



2018年第32期总32期

## 小麦遗传育种专题

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## 学术文献

### 1. Association between presence of *Triticum timopheevii* introgression and D-genome retention in hexaploid/tetraploid wheat crosses (六倍体/四倍体小麦杂交组合中小麦、黑麦侵染与D-基因组保留的关系)

**简介:** 二代黑麦是小麦抵抗多种病害和改良品质性状的基因载体。为了将此基因片段从面包小麦转移到硬粒小麦中,将携带该导入2G片段的面包小麦品系Sunguard与三个四倍体硬粒小麦亲本杂交。在F-2代不同杂交组合中,2G片段的分离率存在显著差异,三个品种中有两个对六倍体2G片段的分离会发生畸变。在这些品种中,2G片段的存在与D染色体的存在密切相关。研究结果在这一品种的F-4代中得到证实。从F-4代中鉴定出6株植株,它们在纯合子条件下保留了渗入的2G片段,并且没有完整的D-基因组集。在F-5代中,其中只有两条染色体具有两条非同源的D-染色体。因此,2G片段和可能的其他易位可以通过六倍体/四倍体杂交转移到硬质小麦中。

**来源:** MOLECULAR BREEDING

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**全文链接:**

<http://agri.ckcest.cn/ass/3754b038-3db7-4ba7-b07c-436f13dca2e7.pdf>

### 2. Optimising Genomic Selection in Wheat: Effect of Marker Density, Population Size and Population Structure on Prediction Accuracy (小麦基因组选择优化:标记密度、种群大小和种群结构对预测精度的影响)

**简介:** Genomic selection applied to plant breeding enables earlier estimates of a line's performance and significant reductions in generation interval. Several factors affecting prediction accuracy should be well understood if breeders are to harness genomic selection to its full potential. We used a panel of 10,375 bread wheat (*Triticum aestivum*) lines genotyped with 18,101 SNP markers to investigate the effect and interaction of training set size, population structure and marker density on genomic prediction accuracy. Through assessing the effect of training set size we showed the rate at which prediction accuracy increases is slower beyond approximately 2,000 lines. The structure of the panel was assessed via principal component analysis and K-means clustering, and its effect on prediction accuracy was examined through a novel cross-validation analysis according to the K-means clusters and breeding cohorts. Here we showed that accuracy can be improved by increasing the diversity within the training set, particularly when relatedness between training and validation sets is low. The breeding cohort analysis revealed that traits with higher selection pressure (lower allelic diversity) can be more accurately predicted by including several previous cohorts in the training set. The effect of marker density and its interaction with population structure was assessed for marker subsets containing between 100 and 17,181 markers. This analysis showed that response to increased marker density is largest when using a diverse training set to predict between poorly related material. These findings

represent a significant resource for plant breeders and contribute to the collective knowledge on the optimal structure of calibration panels for genomic prediction.

来源: Web of Science

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全文链接:

<http://agri.ckcest.cn/ass/39ed6b85-a7dd-470f-bbea-b30b796f01ad.pdf>

### **3. SNP-based pool genotyping and haplotype analysis accelerate fine-mapping of the wheat genomic region containing stripe rust resistance gene Yr26 (基于SNP基因池分型和单倍体分析加速了含有抗条锈病基因Yr26的小麦基因组区域的精细定位)**

简介: NGS-assisted super pooling emerging as powerful tool to accelerate gene mapping and haplotype association analysis within target region uncovering specific linkage SNPs or alleles for marker-assisted gene pyramiding. Conventional gene mapping methods to identify genes associated with important agronomic traits require significant amounts of financial support and time. Here, a single nucleotide polymorphism (SNP)-based mapping approach, RNA-Seq and SNP array assisted super pooling analysis, was used for rapid mining of a candidate genomic region for stripe rust resistance gene Yr26 that has been widely used in wheat breeding programs in China. Large DNA and RNA super-pools were genotyped by Wheat SNP Array and sequenced by Illumina HiSeq, respectively. Hundreds of thousands of SNPs were identified and then filtered by multiple filtering criteria. Among selected SNPs, over 900 were found within an overlapping interval of less than 30 Mb as the Yr26 candidate genomic region in the centromeric region of chromosome arm 1BL. The 235 chromosome-specific SNPs were converted into KASP assays to validate the Yr26 interval in different genetic populations. Using a high-resolution mapping population (> 30,000 gametes), we confined Yr26 to a 0.003-cM interval. The Yr26 target region was anchored to the common wheat IWGSC RefSeq v1.0 and wild emmer WEWSeq v.1.0 sequences, from which 488 and 454 kb fragments were obtained. Several candidate genes were identified in the target genomic region, but there was no typical resistance gene in either genome region. Haplotype analysis identified specific SNPs linked to Yr26 and developed robust and breeder-friendly KASP markers. This integration strategy can be applied to accelerate generating many markers closely linked to target genes/QTL for a trait of interest in wheat and other polyploid species.

来源: THEORETICAL AND APPLIED GENETICS

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<http://agri.ckcest.cn/ass/ab470915-1bba-46bd-849a-bcbbff7181e8.pdf>

### **4. 分子标记在小麦抗条锈病遗传育种中的应用研究进展**

简介: 小麦条锈病是小麦生产上的主要病害, 抗条锈病小麦新品种的选育是综合防治小麦条锈病的最佳途径。分子标记技术具有不受环境和植株正常生长发育影响的特点, 结

合传统抗病性鉴定可在育种早期对植株抗病性进行综合分析,快速有效地进行育种选择,从而大大缩短育种进程,提高育种效率。本综述从小麦抗条锈病基因遗传图谱构建、小麦种质资源抗条锈病状况评价、抗性基因差异表达及抗性材料遗传多样性分析等4个方面论述了3代分子标记在小麦抗条锈病遗传育种中的应用及研究进展,对全基因组关联研究与蛋白质组学技术结合在小麦抗条锈病遗传机制研究中的应用进行了探讨。

**来源:** 分子植物育种

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**全文链接:**

<http://agri.ckcest.cn/ass/7e09e3a7-4c28-4fe7-9bcb-6e9a748ff66a.pdf>

## ➤ 前沿资讯

### 1. Genetic discovery another tool in battle against wheat pests (基因发现是对抗小麦害虫的另一个工具)

**简介:**阿马里洛市的麦二叉蚜和小麦瘿蝇会对得克萨斯州甚至世界范围内小麦产量和质量的降低造成严重的影响。利用标记辅助选择技术进行对抗这两种害虫的育种刚刚从德克萨斯A&M农业研究中心获得了一项新工具。遗传学是减少小麦生产损失最经济的策略,小麦遗传研究专家刘树宇博士两年前开始寻找有利于这两种昆虫繁殖的遗传标记。这一步是正在进行的昆虫抗性遗传工作的延续。多年来,在小麦及其亲缘植物中,通过对不同生物类型(从a到K)不同反应的研究,鉴定出了一些绿色细菌抗性基因。同时还有18种黑穗病蝇的生物类型,由于它具有通过突变克服小麦品种中的抗性基因的能力,因此有必要识别和利用来自不同来源的抗性基因进行小麦育种。科学家们使用遗传标记来识别在特定植物上可以找到特定基因的区域。刘博士发现了一种基因的邻近区域或标记物,该基因具有绿色细菌抗性,即Gb7,以及具有小麦瘿蝇抗性的H32。

**来源:** EurekAlert!

**发布日期:**2018-10-28

**全文链接:**

<http://agri.ckcest.cn/ass/0a377e8b-749b-4d71-9eb2-d69bf137cd73.pdf>