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蔬菜育种专题

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前沿资讯

1. New approach will help geneticists identify genes responsible for complex traits(研究发现识别控制复杂性状基因的新方法)

简介：在生命科学领域中，遗传学家都在追寻与疾病易感性、作物产量和其他性状相关的特定基因。近15年来，这些研究都依赖于全基因组关联分析（GWAS），需要进行大量的统计计算，以搜寻遗传密码的差异。

GWAS的特点是一次测试一个标记与性状的关联强度。然而，性状并非仅由一个基因控制，而是多个基因以附加形式控制着表型变异，并在上位上进行互动。研究人员想要探寻的是在生物学上更为精确的统计方法。他们在寻找一次就有多个标记甚至有多个双向互动效果的统计模型。

来自美国伊利诺伊大学的研究团队测试了新方法——“构建附加上位多基因座模式的分步程序”（Stepwise Procedure for constructing an Additive and Epistatic Multi-Locus model, SPAEML）——能否检测到数据库的模拟性状。研究人员在人类数据库和玉米数据库中都识别出了模拟标记，并在前者中区分出了加性基因座和互作基因座。研究团队花费了近四年的时间研发并改进了处理组合式探索的方法，将数百万个数据点减少至约15,000个，这样SPAEML就能轻松处理了。今后，研究人员计划利用SPAEML解锁未知的基因结构。

来源：AAAS

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全文链接:

http://agri.ckcest.cn/file1/M00/06/5B/CsgkOFwyxy-Acnb7AAGM4qLK_xY210.pdf

学术文献

1. Effects of hormonal and physical treatments on the expression of a putative chlorophyll b reductase gene (BoNYC1) during postharvest senescence of broccoli(激素和物理处理对青花菜采后衰老过程中叶绿素B还原酶（BoNYC1）基因表达的影响)

简介：Senescence and degreening are the most important features that determine loss of quality during postharvest of broccoli. During senescence, chlorophylls are degraded with the purpose of avoiding presence of photoactive molecules. Chlorophyll b must be previously converted to chlorophyll a in order to be catabolized. This reduction process is catalyzed by two enzymes, chlorophyll b reductase (CBR) and hydroxymethyl chlorophyll a reductase (HCAR). In this work, we characterized the expression of a gene encoding a putative CBR (BoNYC1) during postharvest senescence of broccoli and analysed the effect of several postharvest treatments. BoNYC1 expression increased during first days of postharvest, but decreased in advanced senescence stages, simultaneously with chlorophyll degradation. The effect of different growth regulators and an inhibitor of ethylene action (1-MCP) were analyzed. Treatments with cytokinins and 1-MCP delayed the increment of BoNYC1 expression whereas ethylene accelerated the process. In addition, storage in modified

atmosphere, exposure to hot air (45℃, 3 h), UV-C and white light were also employed. These treatments delayed chlorophyll degradation but only hot air and UV-C delayed the increment of BoNYC1 expression whereas modified atmosphere and visible light caused a higher BoNYC1 expression. In conclusion, most of the hormonal and physical treatments that modify the rate of postharvest senescence of broccoli also affect the expression of BoNYC1.

来源： Postharvest Biology and Technology

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全文链接:

http://agri.ckcest.cn/file1/M00/06/5B/CsgkOFwyuyCAfZGWABwrjEIXxBA156.pdf

2. The evaluation of plant extracts, biocontrol agents and hot water as seed treatments to control black rot of rape in South Africa（植物提取物、生物制剂和热水等种子处理方法对南非油菜黑腐病防治效果的评价）

简介： Black rot disease, which is caused by the pathogen Xanthomonas campestris pv. campestris (Xcc), is a major challenge to brassica vegetable production by smallholder farmers. The pathogen is seed-borne making it difficult to control the disease. In this study various plant extracts, commercial biocontrol agents (BCAs) and hot water treatments were evaluated for their antibacterial activity, and as seed treatments of rape (Brassica napus L.) against Xcc in vitro and under greenhouse conditions. The microtitre double-dilution assay showed that acetone extracts of Cymbopogon citratus had strong antimicrobial activity with the lowest minimum inhibitory concentration (MIC) of 0.19 mg/ml, which was comparable to the antibiotic neomycin (0.2 mg/ml). Using the agar well diffusion method the BCA Paenibacillus sp. (3×10^9 cfu/ml) recorded the highest antibacterial activity with a maximum zone of inhibition of 17 mm. Seed treatment with hot water at 50℃ for 30 min reduced the bacterial population to 3.1 cfu/ml compared to the untreated inoculated control (6.0 cfu/ml). Significantly higher germination percentage (84%) was recorded after seed treatments with acetone extracts of Agapanthus caulescens (15 mg/ml) and hot water at 50℃ for 30 min. In the greenhouse trials, acetone extracts of A. caulescens (15 mg/ml), Paenibacillus sp., and hot water at 50℃ for 30 min significantly increased seedling emergence and reduced black rot incidence and severity on rape leaves. The present study showed that plant extracts, commercial BCAs and hot water have potential as seed treatments for the control of Xcc and black rot disease.

来源： Crop Protection

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全文链接:

http://agri.ckcest.cn/file1/M00/06/5B/CsgkOFwywbaAEhooAAZMNi09NPs686.pdf

3. Association mapping of cadmium-tolerant QTLs in Brassica napus L. and insight into their contributions to phytoremediation（甘蓝型油菜耐镉QTL的关联图谱及其对植物修复的贡献）

简介：Cadmium (Cd) contamination in soil is one of the major global environmental issues. Rapeseed (Brassica napus L.), as one of the most important oil crops, bio-energy resources and Cd accumulator, is an ideal plant for phytoremediation. But the Cd tolerance mechanisms in rapeseed are not known. Thus, both phenotypic and genotypic identification of Cd tolerance were conducted in a rapeseed natural population. Twelve Cd-tolerant genotypes were selected among 472 worldwide collection of natural rapeseeds based on the criterion of relative radicle length (RRL) > 60%. Nine associated SNPs localized in four QTLs were identified by genome-wide association study (GWAS) in which 60 K Brassica Infinium® SNP array was used. Seven candidate genes for Cd tolerance, including HIPP27, EXPB4, EMB1793 and CDSP32 orthologues, were obtained in these loci. The expression of these genes were induced by Cd stress in Cd-tolerant genotype and reduced or not affected by Cd stress in Cd-sensitive genotype in qRT-PCR assays. These genes may contribute to Cd tolerance in rapeseed through the regulation of cell wall development, metal chelation, detoxification and antioxidant defense, respectively. In addition, we suggested that Cd tolerance in rapeseed could be improved by gene pyramiding, as our study has demonstrated the additive effect in both intra- and inter-QTL. Collectively, these findings could provide several breeding materials for producing Cd-tolerant rapeseeds that could be utilized in phytoremediation of heavy Cd polluted field.

来源：Environmental and Experimental Botany

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全文链接:

http://agri.ckcest.cn/file1/M00/06/5B/CsgkOFwyxn6AGjziAB59ttYPk8E789.pdf

4. The RNA chaperone Hfq is important for the virulence, motility and stress tolerance in the phytopathogen Xanthomonas campestris(RNA分子伴侣hfq对野油菜黄单胞菌的毒力、活力和抗应激能力具有重要作用)

简介：The RNA chaperone, Hfq, is known to play extensive roles in bacterial growth and development. More recently, it has been shown to be required for virulence in many human and animal bacterial pathogens. Despite these studies little is known about the role Hfq plays in phytopathogenic bacteria. In this study, we show Hfq is required for full virulence of the crucifer black rot pathogen Xanthomonas campestris pv. campestris (Xcc). We demonstrate that an Xcc hfq deletion strain is highly attenuated for virulence in Chinese radish and shows a severe defect in the production of virulence factors including extracellular enzymes and extracellular polysaccharide. Furthermore, the Xcc strain lacking Hfq had significantly reduced cell motility and stress tolerance. These findings suggest that Hfq is a key regulator of important aspects of virulence and adaptation of Xcc. Taken together, our findings are suggestive of a regulatory network placing Hfq at the centre of virulence gene expression control in Xcc.

来源：Environmental Microbiology Reports

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全文链接:

http://agri.ckcest.cn/file1/M00/06/5B/CsgkOFwywHiAEtHoAB0YGOT5tno280.pdf