



2018年第53期总167期

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▶ 前沿资讯

1. Inactivating genes can boost crop genetic diversity (研究发现灭活基因可增强农作物基因多样性)

简介: 法国农艺研究国际合作开发中心 (CIRAD) 和法国国家农业研究院 (INRA) 的最新研究发现, 失活一个基因RECQ4会导致水稻、豌豆和番茄等作物的重组增加三倍。该基因在作物有性生殖过程中抑制重组 (杂交) 遗传物质的交换。这一发表在《自然植物》杂志上的成果可以加速植物育种, 培育更适合特定环境条件 (抗病、适应气候变化) 的品种。

重组是所有有性繁殖生物体共有的自然机制。过去一万年来, 植物育种主要围绕着这种机制进行。例如, 为了获得既美味又抗病虫害的番茄新品种, 育种者通过连续杂交重组培育含有与味道和抗病性相关基因的植物。但这一过程非常漫长, 因为在繁殖过程中重组发生的几率很低。平均每次杂交的染色体中只有一到三个遗传物质交换点。因此, 不可能在一代中结合六个有价值的基因, 这是作物改良的主要障碍。

为了找出限制遗传重组数量的原因, 来自INRA的研究人员在模式植物拟南芥中鉴定并研究了控制重组的基因, 发现RECQ4基因在防止杂交重组方面特别有效。在某种程度上, 失活它可使重组频率倍增至四倍! INRA和CIRAD研究人员在豌豆、番茄和水稻上通过“关闭”RECQ4基因, 成功地使杂交数量平均增加了两倍, 从而获得了更大的染色体改组, 增加了每一代的多样性。

来源: AgroPages

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<http://agri.ckcest.cn/file1/M00/06/5A/Csgk0FwkRUKALP2PAAPyOrzNmBM064.pdf>

▶ 学术文献

1. Effects of genotype and environment on seed quality traits variability in interspecific cross-derived Brassica lines (基因型和环境对种间杂交甘蓝品系种子品质性状变异的影响)

简介: Genotype (G), environment [i.e. year (Y) and location (L)] and their interaction (GYL) play an important role in the final expression of quality attributes. A multi-environment trial in selected interspecific cross-derived Brassica lines was conducted to evaluate the magnitude of G, Y, L and GYL effects on seed quality traits of Brassica genotypes under three locations in Poland, during the 2011-2013 cropping season. The oil, protein, fiber (Acid Detergent Fiber and Neutral Detergent Fiber) as well as glucosinolate contents was determined by near-infrared reflectance spectroscopy (NIRS) and significant differences were observed between tested Brassica genotypes and across harvesting years and growing locations. Generally, all tested hybrid lines displayed wider genetic variability for studied quality traits than control genotypes. Analysis of variance indicated that the main effects of genotypes, years and locations as well as all interactions were significant for all traits of study (except year×location interaction for glucosinolates). However, location had the most significant

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effect on oil, protein and fiber content while genotype had significant impact on glucosinolates content in Brassica seeds. Moreover, the individual lines having combination of desirable traits were also identified from F₅ to F₇ generations of tested hybrids.

来源: Euphytica

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<http://agri.ckcest.cn/file1/M00/06/5A/Csgk0FwkQ1iAC0yMAAfbcx0AhgM168.pdf>

2. Optimizing growth conditions for glucosinolate production in Chinese cabbage (大白菜硫代葡萄糖苷产生条件的优化研究)

简介: Glucosinolates are well known functional food components that were discovered in Cruciferae and have been the object of study from diverse disciplinary perspectives, including metabolism, quantitative analysis, and breeding. However, the effects of the growth environment and post-harvest processes on glucosinolate production in Chinese cabbage are not well studied. Hence, this study aimed to identify the major factors that affect glucosinolate accumulation in Chinese cabbage during growth, and to optimize growth conditions in order to maximize glucosinolate content. Therefore, we measured glucosinolate content in cabbage grown in five environmental conditions that altered electrical conductivity, pH, cultivation time, temperature, and relative humidity. We used principal component analysis (PCA) to identify the variables primarily affecting growth, followed by response surface methodology (RSM) to determine optimal growth conditions that maximize glucosinolate content in Chinese cabbage. Results from PCA indicated that cultivation time, temperature, and relative humidity were the principal components that explained 85.8% of the total variance, suggesting these are the most significant environmental factors that affect glucosinolate accumulation. Moreover, RSM indicated that the total model for evaluating glucosinolate content was significant ($R^2=0.934$) and showed that the optimal temperature and relative humidity for maximizing glucosinolate content are 28°C, and 66%, respectively. This study provided practical information of optimal condition for producing functional Chinese cabbage intensifying glucosinolate.

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<http://agri.ckcest.cn/file1/M00/06/5A/Csgk0FwkRL-AMLnmABPhfEPUixI121.pdf>

3. Differential antioxidative and biochemical responses to aluminium stress in Brassica juncea cultivars (不同芥菜品种对铝胁迫的抗氧化和生化反应差异)

简介: Aluminium (Al) toxicity in acidic soils limits crop production worldwide. We evaluated eleven genotypes of Brassica juncea (Mustard) under Al stress on basis of their growth and shortlisted two best among them for further comparative analysis. Our objective was to elucidate individual and differential oxidative damage and defence response elicited by Al treatment in selected mustard genotypes, 'Pusa Tarak' and 'Pusa Vijay'. Thirty-day-old

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plants of both genotypes were subjected to Al stress for a period of 24 h and 72 h. Concentration of superoxides was visible much higher in leaves of 'Pusa Vijay' both at 24 h and 72 h, also confirmed by oxidative stress marker thiobarbituric acid reactive substances (TBARS). The activities of the enzymatic antioxidants superoxide dismutase (SOD), ascorbate peroxidase (APX), glutathione reductase (GR), glutathione S-transferase (GST), and catalase (CAT) were significantly higher in 'Pusa Tarak' compared to control and 'Pusa Vijay' at both time stages. Levels of non-enzymatic antioxidants glutathiones and ascorbates were already higher in 'Pusa Vijay'; however, Al treatment increased their levels in both genotypes with non-significant changes on inter-genotypes basis. More and significant decline by Al in chlorophylls was observed in 'Pusa Vijay'. Interestingly, increase in proline content by Al was much prominent in 'Pusa Tarak' compared to 'Pusa Vijay'. The in vitro antioxidant capacity estimation of mustard genotypes, evaluated by measuring 2,2-diphenyl-1-picrylhydrazyl (DPPH) radical scavenging and hydroxyl radical scavenging (HRSA) activities proved that extract of 'Pusa Tarak' can detoxify more radicals than 'Pusa Vijay'. We conclude that 'Pusa Tarak' can upregulate cellular antioxidants and osmoregulation, and quench more radicals compared to 'Pusa Vijay'. The results will contribute for selection of better Brassica genus to be grown in Al rich acidic soils, and help in designing strategies for crop breeding and cultivation.

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http://agri.ckcest.cn/file1/M00/06/5A/Csgk0FwkQwKAHTJ_ACA6fsMMYgA789.pdf

4. Comprehensive analysis of CCCH zinc-finger-type transcription factors in the Brassica rapa genome (油菜基因组CHCH锌指型转录因子的综合分析)

简介: The CCCH-type zinc finger proteins are characterized by their signature motif of three cysteine and one histidine residues. These proteins are RNA binding proteins that function in plant growth, developmental processes, and responses to various environmental stress conditions. In this study, a comprehensive analysis using computational methods allowed the identification of 63 functionally important CCCH genes in the Brassica rapa genome. Several analyses were carried out on the identified genes to understand their roles in this plant. Comparative phylogenetic analysis classified CCCH genes into six clusters, while motif and structural analyses revealed four unique CCCH motifs including different functional motifs and intron/exon variations unique to plants compared to those in other species. Real-time qRT-PCR analysis of 10 randomly selected genes indicated they function at the early stages rather than the later stages of cold and salt stress. This study provides a basic understanding of potential candidate CCCH genes in B. rapa, their structural variation, expression patterns, and their roles under different stress conditions.

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