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➤ 前沿资讯

1. Diverging importance of drought stress for maize and winter wheat in Europe (干旱胁迫对欧洲玉米和冬小麦不同影响的重要性)

简介: 为了支持适应规划和应对不断变化的生产风险,有必要研究了解气候变化下作物产量水平的驱动因素。本研究使用空间网格上的作物模型组合,量化了各种气候驱动因素对欧洲作物系统(1984-2009年)中玉米和冬小麦过去产量变化的贡献,以及气候变化对2050年的影响。结果表明,就目前的基因型及水旱混合生产而言,气候变化将导致玉米产量的降低和冬小麦产量的增加。在整个欧洲的雨养系统中,无论哪种作物的平均热应力都不会增加,而只有玉米的干旱应力会加剧。在低产年份,干旱胁迫仍然是两种作物产量下降的主要作用因素,而二氧化碳含量的增加在这些年份并没有带来产量效益。

来源: Nature

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<http://agri.ckcest.cn/ass/f90471b7-785e-4c5f-9131-4d8f4d205c2d.pdf>

➤ 相关专利

1. 小麦-长穗偃麦草抗赤霉病易位系的选育方法及分子标记

简介: 本发明公开了一种小麦-长穗偃麦草抗赤霉病易位系的选育方法及分子标记。同时,本发明还提供扩增该分子标记的引物、该分子标记在小麦遗传育种中的应用。所述分子标记是如下的分子之一:(1)序列如SEQ ID NO. 1所示的核酸分子;或(2)序列如SEQ ID NO. 2所示的核酸分子;或(3)序列如SEQ ID NO. 3所示的核酸分子。本发明对于小麦遗传育种的理论研究和实际应用均有重要价值。

来源: 国家知识产权局专利检索及分析

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<http://agri.ckcest.cn/ass/28c5b72d-8ac3-43da-b048-23d3df71f71f.PDF>

➤ 学术文献

1. Genome-wide association mapping for resistance to leaf rust, stripe rust and tan spot in wheat reveals potential candidate genes (小麦抗叶锈病、条锈病和棕褐色斑点的全基因组关联图揭示了育种的潜在候选基因)

简介: Genome-wide association mapping in conjunction with population sequencing map and Ensembl plants was used to identify markers/candidate genes linked to leaf rust, stripe rust and tan spot resistance in wheat. Leaf rust (LR), stripe rust (YR) and tan spot (TS) are some of the important foliar diseases in wheat (*Triticum aestivum* L.). To identify candidate resistance genes for these diseases in CIMMYT's (International Maize and Wheat

Improvement Center) International bread wheat screening nurseries, we used genome-wide association studies (GWAS) in conjunction with information from the population sequencing map and Ensembl plants. Wheat entries were genotyped using genotyping-by-sequencing and phenotyped in replicated trials. Using a mixed linear model, we observed that seedling resistance to LR was associated with 12 markers on chromosomes 1DS, 2AS, 2BL, 3B, 4AL, 6AS and 6AL, and seedling resistance to TS was associated with 14 markers on chromosomes 1AS, 2AL, 2BL, 3AS, 3AL, 3B, 6AS and 6AL. Seedling and adult plant resistance (APR) to YR were associated with several markers at the distal end of chromosome 2AS. In addition, YR APR was also associated with markers on chromosomes 2DL, 3B and 7DS. The potential candidate genes for these diseases included several resistance genes, receptor-like serine/threonine-protein kinases and defense-related enzymes. However, extensive LD in wheat that decays at about 5×10^7 bps, poses a huge challenge for delineating candidate gene intervals and candidates should be further mapped, functionally characterized and validated. We also explored a segment on chromosome 2AS associated with multiple disease resistance and identified seventeen disease resistance linked genes. We conclude that identifying candidate genes linked to significant markers in GWAS is feasible in wheat, thus creating opportunities for accelerating molecular breeding.

来源: THEORETICAL AND APPLIED GENETICS

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<http://agri.ckcest.cn/ass/75b1395f-d230-480b-ae30-0258422fe80a.pdf>

2. Characterization of wheat endoplasmic reticulum oxidoreductin 1 and its application in Chinese steamed bread (小麦内质网氧化还原蛋白1的表征及其在馒头中的应用)

简介: 本文研究了重组小麦内质网氧化还原蛋白1 (wEro1)的特性及其对馒头品质的影响。纯化后的wEro1单体中含有两个保守的氧化还原活性基位点,与黄酮类、腺嘌呤二核苷酸(FAD)辅因子结合,分子量47 kDa。wEro1催化了结合和自由FAD的还原,其对自由FAD的还原活性达到7.8 U/mg。此外,wEro1催化了二硫苏三醇和小麦蛋白二硫异构酶(wPDI)的氧化。谷胱甘肽和核糖核酸酶均能作为wEro1的电子供体,催化wPDI的氧化。此外,wEro1的添加提高了CSB的质量,增加了CSB的比体积,降低了面包屑硬度,这是由于水溶性小麦蛋白的增加和面筋网的增强。研究结果为wEro1的性能和功能提供了新的认识,有助于wEro1在面粉加工业中的应用。

来源: Food Chemistry

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3. Multi-objective optimized genomic breeding strategies for sustainable food improvement (可持续性食品改良的多目标优化基因组育种策略)

简介: The purpose of breeding programs is to obtain sustainable gains in multiple traits while

controlling the loss of genetic variation. The decisions at each breeding cycle involve multiple, usually competing, objectives; these complex decisions can be supported by the insights that are gained by applying multi-objective optimization principles to breeding. The discussion in this manuscript includes the definition of several multi-objective optimized breeding approaches within the phenotypic or genomic breeding frameworks and the comparison of these approaches with the standard multi-trait breeding schemes such as tandem selection, independent culling and index selection. Proposed methods are demonstrated with two empirical data sets and simulations. In addition, we have described several graphical tools that can aid breeders in arriving at a compromise decision. The results show that the proposed methodology is a viable approach to answer several real breeding problems. In simulations, the newly proposed methods resulted in gains larger than the methods previously proposed including index selection: Compared to the best alternative breeding strategy, the gains from multi-objective optimized parental proportions approaches were about 2030% higher at the end of long-term simulations of breeding cycles. In addition, the flexibility of the multi-objective optimized breeding strategies were displayed with methods and examples covering non-dominated selection, assignment of optimal parental proportions, using genomewide marker effects in producing optimal mating designs, and finally in selection of training populations for genomic prediction.

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<http://agri.ckcest.cn/ass/0ce0ae15-18bf-4b31-95c0-844acba3af7.pdf>