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2024年4月1日

政策法规

1．棉花产业公证检验质效提升助力发展，新疆全覆盖全国超95%

简介：在3月21日举行的2024’CNCE年会上，中国纤维质量监测中心副主任王丹涛发表演讲，深入探讨了如何通过多措并举提升公检质效，综合施策助力棉业发展。王丹涛从产业政策、公检模式、管理体系、技术基础四个方面进行了详细阐述。 公证检验已成为棉花产业新型生态圈的关键环节。受新疆监管棉公检模式的积极影响，甘肃、湖南等地区积极落实内地监管棉试点。目前，公证检验实现了对新疆棉花的全覆盖，全国流通棉花公检覆盖率超过95%。为优化公检模式，中国纤维质量监测中心不断创新，提高棉花公证检验水平。新模式、新技术的引入持续提升了技术水平和工作效率。包括数据自动传输、回潮率针插式检验、智能随机抽样、含杂率仪器权属问题的解决以及含杂率智能检验设备的升级等。 在健全管理体系方面，配合市场监管总局公证检验监督，制定专项整改方案，推进整改。搭建棉花检验信息化平台，实现全面监测。同时，建立可视化监控系统，实时监测检验情况，并强化棉花公检实验室水平监测。为适应我国棉花全产业链发展新阶段，国家标准委委托中国纤维质量监测中心修订棉花强制性国家标准。引入短纤维率指标和仪器化检验方法标准，增加棉花短纤维率指标及检验内容，同时去除机采棉的四分要求，放宽白棉2级级距，并实行分段确定包数的抽样方法。通过这些措施，棉花产业有望实现更高的质量和效率，为二级市场投资者提供新的发展机遇。

来源：和讯

发布日期:2024-03-22

全文链接:http://agri.nais.net.cn/file1/M00/10/3F/Csgk0EGuyVeASCYMAAdNxEXDn7w212.pdf

前沿资讯

1．2023年度新疆棉花生产加工过程质量状况监测结果表明新疆棉花质量持续提升

简介：近日，中国纤维质量监测中心发布2023年度新疆棉花生产加工过程质量状况监测结果。监测结果表明，新疆棉花质量持续提升。此次监测由新疆地区纤维质量监测机构具体实施，监测周期从2023年4月至2024年2月，这是中国纤维质量监测中心连续第6年对新疆棉花生产加工过程质量状况进行监测。2023年度，该中心监测棉花加工企业21家，涉及棉农59户，棉花种植面积6246公顷，棉花品种22个，其中当地主栽品种14个，监测棉花样品1.286万个。从监测情况来看，大垛抽检的综合纤维品质显著好于2021年和2022年。优质品种质量突出，金垦1775品种纤维长度和断裂比强度达到“双31”标准；源棉8号、新塔棉3号、惠远720、新陆中61、新陆早65、新陆中54等品种，纤维长度和断裂比强度均达到“双30”标准。科学的田间管理对棉花质量影响较大，适宜的种植密度和肥水施用是棉纤维正常发育的重要保证。合理的加工工艺有利于保持棉花内在质量，加工工艺对棉花品质影响突出，籽棉清理环节对纤维长度和长度整齐度为负效应，对断裂比强度和马克隆值影响较小，对颜色级正效应显著；轧花环节对纤维断裂比强度为负效应，对纤维长度、长度整齐度、马克隆值和颜色级影响很小；皮清环节对纤维品质为负效应，其中纤维长度、长度整齐度、断裂比强度都有所下降，马克隆值受影响小，颜色级有所改善但幅度较小。

来源：中国质量报

发布日期:2024-03-27

全文链接:http://agri.nais.net.cn/file1/M00/03/6C/Csgk0WYFeaeAGr-hAAq4mchiI1g382.pdf

2. Breakthrough in reviving Pakistani cotton production - PU CEMB has developed a new triple gene cotton variety with resistance to pink bollworm and glyphosate(恢复巴基斯坦棉花生产的突破——PU CEMB已开发出一种新的对红铃虫和草甘膦具有抗性的三基因棉花品种)

简介： The Punjab University-Center of Excellence in Molecular Biology (CEMB), Lahore has developed another new variety of triple gene cotton (CKC-05) under the leadership of Prof. Dr. Idrees Ahmad Nasir and Prof. Dr. Tayyeb Hasnain. CKC-05 has all the characteristics of high yielding good cotton variety. Amenable to control all bollworms including pink bollworm, which is otherwise very costly to control conventionally. Punjab Seed Council has approved the new triple gene variety CKC-5 for general cultivation. CKC technology is a historic achievement of Punjab University scientists to increase cotton production and build Pakistan's economy on a strong foundation. This CKC technology contains double Bt genes (CEMB-Cry1Ac+Cry2A) and one glyphosate resistance gene (CEMB-GTG). CKC varieties help farmers to increase their income by reducing the number of insecticide sprays and saving the cost on hoeing. The scientists explained that the varieties developed by using CKC technology i.e., CKC-1, CKC-3, CKC-5 and CKC-6 have this year covered nearly 70% (rough estimate) of the total area under cotton and are helping farmers to effectively control bollworms and weeds, making Pakistan self-sufficient in cotton production again. This technology will prove to be an important milestone towards the stabilization of the Pakistan economy as Pakistan's largest export revenue depends on cotton and its related value-added products. Minister of Agriculture, Commerce and Industry of the Punjab SM Tanveer and Vice Chancellor of the Punjab University, Prof. Dr. Khalid Mehmood visited various laboratories of the CEMB engaged in the application of biotechnology in the field of agriculture and health. He congratulated the team of scientists for giving another new triple gene variety for the benefit of Pakistan's farming community. The Minister said that the role of scientists in the development of the country is very important; therefore the nation should encourage the research projects of the scientists. Prof. Dr. Khalid Mehmood said that the scientists of CEMB are fully capable of solving the biotechnology related country's problems, but there is a dire need for encouragement and funding for the projects of national interest. On this occasion, Director CEMB Prof. Dr. Moaz ur Rahman gave a briefing about various research projects in the fields of agriculture and health. He said that CEMB will continue to play an active role in solving the various challenges faced by the country in the field of agriculture and health. Prof. Dr. Abdul Qayyum Rao, in-charge Plant Biotechnology Lab said that the initial experiments of genome editing technology are highly encouraging and by applying these findings, Pakistan can revolutionize in the field of agriculture. Lead researcher cotton Breeding programme, Dr. Allah Bakhsh added that we will continue integrating this genome edited lines to CEMB cotton breeding programme as source of germplasm to breed resilient cotton varieties.

来源： University of the Punjab

发布日期:2023-10-15

全文链接:http://agri.nais.net.cn/file1/M00/10/3F/Csgk0EGuz7KAcrGbAAzFyP0o330540.pdf

1．Gibberellic acid promotes single-celled fiber elongation through the activation of two signaling cascades in cotton(赤霉素通过激活两个信号级联促进棉花单细胞纤维伸长)

简 介： The agricultural green revolution spectacularly enhanced crop yield through modification of gibberellin (GA) signaling. However, in cotton, the GA signaling cascades remain elusive, limiting our potential to cultivate new cotton varieties and improve yield and quality. Here, we identified that GA prominently stimulated fiber elongation through the degradation of DELLA protein GhSLR1, thereby disabling GhSLR1's physical interaction with two transcription factors, GhZFP8 and GhBLH1. Subsequently, the resultant free GhBLH1 binds to GhKCS12 promoter and activates its expression to enhance VLCFAs biosynthesis. With a similar mechanism, the free GhZFP8 binds to GhSDCP1 promoter and activates its expression. As a result, GhSDCP1 upregulates the expression of GhPIF3 gene associated with plant cell elongation. Ultimately, the two parallel signaling cascades synergistically promote cotton fiber elongation. Our findings outline the mechanistic framework that translates the GA signal into fiber cell elongation, thereby offering a roadmap to improve cotton fiber quality and yield.
来源： Developmental Cell
发布日期:2024-03-25
全文链接:http://agri.nais.net.cn/file1/M00/03/6C/Csgk0WYFf4aAXRo1AHtv7lVjBgU654.pdf

2．In vivo maternal haploid induction system in cotton(棉花体内母体单倍体诱导系统)

简介： The ghdmp mutant of cotton, generated through the CRISPR system, exhibits a haploid induction rate of 1.06% in F1 progeny as the haploid inducer line.
来源： PLANT PHYSIOLOGY
发布日期:2024-02-29
全文链接:http://agri.nais.net.cn/file1/M00/03/6C/Csgk0WYJagSANaQMAAndXfSf33c872.pdf

3．The BEL1-like transcription factor GhBLH5-A05 participates in cotton response to drought stress(类BEL1转录因子GhBLH5-A05参与棉花对干旱胁迫的响应)

简介： Drought stress impairs crop growth and development. BEL1-like family transcription factors may be involved in plant response to drought stress, but little is known of the molecular mechanism by which these proteins regulate plant response and defense to drought stress. Here we show that the BEL1-like transcription factor GhBLH5-A05 functions in cotton (Gossypium hirsutum) response and defense to drought stress. Expression of GhBLH5-A05 in cotton was induced by drought stress. Overexpression of GhBLH5-A05 in both Arabidopsis and cotton increased drought tolerance, whereas silencing GhBLH5A05 in cotton resulted in elevated sensitivity to drought stress. GhBLH5-A05 binds to cis elements in the promoters of GhRD20-A09 and GhDREB2C-D05 to activate the expression of these genes. GhBLH5A05 interacted with the KNOX transcription factor GhKNAT6-A03. Co -expression of GhBLH5-A05 and GhKNAT6-A03 increased the transcription of GhRD20-A09 and GhDREB2C-D05. We conclude that GhBLH5-A05 acts as a regulatory factor with GhKNAT6-A03 functioning in cotton response to drought stress by activating the expression of the drought-responsive genes GhRD20-A09 and

GhDREB2C-D05.
来源：CROP JOURNAL
发布日期:2024-02-28
全文链接:http://agri.nais.net.cn/file1/M00/03/6C/Csgk0WYJZVGAARivADDqRYGPuBU281.pdf

4. Single-cell transcriptome atlas reveals somatic cell embryogenic differentiation features during regeneration(单细胞转录组图谱揭示再生过程中体细胞胚性分化特征)

简介：Understanding somatic cell totipotency remains a challenge facing scientific inquiry today. Plants display remarkable cell totipotency expression, illustrated by single-cell differentiation during somatic embryogenesis (SE) for plant regeneration. Determining cell identity and exploring gene regulation in such complex heterogeneous somatic cell differentiation have been major challenges. Here, we performed high-throughput single-cell sequencing assays to define the precise cellular landscape and revealed the modulation mode of marker genes during embryogenic differentiation in cotton (Gossypium hirsutum L.) as the crop for biotechnology application. We demonstrated that nonembryogenic calli (NEC) and primary embryogenic calli (PEC) tissues were composed of heterogeneous cells that could be partitioned into four broad populations with six distinct cell clusters. Enriched cell clusters and cell states were identified in NEC and PEC samples, respectively. Moreover, a broad repertoire of new cluster-specific genes and associated expression modules were identified. The energy metabolism, signal transduction, environmental adaptation, membrane transport pathways, and a series of transcription factors were preferentially enriched in cell embryogenic totipotency expression. Notably, the SE-ASSOCIATED LIPID TRANSFER PROTEIN (SELTP) gene dose-dependently marked cell types with distinct embryogenic states and exhibited a parabolic curve pattern along the somatic cell embryogenic differentiation trajectory, suggesting that SELTP could serve as a favorable quantitative cellular marker for detecting embryogenic expression at the single-cell level. In addition, RNA velocity and Scissor analysis confirmed the pseudo-temporal model and validated the accuracy of the scRNA-seq data, respectively. This work provides valuable marker-genes resources and defines precise cellular taxonomy and trajectory atlases for somatic cell embryogenic differentiation in plant regeneration.High-throughput single-cell transcriptomics provide valuable marker genes and precise cellular taxonomy and trajectory atlases for somatic cell embryogenic differentiation in cotton regeneration.
来源：PLANT PHYSIOLOGY
发布日期:2024-02-24
全文链接:http://agri.nais.net.cn/file1/M00/10/3F/Csgk0EGytsOAE4syABhGKUGUPXk695.pdf

5. The elicitor VP2 from Verticillium dahliae triggers defence response in cotton(棉花黄萎病激发子VP2诱导防御反应)

简介：Verticillium dahliae is a widespread and destructive soilborne vascular pathogenic fungus that causes serious diseases in dicot plants. Here, comparative transcriptome analysis showed that the number of genes upregulated in defoliating pathotype V991 was significantly higher than in the non-defoliating pathotype 1cd3-2 during the early response of cotton. Combined with analysis of the secretome during the V991-cotton interaction, an elicitor VP2 was identified, which was highly upregulated at the early stage of V991 invasion, but was barely expressed during the 1cd3-2-cotton interaction. Full-length VP2 could

induce cell death in several plant species, and which was dependent on NbBAK1 but not on NbSOBIR1 in N. benthamiana. Knock-out of VP2 attenuated the pathogenicity of V991. Furthermore, overexpression of VP2 in cotton enhanced resistance to V. dahliae without causing abnormal plant growth and development. Several genes involved in JA, SA and lignin synthesis were significantly upregulated in VP2-overexpressing cotton. The contents of JA, SA, and lignin were also significantly higher than in the wild-type control. In summary, the identified elicitor VP2, recognized by the receptor in the plant membrane, triggers the cotton immune response and enhances disease resistance.
来源：PLANT BIOTECHNOLOGY JOURNAL
发布日期:2024-02-01
全文链接:http://agri.nais.net.cn/file1/M00/10/3F/Csgk0EGyuXKARr8eAD72I-_mXh4615.pdf

6. Long noncoding RNA TRABA suppresses β-glucosidase-encoding BGLU24 to promote salt tolerance in cotton(长链非编码RNA TRABA抑制编码BGLU24的β-葡萄糖苷酶提高棉花耐盐性)

简介：Salt stress severely damages the growth and yield of crops. Recently, long noncoding RNAs (lncRNAs) were demonstrated to regulate various biological processes and responses to environmental stresses. However, the regulatory mechanisms of lncRNAs in cotton (Gossypium hirsutum) response to salt stress are still poorly understood. Here, we observed that a lncRNA, trans acting of BGLU24 by lncRNA (TRABA), was highly expressed while GhBGLU24-A was weakly expressed in a salt-tolerant cotton accession (DM37) compared to a salt-sensitive accession (TM-1). Using TRABA as an effector and proGhBGLU24-A-driven GUS as a reporter, we showed that TRABA suppressed GhBGLU24-A promoter activity in double transgenic Arabidopsis (Arabidopsis thaliana), which explained why GhBGLU24-A was weakly expressed in the salt-tolerant accession compared to the salt-sensitive accession. GhBGLU24-A encodes an endoplasmic reticulum (ER)-localized beta-glucosidase that responds to salt stress. Further investigation revealed that GhBGLU24-A interacted with RING-type E3 ubiquitin ligase (GhRUBL). Virus-induced gene silencing (VIGS) and transgenic Arabidopsis studies revealed that both GhBGLU24-A and GhRUBL diminish plant tolerance to salt stress and ER stress. Based on its substantial effect on ER-related degradation (ERAD)-associated gene expression, GhBGLU24-A mediates ER stress likely through the ERAD pathway. These findings provide insights into the regulatory role of the lncRNA TRABA in modulating salt and ER stresses in cotton and have potential implications for developing more resilient crops.
来源：PLANT PHYSIOLOGY
发布日期:2024-01-31
全文链接:http://agri.nais.net.cn/file1/M00/03/6C/Csgk0WYJbMWAGnc6AB-497qAReY387.pdf

7. C-terminally encoded peptides act as signals to increase cotton root nitrate uptake under nonuniform salinity(C端编码肽在不均匀盐胁迫下促进棉花根系硝酸盐吸收的作用)

简介：Soil salinity is often heterogeneous in saline fields. Nonuniform root salinity increases nitrate uptake into cotton (Gossypium hirsutum) root portions exposed to low salinity, which may be regulated by root portions exposed to high salinity through a systemic long-distance signaling mechanism. However,

the signals transmitted between shoots and roots and their precise molecular mechanisms for regulating nitrate uptake remain unknown. Here, we showed that nonuniform root salinity treatment using split-root systems increases the expression of C-TERMINALLY ENCODED PEPTIDE (GhCEP) genes in high-saline-treated root portions. GhCEP peptides originating in high-saline-treated root portions act as ascending long-distance mobile signals transported to the shoots to promote the expression of CEP DOWNSTREAM (GhCEPD) genes by inducing the expression of CEP receptor (GhCEPR) genes. The shoot-derived GhCEPD polypeptides act as descending mobile signals transported to the roots through the phloem, increasing the expression of nitrate transport genes NITRATE TRANSPORTER 1.1 (GhNRT1.1), GhNRT2.1, and GhNRT1.5 in nonsaline-treated root portions, thereby increasing nitrate uptake in the nonsaline-treated root portions. This study indicates that GhCEP and GhCEPD signals are transported between roots and shoots to increase nitrate uptake in cotton, and the transport from the nonsaline root side is in response to nonuniform root salinity distribution.Nonuniform root salinity increases nitrate uptake from the nonsaline root side in cotton by salt stress-induced C-terminally encoded peptide signals from the high-saline root side.

来源：PLANT PHYSIOLOGY

发布日期:2023-12-30

全文链接:http://agri.nais.net.cn/file1/M00/10/3F/Csgk0EGyvOWAT0EoABfjC3QJSR4838.pdf

8. RVE2, a new regulatory factor in jasmonic acid pathway, orchestrates resistance to Verticillium wilt(茉莉酸途径新调控因子RVE2调控黄萎病抗性)

简介：Verticillium dahliae, one of the most destructive fungal pathogens of several crops, challenges the sustainability of cotton productivity worldwide because very few widely-cultivated Upland cotton varieties are resistant to Verticillium wilt (VW). Here, we report that REVEILLE2 (RVE2), the Myb-like transcription factor, confers the novel function in resistance to VW by regulating the jasmonic acid (JA) pathway in cotton. RVE2 expression was essentially required for the activation of JA-mediated disease-resistance response. RVE2 physically interacted with TPL/TPRs and disturbed JAZ proteins to recruit TPL and TPR1 in NINJA-dependent manner, which regulated JA response by relieving inhibited-MYC2 activity. The MYC2 then bound to RVE2 promoter for the activation of its transcription, forming feedback loop. Interestingly, a unique truncated RVE2 widely existing in D-subgenome (GhRVE2D) of natural Upland cotton represses the ability of the MYC2 to activate GhRVE2A promoter but not GausRVE2 or GbRVE2. The result could partially explain why Gossypium barbadense popularly shows higher resistance than Gossypium hirsutum. Furthermore, disturbing the JA-signalling pathway resulted into the loss of RVE2-mediated disease-resistance in various plants (Arabidopsis, tobacco and cotton). RVE2 overexpression significantly enhanced the resistance to VW. Collectively, we conclude that RVE2, a new regulatory factor, plays a pivotal role in fine-tuning JA-signalling, which would improve our understanding the mechanisms underlying the resistance to VW.

来源：PLANT BIOTECHNOLOGY JOURNAL

发布日期:2023-12-01

全文链接:http://agri.nais.net.cn/file1/M00/03/6C/Csgk0WYJb-qARWvHACL9gHvh4OM809.pdf

9. A truncated ETHYLENE INSENSITIVE3-like protein, GhLYI, regulates senescence in cotton(截短型乙烯不敏感蛋白GhLYI调控棉花衰老)

简介：Numerous endogenous and environmental signals regulate the intricate and highly orchestrated process of plant senescence. Ethylene (ET), which accumulates as senescence progresses, is a major promoter of leaf senescence. The master transcription activator ETHYLENE INSENSITIVE3 (EIN3) activates the expression of a wide range of downstream genes during leaf senescence. Here, we found that a unique EIN3-LIKE 1 (EIL1) gene, cotton LINT YIELD INCREASING (GhLYI), encodes a truncated EIN3 protein in upland cotton (Gossypium hirsutum L.) that functions as an ET signal response factor and a positive regulator of senescence. Ectopic expression or overexpression of GhLYI accelerated leaf senescence in both Arabidopsis (Arabidopsis thaliana) and cotton. Cleavage under targets and tagmentation (CUT & Tag) analyses revealed that SENESCENCE-ASSOCIATED GENE 20 (SAG20) was a target of GhLYI. Electrophoretic mobility shift assay (EMSA), yeast 1-hybrid (Y1H), and dual-luciferase transient expression assay confirmed that GhLYI directly bound the promoter of SAG20 to activate its expression. Transcriptome analysis revealed that transcript levels of a series of senescence-related genes, SAG12, NAC-LIKE, ACTIVATED by APETALA 3/PISTILLATA (NAP/ANAC029), and WRKY53, are substantially induced in GhLYI overexpression plants compared with wild-type (WT) plants. Virus-induced gene silencing (VIGS) preliminarily confirmed that knockdown of GhSAG20 delayed leaf senescence. Collectively, our findings provide a regulatory module involving GhLYI-GhSAG20 in controlling senescence in cotton.Cotton LINT YIELD INCREASING encodes a truncated ETHYLENE INSENSITIVE3 protein that modulates senescence by activating senescence-associated genes.
来源：PLANT PHYSIOLOGY
发布日期:2023-09-22
全文链接:http://agri.nais.net.cn/file1/M00/10/3F/Csgk0EGyvuuAd0U5AB7-H6LIsKs628.pdf

10. Cotton leaf curl Multan virus C4 protein suppresses autophagy to facilitate viral infection(棉花曲叶木尔坦病毒C4蛋白抑制自噬促进病毒感染)

简介：Autophagy plays an important role in plant antiviral defense. Several plant viruses are reported to encode viral suppressor of autophagy (VSA) to prevent autophagy for effective virus infection. However, whether and how other viruses, in particular DNA viruses, also encode VSAs to affect viral infection in plants is unknown. Here, we report that the C4 protein encoded by Cotton leaf curl Multan geminivirus (CLCuMuV) inhibits autophagy by binding to the autophagy negative regulator eukaryotic translation initiation factor 4A (eIF4A) to enhance the eIF4A-Autophagy-related protein 5 (ATG5) interaction. By contrast, the R54A or R54K mutation in C4 abolishes its capacity to interact with eIF4A, and neither C4(R54A) nor C4(R54K) can suppress autophagy. However, the R54 residue is not essential for C4 to interfere with transcriptional gene silencing or post-transcriptional gene silencing. Moreover, plants infected with mutated CLCuMuV-C4(R54K) develop less severe symptoms with decreased levels of viral DNA. These findings reveal a molecular mechanism underlying how the DNA virus CLCuMuV deploys a VSA to subdue host cellular antiviral autophagy defense and uphold viral infection in plants.A geminiviral protein suppresses autophagy by enhancing the interaction between the autophagy negative regulator eIF4A and ATG5 to facilitate virus infection.
来源：PLANT PHYSIOLOGY
发布日期:2023-08-31
全文链接:http://agri.nais.net.cn/file1/M00/10/3F/Csgk0EGywfCAaaotAKfKSnHZgpE660.pdf

11. Cotton 4-coumarate-CoA ligase 3 enhanced plant resistance to Verticillium dahliae by promoting jasmonic acid signaling-mediated vascular lignification and metabolic flux(棉花4-香豆酸-CoA连接酶3通过促进茉莉酸信号介导的维管木质化和代谢通量增强植物对大丽轮枝菌的抗性)

简 介： Lignins and their antimicrobial-related polymers cooperatively enhance plant resistance to pathogens. Several isoforms of 4-coumarate-coenzyme A ligases (4CLs) have been identified as indispensable enzymes involved in lignin and flavonoid biosynthetic pathways. However, their roles in plant-pathogen interaction are still poorly understood. This study uncovers the role of Gh4CL3 in cotton resistance to the vascular pathogen Verticillium dahliae. The cotton 4CL3-CRISPR/Cas9 mutant (CR4cl) exhibited high susceptibility to V. dahliae. This susceptibility was most probably due to the reduction in the total lignin content and the biosynthesis of several phenolic metabolites, e.g., rutin, catechin, scopoletin glucoside, and chlorogenic acid, along with jasmonic acid (JA) attenuation. These changes were coupled with a significant reduction in 4CL activity toward p-coumaric acid substrate, and it is likely that recombinant Gh4CL3 could specifically catalyze p-coumaric acid to form p-coumaroyl-coenzyme A. Thus, overexpression of Gh4CL3 (OE4CL) showed increasing 4CL activity that augmented phenolic precursors, cinnamic, p-coumaric, and sinapic acids, channeling into lignin and flavonoid biosyntheses and enhanced resistance to V. dahliae. Besides, Gh4CL3 overexpression activated JA signaling that instantly stimulated lignin deposition and metabolic flux in response to pathogen, which all established an efficient plant defense response system, and inhibited V. dahliae mycelium growth. Our results propose that Gh4CL3 acts as a positive regulator for cotton resistance against V. dahliae by promoting JA signaling-mediated enhanced cell wall rigidity and metabolic flux.

来源：PLANT JOURNAL
发布日期:2023-07-01
全文链接:http://agri.nais.net.cn/file1/M00/03/6C/Csgk0WYJcoyANl1bABsbPhllVjY630.pdf