2024年第1期总2期

棉花遗传育种专题

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前沿资讯

1．华盛顿州立大学研究人员开发出能导电的新型棉纤维

简介：研究人员开发出一种新型纤维，它既有棉花的柔韧性，又有聚合物聚苯胺的导电性。这种创新材料在《碳水化合物聚合物》（Carbohydrate Polymers）期刊中做了详细介绍，它显示出了制造可穿戴电子纺织品的潜力，可用于健康监测和危险暴露检测等应用。华盛顿州立大学开发的一种单股纤维同时具有棉花的柔韧性和一种名为聚苯胺的聚合物的导电性，显示出在可穿戴电子纺织品方面的巨大潜力。华盛顿州立大学的研究人员用一个为 LED 灯供电的系统和另一个感应氨气的系统测试了这种纤维，并在《碳水化合物聚合物》杂志上详细介绍了他们的研究成果。华盛顿州立大学纺织品研究员、该研究的通讯作者刘航（音译）说："我们将一种纤维分为两部分：一部分是传统的棉花：柔韧性和强度足以满足日常使用，而另一面则是导电材料。棉花可以支撑导电材料，而导电材料可以提供所需的功能。"可穿戴技术的潜在应用虽然还需要更多的开发工作，但研究人员的想法是将这样的纤维集成到服装中，作为带有柔性电路的传感器贴片。这些贴片可以成为消防员、士兵或处理化学品的工人制服的一部分，以检测是否接触到危险物质。其他应用还包括健康监测或运动衬衫，它们比目前的健身监测器能做得更多。刘说："我们现在有一些智能可穿戴设备，比如智能手表可以跟踪你的运动和人体生命体征，但我们希望将来你的日常服装也能实现这些功能。时尚并不像很多人认为的那样只是颜色和款式，时尚就是科学本身。"技术挑战与解决方案在这项研究中，华盛顿州立大学团队努力克服将导电聚合物与棉纤维素混合的难题。聚合物是一种具有重复模式的大分子物质。在这种情况下，研究人员使用了聚苯胺（又称 PANI），这是一种具有导电性能的合成聚合物，已被用于印刷电路板制造等应用中。虽然聚苯胺本身具有导电性，但它比较脆，无法制成纺织品纤维。为了解决这个问题，西悉尼大学的研究人员将从回收的 T 恤衫中提取的棉纤维素溶解到一种溶液中，并将导电聚合物溶解到另一种单独的溶液中。然后将这两种溶液并排合并在一起，挤出材料制成一根纤维。结果显示界面结合良好，这意味着不同材料的分子在拉伸和弯曲过程中都能保持在一起，在棉纤维素和聚苯胺的界面上实现适当的混合是一个微妙的平衡。刘说："我们希望这两种溶液能够发挥作用，这样当棉花和导电聚合物相互接触时，它们就会在一定程度上混合在一起，形成一种粘合剂，但我们又不希望它们混合得太多，否则导电性能就会降低。"参考文献：《用于可穿戴电子纺织品的纤维素基导电复合纤维的新型结构设计》，作者：Wangcheng Liu、Hang Liu、Zihui Zhao、Dan Liang、Wei-Hong Zhong 和 Jinwen Zhang，2023 年 8 月 18 日，《碳水化合物聚合物》。

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2．超一千三百个水稻、玉米、大豆、棉花新品种获审定通过——中国农作物品种创新有新突破

简介：优质绿色水稻、耐密宜机收玉米、高油高产大豆——近日，农业农村部发布品种审定公告，第五届国家农作物品种审定委员会（以下简称国家品审委）根据《种子法》《主要农作物品种审定办法》有关规定，审定通过了1304个水稻、玉米、大豆、棉花新品种。这些新品种有啥特点？对保障粮食安全有何帮助？农业农村部有关负责人表示，从审定品种情况看，相关作物品种创新取得了一系列新进展、新突破，这些品种推广应用将有利于持续提升我国粮食大面积单产和品质水平。水稻是此次新品种中数量较多的一类，共409个，优质绿色是其突出特点。此次审定通过米质达到国标1级优质米品种50个，较上年增加6个；兼具高产、优质、绿色的“三好品种”28个，同比增加6

个。由湖南杂交水稻研究中心育种并提出申请的“西子3号”是其中之一。中国工程院院士、湖南省农业科学院党委书记柏连阳介绍，经检测，“西子3号”在区域试验中的糙米镉含量为每千克0.000至0.098毫克，低于每千克0.2毫克的国家限量标准。“作为籼型常规稻品种，‘西子3号’可在长江中下游做双季晚稻种植，将有利于部分受重金属污染的地区解决‘镉大米’问题，提升我国粮食安全的保障能力。”柏连阳说。大豆是另一个重要品类。数据显示，此次审定通过17个高油高产大豆新品种，占比达到1/5，亩产最高达到240公斤，含油率最高达到22.97%，同时筛选推荐了7个适合大豆玉米带状复合种植的大豆品种。国家品审委负责人介绍，围绕加强高油大豆品种培育和大面积单产提升，国家品审委日前对外发布《国家级大豆品种审定标准（2023年修订）》。此次标准修订提高了品种DNA指纹差异要求，推动解决品种同质化问题，同时提高了品种产量、品质要求以及品种抗病性要求。“聚焦大豆品种审定，我们还将在对照品种、种植密度、试验布局等方面对品种试验实施方案进行完善。”上述负责人说，明年将先行调整北方春大豆中早熟和中晚熟组、黄淮海夏大豆南片等生态区组对照品种，引导高产大豆品种选育；在2022年大豆品种试验种植密度普遍提高10%的基础上，明年将北方春大豆早熟区、黄淮海夏大豆北片等部分生态区试验种植密度再提高10%，引导耐密大豆品种选育；按照主要农作物品种审定办法规定，同一生态类型区试验点，国家级不少于10个，目前试验点一般在10-13个，明年将北方春大豆等生态区试验点数增加10%以上，进一步强化对品种稳产性的试验评价。此次审定推出的优质高产新品种还包括764个玉米品种、51个棉花品种。具体来看：审定通过15个籽粒机收品种，覆盖三大主产区，籽粒含水量平均为23.7%，同比下降0.56个百分点；耐密品种选育初现苗头，郑原玉333、郑品玉608等品种在西北种植密度每亩可达6000株以上。审定通过纤维品质优质I型和II型品种26个，占比达到51%；生育期小于110天且品质不低于Ⅱ型的短季棉品种2个，可用于黄河流域棉区麦后直播棉种植和长江流域棉区扩种油菜茬口衔接。农业农村部表示，国家品审委按照种业振兴市场净化行动安排部署，正组织持续推进品种审定绿色通道和联合体试验整治，不断规范品种审定试验，同时加快修订小麦、棉花品种审定标准，多措并举为粮油等主要作物大面积单产提升提供有力品种支撑。

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3． How a moth’s taste preferences change with age——Researchers have characterised the molecular basis for the change in food selection among cotton bollworms that occurs between their larval and adult stages.(蛾类的味觉偏好性如何随年龄变化——研究人员描述了棉铃虫在幼虫期和成虫期之间发生食物选择变化的分子基础)

简 介： The larvae and adult forms of the cotton bollworm (Helicoverpa armigera) adopt different sugar-sensing systems to satisfy their requirements for food selection, according to new research. Published today as a Reviewed Preprint in eLife, the study is described as important by the editors, who say it offers convincing evidence that two different gustatory receptors for sugar sensing underlie the change in diet preference between the larval and adult cotton bollworm.The findings, combined with further research, could suggest a new approach for pest control to increase crop yields across the globe.The cotton bollworm is a notorious, world-wide crop pest that contributes to approximately USD$3bn worth of economic loss every year. In its juvenile, larval stage the cotton bollworm mostly feeds on the leaves, flower buds and fruits of plants, which have a relatively low sugar concentration. As an adult, it mostly feeds on the sugar-rich nectar of plants. Previous studies have shown that the cotton

bollworm has external gustatory sensory neurons (GSNs) specialised nerve cells responsible for detecting and transmitting taste signals to the brain that are sensitive to sucrose and fructose. In larvae, these GSNs are located in specialised structures around their mouth, and in adults they are found in their antennae, the tarsi (the segments of the leg that are furthest from the body) and a specialised feeding structure called the proboscis, which serves a similar function as the human tongue. “The larval and adult diets of the cotton bollworm vary dramatically in their variety and concentration of sugars. Sucrose is the major sugar found in plant tissues, whereas nectar mainly contains sucrose, fructose and glucose,” explains lead author Shuai-Shuai Zhang, a PhD student at the State Key Laboratory of Integrated Management of Pest Insects and Rodents, Institute of Zoology, Chinese Academy of Sciences, Beijing, China. “We aimed to characterise the molecular basis for the change in diet seen between the cotton bollworm’s two life phases.” Zhang and colleagues first compared the electrophysiological and behavioural responses of cotton bollworm larvae and adults to seven sugars found in plants, including sucrose, fructose and glucose. They confirmed that both larvae and adults have sugar-detecting GSNs, but that their response profile, intensity and sensitivity differed markedly. The sugar GSNs in larvae responded strongly to sucrose with high sensitivity between 1001,000 times more sensitive to sucrose than adult GSNs, which responded to sucrose, fucose and fructose with lower intensity and sensitivity. This high sensitivity in larvae may help them locate sucrose in the sugar-sparse tissues of plants. Next, the team analysed the expression and function of nine candidate sugar gustatory receptor (GR) genes in larval and adult taste organs; Gr4Gr12 inclusively. Since the function of Gr9 is known, they tested the function of other eight GRs using Xenopus oocytes the unfertilised eggs of the African clawed frog, which are widely used in scientific research as they are large and relatively easy to manipulate. The team inserted DNA sequences for each GR gene into an individual oocyte, and then tested each oocyte’s response to 11 different sugar compounds. Most oocytes had no response, but the oocytes expressing Gr10 and Gr6 were responsive to one or more sugars, indicating their role in food recognition. Gr10 was found to be tuned to sucrose specifically, whereas Gr6 responded to sucrose, fucose and fructose. Finally, Zhang and colleagues used CRISPR/Cas9 DNA modifying techniques to create two homozygous mutants of cotton bollworms for Gr6 and Gr10, respectively meaning they do not possess the function of the Gr6 or Gr10 gene any more. The team sought to identify any changes in the electrophysiological and behavioural responses of the mutant larvae and adults to sugars compared to typical cotton bollworms. From their analysis, the team determined that Gr10 plays a key role in sucrose reception by the sugar GSNs in larvae, and mediates the larvae’s preference for sucrose. On the other hand, Gr6 is responsible for sensing sucrose, fucose and fructose in the GSNs of the adult cotton bollworm. Taken together, the results demonstrate that larval and adult cotton bollworms use different gustatory receptor genes to detect sucrose in food. Larvae mainly use Gr10 to detect the low amount of sucrose found in plant tissues, whereas adults primarily use Gr6 to detect a variety of sugars with high content, including sucrose in nectar. Both the authors and the editors note that, to thoroughly reveal the mechanisms of sugar sensing to design a new approach for pest control, it is crucial to first comprehensively study the function of all of the GRs involved in sucrose sensation. “We’ve reported the molecular basis of sucrose reception in the eternal taste neurons of the cotton bollworm, and discovered that different taste receptors underlie the difference in food selection between the adult and larval stages,” concludes senior author Chen-Zhu Wang, a professor at the State Key Laboratory of Integrated Management of Pest Insects and Rodents, Institute of Zoology, Chinese Academy of Sciences. “GRs closely associated with Gr10 and Gr6 are also found in other moth and butterfly species. We therefore speculate that

similar sugar-sensing mechanisms may also exist in these species, which is worth verifying with future research."

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学术文献

1. GhXB38D represses cotton fibre elongation through ubiquitination of ethylene biosynthesis enzymes GhACS4 and GhACO1(GhXB38D通过泛素化乙烯生物合成酶GhACS4和GhACO1抑制棉纤维伸长)

简介： Ethylene plays an essential role in the development of cotton fibres. Ethylene biosynthesis in plants is elaborately regulated by the activities of key enzymes, 1-aminocyclopropane-1-carboxylate oxidase (ACO) and 1-aminocyclopropane-1-carboxylate synthase (ACS); however, the potential mechanism of post-translational modification of ACO and ACS to control ethylene synthesis in cotton fibres remains unclear. Here, we identify an E3 ubiquitin ligase, GhXB38D, that regulates ethylene biosynthesis during fibre elongation in cotton. GhXB38D gene is highly expressed in cotton fibres during the rapid elongation stage. Suppressing GhXB38D expression in cotton significantly enhanced fibre elongation and length, accompanied by the up-regulation of genes associated with ethylene signalling and fibre elongation. We demonstrated that GhXB38D interacts with the ethylene biosynthesis enzymes GhACS4 and GhACO1 in elongating fibres and specifically mediates their ubiquitination and degradation. The inhibition of GhXB38D gene expression increased the stability of GhACS4 and GhACO1 proteins in cotton fibres and ovules, resulting in an elevated concentration of ethylene. Our findings highlight the role of GhXB38D as a regulator of ethylene synthesis by ubiquitinating ACS4 and ACO1 proteins and modulating their stability. GhXB38D acts as a negative regulator of fibre elongation and serves as a potential target for enhancing cotton fibre yield and quality through gene editing strategy.

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2. Cotton GhNAC4 promotes drought tolerance by regulating secondary cell wall biosynthesis and ribosomal protein homeostasis(棉花GhNAC4通过调控次生细胞壁生物合成和核糖体蛋白稳态来促进耐旱性)

简介： Drought has a severe impact on the quality and yield of cotton. Deciphering the key genes related to drought tolerance is important for understanding the regulation mechanism of drought stress and breeding drought-tolerant cotton cultivars. Several studies have demonstrated that NAC transcription factors are crucial in the regulation of drought stress, however, the related functional mechanisms are still largely unexplored. Here, we identified that NAC transcription factor GhNAC4 positively regulated drought stress tolerance in cotton. The expression of GhNAC4 was significantly induced by abiotic stress and plant hormones. Silencing of GhNAC4 distinctly impaired the resistance to drought stress and overexpressing GhNAC4 in cotton significantly enhanced the stress tolerance. RNA-seq analysis revealed

that overexpression of GhNAC4 enriched the expression of genes associated with the biosynthesis of secondary cell walls and ribosomal proteins. We confirmed that GhNAC4 positively activated the expressions of GhNST1, a master regulator reported previously in secondary cell wall formation, and two ribosomal protein-encoding genes GhRPL12 and GhRPL18p, by directly binding to their promoter regions. Overexpression of GhNAC4 promoted the expression of downstream genes associated with the secondary wall biosynthesis, resulting in enhancing secondary wall deposition in the roots, and silencing of GhRPL12 and GhRPL18p significantly impaired the resistance to drought stress. Taken together, our study reveals a novel pathway mediated by GhNAC4 that promotes secondary cell wall biosynthesis to strengthen secondary wall development and regulates the expression of ribosomal protein-encoding genes to maintain translation stability, which ultimately enhances drought tolerance in cotton.

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3. GhMYB30-GhMUR3 affects fiber elongation and secondary wall thickening in cotton(GhMYB30-GhMUR3对棉花纤维伸长和次生壁增厚的影响)

简介： Xyloglucan, an important hemicellulose, plays a crucial role in maintaining cell wall structure and cell elongation. However, the effects of xyloglucan on cotton fiber development are not well understood. GhMUR3 encodes a xyloglucan galactosyltransferase that is essential for xyloglucan synthesis and is highly expressed during fiber elongation. In this study, we report that GhMUR3 participates in cotton fiber development under the regulation of GhMYB30. Overexpression GhMUR3 affects the fiber elongation and cell wall thickening. Transcriptome showed that the expression of genes involved in secondary cell wall synthesis was prematurely activated in OE-MUR3 lines. In addition, GhMYB30 was identified as a key regulator of GhMUR3 by Y1H, Dual-Luc, and electrophoretic mobility shift assay (EMSA) assays. GhMYB30 directly bound the GhMUR3 promoter and activated GhMUR3 expression. Furthermore, DAP-seq of GhMYB30 was performed to identify its target genes in the whole genome. The results showed that many target genes were associated with fiber development, including cell wall synthesis-related genes, BR-related genes, reactive oxygen species pathway genes, and VLCFA synthesis genes. It was demonstrated that GhMYB30 may regulate fiber development through multiple pathways. Additionally, GhMYB46 was confirmed to be a target gene of GhMYB30 by EMSA, and GhMYB46 was significantly increased in GhMYB30-silenced lines, indicating that GhMYB30 inhibited GhMYB46 expression. Overall, these results revealed that GhMUR3 under the regulation of GhMYB30 and plays an essential role in cotton fiber elongation and secondary wall thickening. Additionally, GhMYB30 plays an important role in the regulation of fiber development and regulates fiber secondary wall synthesis by inhibiting the expression of GhMYB46.

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4. The transcription factor ERF108 interacts with AUXIN RESPONSE FACTORs to mediate cotton fiber secondary cell wall biosynthesis(转录因子ERF108与生长素反应因子相互作用介导棉花纤维次生细胞壁生物合成)

简介：Transcription factors GhERF108 and GhARF7 interact to establish ethylene-auxin crosstalk, which activates downstream secondary cell wall (SCW)-related genes to facilitate fiber SCW formation in cotton.Phytohormones play indispensable roles in plant growth and development. However, the molecular mechanisms underlying phytohormone-mediated regulation of fiber secondary cell wall (SCW) formation in cotton (Gossypium hirsutum) remain largely underexplored. Here, we provide mechanistic evidence for functional interplay between the APETALA2/ethylene response factor (AP2/ERF) transcription factor GhERF108 and auxin response factors GhARF7-1 and GhARF7-2 in dictating the ethylene-auxin signaling crosstalk that regulates fiber SCW biosynthesis. Specifically, in vitro cotton ovule culture revealed that ethylene and auxin promote fiber SCW deposition. GhERF108 RNA interference (RNAi) cotton displayed remarkably reduced cell wall thickness compared with controls. GhERF108 interacted with GhARF7-1 and GhARF7-2 to enhance the activation of the MYB transcription factor gene GhMYBL1 (MYB domain-like protein 1) in fibers. GhARF7-1 and GhARF7-2 respond to auxin signals that promote fiber SCW thickening. GhMYBL1 RNAi and GhARF7-1 and GhARF7-2 virus-induced gene silencing (VIGS) cotton displayed similar defects in fiber SCW formation as GhERF108 RNAi cotton. Moreover, the ethylene and auxin responses were reduced in GhMYBL1 RNAi plants. GhMYBL1 directly binds to the promoters of GhCesA4-1, GhCesA4-2, and GhCesA8-1 and activates their expression to promote cellulose biosynthesis, thereby boosting fiber SCW formation. Collectively, our findings demonstrate that the collaboration between GhERF108 and GhARF7-1 or GhARF7-2 establishes ethylene-auxin signaling crosstalk to activate GhMYBL1, ultimately leading to the activation of fiber SCW biosynthesis.
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5．LIPID TRANSFER PROTEIN4 regulates cotton ceramide content and activates fiber cell elongation(LIPID TRANSFER PROTEIN4调控棉花神经酰胺含量，激活纤维细胞伸长)

简介：Cell elongation is a fundamental process for plant growth and development. Studies have shown lipid metabolism plays important role in cell elongation; however, the related functional mechanisms remain largely unknown. Here, we report that cotton (Gossypium hirsutum) LIPID TRANSFER PROTEIN4 (GhLTP4) promotes fiber cell elongation via elevating ceramides (Cers) content and activating auxin-responsive pathways. GhLTP4 was preferentially expressed in elongating fibers. Over-expression and down-regulation of GhLTP4 led to longer and shorter fiber cells, respectively. Cers were greatly enriched in GhLTP4-overexpressing lines and decreased dramatically in GhLTP4 down-regulating lines. Moreover, auxin content and transcript levels of indole-3-acetic acid (IAA)-responsive genes were significantly increased in GhLTP4-overexpressing cotton fibers. Exogenous application of Cers promoted fiber elongation, while NPA (N-1-naphthalic acid, a polar auxin transport inhibitor) counteracted the promoting effect, suggesting that IAA functions downstream of Cers in regulating fiber elongation. Furthermore, we identified a basic helix-loop-helix transcription factor, GhbHLH105, that binds to the E-box element in the GhLTP4 promoter region and promotes the expression of GhLTP4. Suppression of GhbHLH105 in cotton reduced the transcripts level of GhLTP4, resulting in smaller cotton bolls and decreased fiber length. These results provide insights into the complex interactions between lipids and auxin-signaling pathways to promote plant cell elongation.

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6. GoSTR, a negative modulator of stem trichome formation in cotton(棉花茎秆表皮毛形成的负调控因子GoSTR)

简介：Trichomes, the outward projection of plant epidermal tissue, provide an effective defense against stress and insect pests. Although numerous genes have been identified to be involved in trichome development, the molecular mechanism for trichome cell fate determination is not well enunciated. Here, we reported GoSTR functions as a master repressor for stem trichome formation, which was isolated by map-based cloning based on a large F-2 segregating population derived from a cross between TM-1 (pubescent stem) and J220 (smooth stem). Sequence alignment revealed a critical G-to-T point mutation in GoSTR's coding region that converted codon 2 from GCA (Alanine) to TCA (Serine). This mutation occurred between the majority of Gossypium hirsutum with pubescent stem (GG-haplotype) and G. barbadense with glabrous stem (TT-haplotype). Silencing of GoSTR in J220 and Hai7124 via virus-induced gene silencing resulted in the pubescent stems but no visible change in leaf trichomes, suggesting stem trichomes and leaf trichomes are genetically distinct. Yeast two-hybrid assay and luciferase complementation imaging assay showed GoSTR interacts with GoHD1 and GoHOX3, two key regulators of trichome development. Comparative transcriptomic analysis further indicated that many transcription factors such as GhMYB109, GhTTG1, and GhMYC1/GhDEL65 which function as positive regulators of trichomes were significantly upregulated in the stem from the GoSTR-silencing plant. Taken together, these results indicate that GoSTR functions as an essential negative modulator of stem trichomes and its transcripts will greatly repress trichome cell differentiation and growth. This study provided valuable insights for plant epidermal hair initiation and differentiation research.
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7. Down-regulation of xylan biosynthetic GhGT47Bs in cotton impedes fibre elongation and secondary wall thickening during fibre transition(棉花木聚糖生物合成GhGT47Bs下调对纤维伸长和次生壁增厚的影响)

简介：Cotton provides abundant natural fibres for the textile industry. Cotton fibre development can be divided into five stages: fibre initiation, elongation, transition, secondary cell wall (SCW) thickening and maturation. Fibre initiation and elongation have been extensively studied, but the transition stage remains less investigated. Although cellulose accounts for >90% of mature fibres, non-cellulosic polysaccharides also contribute to fibre development. Little is known about the roles of these carbohydrates during this process. The hemicellulosic polysaccharide xylan peaked in 17 days postanthesis (dpa) fibres in four cotton species with contrasting fibre characteristics, indicating that xylan may function in the transition stage.GhFSN1 and GhMYB46_D13 positively regulate SCW synthesis in cotton fibres (Huang et al., 2021; Zhang et al., 2018), and overexpression of GhFSN1 or GhMYB46_D13 up-regulated the expression of a set of cell wall-related genes. Two GhGT47B genes (Gh_A13G2031 and Gh_D13G2434, designated as GhGT47B_A13 and GhGT47B_D13, respectively) caught our attention as

they are annotated as homologues of AtFRA8, which is involved in xylan biosynthesis in Arabidopsis (Chen et al., 2020; Zhong et al., 2005). A yeast one-hybrid analysis coupled with transactivation assay confirmed that both GhGT47B genes can be activated by GhFSN1 and GhMYB46_D13 (Figure S1ad). RT-qPCR analysis showed that GhGT47B expression peaked in 15, 18 and 20 dpa cotton fibres, and they represent the most abundantly expressed GhGT47B subclade during fibre transition (Figures S2a and S3). Subcellular localization assays indicated that both GhGT47B proteins were located in the Golgi, where xylan is synthesized (Figure S2b).Next, we silenced both GhGT47B genes in cotton. Fibre phenotype analysis in the T1 and T2 generations revealed that mature fibres of RNAi lines were significantly shorter than those of the wild type (Figure S4). We confirmed these results in two independent RNAi lines of the T3 generation (Figure 1ac). In addition, the cell wall thickness of mature cotton fibres of RNAi lines was significantly thinner than that of wild type (Figure 1d,e). Fibre quality parameters analyses showed that the length, breaking strength, elongation and micronaire value of fibres in RNAi lines significantly decreased (Table S1). Moreover, the degree of twisting of most cotton fibres of GhGT47B RNAi lines was largely reduced (Figure 1f,g), suggesting that the breaking strength in RNAi fibres declined.We next examined xylan abundance in the RNAi lines by immunolabelling. We found weaker fluorescence intensity of 15 dpa and 21 dpa cotton fibre cell walls of RNAi compared with wild type (Figure 1h). Monosaccharide composition analysis validated that the xylose content significantly decreased in RNAi fibres (Figure 1k). Further NMR analysis showed that the xylan structure in wild-type cotton fibre and Arabidopsis stem appeared largely similar. Interestingly, there is a new peak in the spectrum of cotton (highlighted in the blue rectangular box), which is absent in the Arabidopsis xylan (Figure 1i). Nevertheless, the structure of xylan reducing end sequence (RES) in cotton fibre and Arabidopsis stem is different. G1, R1 and X1 are peaks represented by different monosaccharides constituting the RES. R1 and X1 of cotton fibre can hardly be detected, but the G1 peak is more pronounced, while there is little difference in the height of G1, R1 and X1 peaks in Arabidopsis stem (Figure 1i). Through calculation, the relative abundance of RES in the GhGT47B RNAi lines was 21% lower than that of wild type, implicating GhGT47B activity in the synthesis of xylan RES in cotton fibre.To explore whether the decrease of xylan content impacts cellulose synthesis, we used cellulose-specific fluorescent dye pontamine fast scarlet 4B to stain the fibre resin slices. The fluorescence of 15 dpa, 21 dpa and mature cotton fibres of RNAi transgenic lines was obviously fainter than those of wild type (Figure 1j). These results were corroborated by crystalline cellulose measurements (Figure 1l) and indicate that cotton fibres produce less cellulose when GhGT47B is down-regulated.To further investigate genes and pathways affected by GhGT47B, we sequenced the transcriptome of 18 dpa fibre of GhGT47B RNAi cotton and the wild type. Gene Ontology (GO) enrichment analysis showed that several terms involved in cell wall synthesis and modification were enriched, confirming that GhGT47B is associated with cell wall biogenesis and/or organization (Figure S5ad). Further analysis showed that genes related to synthesis of xylan backbone, side chain modification and genes involved in cellulose synthesis are among the differentially expressed genes (Figure S5e,f). It is plausible cell wall change is sensed by a monitoring pathway that then regulates growth to ensure sufficient strength during fibre development. Based on the transcriptome analysis, we summarized the mode in which down-regulation of GhGT47B might affect cell wall components (Figure S6).Fibre development requires many cell wall-related genes. Exploring these genes will provide insights into cell wall modifications, with the aim to ultimately make unique cotton fibres to better suit our needs. Our findings support the involvement of xylan in fibre development and might work as a template to manipulate xylan synthesis to fine-tune cell wall composition for fibre improvement.

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8．Identification of candidate genes for aphid resistance in upland cotton by QTL mapping and expression analysis(陆地棉抗蚜候选基因的QTL定位及表达分析)

简介：Lignin is one of the main components of cell walls and is essential for resistance to insect pests in plants. Cotton plants are damaged by aphid (Aphis gossypii) worldwide but resistant breeding is undeveloped due to scarce knowledge on resistance genes and the mechanism. This study reported a lignin biosynthesis related gene identified in the F2 population derived from the cross between cotton cultivars Xinluzao 61 (resistant to aphid) and Xinluzao 50 (susceptible to aphid). A quantitative trait locus was mapped on chromosome D04 with a logarithm of odds (LOD) score of 5.99 and phenotypic effect of 27%. RNA-seq analysis of candidate intervals showed that the expression level of GH_D04G1418 was higher in the resistant cultivar than in the susceptible cultivar. This locus is close to AtLAC4 in the phylogenetic tree and contains a conserved laccase domain. Hence, it was designated GhLAC4-3. Silencing of GhLAC4-3 in Xinluzao 61 via virus-induced gene silencing (VIGS) resulted in decreased lignin content and increased susceptibility to aphids. These results suggest that GhLAC4-3 might enhance aphid resistance by regulating lignin biosynthesis in cotton.(c) 2023 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. This is an open access article under the CC BY-NC ND license.
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9． The R2R3-MYB transcription factor GaPC controls petal coloration in cotton(R2R3-MYB转录因子GaPC调控棉花花瓣着色)

简介：Although a few cases of genetic epistasis in plants have been reported, the combined analysis of genetically phenotypic segregation and the related molecular mechanism remains rarely studied. Here, we have identified a gene (named GaPC) controlling petal coloration in Gossypium arboreum and following a heritable recessive epistatic genetic model. Petal coloration is controlled by a single dominant gene, GaPC. A loss-of-function mutation of GaPC leads to a recessive gene Gapc that masks the phenotype of other color genes and shows recessive epistatic interactions. Map-based cloning showed that GaPC encodes an R2R3-MYB transcription factor. A 4814-bp long terminal repeat retrotransposon insertion at the second exon led to GaPC loss of function and disabled petal coloration. GaPC controlled petal coloration by regulating the anthocyanin and flavone biosynthesis pathways. Expression of core genes in the phenylpropanoid and anthocyanin pathways was higher in colored than in white petals. Petal color was conferred by flavonoids and anthocyanins, with red and yellow petals rich in anthocyanin and flavonol glycosides, respectively. This study provides new insight on molecular mechanism of recessive epistasis, also has potential breeding value by engineering GaPC to develop colored petals or fibers for multifunctional utilization of cotton.(c) 2023 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. This is an open access article under the CC BY-NC ND license.

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10. Jurassic NLR: Conserved and dynamic evolutionary features of the atypically ancient immune receptor ZAR1(侏罗纪NLR：非典型古免疫受体ZAR1的保守和动态演化特征)

简介： The evolutionary history of HOPZ-ACTIVATED RESISTANCE1 (ZAR1) traces its origin to early flowering plant lineages.Plant nucleotide-binding leucine-rich repeat (NLR) immune receptors generally exhibit hallmarks of rapid evolution, even at the intraspecific level. We used iterative sequence similarity searches coupled with phylogenetic analyses to reconstruct the evolutionary history of HOPZ-ACTIVATED RESISTANCE1 (ZAR1), an atypically conserved NLR that traces its origin to early flowering plant lineages & SIM;220 to 150 million yrs ago (Jurassic period). We discovered 120 ZAR1 orthologs in 88 species, including the monocot Colocasia esculenta, the magnoliid Cinnamomum micranthum, and most eudicots, notably the Ranunculales species Aquilegia coerulea, which is outside the core eudicots. Ortholog sequence analyses revealed highly conserved features of ZAR1, including regions for pathogen effector recognition and cell death activation. We functionally reconstructed the cell death activity of ZAR1 and its partner receptor-like cytoplasmic kinase (RLCK) from distantly related plant species, experimentally validating the hypothesis that ZAR1 evolved to partner with RLCKs early in its evolution. In addition, ZAR1 acquired novel molecular features. In cassava (Manihot esculenta) and cotton (Gossypium spp.), ZAR1 carries a C-terminal thioredoxin-like domain, and in several taxa, ZAR1 duplicated into 2 paralog families, which underwent distinct evolutionary paths. ZAR1 stands out among angiosperm NLR genes for having experienced relatively limited duplication and expansion throughout its deep evolutionary history. Nonetheless, ZAR1 also gave rise to noncanonical NLRs with integrated domains and degenerated molecular features.
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11. Cell cycle-dependent kinase inhibitor GhKRP6, a direct target of GhBES1.4, participates in BR regulation of cell expansion in cotton(细胞周期依赖性激酶抑制剂GhKRP6是GhBES1.4的直接靶点，参与BR对棉花细胞增殖的调控)

简介：The steroidal hormone brassinosteroid (BR) has been shown to positively regulate cell expansion in plants. However, the specific mechanism by which BR controls this process has not been fully understood. In this study, RNA-seq and DAP-seq analysis of GhBES1.4 (a core transcription factor in BR signaling) were used to identify a cotton cell cycle-dependent kinase inhibitor called GhKRP6. The study found that GhKRP6 was significantly induced by the BR hormone and that GhBES1.4 directly promoted the expression of GhKRP6 by binding to the CACGTG motif in its promoter region. GhKRP6-silenced cotton plants had smaller leaves with more cells and reduced cell size. Furthermore, endoreduplication was inhibited, which affected cell expansion and ultimately decreased fiber length and seed size in GhKRP6-silenced plants compared with the control. The KEGG enrichment results of control and

VIGS-GhKRP6 plants revealed differential expression of genes related to cell wall biosynthesis, MAPK, and plant hormone transduction pathways - all of which are related to cell expansion. Additionally, some cyclin-dependent kinase (CDK) genes were upregulated in the plants with silenced GhKRP6. Our study also found that GhKRP6 could interact directly with a cell cycle-dependent kinase called GhCDKG. Taken together, these results suggest that BR signaling influences cell expansion by directly modulating the expression of cell cycle-dependent kinase inhibitor GhKRP6 via GhBES1.4.

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12． A cell wall-localized β-1,3-glucanase promotes fiber cell elongation and secondary cell wall deposition(细胞壁定位β-1,3-葡聚糖酶促进纤维细胞伸长和次生细胞壁沉积)

简介： A cell wall-localized & beta;-1,3-glucanase enhances polysaccharide metabolism and cell wall synthesis to promote fiber cell elongation and thickening.& beta;-1,3-glucanase functions in plant physiological and developmental processes. However, how & beta;-1,3-glucanase participates in cell wall development remains largely unknown. Here, we answered this question by examining the role of GhGLU18, a & beta;-1,3-glucanase, in cotton (Gossypium hirsutum) fibers, in which the content of & beta;-1,3-glucan changes dynamically from 10% of the cell wall mass at the onset of secondary wall deposition to <1% at maturation. GhGLU18 was specifically expressed in cotton fiber with higher expression in late fiber elongation and secondary cell wall (SCW) synthesis stages. GhGLU18 largely localized to the cell wall and was able to hydrolyze & beta;-1,3-glucan in vitro. Overexpression of GhGLU18 promoted polysaccharide accumulation, cell wall reconstruction, and cellulose synthesis, which led to increased fiber length and strength with thicker cell walls and shorter pitch of the fiber helix. However, GhGLU18-suppressed cotton resulted in opposite phenotypes. Additionally, GhGLU18 was directly activated by GhFSN1 (fiber SCW-related NAC1), a NAC transcription factor reported previously as the master regulator in SCW formation during fiber development. Our results demonstrate that cell wall-localized GhGLU18 promotes fiber elongation and SCW thickening by degrading callose and enhancing polysaccharide metabolism and cell wall synthesis.

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