



2019年第31期总71期

小麦遗传育种专题

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1. 鉴定小麦产量相关性状的分子标记与方法

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▶ 前沿资讯

1. Discovering consensus genomic regions in wheat for root-related traits by QTL meta-analysis (通过QTL元分析发现小麦根系相关性状的共识基因组区域)

简介: Root system architecture is crucial for wheat adaptation to drought stress, but phenotyping for root traits in breeding programmes is difficult and time-consuming owing to the belowground characteristics of the system. Identifying quantitative trait loci (QTLs) and linked molecular markers and using marker-assisted selection is an efficient way to increase selection efficiency and boost genetic gains in breeding programmes. Hundreds of QTLs have been identified for different root traits in the last few years. In the current study, consensus QTL regions were identified through QTL meta-analysis. First, a consensus map comprising 7352 markers was constructed. For the meta-analysis, 754 QTLs were retrieved from the literature and 634 of them were projected onto the consensus map. Meta-analysis grouped 557 QTLs in 94 consensus QTL regions, or meta-QTLs (MQTLs), and 18 QTLs remained as singletons. The recently published genome sequence of wheat was used to search for gene models within the MQTL peaks. As a result, gene models for 68 of the 94 Root_MQTLs were found, 35 of them related to root architecture and/or drought stress response. This work will facilitate QTL cloning and pyramiding to develop new cultivars with specific root architecture for coping with environmental constraints.

来源: Nature

发布日期: 2019-07-22

全文链接:

http://agri.ckcest.cn/file1/M00/06/8C/Csgk0F0-VJaAHm08ABiknS_j5co122.pdf

▶ 学术文献

1. Powdery mildew susceptibility of spring wheat cultivars as a major constraint on grain yield (春小麦品种白粉病易感性是影响籽粒产量的主要因素)

简介: Powdery mildew infection caused by *Blumeria graminis* f. sp. *tritici* and grain yield of 23 spring wheat cultivars were investigated under controlled and natural conditions during two growing seasons (2016/17 and 2017/18). Under controlled greenhouse conditions, seedling infection types of 9 cultivars, Sids-12, Sids-13, Gemmeiza-3, Gemmeiza-10, Sakha-61, Sakha-93, Sakha-94, Giza-160 and Giza-163 revealed susceptibility to the disease, while 14 cultivars, Misr-1, Misr-2, Sids-1, Gemmeiza-1, Gemmeiza-5, Gemmeiza-7, Gemmeiza-9, Gemmeiza-11, Gemmeiza-12, Sakha-8, Sakha-69, Giza-167, Giza-168 and Giza-171 showed resistance during both seasons. In the field, adult plant infections revealed susceptibility of 8 cultivars, Gemmeiza-3, Gemmeiza-5, Gemmeiza-7, Sakha-8, Sakha-61, Sakha-93, Giza-160 and Giza-163, while 7 cultivars, Misr-2, Sids-13, Gemmeiza-11, Gemmeiza-12, Giza-167, Giza-168 and Giza-171 exhibited resistance during both seasons.

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These last-mentioned 7 cultivars also showed best resistance in seedling infection tests during both seasons. The highest levels of disease severity were recorded with Gemmeiza-3, Sakha-61 and Sakha-94, while the lowest ones were in Giza-167 and Giza-168 as resistant cultivars. Significant losses in grain yield (1000-kernel weight) were recorded with highly susceptible cultivars, reaching 26.68% in Gemmeiza-3, while insignificant loss was recorded with resistant cultivars, 2.06% in Giza-168. A strong positive correlation was observed between % disease severity and % loss in 1000-kernel weight, recording $r = 0.9195$ in the first season and $r = 0.9402$ in the second season. In susceptible cultivars, disease was an important yield constraint. Resistant cultivars may be incorporated in breeding programs to prevent yield losses.

来源: Science Direct

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/8C/Csgk0F0-WTGAByiiAAg0xUs8Ck0171.pdf>

2. Seedling and adult plant resistance to leaf rust in 46 Chinese bread wheat landraces and 39 wheat lines with known Lr genes (46个中国面包小麦地方品种和39个已知Lr基因小麦系的幼苗和成株对叶锈病的抗性)

简介: Wheat leaf rust, caused by *Puccinia triticina* (Pt), is an important foliar disease that has an important influence on wheat yield. The most economic, safe and effective way to control the disease is growing resistant cultivars. In the present study, a total of 46 wheat landraces and 34 wheat lines with known Lr (leaf rust resistance) genes were inoculated with 16 Pt pathotypes for postulating seedling resistance gene(s) in the greenhouse. These cultivars and five wheat differential lines with adult plant resistance (APR) genes (Lr12, Lr22b, Lr34, Lr35 and Lr37) were also evaluated for identification of slow rusting resistance in the field trials in Baoding, Hebei Province of China in the 20142015 and 20152016 cropping seasons. Furthermore, 10 functional molecular markers closely linked to 10 known Lr genes were used to detect all the wheat genotypes. Results showed that most of the landraces were susceptible to most of the Pt pathotypes at seedling stage. Nonetheless, Lr1 was detected only in Hongtangliangmai. The field experimental test of the two environments showed that 38 landraces showed slow rusting resistance. Seven cultivars possessed Lr34 but none of the landraces contained Lr37 and Lr46. Lr genes namely, Lr9, Lr19, Lr24, Lr28, Lr29, Lr47, Lr51 and Lr53 were effective at the whole plant stage. Lr18, Lr36 and Lr45 had lost resistance to part of pathotypes at the seedling stage but showed high resistance at the adult plant stage. Lr34 as a slowing rusting gene showed good resistance in the field. Four race-specific APR genes Lr12, Lr13, Lr35 and Lr37 conferred good resistance in the field experiments. Seven race-specific genes, Lr2b, Lr2c, Lr11, Lr16, Lr26, Lr33 and LrB had lost resistance. The 38 landraces showed slow rusting resistance to wheat leaf rust can be used as resistance resources for wheat resistance breeding in China.

来源: Science Direct

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/8C/Csgk0F0-WGKAQc j4AAZVDPB7xUM854.pdf>

3. Genetic modification of spikelet arrangement in wheat increases grain number without significantly affecting grain weight (小麦穗排列的遗传修饰增加了籽粒数, 但对籽粒重没有显著影响)

简介: 作物产量是由光合同化物质在库器官的获取和分配决定的。因此, 库大小的遗传修饰对于理解调控库强度和源活动的复杂信号网络是至关重要的。小麦的粒库大小与穗粒数、小穗数、籽粒重和干物质积累有关。因此, 增加小穗数和改善小穗基因库是小麦育种的目标。本研究的主要目的是对小麦穗结构进行基因修饰, 即: 通过将“奇迹小麦”(Miracle wheat)或bht-A1等位基因导入到一种优质硬粒小麦cv. Floradur中, 这种基因库的大小就可以确定了。通过与复归亲本Floradur (FL)的四代回交, 我们成功地培育出近等基因系(NILs), 利用一种改良的小穗排列, 从而增加了小穗数和每穗粒数。采用基因型测序法对bht-A1 NILs进行基因分型, 发现携带bht-A1基因的外源供体片段大小在2.3 ~ 38 cM之间。进入bht-A1 NILs的最短供体片段的大小估计为9.8百万碱基对(Mbp)。表型分析表明, FL-bht-A1-NILs (BC3F2和BC3F3)每穗可携带多达7个额外的小穗, 导致收获时穗干重(SDWh)增加高达29%。

来源: Springer

发布日期: 2019-04-01

全文链接:

<http://agri.ckcest.cn/file1/M00/06/8C/Csgk0F0-Vv-AE-mCADJbBHBLA24439.pdf>

➤ 相关专利

1. 鉴定小麦产量相关性状的分子标记与方法

简介: 本发明公开了鉴定小麦产量相关性状的分子标记与方法。本发明公开的鉴定小麦产量相关性状的分子标记为小麦基因组中的H和J位点, H位点为序列表序列1自5'末端的第31位, J位点为序列表序列2自5'末端的第21位, H位点为T的小麦穗长长于或候选长长于H位点为G的小麦穗长; J位点为C的小麦每穗小穗数多于或候选多于J位点为T的小麦每穗小穗数。通过检测H和J位点的核苷酸, 即可找到穗长和每穗小穗数相对较高的小麦。本发明为小麦分子标记辅助选择育种提供了一个新方法, 在培育高产小麦品种或研究中具有重要意义。

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/8C/Csgk0F0-X7OAPGrJABR1XyYnRNQ399.PDF>