



2019年第39期总206期

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政策法规

1. 美国修订阿维菌素在部分蔬菜中的残留限量要求

简介: 据美国联邦公报消息, 2019年9月9日, 美国环保署发布2019-19400号文件, 修订阿维菌素 (Abamectin) 在部分蔬菜中的残留限量。美国环保署对阿维菌素开展了风险评估, 分别评估了毒理性、饮食暴露量以及对婴幼儿的影响。

来源: 世界农化网

发布日期: 2019-09-11

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/C9/Csgk0F2JyFiACIfdAAhxUDZXnvs988.pdf>

前沿资讯

1. Harnessing tomato jumping genes could help speed-breed drought-resistant crops (利用番茄跳跃基因有助于快速培育抗旱作物)

简介: 近日, 剑桥大学塞恩斯伯里实验室 (SLCU) 和植物科学系的研究人员发现, 干旱胁迫触发了一个跳跃基因家族 (Rider反转录转座子) 的活性, 该家族与番茄的果实形状和颜色有关。发表在《PLOS Genetics》杂志上的Rider的特征表明, Rider家族也存在并可能活跃在其他植物中, 包括如油菜籽、甜菜根和藜麦等重要经济作物。番茄中发现的跳跃基因家族作为一种潜在的新性状变异来源, 有望加速作物育种, 提高抗旱性等性状, 帮助植物更好应对气候变化导致的极端的条件。

跳跃基因具有作物改良潜力。转座子 (通常被称为跳跃基因) 是DNA编码的移动片段, 可以将自身复制到基因组中的新位置, 它们可以改变、破坏或扩增基因, 在进化过程中以及在改变植物基因表达和生理特性中起着重要作用。它们是性状多样性的强大驱动力, 利用植物中已经存在的跳跃基因产生新特性将是传统育种技术的重要一步, 使得在传统培育生产出形状、颜色和尺寸统一的作物中产生新的性状成为可能, 从而提高收获效率并实现产量最大化。

跳跃基因调控机制研究将加速作物新性状的产生。转座子的广泛存在促使研究人员进一步研究如何以受控方式激活Rider, 或者将其重新激活或重新引入当前具有非活性Rider元素的植物中, 从而恢复其性状多样化潜力。与传统方法相比, 该方法有可能显著缩短育种时间。在一个庞大的群体中, 每个个体的转座子都被激活, 产生不同的新性状。通过控制植物内的这种“随机突变”过程, 可以加速这一过程, 产生超出想象的新表型。

利用跳跃基因育种是一种无转基因育种方法。当今的基因靶向技术非常强大, 但通常需要对基础基因有一定的功能了解才能产生有用的结果, 并且通常只靶向一个或几个基因。转座子活性是植物中已经存在的一种天然工具, 可以利用其产生新表型或抗性并补充基因靶向作用。使用转座子产生新的突变提供了一种无转基因的育种方法, 该方法合乎当前欧盟有关转基因生物的法律规定。

利用Rider可以培育出抗旱作物。确定Rider活性是由干旱触发的研究表明Rider可以创建新的基因调控网络, 从而帮助植物应对干旱, 这意味着我们可以利用

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Rider来对作物中已有的基因提供干旱响应，从而培育出更适合干旱胁迫的作物。在全球变暖时期迫切需要培育更具适应力的农作物。

来源: SeedQuest

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全文链接:

<http://agri.ckcest.cn/file1/M00/0E/C9/Csgk0F2JvwOASkuSAAQUs7UiDOY214.pdf>

2. CABI collaborates to improve resistance of Kenya's cabbage and kale crops to TuMV disease (CABI协同提高肯尼亚甘蓝和羽衣甘蓝作物对TuMV疾病的抗性)

简介: A team of international scientists from CABI, the Kenyan Agricultural and Livestock Research Organisation (KALRO), NIAB EMR (UK), University of Warwick (UK) and Syngenta (Netherlands) are seeking to improve the resistance of Kenya's cabbage and kale crops to Turnip mosaic virus (TuMV).

In the distantly-related Chinese cabbage (*Brassica rapa*), a potentially durable TuMV disease resistance trait was identified by Prof John Walsh at the University of Warwick while work by Dr Charlotte Nellist, of NIAB EMR, UK, Dr Bill Briggs, of Syngenta, and Prof Walsh elucidated the novel mechanism of TuMV resistance.

The scientists are now working to employ conventional breeding methods to move the resistance trait from Chinese cabbage to Kenyan cabbage and kale varieties in the anticipation that providing durable disease resistance in Kenyan cabbage and kale cultivars will help reduce yield losses.

The lower cost of production, the researchers believe, will hopefully result in cheaper retail prices-making the crops more available for consumption and helping in the fight against malnutrition.

In addition, the project aims to survey the prevalence of TuMV from multiple regions in Kenya and provide data on the efficacy of the Chinese cabbage resistance against contemporary Kenyan TuMV isolates.

来源: SeedQuest

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全文链接:

http://agri.ckcest.cn/file1/M00/0E/C9/Csgk0F2Jx0WAQNejAHy_KZh5rIw602.pdf

学术文献

1. 青花菜茎粗性状的遗传及QTL定位分析

简介: 本研究通过茎粗细差异极大的双亲构建六世代和DH群体, 研究青花菜茎粗性状的遗传规律及QTL初定位。以粗茎与细茎的两个青花菜DH系为亲本, 构建了F1、BCP1、BCP2和F2群体, 采用植物数量性状主基因+多基因混合遗传模型分析法, 对早播种和晚播种两个环境下的青花菜茎粗性状进行了遗传分析。对F1进行小孢子培养构建了DH作图群体, 通过特异性位点扩增片段测序 (SLAF) 构建了高密度遗传图谱, 并对茎粗性状进行了

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QTL定位分析。结果显示，两种环境下的青花菜茎粗性状均是由两对加性主基因+加性-显性多基因遗传控制；在两个环境下的F₂中遗传力均较高，分别是87.93%和93.37%，表明青花菜茎粗性状主要受遗传因子控制，受一定的环境因素影响；通过IciMapping 4.0软件分析，在青花菜6和9号连锁群上检测到2个QTLs (qBSM.C06, qBSM.C09)，表型变异贡献率分别为24.3%和18.4%。本研究结果为青花菜茎粗性状的相关基因挖掘以及为茎粗QTL应用于青花菜新品种培育提供了基础数据。

来源：分子植物育种

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<http://agri.ckcest.cn/file1/M00/OE/C9/Csgk0F2Ju4iAeKjDAA8p74seYyM842.pdf>

2. Detection of First Marker Trait Associations for Resistance Against *Sclerotinia sclerotiorum* in Brassica juncea-Erucastrum cardaminoides Introgression Lines (芥菜-Erucastrum cardaminoides 基因渗入系对核盘菌抗性的第一标记性状关联检测)

简介：A set of 96 Brassica juncea-Erucastrum cardaminoides introgression lines (ILs) were developed with genomic regions associated with Sclerotinia stem rot (*Sclerotinia sclerotiorum*) resistance from a wild Brassicaceous species *E. cardaminoides*. ILs were assessed for their resistance responses to stem inoculation with *S. sclerotiorum*, over three crop seasons (season I, 2011/2012; II, 2014/2015; III, 2016-2017). Initially, ILs were genotyped with transferable SSR markers and subsequently through genotyping by sequencing. SSR based association mapping identified six marker loci associated to resistance in both A and B genomes. Subsequent genome-wide association analysis (GWAS) of 84 ILs recognized a large number of SNPs associated to resistance, in chromosomes A03, A06, and B03. Chromosomes A03 and A06 harbored the maximum number of resistance related SNPs. Annotation of linked genomic regions highlighted an array of resistance mechanisms in terms of signal transduction pathways, hypersensitive responses and production of anti-fungal proteins and metabolites. Of major importance was the clustering of SNPs, encoding multiple resistance genes on small regions spanning approximately 885 kb region on chromosome A03 and 74 kb on B03. Five SNPs on chromosome A03 (6,390,210-381) were associated with LRR-RLK (receptor like kinases) genes that encode LRR-protein kinase family proteins. Genetic factors associated with pathogen-associated molecular patterns (PAMPs) and effector-triggered immunity (ETI) were predicted on chromosome A03, exhibiting 11 SNPs (6,274,763-994). These belonged to three R-Genes encoding TIR-NBS-LRR proteins. Marker trait associations (MTAs) identified will facilitate marker assisted introgression of these critical resistances, into new cultivars of *B. juncea* initially and, subsequently, into other crop Brassica species.

来源：Frontiers in Plant Science

发布日期:2019-08-06

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/C9/Csgk0F2Jum6A0QAeAILdZvKRdXo105.pdf>

3. Potential for Seed Transmission of *Verticillium longisporum* in Oilseed Rape (*Brassica napus*) (油菜(*Brassica napus*) 中长孢轮枝菌(*Verticillium longisporum*) 的种子传播潜力)

简介: *Verticillium longisporum* is a soil-borne vascular fungal pathogen that has spread throughout the European oilseed rape cultivation area since the 1980s and was detected in canola fields in Canada in 2014. In a series of greenhouse and field inoculation experiments using *V. longisporum*-resistant and susceptible cultivars of winter and spring types of oilseed rape, the present study investigated the potential of *V. longisporum* dissemination by seeds of *Brassica napus*. Greenhouse inoculation studies with a DsRed-labeled isolate of *V. longisporum* confirmed the systemic growth of the pathogen from roots to seeds. Further monitoring of plant colonization in the greenhouse with a species-specific real-time polymerase chain reaction assay verified the pathogen growth from roots to stem bases, pods, and seeds in root-inoculated plants. The frequency of recovery of viable colonies of *V. longisporum* from seeds harvested from greenhouse-grown inoculated plants ranged from 0.08 to 13.3%. The frequency of seed transmission in the greenhouse differed in oilseed rape cultivars varying in susceptibility to *V. longisporum*. Subsequent studies on transmission of the disease into the offspring revealed that only 1.7 to 2.3% of plants showed disease symptoms as confirmed by the formation of microsclerotia in the stems. Results from field-grown plants differed from the greenhouse studies. The degree of seed transmission in the field was dependent on the crop type. Although only low concentrations of DNA of *V. longisporum* were detectable in seeds harvested from severely infected winter oilseed rape, significantly greater concentrations of fungal DNA were found in seeds of spring-type oilseed rape, at similar soil conditions and inoculum densities. Correspondingly, plating seeds that were harvested from infected plants on agar yielded viable *V. longisporum* colonies only from seeds of the spring-type but not of the winter-type plants. Lack of seed infection in the winter-type crop was confirmed in two seasons. Equally, none of the offspring grown from seeds from severely diseased winter oilseed rape plants developed symptoms of *Verticillium* stem striping. The results suggest that the rate of seed transmission of *V. longisporum* depends on the degree of plant colonization, which is significantly faster under greenhouse than field conditions and in a spring-sown crop compared with an autumn-sown oilseed rape crop. According to our studies, disease transmission by seeds from European winter oilseed rape production cannot be confirmed.

来源: Plant Disease

发布日期: 2019-05-20

全文链接:

http://agri.ckcest.cn/file1/M00/0E/C9/Csgk0F2JuSeAR1UmAA0uS_nfV2s206.pdf

4. Competitive Biomass Allocation Between the Main Shoot and Lateral Branches of Broccoli (*Brassica oleracea* L. var. *italica*) (西兰花 (*Brassica oleracea* L. var. *italica*) 主要枝条和侧枝之间的竞争生物量分配)

简介: The branching habit and stalk proportion of heading type broccoli (*Brassica oleracea* L.

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var. italica) differs based on the cultivar, but the extent of the effects of these factors on the apical head weight is unknown. The main objectives of this study were to elucidate the relationships between the apical head weight and the branching habit or the stalk proportion. Firstly, the shoots of broccoli from six cultivars were divided into four parts (apical head, leaves on the main stem, lateral branches, and the rest of the main stem), and the weight proportions of each part were investigated. The results showed that the cultivars showing higher branching tended to produce smaller apical heads. Furthermore, apical head weights showed a positive relationship with the area of the leaves on the main stem, but a negative relationship with those on the branches. Secondly, four cultivars were grown with lateral bud nipping. This significantly increased the apical head weight in the cultivars showing higher lateral branching, but did not significantly change the weight of the whole shoot. These results suggest competitive biomass allocation between the main shoot and lateral branches. The difference in the weight of lateral branches depended on the probability of axillary bud presence rather than on the number of internodes or weight per branch. Finally, a strong correlation between the apical head weights and the square of the stalk diameter was demonstrated by generalized linear models ($R^2=0.95$). These findings will contribute to the knowledge base on diverse methods of broccoli cultivation.

来源: The Horticulture Journal

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全文链接:

<http://agri.ckcest.cn/file1/M00/0E/C9/Csgk0F2JtqgAbBFsABAs0-g1GTM667.pdf>

5. Current understanding of male sterility systems in vegetable Brassicas and their exploitation in hybrid breeding (芸薹属蔬菜雄性不育系的研究现状及其在杂交育种中的应用)

简介: **Key message** Overview of the current status of GMS and CMS systems available in Brassica vegetables, their molecular mechanism, wild sources of sterile cytoplasm and exploitation of male sterility in hybrid breeding.

Abstract The predominantly herbaceous family Brassicaceae (crucifers or mustard family) encompasses over 3700 species, and many of them are scientifically and economically important. The genus Brassica is an economically important genus within the tribe Brassicaceae that comprises important vegetable, oilseed and fodder crops. Brassica vegetables display strong hybrid vigor, and heterosis breeding is the integral part in their improvement. Commercial production of F1 hybrid seeds in Brassica vegetables requires an effective male sterility system. Among the available male sterility systems, cytoplasmic male sterility (CMS) is the most widely exploited in Brassica vegetables. This system is maternally inherited and studied intensively. A limited number of reports about the genic male sterility (GMS) are available in Brassica vegetables. The GMS system is reported to be dominant, recessive and trirecessive in nature in different species. In this review, we discuss the available male sterility systems in Brassica vegetables and their potential use in hybrid breeding. The molecular mechanism of mt-CMS and causal mitochondrial genes of CMS has been discussed in detail. Finally, the exploitation of male sterility system in heterosis

breeding of Brassica vegetables, future prospects and need for further understanding of these systems are highlighted.

来源: Plant Reproduction

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