



2018年第36期总36期

小麦遗传育种专题

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▶ 前沿资讯

1. Flour power to boost food security (面粉可以提高粮食安全)

简介: 寻找小麦中决定面粉产量的基因,可以增加面粉的产量,同时提高粮食安全,生产出更健康的面粉。昆士兰大学(University of Queensland)的研究人员认为,这一发现可能使小麦生产的面粉数量增加10%。小麦是全球主要的温带气候作物,提供了全球消耗总热量和蛋白质的20%。麦粒碾碎后,可以用来制作面包和其他食品的面粉。昆士兰大学农业与食品创新联盟(UQ Queensland Alliance for Agriculture and Food Innovation)主任罗伯特·亨利(Robert Henry)教授表示,他的研究团队已经确定了控制细胞蛋白的基因。细胞蛋白的作用类似胶水,将小麦籽粒的胚乳、小麦胚芽和麸皮层粘合在一起。生产这种胶状蛋白质较少的小麦在碾磨过程中更容易分解。这样就提高了加工效率,改善了面粉的营养状况,因为更多的胚乳外层部分——富含维生素和矿物质被加入到了面粉中。

来源: EurekAlert!

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<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0Fv8pL6AAFpuAABYHx8193g333.pdf>

▶ 学术文献

1. Dynamic Evolution of α -Gliadin Prolamin Gene Family in Homeologous Genomes of Hexaploid Wheat (六倍体小麦部分同源基因组中的动态演化 α -醇溶谷蛋白基因家族)

简介: 小麦Gli-2基因位点编码 α -醇溶谷蛋白复合群对于面包的制作尤为重要,同时它也是乳糜泻病(CD)的主要诱因。 α -醇溶谷蛋白进化的阐明为生产出具有更好终端用途特性和降低免疫原性潜力的小麦提供了认知。Gli-2基因位点包含大量串联复写的基因和高度重复的DNA,使得基因组区域的序列编译具有挑战性。这里,我们通过将基于PacBio的序列连接物与生物纳米基因组图谱对准,构建了跨越三个小麦同源 α -醇溶谷蛋白位点的高质量序列。共鉴定出47个 α -醇溶谷蛋白基因,其中只有26个编码完整的全长蛋白产物。对 α -醇溶谷蛋白基因位点和系统发育树重建的分析表明,在A、B、D基因组分化后的最近250万年中, α -醇溶谷蛋白基因发生了显著的重复,支持其在不同小麦基因组中快速的独立谱系扩增。我们发现, α -醇溶谷蛋白基因表达的显著差异不能归因于启动子区域的序列变化。该研究还深入了解了乳糜泻病(CD)表位的演变,并确定了六倍体小麦D基因组中的一个单指数事件,该事件可能引起33个高毒性单体CD表位的产生。

来源: Nature

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<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0Fv8rPiATet9ADJPDPrdo3U096.pdf>

2. Molecular marker assisted breeding and genome composition

analysis of Zhengmai 7698, an elite winter wheat cultivar (冬小麦优良品种郑麦7698的分子标记辅助选育及基因组组成分析)

简介: Zhengmai 7698 is an elite winter wheat variety widely cultivated in the Southern regions of the Yellow-Huai River Valley of China. Here, we report the molecular markers used for breeding Zhengmai 7698 and the genome composition of this cultivar revealed using genome-wide SNPs. A total of 26 DNA markers derived from the genes controlling gluten protein quality, grain hardness, flour color, disease resistance, or pre-harvesting sprouting resistance were used during breeding. Consequently, Zhengmai 7698 had strong gluten, high grain hardness index, white flour color, and high levels of resistance to powdery mildew, stripe rust infections, and pre-harvesting sprouting. Using genome complexity reduction, 28,996 high-quality SNPs distributed on 21 wheat chromosomes were identified among Zhengmai 7698 and its three parental lines (4B269, Zhengmai 9405 and Zhoumai 16). Zhengmai 7698 shared 12,776, 14,411 and 16,085 SNPs with 4B269, Zhengmai 9405 and Zhoumai 16, respectively. Thus, the contributions of 4B269, Zhengmai 9405 and Zhoumai 16 to the genome of Zhengmai 7698 were comparable. Interestingly, Zhengmai 7698 had 307 unique SNPs that are absent in all three parents. We suggest that molecular markers facilitate selection of a wheat cultivar with multiple elite traits. Analysis of genome composition with SNPs may provide useful clues for further dissecting the genetic basis of improved wheat performance.

来源: Nature

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<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0Fv8p8qAGRd2ABXLCIxi5tc877.pdf>

➤ 相关专利

1. 一种抗病的小麦-黑麦7BS .7RL染色体易位系的培育方法及应用

简介: 本发明公开了一种抗病的小麦-黑麦7BS .7RL染色体易位系的培育方法, 该方法包括以下步骤: 以绵阳11为受体, 白粒黑麦为供体进行杂交, 得到F1代材料, 进行染色体数目加倍处理, 得到小麦-黑麦双二倍体材料, 然后与绵阳11连续回交2次, 选出小麦-黑麦7R单体附加系, 然后进行自交, 获得7BS .7RL易位系, 本发明还公开了一种由上述培育方法选育得到的抗病的小麦-黑麦7BS .7RL染色体易位系以及该易位系在小麦育种中的应用。本发明有利于新抗病基因的转移和利用, 由于7RL不含黑麦碱基因, 对小麦的加工品质不会造成负面影响。

来源: 国家知识产权局专利检索及分析

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<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0Fv8rbyAC4DrABN3jrL5Bmw907.PDF>

➤ 科技报告

1. Genotyping-by-Sequencing Derived High-Density Linkage Map and its Application to QTL Mapping of Flag Leaf Traits in Bread Wheat (通过测序得到的高密度连锁图谱及其在面包小麦剑叶性状QTL定位中的应用)

简介: Winter wheat parents ‘Harry’ (drought tolerant) and ‘Wesley’ (drought susceptible) were used to develop a recombinant inbred population with future goals of identifying genomic regions associated with drought tolerance. To precisely map genomic regions, high-density linkage maps are a prerequisite. In this study genotyping-by-sequencing (GBS) was used to construct the high-density linkage map. The map contained 3,641 markers distributed on 21 chromosomes and spanned 1,959 cM with an average distance of 1.8 cM between markers. The constructed linkage map revealed strong collinearity in marker order across 21 chromosomes with POPSEQ-v2.0, which was based on a high-density linkage map. The reliability of the linkage map for QTL mapping was demonstrated by co-localizing the genes to previously mapped genomic regions for two highly heritable traits, chaff color, and leaf cuticular wax. Applicability of linkage map for QTL mapping of three quantitative traits, flag leaf length, width, and area, identified 21 QTLs in four environments, and QTL expression varied across the environments. Two major stable QTLs, one each for flag leaf length (Qfl.l.hww-7A) and flag leaf width (Qfl.w.hww-5A) were identified. The map constructed will facilitate QTL and fine mapping of quantitative traits, map-based cloning, comparative mapping, and in marker-assisted wheat breeding endeavors.

来源: Nature

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<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0Fv8poGAHKG0AEnFZpxhL-M394.pdf>