蔬菜育种专题

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前沿资讯

1. Connecting the pieces: uncovering the molecular basis for long‑distance communication through plant grafting（通过植物嫁接揭示远距离通信的分子基础）

简介：维管植物具有非常独特的长距离通讯系统。该网络在不同物种中的尺度差异巨大，从拟南芥中的几厘米到红杉中的数百米，这些网络连接着植物不同部位的器官，形成一个整体的、多细胞生物。嫁接是一项十分重要的技术。借用这一技术，研究人员可以将植物打断，然后再重组长距离运输系统，进而可以研究植物不同器官间通讯的分子信号。目前，来自美国康奈尔大学的研究人员在《新植物学家》杂志上发表论文，综述了植物嫁接是如何用于鉴定植物长距离信号分子的发现，这些信号分子作用于植物的发育状态转变、生物和非生物胁迫响应以及不同物种间的互作。该领域的快速发展为试验、大田、果园等植物的表型改良提供了可行的方法和可持续的解决方案。

来源： New Phytologist

发布日期： 2019-03-04

全文链接：

http://agri.ckcest.cn/file1/M00/06/60/Csgk0FyLQU6AX2dEAAaYIboqHK8558.pdf

学术文献

1. Comparative Mapping Combined With Map-Based Cloning of the Brassica juncea Genome Reveals a Candidate Gene for Multilocular Rapeseed（比较图谱结合油菜基因组的图位克隆（map-based cloning）揭露多室油菜的候选基因）

简介： Multilocular traits exist in a variety of plants and exert important effects on plant yield. Previous genetic studies have shown that multilocular trait of the Brassica juncea cultivar Duoshi is controlled by two recessive genes, Bjln1 and Bjln2. In previous studies, the Bjln1 gene is located on chromosome A07, and the Bjln1 candidate gene is BjuA07.CLV1. In this study, a BC4 mapping population for the Bjln2 gene was generated. This population was used to construct genetic linkage maps of the Bjln2 gene using amplified fragment length polymorphism (AFLP), intron length polymorphism (IP) and simple sequence repeat (SSR) methodology. The results showed that the Bjln2 gene was restricted to a 0.63 cM interval. BLAST alignment with B. juncea revealed the Bjln2 gene was located within a 11.81-16.65 Mb region on chromosome B07. Moreover, the candidate gene BjuB07.CLV1 (equivalent to Bjln2) was cloned by comparing mapping and map-based cloning, and BjuB07.CLV1 gene was shown to have the ability to restore the bilocular traits in a genetic complementation experiment. The sequencing revealed that a 4961 bp insertion interrupted the coding sequence of the BjuB07.CLV1 gene, resulting in an increase in locule number. Expression analysis revealed that BjuB07.CLV1 was expressed in all tissues and the expression level in bilocular plants was significantly higher than that in multilocular plants. In addition, markers closely linked to the Bjln2 gene were developed and used for molecular marker-assisted

breeding of multilocular traits.

来源：Frontiers in Plant Science

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全文链接：

http://agri.ckcest.cn/file1/M00/06/60/Csgk0FyLPiWAXq19ADFlqZLPHAg979.pdf

2．Partial stem resistance in Brassica napus to highly aggressive and genetically diverse Sclerotinia sclerotiorum isolates from Australia（欧洲油菜部分茎对来自澳大利亚的高侵袭性和基因多样性的核盘菌分离株的抗性）

简介：Sclerotinia sclerotiorum is a fungal pathogen that causes stem rot in oilseed rape (Brassica napus). Previously, B. napus accessions with partial stem resistance to a Canadian S. sclerotiorum isolate (#321) were identified using a stem test in which flowering plants were inoculated with mycelium plugs. The present study examined the partial stem resistance of four of these accessions, PAK54, PAK93, DC21 and K22, following inoculation with Australian isolates. Mycelial compatibility groups and intergenic spacer (IGS) region haplotypes were identified among 71 isolates from Australian oilseed rape and lupin fields. Eleven genetically diverse isolates showed differences in aggressiveness when inoculated onto nine oilseed rape varieties and one Chinese accession. Isolates CU8.24, CU10.17 and CU11.19 were selected based on genetic diversity, growth rate in vitro and high aggressiveness in the initial screen and subsequently inoculated onto the four B. napus accessions. These accessions developed significantly smaller lesions compared with the susceptible control varieties ('AV Garnet' and 'Westar'), with the average frequency of soft and collapsed lesions being less than 20% in PAK54, DC21 and K22, 29% in PAK93 and greater than 88% in the susceptible controls. Microscopic examination revealed that hyphae were typically confined to the stem cortex in the smallest lesions, but could be found in the stem pith in larger lesions. These results show that B. napus accessions PAK54, PAK93, DC21 and K22 can be used in Australia for development of varieties with partial stem resistance to S. sclerotiorum.

来源：Canadian Journal of Plant Pathology

发布日期：2018-10-10

全文链接：

http://agri.ckcest.cn/file1/M00/06/60/Csgk0FyK_CyAVTwnABrlITxAruo488.pdf

3．Genomic Prediction Using Prior Quantitative Trait Loci Information Reveals a Large Reservoir of Underutilised Blackleg Resistance in Diverse Canola (Brassica napus L.) Lines（利用先验QTL进行基因组预测揭示了不同甘蓝型油菜品系中存在大量未充分利用的黑腿病抗性）

简介：Genomic prediction is becoming a popular plant breeding method to predict the genetic merit of lines. While some genomic prediction results have been reported in canola, none

have been evaluated for blackleg disease. Here, we report genomic prediction for seedling emergence, survival rate, and internal infection), using 532 Spring and Winter canola lines. These lines were phenotyped in two replicated blackleg disease nurseries grown at Wickliffe and Green Lake, Victoria, Australia. A transcriptome genotyping-by-sequencing approach revealed 98,054 single nucleotide polymorphisms (SNPs) after quality control. We assessed various genomic prediction scenarios based on Genomic Best Linear Unbiased Prediction (GBLUP), BayesR and BayesRC, which can make use of prior quantitative trait loci information, via cross-validation. Clustering based on genomic relationships showed that Winter and Spring lines were genetically distinct, indicating limited gene flow between sets. Genetic correlations within traits between Spring and Winter lines ranged from 0.68 and 0.90 (mean = 0.76). Based on GBLUP in the whole population, moderate to high genomic prediction accuracies were achieved within environments (0.35-0.74) and were reduced across environments (0.28-0.58). Prediction accuracy within the Spring set ranged from 0.30-0.69, and from 0.19-0.71 within the Winter set. The BayesR model resulted in slightly lower accuracy to GBLUP. The proportion of genetic variance explained by known blackleg quantitative trait loci (QTL) was < 30%, indicating that there is a large reservoir of genetic variation in blackleg traits that remains to be discovered, but can be captured with genomic prediction. However, providing prior information of known QTL in the BayesRC method resulted in an increased prediction accuracy for survival and internal infection, particularly with Spring lines. Overall, these promising results indicate that genomic prediction will be a valuable tool to make use of all genetic variation to improve blackleg resistance in canola.

来源：The Plant Genome

发布日期：2018-05-17

全文链接：

http://agri.ckcest.cn/file1/M00/06/60/Csgk0FyLGOOANn7UAD06aM3msQ0974.pdf

4．Effective Genomic Selection in a Narrow-Genepool Crop with Low-Density Markers: Asian Rapeseed as an Example（低密度标记、基因库狭小作物的有效基因组选择：以亚洲油菜为例）

简介：Genomic selection (GS) has revolutionized breeding for quantitative traits in plants, offering potential to optimize resource allocation in breeding programs and increase genetic gain per unit of time. Modern high-density single nucleotide polymorphism (SNP) arrays comprising up to several hundred thousand markers provide a user-friendly technology to characterize the genetic constitution of whole populations and for implementing GS in breeding programs. However, GS does not build upon detailed genotype profiling facilitated by maximum marker density. With extensive genome-wide linkage disequilibrium (LD) being a common characteristic of breeding pools, fewer representative markers from available high-density genotyping platforms could be sufficient to capture the association between a genomic region and a phenotypic trait. To examine the effects of reduced marker density on genomic prediction accuracy, we collected data on three traits across 2 yr in a panel of 203 homozygous Chinese semiwinter rapeseed (Brassica napus L.) inbred lines, broadly encompassing allelic variability in the Asian B. napus genepool. We investigated two

approaches to selecting subsets of markers: a trait-dependent strategy based on genome-wide association study (GWAS) significance thresholds and a trait-independent method to detect representative tag SNPs. Prediction accuracies were evaluated using cross-validation with ridge-regression best linear unbiased predictions (rrBLUP). With semiwinter rapeseed as a model species, we demonstrate that low-density marker sets comprising a few hundred to a few thousand markers enable high prediction accuracies in breeding populations with strong LD comparable to those achieved with high-density arrays. Our results are valuable for facilitating routine application of cost-efficient GS in breeding programs.

来源：The Plant Genome

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全文链接：

http://agri.ckcest.cn/file1/M00/06/60/Csgk0FyLGd6AcOx9ABVBkDeCXrM555.pdf