



2023年第1期总1期

# 棉花遗传育种专题

## 本期导读

### ▶ 前沿资讯

1. 美国植物病理学会研究发现棉花中的基因B赋予了棉花对白叶枯病高且广泛的抗性并产生大量的倍半萜抗毒素
2. 美国DePaul大学计算机科学家重建了非洲驯化的棉花品种Wagad完整的基因组
3. 美国农业部(USDA)的一个研究团队培育了天然耐燃的棉花新品系

### ▶ 学术文献

1. 单细胞转录组分析揭示了比克氏棉色素腺体的发育轨迹和转录调控网络
2. 中国棉花育种遗传基础的基因组学的思考
3. 9个陆地棉优良品种的高分辨测序揭示了基因变异和育种改良目标
4. 西北内陆早熟陆地棉品种的综合评价及育种演化
5. 鉴定棉花中与特定种子性状相关的候选基因及其在拟南芥中的初步功能表征
6. 超长链脂肪酸合成基因SD38通过激活水稻乙烯生物合成影响株高

更多资讯 尽在农业专业知识服务系统:<http://agri.nais.net.cn/>

7. 纤维伸长过程中表达基因及其新等位基因的鉴定揭示了棉花纤维长度改良的遗传因素
8. GhOMT1功能缺失导致棉花(陆地棉)花青素过度积累及纤维颜色多样化
9. GhBZR3通过抑制超长链脂肪酸生物合成抑制棉花纤维伸长
10. 陆地棉的入侵是海岛棉种群分化和遗传多样性的驱动因素
11. 基因组和GWAS分析证明了中国海岛棉的系统发育关系以及纤维长度、衣分和枯萎病抗性的选择
12. 异源四倍体栽培棉纤维增强用磷脂酶A基因的敲除
13. 棉花GhBRC1通过整合多种激素途径调控分枝、开花和生长

中国农业科学院农业信息研究所

联系人：张毅

联系电话：010-82109921

邮箱：[agri@ckcest.cn](mailto:agri@ckcest.cn)

2023年11月30日

## ▶ 前沿资讯

### 1. Gene grants powerful resistance to resurging plant disease (美国植物病理学会研究发现棉花中的基因B赋予了棉花对白叶枯病高且广泛的抗性并产生大量的倍半萜抗毒素)

简介: While wrapping oneself in 100% Egyptian cotton bedsheets is a delightful luxury on a warm summer night, cotton provides much more than breathable, soft fabric. In addition to textiles, the cotton plant is grown for food, fuel, and daily-use consumer products—such as coffee filters, currency, and moisturizers. However, a resurging plant disease called bacterial blight is currently threatening cotton production worldwide. Bacterial blight is best controlled through natural, genetic resistance. Although several genes for natural resistance to bacterial blight of cotton were discovered in northeast Africa during the mid-twentieth century, one of these genes, found in Egyptian cotton, had been overlooked until a team of researchers led by Margaret Essenberg from Oklahoma State University began studying the gene. One of their recent studies, published by the American Phytopathological Society in a special focus issue of its journal *Phytopathology*, unveiled that gene B5 confers powerful resistance to bacterial blight. Essenberg and colleagues observed puzzling behavior from gene B5 after it was crossed into the DNA of upland cotton—a variety used in most clothing fabrics—as it did not appear to follow typical Mendelian genetics. Further investigation revealed an explanation for this peculiarity: upland cotton (AcB5) appears to carry gene B5 at two locations in its genome versus the typical single location. Under Oklahoma field conditions, the gene at either location enabled strong resistance to bacterial blight. In the lab, AcB5 exhibited resistance to the predominant and widely virulent strain of the disease’s causal pathogen, race 18, in addition to nine other pathogen races. These findings have positive implications for bacterial blight resistance in agriculture. “Natural, heritable disease resistance is an economical and environmentally safe means of maintaining plant health,” corresponding author Melanie Bayles explains. “Resistance genes trigger synthesis of natural defense chemicals at sites of infection. AcB5 cotton is a champion in this activity; it accumulated at least ten-fold more defense chemicals than cotton lines with four other single resistance genes.” Because pathogens often evolve to overcome such resistance, relying only on a single gene for disease resistance is precarious. The researchers propose that plant breeders combine this valuable B5 gene with other strong, broadly specific genes, such as B12, to develop durable resistance to bacterial blight. In addition to plant breeding, Bayles states that this research can benefit disciplines such as molecular plant-microbe interactions and phytochemistry, since the “signal transduction pathways of five different major genes for bacterial disease resistance in cotton are shown to lead in part to production of the same set of defense chemicals.” AcB5 is available for other researchers to use, along with a near-isogenic susceptible parent line. Essenberg and colleagues’ new, quick method for estimating amounts of defense chemicals in cotton plants, reported in *Phytopathology*, offers a “blight bulb” idea for improving resistance to this prevalent disease. For further details, read *Gene B5 in Cotton Confers High and Broad Resistance to Bacterial Blight and Conditions High Amounts of Sesquiterpenoid Phytoalexins*, published in the *Phytopathology* Focus Issue “Plant Disease Resistance at the Dawn of the New Era”—Volume 113, Number 5 / May 2023.

来源: EurekaAlert

发布日期: 2023-08-07

全文链接: [http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVm\\_2yACoF1AAVEk-LtyG4704.pdf](http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVm_2yACoF1AAVEk-LtyG4704.pdf)

更多资讯 尽在农业专业知识服务系统: <http://agri.nais.net.cn/>

## 2. Computer scientists sequence cotton genome (美国DePaul大学计算机科学家重建了非洲驯化的棉花品种Wagad完整的基因组)

简介: Cotton is the primary source of natural fiber on Earth, yet only four of 50 known species are suitable for textile production. Computer scientists at DePaul University applied a bioinformatics workflow to reconstruct one of the most complete genomes of a top cotton species, African domesticated *Gossypium herbaceum* cultivar Wagad. Experts say the results give scientists a more complete picture of how wild cotton was domesticated over time and may help to strengthen and protect the crop for farmers in the U.S., Africa and beyond. The findings are published in the journal *G3 Genes|Genomes|Genetics*. Thiru Ramaraj, assistant professor of computer science in DePaul's Jarvis College of Computing and Digital Media, is lead author on the publication. Leaps in technological advancement in the past decade made it possible for Ramaraj to analyze the genome in his Chicago lab. "The power of this technology is it allows us to create high-quality genomes that supply a level of detail that simply wasn't possible before," says Ramaraj, who specializes in bioinformatics. "This opens up the possibility for more researchers to sequence many crops that are important to the global economy and to feeding the population." The work is part of a collaboration that includes Jonathan Wendel, distinguished professor in the Department of Ecology, Evolution, and Organismal Biology at Iowa State University; and Joshua Udall, research leader for the Crop Germplasm Research Unit at the U.S. Department of Agriculture Agricultural Research Service. According to Udall, Wagad cotton is a diploid strain grown predominantly in African countries. "This has the potential to provide a genetic map that could improve their cotton crop," Udall said. Advanced computational methodologies bring forward genome. The team's work began with crunching DNA sequence data. They began reconstructing the Wagad genome by assembling high quality long DNA sequence data generated using Pacific Biosciences sequencing technology. As a next step, whole genome maps from Bionano genomics were used to order and orient the initial assembly. Lastly Hi-C sequence data from Phase genomics were used to construct chromosome level genome. Ramaraj then turned to Azalea Mendoza, a graduate student in computer science who also holds a bachelor's degree in environmental studies from DePaul. "Azalea had the biology background and knowledge to dive into this research," Ramaraj said. Mendoza began by researching the history of cotton to zoom out and understand "the big picture." No matter where cotton is grown, it's primarily used for fiber. Using comparative genomics, she looked for variations against its closet relative and to an outgroup. Mendoza also delved into annotated genes and noted their functions. "As we were studying the regions of the genome, we found many genes that were related to the content of fiber," Mendoza says. "It was incredible to see the real-life application of the work." Protecting crops in the U.S. and beyond. The impact of cotton genomics on U.S. agriculture and economy are clear to Udall, who has worked with Ramaraj since 2015. Udall leads the Crop Germplasm Research Unit and examines some of the 10,000 accessions of various species that the USDA holds in its repository. Their goal is to maintain the country's genetic food and feed security, and part of that is understanding the resilience and weaknesses of crops from around the world. "When new diseases come to the U.S., or there's new invasive pests, one of the first things we do is screened the genetic diversity of cotton to see if any of the previous varieties are resistant to it," Udall says. This can give farmers a chance to cross breed those genes and improve modern varieties of cotton, potentially avoiding catastrophic loss of agriculture. Udall relies on computational biologists like Ramaraj to further this work. While the cost of sequencing genomes has come down, this study still took nearly two years of work across disciplines. "This

is a good step in identifying future cotton genomes to sequence," Udall says. Ramaraj hopes the project will inspire other faculty and student collaborators to approach CDM with ideas for bioinformatics projects. For Mendoza, now an alumna working as a data analyst, the experience working in bioinformatics at DePaul is inspiring her career goals. "I love research and work that helps me grow on multiple levels," Mendoza says. "This is the kind of work that is going to affect humans and sustainability into the future."

来源: DePaul University

发布日期: 2023-06-22

全文链接: <http://agri.nais.net.cn/file1/M00/10/34/Csgk0GVnAwCArRAnAAIngPkkkeU240.pdf>

### **3. Watch: Scientists breed flame-resistant cotton, without added chemicals (美国农业部(USDA)的一个研究团队培育了天然耐燃的棉花新品系)**

简介: A research team at the USDA has developed new lines of cotton that are naturally flame-resistant — even putting themselves out when lit. How do researchers study the prevalence of mental illnesses? The ability could help cut back on the use of flame retardants, chemicals applied to a vast array of commercial products, like clothing, carpets, upholstery, and mattresses, to prevent cotton's flammable fibers from burning people if there's a fire — but which come with a variety of negative health and environmental impacts. Chemicals and fire: While flame retardants are effective and have improved fire safety, many of them come with environmental and health costs. According to the NIH, a growing body of research associates them with, among other things, higher risks of cancer, immune system disruption, and adverse effects on fetal development. Despite many of them being phased out of production, their hardness means they can build up in the environment, causing damage to places, people, and animals. USDA researchers have developed new lines of cotton that are naturally flame-resistant — even putting themselves out when lit. Natural flame retardants: The self-extinguishing cotton lines, published in PLOS One, were bred by using existing lines of cotton, with no recombinant genetic modification — or the extra rules and regulations that come with it. FEATURED VIDEO That means, as the Daily Beast's Maddie Bender pointed out, that it can be grown without the arduous approval process for GMOs. "Use of these lines to develop commercial cultivars creates an opportunity to improve the safety of cotton products while reducing the economic and environmental impacts of chemical flame retardants," said study senior author Brian Condon, the retired research leader at the USDA's Agricultural Research Service (ARS) Cotton Chemistry and Utilization Research Unit. Scientists have known that brown-colored cotton can be flame resistant, but the team's new lines are "the first report of a white cotton line with the property," USDA cotton chemistry researcher Gregory Thyssen told the Daily Beast. The self-extinguishing cotton lines were bred by using existing lines of cotton, with no recombinant genetic modification. ARS researchers Johnnie Jenkins and Jack McCarty began with 11 parent cultivars, none of which possessed flame resistance traits. Breeding these 11 different cultivars together in a variety of combinations, the team developed 257 new lines. They winnowed these down to the best 30 candidates for the next year's breeding season, per the Daily Beast, then made cuts again, selecting the best ten to work with the year after that. They then wove five textiles using the most flame-resistant varieties. "Of the textiles fabricated from the five superior [lines], four exhibited the novel characteristic of inherent flame resistance," the authors wrote in their study. (The others were "rapidly and completely consumed by flame.") When put through a standard 45° incline flammability test, the four fabrics self-extinguished — actually putting themselves out. The natural flame retardants the team bred did not derive their resistance from one simple trait; instead it was "obviously due to an uncommon

更多资讯 尽在农业专业知识服务系统: <http://agri.nais.net.cn/>

combination of alleles” — a bunch of genetic mixing and matching across sundry regions of the genome. The complex formula for flame resistance meant old-school breeding was actually a better choice than more targeted genetic engineering.

来源: Freethink

发布日期: 2023-03-11

全文链接: <http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVnAzGA0HVqAH1x4d26fZY442.pdf>

## 学术文献

### 1. Single-cell transcriptomic analysis reveals the developmental trajectory and transcriptional regulatory networks of pigment glands in *Gossypium bickii* (单细胞转录组分析揭示了比克氏棉色素腺体的发育轨迹和转录调控网络)

简介: Comprehensive utilization of cottonseeds is limited by the presence of pigment glands and its inclusion gossypol. The ideal cotton has glandless seeds but a glanded plant, a trait found in only a few Australian wild cotton species, including *Gossypium bickii*. Introgression of this trait into cultivated species has proved to be difficult. Understanding the biological processes toward pigment gland morphogenesis and the associated underlying molecular mechanisms will facilitate breeding of cultivated cotton varieties with the trait of glandless seeds and glanded plant. In this study, single-cell RNA sequencing (scRNA-seq) was performed on 12 222 protoplasts isolated from cotyledons of germinating *G. bickii* seeds 48 h after imbibition. Clustered into 14 distinct clusters unsupervisedly, these cells could be grouped into eight cell populations with the assistance of known cell marker genes. The pigment gland cells were well separated from others and could be separated into pigment gland parenchyma cells, secretory cells, and apoptotic cells. By integrating the pigment gland cell developmental trajectory, transcription factor regulatory networks, and core transcription factor functional validation, we established a model for pigment gland formation. In this model, light and gibberellin were verified to promote the formation of pigment glands. In addition, three novel genes, GbiERF114 (ETHYLENE RESPONSE FACTOR 114), GbiZAT11 (ZINC FINGER OF ARABIDOPSIS THALIANA 11), and GbiNTL9 (NAC TRANSCRIPTION FACTOR-LIKE 9), were found to affect pigment gland formation. Collectively, these findings provide new insights into pigment gland morphogenesis and lay the cornerstone for future cotton scRNA-seq investigations.

来源: MOLECULAR PLANT

发布日期: 2023-04-03

全文链接: <http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVn45uAR5ZhADUb0zUYdWg927.pdf>

### 2. Genomic insights into the genetic basis of cotton breeding in China (中国棉花育种遗传基础的基因组学的思考)

简介: The excellent Upland cotton (*Gossypium hirsutum*) cultivars developed since 1949 have made a huge contribution to cotton production in China, the world's largest producer and consumer of cotton. However, the genetic and genomic basis for the improvements of these cotton cultivars remains largely unclear. In this study, we selected 16 Upland cotton cultivars with important historical status in Chinese cotton breeding and constructed a multiparent, advanced generation, intercross (MAGIC) population comprising 920 recombinant inbred lines. A genome-wide association study using the MAGIC population identified 54

更多资讯 尽在农业专业知识服务系统: <http://agri.nais.net.cn/>

genomic loci associated with lint yield and fiber quality. Of them, 25 (46.30%) pleiotropic genomic loci cause simultaneous changes of lint yield and/or fiber quality traits, revealing complex trade-offs and linkage drags in Upland cotton agronomic traits. Deep sequencing data of 11 introduced ancestor cultivars and publicly available resequencing datasets of 839 cultivars developed in China during the past 70 years were integrated to explore the historical distribution and origin of the elite or selected alleles. Interestingly, 85% of these elite alleles were selected and fixed from different American ancestors, consistent with cotton breeding practices in China. However, seven elite alleles of native origin that are responsible for Fusarium wilt resistance, early maturing, good-quality fiber, and other characteristics were not found in American ancestors but have greatly contributed to Chinese cotton breeding and wide cultivation. Taken together, these results provide a genetic basis for further improving cotton cultivars and reveal that the genetic composition of Chinese cotton cultivars is narrow and mainly derived from early introduced American varieties.

来源: MOLECULAR PLANT

发布日期: 2023-04-03

全文链接: <http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVn4nmARp19ACi5eMtJWXQ269.pdf>

### 3. High-resolution sequencing of nine elite upland cotton cultivars uncovers genic variations and breeding improvement targets (9个陆地棉优良品种的高分辨测序揭示了基因变异和育种改良目标)

简介: Structural variations (SVs) are critical factors affecting genome evolution and important traits. However, identification results and functional analyses of SVs in upland cotton are rare. Here, based on the genetic relationships, breeding history and cumulative planting area of upland cotton in China, nine predominant cultivars from the past 60 years (1950s-2010s) were selected for long read sequencing to uncover genic variations and breeding improvement targets for this crop. Based on the ZM24 reference genome,  $0.88-1.47 \times 10^4$  SVs per cultivar were identified, and an SV set was constructed. SVs affected the expression of a large number of genes during fiber elongation, and a transposable element insertion resulted in the glandless phenotype in upland cotton. Six widespread inversions were identified based on nine draft genomes and high-throughput chromosome conformation capture data. Multiple haplotype blocks that were always associated with aggregated SVs were demonstrated to play a pivotal role in the agronomic traits of upland cotton and drove its adaptation to the northern planting region. Exotic introgression was the source of these haplotype blocks and increased the genetic diversity of upland cotton. Our results enrich the genome resources of upland cotton, and the identified SVs will promote genetic and breeding research in cotton.

来源: PLANT JOURNAL

发布日期: 2023-01-01

全文链接: <http://agri.nais.net.cn/file1/M00/10/34/Csgk0GVn3s0AVSvAADe-LEoIdrU318.pdf>

### 4. 西北内陆早熟陆地棉品种的综合评价及育种演化

简介: 【目的】综合评价近30年西北内陆棉区审定的早熟陆地棉品种, 阐述该区域育成品种主要性状的育种演变规律, 为西北内陆棉花新品种选育和主栽品种推荐提供参考依据。【方法】2020年和2021年分别在甘肃敦煌和新疆石河子对110个1988—2021年西北内陆棉区审定的早熟陆地棉品种与早熟、产量、纤维品质和株型相关的12个主要性状的表型进行鉴定; 利用聚类分析、相关性分析和主成分分

更多资讯 尽在农业专业知识服务系统: <http://agri.nais.net.cn/>

析等方法,对品种表型特征进行综合评分,筛选优良品种,并对其主要性状进行育种演化分析。【结果】110个早熟陆地棉参试品种的12个主要性状表型值分布范围较大,变异系数由大到小依次为:果枝长度>单株结铃数>吐絮率>单铃重>马克隆值>纤维强度>衣分>纤维长度>开花时间>果枝夹角>伸长率>整齐度。通过聚类分析将110个早熟陆地棉品种分为I、II、III和IV4个类群,它们分别为优良纤维品质、早熟、松散株型和高产的品种类群。相关性分析表明,早熟性与产量和纤维品质相关性状均呈负相关,产量构成性状与纤维品质性状呈正相关,且多数性状之间达显著或极显著水平。利用主成分分析将12个主要性状简化为4个主成分,其累积贡献率达66.92%;并对110份早熟陆地棉品种进行综合评分,评分排名第一的品种为中棉113(0.67),该品种具有早熟、高产、纤维品质优良和株型相对松散等特征。进一步分析发现,甘肃审定品种的早熟性显著优于西北内陆和新疆审定品种,产量和纤维品质相关性状显著低于西北内陆和新疆审定品种。西北内陆早熟陆地棉品种在30多年的演化过程中,多数产量和纤维品质相关性状呈显著上升的变化趋势,株型向更为紧凑的趋势演变;早期育成品种的单株结铃数与单铃重、衣分、纤维长度和强度呈负相关,而近期育成品种单株结铃数与单铃重、衣分、纤维长度和强度呈正相关。【结论】西北内陆早熟陆地棉品种在育种改良过程中,与产量和纤维品质相关的主要性状指标分布广泛,逐年呈显著提升的演变趋势;近期育成品种已实现了单株结铃数与纤维长度和强度的协同提高。

来源: 中国农业科学

发布日期:2023-01-01

全文链接:<http://agri.nais.net.cn/file1/M00/10/34/Csgk0GVn2dSAdFHKAEPHe4y8dY390.pdf>

## 5. Identification of candidate genes in cotton associated with specific seed traits and their initial functional characterization in Arabidopsis (鉴定棉花中与特定种子性状相关的候选基因及其在拟南芥中的初步功能表征)

简介: Oilseed crops are used to produce vegetable oil to satisfy the requirements of humans and livestock. Cotton (*Gossypium* spp.) is of great economic value because it is used as both an important textile commodity and a nutrient-rich resource. Cottonseed oil is rich in polyunsaturated fatty acids and does not contain trans fatty acids; hence, it is considered a healthy vegetable oil. However, research on the genetic basis for cottonseed protein content, oil production, and fatty acid composition is lacking. Here, we investigated the protein content, oil content, and fatty acid composition in terms of oleic acid (C18:1) and linoleic acid (C18:2) in mature cottonseeds from 318 *Gossypium hirsutum* accessions. Moreover, we examined the dynamic change of protein content and lipid composition including palmitic acid (C16:0), stearic acid (C18:0), oleic acid (C18:1), linoleic acid (C18:2), and linolenic acid (C18:3) in developing seeds from 258 accessions at 10 and 20 days post-anthesis. Then, we conducted a genome-wide association study and identified 152 trait-associated loci and 64 candidate genes responsible for protein and oil-related contents in mature cottonseeds and ovules. Finally, six candidate genes were experimentally validated to be involved in the regulation of fatty acid biosynthesis through heterologous expression in *Arabidopsis*. These results comprise a solid foundation for expanding our understanding of lipid biosynthesis in cotton, which will help breeders manipulate protein and oil contents to make it a fully developed 'fiber, food, and oil crop'.

来源: PLANT JOURNAL

发布日期:2022-11-01

全文链接:[http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVn5paARq\\_hAAeEWDpvh1k933.pdf](http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVn5paARq_hAAeEWDpvh1k933.pdf)

更多资讯 尽在农业专业知识服务系统:<http://agri.nais.net.cn/>



## 6. A very-long-chain fatty acid synthesis gene, SD38, influences plant height by activating ethylene biosynthesis in rice (超长链脂肪酸合成基因SD38通过激活水稻乙烯生物合成影响株高)

**简介:** As an important trait in crop breeding, plant height is associated with lodging resistance and yield. With the identification and cloning of several semi-dwarfing genes, increasing numbers of semi-dwarf cultivars have emerged, which has led to a 'green revolution' in rice (*Oryza sativa*) production. In this study, we identified a rice semi-dwarf mutant, semi-dwarf 38 (sd38), which showed significantly reduced cell length. SD38 encodes a fatty acid elongase, beta-ketoacyl-CoA synthase, which is involved in the synthesis of very-long-chain fatty acids (VLCFAs). Expression analysis showed that SD38 was localized on the membrane of the endoplasmic reticulum, and was expressed in all analyzed tissues with differential abundance. The mutation of SD38 affected lipid metabolism in the sd38 mutant. A functional complementarity test in *Saccharomyces cerevisiae* indicated that SD38 was capable of complementing the deficiency of ELO3p activity in BY4741-elo3 knockout yeast cells by participating in the synthesis of C24:0 VLCFA. Significant changes were observed in the expression of genes involved in ethylene synthesis, which resulted in reduced content of the ethylene precursor 1-aminocyclopropane-1-carboxylic acid (ACC) in the sd38 mutant. Exogenously supplied VLCFA (C24:0) increased the expression levels of OsACS3, OsACS4, and OsACO7 and the plant height of sd38 mutant seedlings, similar to the effect of exogenous application of ACC and ethephon. These results reveal a relationship among VLCFAs, ethylene biosynthesis, and plant height and improve our understanding of plant height development in crops.

**来源:** PLANT JOURNAL

**发布日期:** 2022-11-01

**全文链接:** <http://agri.nais.net.cn/file1/M00/10/34/Csgk0GVn4EmANTV1AF2pBCrsZX4994.pdf>

## 7. Expressed genes and their new alleles identification during fibre elongation reveal the genetic factors underlying improvements of fibre length in cotton (纤维伸长过程中表达基因及其新等位基因的鉴定揭示了棉花纤维长度改良的遗传因素)

**简介:** Interspecific breeding in cotton takes advantage of genetic recombination among desirable genes from different parental lines. However, the expression new alleles (ENAs) from crossovers within genic regions and their significance in fibre length (FL) improvement are currently not understood. Here, we generated resequencing genomes of 191 interspecific backcross inbred lines derived from CRI36 (*Gossypium hirsutum*) x Hai7124 (*Gossypium barbadense*) and 277 dynamic fibre transcriptomes to identify the ENAs and extremely expressed genes (eGenes) potentially influencing FL, and uncovered the dynamic regulatory network of fibre elongation. Of 35 420 eGenes in developing fibres, 10 366 ENAs were identified and preferentially distributed in chromosomes subtelomeric regions. In total, 1056-1255 ENAs showed transgressive expression in fibres at 5-15 dpa (days post-anthesis) of some BILs, 520 of which were located in FL-quantitative trait locus (QTLs) and GhFLA9 (recombination allele) was identified with a larger effect for FL than GhFLA9 of CRI36 allele. Using ENAs as a type of markers, we identified three novel FL-QTLs. Additionally, 456 extremely eGenes were identified that were preferentially distributed in recombination hotspots. Importantly, 34 of them were significantly associated with FL. Gene expression quantitative trait locus analysis identified 1286, 1089 and 1059 eGenes that were colocalized with the FL trait at 5, 10 and 15 dpa, respectively. Finally, we verified the Ghir\_D10G011050 gene linked to fibre elongation by the

更多资讯 尽在农业专业知识服务系统:<http://agri.nais.net.cn/>

CRISPR-cas9 system. This study provides the first glimpse into the occurrence, distribution and expression of the developing fibres genes (especially ENAs) in an introgression population, and their possible biological significance in FL.

来源: PLANT BIOTECHNOLOGY JOURNAL

发布日期:2022-10-01

全文链接:[http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVn55CAAu\\_1AIeHZRWxo1M497.pdf](http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVn55CAAu_1AIeHZRWxo1M497.pdf)

## **8. Function deficiency of GhOMT1 causes anthocyanidins over-accumulation and diversifies fibre colours in cotton (*Gossypium hirsutum*) (GhOMT1功能缺失导致棉花(陆地棉)花青素过度积累及纤维颜色多样化)**

简介: Naturally coloured cotton (NCC) fibres need little or no dyeing process in textile industry to low-carbon emission and are environment-friendly. Proanthocyanidins (PAs) and their derivatives were considered as the main components causing fibre coloration and made NCCs very popular and healthy, but the monotonous fibre colours greatly limit the wide application of NCCs. Here a *G. hirsutum* emurpled mutant (HS2) caused by T-DNA insertion is found to enhance the anthocyanidins biosynthesis and accumulate anthocyanidins in the whole plant. HPLC and LC/MS-ESI analysis confirmed the anthocyanidins methylation and peonidin, petunidin and malvidin formation are blocked. The deficiency of GhOMT1 in HS2 was associated with the activation of the anthocyanidin biosynthesis and the altered components of anthocyanidins. The transcripts of key genes in anthocyanidin biosynthesis pathway are significantly up-regulated in HS2, while transcripts of the genes for transport and decoration were at similar levels as in WT. To investigate the potential mechanism of GhOMT1 deficiency in cotton fibre coloration, HS2 mutant was crossed with NCCs. Surprisingly, offsprings of HS2 and NCCs enhanced PAs biosynthesis and increased PAs levels in their fibres from the accumulated anthocyanidins through up-regulated GhANR and GhLAR. As expected, multiple novel lines with improved fibre colours including orange red and navy blue were produced in their generations. Based on this work, a new strategy for breeding diversified NCCs was brought out by promoting PA biosynthesis. This work will help shed light on mechanisms of PA biosynthesis and bring out potential molecular breeding strategy to increase PA levels in NCCs.

来源: PLANT BIOTECHNOLOGY JOURNAL

发布日期:2022-08-01

全文链接:[http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVn61GAXaVaACy1\\_h90ErQ338.pdf](http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVn61GAXaVaACy1_h90ErQ338.pdf)

## **9. GhBZR3 suppresses cotton fiber elongation by inhibiting very-long-chain fatty acid biosynthesis (GhBZR3通过抑制超长链脂肪酸生物合成抑制棉花纤维伸长)**

简介: The BRASSINAZOLE-RESISTANT (BZR) transcription factor is a core component of brassinosteroid (BR) signaling and is involved in the development of many plant species. BR is essential for the initiation and elongation of cotton fibers. However, the mechanism of BR-regulating fiber development and the function of BZR is poorly understood in *Gossypium hirsutum* L. (cotton). Here, we identified a BZR family transcription factor protein referred to as GhBZR3 in cotton. Overexpression of GhBZR3 in *Arabidopsis* caused shorter root hair length, hypocotyl length, and hypocotyl cell length, indicating that GhBZR3 negatively regulates cell elongation. Pathway enrichment analysis from VIGS-GhBZR3 cotton plants found that fatty acid metabolism and degradation might be the regulatory pathway that is primarily controlled by GhBZR3. Silencing GhBZR3 expression in cotton resulted in taller plant height as well as longer fibers. The

更多资讯 尽在农业专业知识服务系统:<http://agri.nais.net.cn/>

very-long-chain fatty acid (VLCFA) content was also significantly increased in silenced GhBZR3 plants compared with the wild type. The GhKCS13 promoter, a key gene for VLCFA biosynthesis, contains two GhBZR3 binding sites. The results of yeast one-hybrid, electrophoretic mobility shift, and luciferase assays revealed that GhBZR3 directly interacted with the GhKCS13 promoter to suppress gene expression. Taken together, these results indicate that GhBZR3 negatively regulates cotton fiber development by reducing VLCFA biosynthesis. This study not only deepens our understanding of GhBZR3 function in cotton fiber development, but also highlights the potential of improving cotton fiber length and plant growth using GhBZR3 and its related genes in future cotton breeding programs.

来源: PLANT JOURNAL

发布日期:2022-08-01

全文链接:<http://agri.nais.net.cn/file1/M00/10/34/Csgk0GVn5PyAGP22AIwsk8BxHUQ709.pdf>

## **10. Introgression from *Gossypium hirsutum* is a driver for population divergence and genetic diversity in *Gossypium barbadense* (陆地棉的入侵是海岛棉种群分化和遗传多样性的驱动因素)**

简介: Interspecific introgression from *Gossypium hirsutum* has reorganized the genomic architecture of *Gossypium barbadense*. In this study, the genetic basis of population differentiation and the genetic diversity were deciphered and the introgression events and haplotype selection affecting associated fiber quality and environmental adaptation traits were illuminated in *Gossypium barbadense*. This study provides new insights into the breeding history of *Gossypium barbadense* and will guard the breeding programs of modern cultivated *Gossypium barbadense*.

来源: PLANT JOURNAL

发布日期:2022-05-01

全文链接:[http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVn7GCALNb1ACx1W\\_2z-7M375.pdf](http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVn7GCALNb1ACx1W_2z-7M375.pdf)

## **11. Genomic and GWAS analyses demonstrate phylogenomic relationships of *Gossypium barbadense* in China and selection for fibre length, lint percentage and *Fusarium* wilt resistance (基因组和GWAS分析证明了中国海岛棉的系统发育关系以及纤维长度、衣分和枯萎病抗性的选择)**

简介: Sea Island cotton (*Gossypium barbadense*) is the source of the world's finest fibre quality cotton, yet relatively little is understood about genetic variations among diverse germplasms, genes underlying important traits and the effects of pedigree selection. Here, we resequenced 336 *G. barbadense* accessions and identified 16 million SNPs. Phylogenetic and population structure analyses revealed two major gene pools and a third admixed subgroup derived from geographical dissemination and interbreeding. We conducted a genome-wide association study (GWAS) of 15 traits including fibre quality, yield, disease resistance, maturity and plant architecture. The highest number of associated loci was for fibre quality, followed by disease resistance and yield. Using gene expression analyses and VIGS transgenic experiments, we confirmed the roles of five candidate genes regulating four key traits, that is disease resistance, fibre length, fibre strength and lint percentage. Geographical and temporal considerations demonstrated selection for the superior fibre quality (fibre length and fibre strength), and high lint percentage in improving *G. barbadense* in China. Pedigree selection breeding increased *Fusarium* wilt disease resistance

更多资讯 尽在农业专业知识服务系统:<http://agri.nais.net.cn/>

and separately improved fibre quality and yield. Our work provides a foundation for understanding genomic variation and selective breeding of Sea Island cotton.

来源: PLANT BIOTECHNOLOGY JOURNAL

发布日期:2022-04-01

全文链接:[http://agri.nais.net.cn/file1/M00/10/34/Csgk0GVn6lyAN\\_omAJJ\\_aWTlkVI671.pdf](http://agri.nais.net.cn/file1/M00/10/34/Csgk0GVn6lyAN_omAJJ_aWTlkVI671.pdf)

## **12. Retrieving a disrupted gene encoding phospholipase A for fibre enhancement in allotetraploid cultivated cotton (异源四倍体栽培棉纤维增强用磷脂酶A基因的敲除)**

简介: After polyploidization originated from one interspecific hybridization event in *Gossypium*, *Gossypium barbadense* evolved to produce extra-long staple fibres than *Gossypium hirsutum* (Upland cotton), which produces a higher fibre yield. The genomic diversity between *G. barbadense* and *G. hirsutum* thus provides a genetic basis for fibre trait variation. Recently, rapid accumulation of gene disruption or deleterious mutation was reported in allotetraploid cotton genomes, with unknown impacts on fibre traits. Here, we identified gene disruptions in allotetraploid *G. hirsutum* (18.14%) and *G. barbadense* (17.38%) through comparison with their presumed diploid progenitors. Relative to conserved genes, these disrupted genes exhibited faster evolution rate, lower expression level and altered gene co-expression networks. Within a module regulating fibre elongation, a hub gene experienced gene disruption in *G. hirsutum* after polyploidization, with a 2-bp deletion in the coding region of GhNPLA1D introducing early termination of translation. This deletion was observed in all of the 34 *G. hirsutum* landraces and 36 *G. hirsutum* cultivars, but not in 96% of 57 *G. barbadense* accessions. Retrieving the disrupted gene GhNPLA1D using its homoeolog GhNPLA1A achieved longer fibre length in *G. hirsutum*. Further enzyme activity and lipids analysis confirmed that GhNPLA1A encodes a typical phospholipase A and promotes cotton fibre elongation via elevating intracellular levels of linolenic acid and 34:3 phosphatidylinositol. Our work opens a strategy for identifying disrupted genes and retrieving their functions in ways that can provide valuable resources for accelerating fibre trait enhancement in cotton breeding.

来源: PLANT BIOTECHNOLOGY JOURNAL

发布日期:2022-04-01

全文链接:<http://agri.nais.net.cn/file1/M00/10/34/Csgk0GVn5FOAPMBUAHIL3HhY8gw345.pdf>

## **13. Cotton GhBRC1 regulates branching, flowering, and growth by integrating multiple hormone pathways (棉花GhBRC1通过整合多种激素途径调控分枝、开花和生长)**

简介: Cotton architecture is partly determined by shoot branching and flowering patterns. GhBRC1 was previously identified by RNA-seq analysis of nulliplex-branching and normal-branching cotton. However, the roles of GhBRC1 in cotton remain unclear. In the present study, investigations of nuclear localization and transcriptional activity indicated that GhBRC1 has characteristics typical of transcription factors. Gene expression analysis showed that GhBRC1 was highly expressed in axillary buds but displayed different expression patterns between the two branching types. Overexpression of GhBRC1 in *Arabidopsis* significantly inhibited the number of branches and promoted flowering. In contrast, silencing GhBRC1 in cotton significantly promoted seedling growth. GhBRC1 was induced by multiple hormones, including

更多资讯 尽在农业专业知识服务系统:<http://agri.nais.net.cn/>

strigolactones, which promoted seedling growth and seed germination of Arabidopsis plants overexpressing GhBRC1. Consistent with these findings, RNA-seq analysis of virus-induced gene silencing treated cotton revealed that a large number of genes were differentially expressed between GhBRC1-silenced and control plants, and these genes were significantly enriched in plant hormone signalling pathways. Together, our data indicates that GhBRC1 regulates plant branching and flowering through multiple regulatory pathways, especially those regulating plant hormones, with functions partly differing from those of Arabidopsis BRC1. These results provide insights into the molecular mechanisms controlling plant architecture, which is important for breeding cotton with ideal plant architecture and high yield. (C) 2021 Crop Science Society of China and Institute of Crop Science, CAAS. Production and hosting by Elsevier B.V. on behalf of KeAi Communications Co., Ltd.

来源: CROP JOURNAL

发布日期:2022-02-01

全文链接:[http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVn70GALbnSAEbBDLyR\\_g0574.pdf](http://agri.nais.net.cn/file1/M00/03/61/Csgk0WVn70GALbnSAEbBDLyR_g0574.pdf)