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蔬菜育种专题

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▶ 前沿资讯

1. Models give synthetic biologists a head start (合成生物学家开发出可预测定制遗传线路输出的模型)

简介: 美国莱斯大学 (Rice University) 合成生物学家马修·贝内特 (Matthew Bennett) 和休斯敦大学数学家威廉·奥特 (William Ott) 牵头开发了可预测定制遗传线路输出的模型。这些线路可用于启动或停止蛋白质产生等活动。研究成果发表在美国化学学会期刊《ACS合成生物学》上。

合成生物线路由蛋白质和配体组成, 可根据细胞内特定条件开启或关闭基因表达。这些线路可用于设计细菌和其他有机体来管理细胞系统。这将使得微生物基因编码变得非常精确, 生物传感领域也预计会迎来变革。

几百个基因元件有几千种组合形式, 由于细胞环境不同, 同样的组合会导致不同的结果。新研究就是要解决这些问题, 通过不断尝试排除错误选项。

贝内特和奥特的建模主要针对多输入合成启动子。这些启动子相当于开关, 在不止一个条件 (如检测到两种化学物质) 得到满足的情况下才能启动或停止特定蛋白质的产生。多输入启动子是DNA上开闭基因的元件, 可以通过多种方式构建。构建出的启动子线路可让细胞同时感知多种环境条件, 从而决定基因开闭。团队探索了不同的系统模拟方法来预测系统性能。通过了解单个简易线路的输入和输出关系, 模型可以预测它们组合起来将如何发挥作用。

首个“naïve”模型利用来自单输入系统的数据, 这些系统能感知是否存在抑制嵌合转录因子转录的配体。综合研究几条线路产生的数据, 研究人员可以精确预测包含两个嵌合体的双输入线路的开闭反应。研究人员设计出基于“嵌合AND门”逻辑的细菌, 需要两个配体才能诱导荧光蛋白产生。配体水平的改变引起荧光蛋白输出的变化, 实际变化曲线和模型预测相差不大。

还有一种更加精密的模型可根据全部输入组合情况预测线路输出。这需要将实验性双输入系统产生的一小组数据“告知”模型, 还需要进行更多实验来证实模型预测是否准确。实验室也测试了两种模型在预测包含激活子 (开) 和抑制子 (闭) 的多输入混合启动子线路时的表现。信号分子之间互相干扰时, naïve模型无能为力, 但“知情”模型仍能做出准确预测。

这为更快设计和构建大型合成基因线路奠定了基础。该naïve模型可用于预测已被充分认识的单输入装置, 研究人员无需再做实验; “知情”模型将帮助研究人员设计出能够适应肠道菌群或土壤等复杂多变环境的微生物。

来源: ScienceDaily

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<http://agri.ckcest.cn/ass/ee7c3958-3a55-4ef1-8711-9d1911f7452a.pdf>

▶ 学术文献

1. MYBs Drive Novel Consumer Traits in Fruits and Vegetables (MYBs等位基因可推动果蔬性状创新)

简介: Eating plant-derived compounds can lead to a longer and healthier life and also benefits the environment. Innovation in the fresh food sector, as well as new cultivars, can improve consumption of fruit and vegetables, with MYB transcription factors being a target to drive this novelty. Plant MYB transcription factors are implicated in diverse roles including development, hormone signalling, and metabolite biosynthesis. The reds and blues of fruit and vegetables provided by anthocyanins, phlobaphenes, and betalains are controlled by specific R2R3 MYBs. New studies are now revealing that MYBs also control carotenoid biosynthesis and other quality traits, such as flavour and texture. Future breeding techniques may manipulate or create alleles of key MYB transcription factors.

来源: Trends in Plant Science

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<http://agri.ckcest.cn/ass/981217a8-07f4-4efa-b691-fb0f9d951238.pdf>

2 . Genome-Wide Analysis of the PYL Gene Family and Identification of PYL Genes That Respond to Abiotic Stress in Brassica napus (PYL基因家族的全基因组分析和甘蓝型油菜中可对非生物胁迫作出反应的PYL基因的认识)

简介: Abscisic acid (ABA) is an endogenous phytohormone that plays important roles in the regulation of plant growth, development, and stress responses. The pyrabactin resistance 1-like (PYR/PYL) protein is a core regulatory component of ABA signaling networks in plants. However, no details regarding this family in Brassica napus are available. Here, 46 PYLs were identified in the B. napus genome. Based on phylogenetic analysis, BnPYR1 and BnPYL1-3 belong to subfamily I, BnPYL7-10 belong to subfamily II, and BnPYL4-6 and BnPYL11-13 belong to subfamily III. Analysis of BnPYL conserved motifs showed that every subfamily contained four common motifs. By predicting cis-elements in the promoters, we found that all BnPYL members contained hormone and stress-related elements and that expression levels of most BnPYLs were relatively higher in seeds at the germination stage than those in other organs or at other developmental stages. Gene Ontology (GO) enrichment showed that BnPYL genes mainly participate in responses to stimuli. To identify crucial PYLs mediating the response to abiotic stress in B. napus, expression changes in 14 BnPYL genes were determined by quantitative real-time RT-PCR after drought, heat, and salinity treatments, and identified BnPYR1-3, BnPYL1-2, and BnPYL7-2 in response to abiotic stresses. The findings of this study lay a foundation for further investigations of PYL genes in B. napus.

来源: Genes

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<http://agri.ckcest.cn/ass/8e8db87b-c938-4c25-8ca6-c1de7cc64d06.pdf>

3. Identification of genomic ATP binding cassette (ABC) transporter genes and Cd-responsive ABCs in Brassica napus (甘蓝型油菜中的)

基因组腺苷三磷酸结合盒（ABC）转运蛋白基因和镉响应性ABC的鉴定

简介: The plant ATP binding cassette (ABC) transporters are one of the integral membrane proteins responsible for uptake and allocation of a wide range of metabolites and xenobiotics including heavy metals (e.g. zinc, manganese and cadmium). They play multiple roles in plant growth, development and environmental stress responses. Although the ABC transporters have been identified in model plants such as Arabidopsis and rice, they have not been annotated and identified in rapeseed (*Brassica napus*) and also, little is known about functionality of these metal transporters. *B. napus* is an important oil crop ranking the third largest source of vegetable oil worldwide. Importantly, it is long considered as a desirable candidate for phytoremediation owing to its massive dry weight productivity and moderate Cd accumulation. In this study, we identified 314 ABC protein genes from *B. napus* using bioinformatics and high-throughput sequencing. Eight subfamilies including ABCA-G and ABCI have been categorized. The ABCG proteins constitute the largest subfamily with 116 members, and the ABCB and ABCC subfamilies ranks second and third with 69 and 47 members, respectively. Analyses of ABCs in *B. napus* genome reveal that their evolutionary expansion was through localized allele duplications. Most of the ABC genes (74.2%, 233/314) were validated by RNA-sequencing rapeseed seedlings. Among the 233 profiled BnaABCs, 132 genes were differentially expressed (> 1.5 fold change, $p < 0.05$) and 84 genes were significantly induced under Cd stress. Analyses of specific cis-elements in the upstream of eight representative genes show diverse motifs, which potentially respond to environmental stress, hormone responsiveness and other development signals.

来源: Gene

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<http://agri.ckcest.cn/ass/dede25ea-9ce2-46dc-8337-15c273e13bb6.pdf>

4. Oilseed rape cultivation increases the microbial richness and diversity in soils contaminated with cadmium (油菜种植增加了镉污染土壤中的微生物丰度和多样性)

简介: **Purpose** This investigation aimed to estimate and characterize the microbial diversity in soils with cadmium (Cd) at different concentrations and to evaluate whether *Brassica napus* can restore the soil microbial diversity.

Materials and methods We conducted the pot experiment to analyze the composition of microbial communities in the soil contaminated with 0, 1, and 2 mg/kg Cd, as well as planted with oilseed rape. The bacterial and fungal communities were characterized via next-generation sequencing based on 16S and 18S rRNA gene fragments pyrosequencing, respectively.

Results and discussion The results show that cadmium contamination decreased both the microbial richness and diversity in the soil, while the cultivation of oilseed rape increased the richness and diversity. In bacteria, Proteobacteria was the most abundant phylum in all the samples accounting for 39.62 to 46.14%, followed by Bacteroidetes, Actinobacteria, and

Chloroflexi. These phyla collectively comprised more than 70% of all phyla. Ascomycota was the most abundant phylum in all samples in fungi (89.65 to 96.00%), and it was the only phylum whose abundance was increased with the rise of Cd concentration.

Conclusions Microbial richness and diversity were affected by the combined action of Cd and *B. napus*. Cd contamination decreased the microbial richness and diversity, while cropping with oilseed rape increased the microbial richness and diversity, which alleviated the deleterious effect of the Cd pollution in soils. These reflected that oilseed rape played a positive role in maintaining species diversity of microorganism from the side.

来源: Journal of Soils and Sediments

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<http://agri.ckcest.cn/ass/dcbba0ca-b071-45c0-a543-9a4afeaa2a7b.pdf>

5. Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid *Brassica napus* (同源交换是双二倍体甘蓝型油菜基因存在/缺失变化的主要原因)

简介: Homoeologous exchanges (HEs) have been shown to generate novel gene combinations and phenotypes in a range of polyploid species. Gene presence/absence variation (PAV) is also a major contributor to genetic diversity. In this study, we show that there is an association between these two events, particularly in recent *Brassica napus* synthetic accessions, and that these represent a novel source of genetic diversity, which can be captured for the improvement of this important crop species. By assembling the pangenome of *B. napus*, we show that 38% of the genes display PAV behaviour, with some of these variable genes predicted to be involved in important agronomic traits including flowering time, disease resistance, acyl lipid metabolism and glucosinolate metabolism. This study is a first and provides a detailed characterization of the association between HEs and PAVs in *B. napus* at the pangenome level.

来源: Plant Biotechnology Journal

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