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蔬菜育种专题

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➤ 前沿资讯

1. Plant growth-promoting bacteria enhance plant salinity tolerance (植物促生细菌可提高农作物的耐盐性)

简介: 土壤盐分是影响农业生产力的非生物胁迫因子之一，尤其对盐敏感的作物如水稻和小麦的产量有严重影响。植物促生细菌（PGPB）具有在土壤盐渍化条件下提高作物生产力的巨大潜力，但由于缺乏非侵入性方法检测不同细菌提高植物抵抗盐渍化的效率，PGPB的应用进展十分缓慢。目前，韩国和爱沙尼亚的科研人员开展的合作研究将叶片挥发性排放和光合特性作为潜在的非侵入性标记，以评估水稻在接种植物根际促生细菌（PGPR）亚麻短杆菌RS16之后耐盐度的改善情况。

该团队主要研究了植物的挥发性有机化合物（VOC）的排放控制。VOC是植物防御的一部分，但是对环境和气候变化的影响很大。土壤盐度增加会引发植物中的氧化应激，最终导致光合作用显著降低。盐胁迫对光合特性和挥发性排放有很强影响，因此可以在盐胁迫条件下筛选出光合特性和挥发性排放作为非侵入性工具。

本研究以IR29（盐敏感型）和FL478（中度耐盐型）两个水稻品种为材料，研究了盐胁迫下接种耐盐PGPB亚麻短杆菌RS16后，对叶片碳同化速率和应激挥发物排放速率的影响。水稻植株接种亚麻短杆菌RS16可以缓解盐胁迫程度，其特点是增强叶片光合特性，减少胁迫下的挥发性排放。盐敏感型品种IR29比中度耐盐基因型FL478检测到的变化更大。结果表明，盐胁迫对两种水稻品种的叶片光合特性均有不利影响。此外，盐度提高了叶片胁迫挥发的排放率。因此，与对照植物相比，亚麻短杆菌RS16能显著改善盐胁迫水稻品种的光合特性，减少挥发性排放。

来源: ScienceDaily

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全文链接:

<http://agri.ckcest.cn/ass/ab331340-2ff8-488c-8028-349a383bb161.pdf>

➤ 学术文献

1. Whole-transcriptome analysis reveals genetic factors underlying flowering time regulation in rapeseed (*Brassica napus* L.) (全转录组分析揭示了甘蓝型油菜花期控制的遗传因素)

简介: Rapeseed (*Brassica napus* L.), one of the most important sources of vegetable oil and protein-rich meals worldwide, is adapted to different geographical regions by modification of flowering time. Rapeseed cultivars have different day length and vernalization requirements, which categorize them into winter, spring, and semiwinter ecotypes. To gain a deeper insight into genetic factors controlling floral transition in *B. napus*, we performed RNA sequencing (RNA-seq) in the semiwinter doubled haploid line, Ningyou7, at different developmental stages and temperature regimes. The expression profiles of more than 54,000 gene models were compared between different treatments and developmental stages, and the differentially expressed genes were considered as targets for association analysis and genetic mapping to confirm their role in floral transition. Consequently, 36 genes with association to flowering

time, seed yield, or both were identified. We found novel indications for neofunctionalization in homologs of known flowering time regulators like VIN3 and FUL. Our study proved the potential of RNA-seq along with association analysis and genetic mapping to identify candidate genes for floral transition in rapeseed. The candidate genes identified in this study could be subjected to genetic modification or targeted mutagenesis and genotype building to breed rapeseed adapted to certain environments.

来源: Plant Cell & Environment

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<http://agri.ckcest.cn/ass/2b3a17cb-6626-4870-9332-b55e1e4d5d0b.pdf>

2. Multi-year linkage and association mapping confirm the high number of genomic regions involved in oilseed rape quantitative resistance to blackleg (多年连锁及关联作图证实大量基因组区域与油菜黑胫病的数量抗性有关)

简介: *Key message* A repertoire of the genomic regions involved in quantitative resistance to *Leptosphaeria maculans* in winter oilseed rape was established from combined linkage-based QTL and genome-wide association (GWA) mapping.

Abstract Linkage-based mapping of quantitative trait loci (QTL) and genome-wide association studies are complementary approaches for deciphering the genomic architecture of complex agronomical traits. In oilseed rape, quantitative resistance to blackleg disease, caused by *L. maculans*, is highly polygenic and is greatly influenced by the environment. In this study, we took advantage of multi-year data available on three segregating populations derived from the resistant cv Darmor and multi-year data available on oilseed rape panels to obtain a wide overview of the genomic regions involved in quantitative resistance to this pathogen in oilseed rape. Sixteen QTL regions were common to at least two biparental populations, of which nine were the same as previously detected regions in a multi-parental design derived from different resistant parents. Eight regions were significantly associated with quantitative resistance, of which five on A06, A08, A09, C01 and C04 were located within QTL support intervals. Homoeologous *Brassica napus* genes were found in eight homoeologous QTL regions, which corresponded to 657 pairs of homoeologous genes. Potential candidate genes underlying this quantitative resistance were identified. Genomic predictions and breeding are also discussed, taking into account the highly polygenic nature of this resistance.

来源: Theoretical and Applied Genetics

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全文链接:

<http://agri.ckcest.cn/ass/124c56fb-6f52-4315-a974-400ce3bb11ce.pdf>

3. Increasing genetic variability in oilseed rape (*Brassica napus*) – Genotypes and phenotypes of oilseed rape transformed by wild type *Agrobacterium rhizogenes* (提高甘蓝型油菜遗传变异性——野生型)

毛根农杆菌改变油菜的基因型和表现型)

简介: Brassica napus (oilseed rape) is a major oil crop worldwide. Due to the short domestication period of oilseed rape the genetic variability is limited compared to other crops. Transfer of rol and aux genes from Agrobacterium rhizogenes is used in horticulture to increase genetic variability. In the current study, we explore transformation by A. rhizogenes as a biotechnological approach in breeding for more branched and shorter oilseed rape. In the 2nd generation of transformed oilseed rape, branch numbers increased significantly by 49% from 7.7 ± 0.4 to 11.5 ± 1.9 when comparing rol+/aux+ plants with WT. Simultaneously, the apical height of plants was reduced by 25% from 81.3 ± 1.9 cm to 62.4 ± 6.7 cm in rol+/aux+ plants at the onset of flowering. Reproductive parameters affecting yield as seed size and number were negatively affected in rol+/aux+ plants. Interestingly, oil composition was changed in rol+/aux+ seeds. Oleic acid ($\omega 9$) contents were reduced by more than 3% whereas α -linolenic acid ($\omega 6$) increased by more than 25% in mature seeds. To obtain shorter and more branched breeding material of oilseed rape we suggest crossing plants with the rol+/aux+ genotype back into the parental breeding line. This could reduce the negative impact of rol+/aux+ on yield.

来源: Plant Science

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<http://agri.ckcest.cn/ass/276c14c7-1516-445c-ab6c-66df4d34ba2c.pdf>

4. Earliness traits in rapeseed (Brassica napus): SNP loci and candidate genes identified by genome-wide association analysis (甘蓝型油菜早熟性状: 全基因组关联分析确认SNP位点和候选基因)

简介: Life cycle timing is critical for yield and productivity of Brassica napus (rapeseed) cultivars grown in different environments. To facilitate breeding for earliness traits in rapeseed, SNP loci and underlying candidate genes associated with the timing of initial flowering, maturity and final flowering, as well as flowering period (FP) were investigated in two environments in a diversity panel comprising 300 B. napus inbred lines. Genome-wide association studies (GWAS) using 201,817 SNP markers previously developed from SLAF-seq (specific locus amplified fragment sequencing) revealed a total of 131 SNPs strongly linked ($P < 4.96E-07$) to the investigated traits. Of these 131 SNPs, 40 fell into confidence intervals or were physically adjacent to previously published flowering time QTL or SNPs. Phenotypic effect analysis detected 35 elite allelic variants for early maturing, and 90 for long FP. Candidate genes present in the same linkage disequilibrium blocks ($r^2 > 0.6$) or in 100 kb regions around significant trait-associated SNPs were screened, revealing 57 B. napus genes (33 SNPs) orthologous to 39 Arabidopsis thaliana flowering time genes. These results support the practical and scientific value of novel largescale SNP data generation in uncovering the genetic control of agronomic traits in B. napus, and also provide a theoretical basis for molecular marker-assisted selection of earliness breeding in rapeseed.

来源: DNA Research

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全文链接:

<http://agri.ckcest.cn/ass/2406931c-12c0-4064-bab9-472698351ff8.pdf>