stripe rust resistance gene Yr5 (由野生小黑麦 (*Triticum turgidum* var. *dicoccoides*) 衍生而来的小麦白粉病抗性基因Pm64与小麦条锈病抗性基因Yr5的排斥作用密切相关)

简介: Stripe rust and powdery mildew are both devastating diseases for durum and common wheat. Pyramiding of genes conferring resistance to one or more diseases in a single cultivar is an important breeding approach to provide broader spectra of resistances in wheat improvement. A new powdery mildew resistance gene originating from wild emmer (*Triticum turgidum* var. *dicoccoides*) backcrossed into common wheat (*T. aestivum*) line WE35 was identified. It conferred an intermediate level of resistance to *Blumeria graminis* f. sp. *tritici* isolate E09 at the seedling stage and a high level of resistance at the adult plant stage. Genetic analysis showed that the powdery mildew resistance in WE35 was controlled by a dominant gene designated Pm64. Bulk segregant analysis (BSA) and molecular mapping indicated that Pm64 was located in chromosome bin 2BL4-0.500.89. Polymorphic

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markers were developed from the corresponding genomic regions of Chinese Spring wheat and wild emmer accession Zavitan to delimit Pm64 to a 0.55 cM genetic interval between markers WGGBH1364 and WGGBH612, corresponding to a 15 Mb genomic region on Chinese Spring and Zavitan 2BL, respectively. The genetic linkage map of Pm64 is critical for fine mapping and cloning. Pm64 was completely linked in repulsion with stripe rust resistance gene Yr5. Analysis of a larger segregating population might identify a recombinant line with both genes as a valuable resource in breeding for resistance to powdery mildew and stripe rust.

来源: Science Direct

发布日期: 2019-03-11

全文链接:

<http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0RuJGAC1HQABP-Q9rBa90649.pdf>

▶ 专业会议

1. 中国作物学会第十一次全国会员代表大会暨2019年学术年会 第一轮通知

简介: “中国作物学会第十一次全国会员代表大会暨2019年学术年会”将于10月27日~30日在浙江杭州召开。大会将邀请国内作物科学领域取得突出成果并具有重要学术影响力的专家学者进行学术报告。组委会诚挚邀请国内外同行参加本次大会。

来源: 中国作物学会

发布日期: 2019-06-14

全文链接:

<http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0RvC6ASAzAA-dfy4hxgo111.pdf>