



2019年第27期总67期

小麦遗传育种专题

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▶ 前沿资讯

1. **Wheat myth debunked (揭开小麦的谜底)**

简介: The myth that modern wheat varieties are more heavily reliant on pesticides and fertilisers is debunked by new research published in Nature Plants today. Lead author on the paper, Dr Kai Voss-Fels, a research fellow at The University of Queensland, said modern wheat cropping varieties actually out-perform older varieties in both optimum and harsh growing conditions.

来源: EurekAlert

发布日期: 2019-07-01

全文链接:

<http://agri.ckcest.cn/file1/M00/06/87/Csgk0F0bEDKAFxPuAABc3A-7XzE818.pdf>

2. **Genebank genomics bridges the gap between the conservation of crop diversity and plant breeding (基因库基因组学填补了作物多样性保护和植物育种之间的空白)**

简介: 基因库的长期任务是保护植物遗传资源，作为未来作物改良的农业遗产。种子贮藏和植物繁殖的操作程序已经实施了几十年，从陆地种族和野生亲属到现代品种，但缺乏有效的手段来发现和转移有益的等位基因，在这里，我们回顾了利用来自基因组序列信息的分子护照数据作为一种通用的监测工具在单植物水平上的应用前景。随着育种方法的最新进展，将基因库转化为生物数字资源中心将有助于选择有用的遗传变异及其在育种项目中的应用，从而方便获得过去的作物多样性。我们建议将自然遗传变异目录与植物性能生物学机制的研究联系起来，作为基因库、植物遗传学家和育种家的长期共同研究目标。

来源: Nature

发布日期: 2019-06-28

全文链接:

<http://agri.ckcest.cn/file1/M00/06/87/Csgk0F0bGquADWRIABgkt0iUnf0648.pdf>

▶ 学术文献

1. **Identification of powdery mildew resistance loci in wheat by integrating genome-wide association study (GWAS) and linkage mapping (结合全基因组关联研究(GWAS)和连锁作图法对小麦白粉病抗性基因座进行鉴定)**

简介: Wheat powdery mildew (*Blumeria graminis* f. sp. *tritici*, Bgt) is a disease of increasing importance globally due to the adoption of high yielding varieties and modern sustainable farming technologies. Growing resistant cultivars is a preferred approach to managing this disease, and novel powdery mildew resistance genes are urgently needed for new cultivar development. A genome-wide association study was performed on a panel of 1292 wheat

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landraces and historical cultivars using 5011 single nucleotide polymorphism (SNP) markers. The association panel was evaluated for reactions to three Bgt inoculants, OKS(14)-B-3-1, OKS(14)-C-2-1, and Bgt15. Linkage disequilibrium (LD) analysis indicated that genome-wide LD decayed to 0.1 at 23 Mb, and population structure analysis revealed seven subgroups in the panel. Association analysis using a mixed linear model (MLM) identified three loci for powdery mildew resistance on chromosome 2B, designated QPm.stars-2BL1, QPm.stars-2BL2, and QPm.stars-2BL3. To evaluate the efficacy of GWAS in gene discovery, QPm.stars-2BL2 was validated using F2 and F2:3 populations derived from PI 420646 × OK1059060-126135-3. Linkage analysis delimited the powdery mildew resistance gene in PI 420646 to an interval where QPm.stars-2BL2 was located, lending credence to the GWAS results. QPm.stars-2BL1 and QPm.stars-2BL3, which were associated with four SNPs located at 457.7461.7 Mb and two SNPs located at 696.6715.9 Mb in the Chinese Spring reference IWGSC RefSeq v1.0, respectively, are likely novel loci for powdery mildew resistance and can be used in wheat breeding to improve powdery mildew resistance.

来源: ScienceDirect

发布日期: 2019-06-01

全文链接:

<http://agri.ckcest.cn/file1/M00/06/87/Csgk0F0bEu6AQeRzACBIeQ6xU1o695.pdf>

2. Preharvest sprouting and α -amylase activity in soft winter wheat (软粒冬小麦收获前发芽与 α -淀粉酶活性)

简介: The wheat value chain is vulnerable to reduced grain quality caused by preharvest sprouting. The Great Lakes region and the Pacific Northwest are particularly vulnerable to sprouting related quality issues because precipitation events near or at the time of harvest are common and are the leading cause of sprout related losses. Both visual preharvest sprouting (PHS) and alpha-amylase activity (α Amy) influence grain quality. In this study, standardized methods for phenotyping PHS and α Amy have been implemented in soft winter wheat varieties and advanced breeding lines. The methods utilized here for rating visual PHS and α Amy using a scaled down Ceralpha method produce consistent and reliable results across years and can be implemented in screening large wheat breeding populations. The populations phenotyped for PHS and α Amy were also genotyped at grain color (R), photoperiod (Ppd), and reduced height (Rht) genes to determine their influence on PHS and α Amy. Phenotypic variation for PHS and α Amy is present in both soft red and soft white wheat market classes. Soft red winter wheat genotypes were identified that have PHS susceptibility and moderate levels of α Amy. Conversely, genotypes of soft white winter wheat were identified that have PHS resistance and low levels of α Amy. As variation exists for PHS and α Amy in soft wheat germplasm, progress can be made using phenotypic selection for these traits in breeding programs. Development of varieties with improved sprouting resistance will mitigate the risk of sprouting and increase the production of high quality wheat.

来源: ScienceDirect

发布日期: 2018-01-01

全文链接:

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http://agri.ckcest.cn/file1/M00/06/87/Csgk0F0bFB-ATH4_AA3D6xbvavA724.pdf

➤ 相关专利

1. 小麦品种水反应特征表示方法及应用

简介：小麦品种水反应特征表示方法，根据灌溉量将小麦灌水量分成I区、II区、III区、IV区四个区域，根据每个区域的特征进行灌溉，所述灌溉量根据水分生产效率的方程、籽粒产量水反应方程、生物产量水反应方程计算获得；其中，I区为0~最大水分生产效率对应的灌溉量；II区为最大水分生产效率对应的灌溉量~籽粒产量最大值对应的灌溉量；III区为籽粒产量最大值对应的灌溉量-生物产量最大值对应的灌溉量；IV区为大于生物产量最大值的灌溉量。可应用于小麦育种，明确了不同品种的水反应特征参数及分区，这可以作为不同种质资源特性鉴定。另外小麦的三个特征参数及其与各自灌溉量比值均处于临界区域，可通过育种改变临界特征值，这为育种改良方向可以明确。

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<http://agri.ckcest.cn/file1/M00/06/87/Csgk0F0bFn0AWLLHAAqVozN7JZo822.PDF>