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Abstract

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Mechanisms and applications of the plant wound response

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Abstract

Crop breeding faces two key bottlenecks. Widespread adaptive compensation causes an inherent growth-defense trade-off in plants, making it challenging to simultaneously improve crop yield and stress resistance. Meanwhile, plant regeneration capacity is highly genotype-dependent, which severely restricts the application of genome-editing and transgenic technologies in breeding. Solving these bottlenecks requires major advances in the fundamental mechanisms of plant immunity and organ regeneration. To address these challenges, we use tomato wound response as a model to explore the regulatory mechanisms of plant immune homeostasis and organ regeneration. A critical conceptual innovation from the lab is the division of plant wound responses into two interconnected physiological processes: immunity and regeneration. Through systematic investigations, the lab deciphered a novel mechanism wherein plants employ functionally antagonistic systemin receptors (SYR1 and SYR2) as sensors of wound severity to fine-tune immune homeostasis. Additionally, the lab identified the peptide REF1 (Regeneration Factor 1) as the primary wound signal that triggers tissue repair and organ regeneration. These findings not only provide theoretical foundations and molecular targets for the synergistic improvement of crop yield and resistance, but also offer a convenient and universal technical approach for establishing high-efficiency genetic transformation systems independent of genotype constraints.

Decoding citrus aroma *via* molecular sensory techniques

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Abstract

Fruit quality is determined by primary and secondary metabolites, and sensory characteristics including appearance, aroma, taste and texture are closely related to consumer preference and industrial value. In this study, diverse citrus germplasms such as mandarin, sweet orange, brown orange and Guangchenpi were used as materials. Combining molecular sensory science, multi-omics and functional verification, we systematically identified characteristic aroma compounds and their biosynthetic and regulatory mechanisms. We constructed two-dimensional and three-dimensional aroma wheels of citrus, and clarified that *d*-limonene, γ -terpinene, β -myrcene, dimethyl anthranilate (NMM) are key aroma-active compounds. CreTPS3 was verified as the key gene for γ -terpinene biosynthesis, and a solo-LTR insertion in its promoter significantly affects γ -terpinene accumulation and consumer preference. CreSAMT1 is responsible for NMM biosynthesis, regulated by CreERF35 and CreZAT11. Furthermore, γ -terpinene enhances plant resistance to pests, while excessive content reduces sensory acceptance. This study provides a theoretical basis and genetic resources for citrus flavor improvement, quality breeding and industrial application.

MdARF16/17 Link Auxin Signaling to Ma1-Independent Control of Vacuolar Malate Transport in Apple

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Abstract

Auxin is a central plant hormone, and organic acids are key determinants of fruit acidity and flavor; however, the molecular mechanism connecting auxin signaling to organic acids remains elusive. Here, we report a negative correlation between auxin levels and malate, the predominant organic acid in apple, in progenies of ‘Gala’ × ‘Mato 1’ and across fruit developmental stages, suggesting that auxin reduces malate levels independently of Ma1, the major-effect genotype. Integrated BSA and RNA-seq identified MdARF16 and MdARF17 as auxin-responsive transcription factors that repress malate accumulation. Auxin represses two tonoplast-localized malate transporters MdALMT9L and the functionally distinct MATE protein MdMATEL2, but not Ma1, through the cooperative action of MdARF16 and MdARF17, which directly bind their promoters to inhibit transcription and restrict cytosolic-to-vacuolar malate transport. These findings reveal a Ma1-independent auxin-MdARF16/17 pathway controlling vacuolar malate transport in apple, offering a molecular framework for auxin-responsive improvement of organic acid traits.

New Insights into the Asexual Reproduction Mechanism and Molecular Switch in Woodland Strawberry

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Abstract

The developmental fate of strawberry axillary meristems determines the formation of branch crowns or stolons, directly shaping plant architecture, asexual reproduction and fruit yield. Gibberellin (GA) is the core hormone driving stolon development, while the molecular mechanism controlling axillary meristem fate decision remains largely unclear. In this study, the juvenile-to-adult transition of axillary meristems was characterized by elevated expression of the GA biosynthesis gene GA20ox4 and subsequent stolon initiation. Transcriptome analysis identified the zinc-finger transcription factor ZFP6, which was highly co-expressed with GA20ox4. CRISPR-mediated knockout of ZFP6 eliminated GA20ox4 expression and completely inhibited stolon growth, and this defective phenotype was fully restored by exogenous GA application, confirming ZFP6 as a key upstream activator of GA biosynthesis and stolon formation. Combined genetic analysis of PhyB, GA biosynthesis and signaling mutants revealed that red light and the red-light receptor PhyB positively regulate axillary meristem maturation, a novel developmental stage prior to fate determination. This study clarifies the integration of internal developmental signals and external environmental cues in modulating axillary meristem development. It also reveals a stage-specific regulatory module governing stolon formation, providing new molecular insights for optimizing strawberry vegetative propagation and crop improvement.

Exploration of Rose Pan-genome

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Abstract

Roses are economically important ornamental plants, with widespread applications in the cut flowers, garden and cosmetics industries. The genomic evolution and diversity of the subgenus *Rosa* remain understudied, limiting exploitation of its diversity in breeding. Here we assembled genomes of 23 accessions, comprising 51 haplotypes that capture the subgenus's high genetic diversity. Extensive introgression across accessions from different sections highlights crossbreeding potential. Pangenome analysis revealed 1,801,537 structural variations, providing insights into the genetic basis and key regulators controlling key traits such as continuous flowering, petal number and discoloration. A key finding was the identification of a CCD4 homolog as the main regulator of petal discoloration. Additional subgenomic analysis of the allopolyploid *Rosa gallica* and the triploid *Rosa hybrida* 'La France', two important breeding materials of modern roses, revealed their hybrid origins. Overall, this study advances understanding of rose genomics and provides valuable resources for future breeding and trait improvement.

Section-Wide Potato NLRome Empowers Discovery of Late Blight Disease Resistance Genes

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Abstract

Potato late blight, caused by *Phytophthora infestans* and responsible for the Irish Potato Famine, remains a major threat to global food security. Most late blight resistance (*R*) genes encode nucleotide-binding domain and leucine-rich repeat (NLR) proteins, yet many have been overcome by the rapid evolution of *P. infestans*. Deploying *R* genes through hybrid potato breeding offers an opportunity to counteract *P. infestans* evolution. Here, we construct a section-wide NLRome comprising 39,211 NLR genes from 31 wild and 21 cultivated potato genomes, representing *Solanum* section *Petota*, the tuber-bearing clade. This includes newly sequenced genomes of seven wild species with strong resistance to late blight. Phylogenomic analysis reveals asymmetric evolutionary patterns that may distinguish sensor and helper NLRs. Mining the NLRome results in the cloning of *Rpi-cph1*, whose ortholog was previously identified only in American black nightshade, and *Rpi-cjml*, the first toll/interleukin-1 receptor (TIR) domain-containing NLR against late blight. Our findings show that the non-canonical NLR integrated domains (IDs) have potentially evolved from integrating pathogen effector targets. We unveil the evolutionary trajectory of NLR IDs in *Petota*, leading to the discovery of *Rpi-brkl* with a heavy-metal-associated (HMA) domain. We demonstrate that the immune function of *Rpi-brkl* necessitates HMA-effector interactions, and that incorporating the HMA domain into the potato NLR R1 expands its resistance spectrum, thereby proposing a domain “plug-in” strategy to engineer disease resistance in potatoes. These findings offer a paradigm for *R* gene discovery through comparative and evolutionary genomics as well as a new strategy for *R* gene engineering.

Genetics and epigenetics underlie domestication and divergence of *Lactuca* genus

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Abstract

Lettuce (*Lactuca sativa* L.) is an economically important vegetable crop worldwide and believed to be domesticated from *Lactuca serriola* and subsequently diverged into morphologically distinct vegetable types. However, the role of genetics and epigenetic variation remains largely unknown. Here, we unite a chromosome-scale graph-based super-pangenome of *Lactuca sativa*, comprising 12 representative cultivated, landrace, and wild genomes, with single-base resolution DNA methylomes from 52 diverse accessions to dissect the evolutionary forces shaping lettuce. Assemblies reveal extensive genome size variation (2.1–5.5 Gb) primarily driven by repeat expansion correlated with localized hypomethylation. A comprehensive structural variation landscape identifies a *FLOWERING LOCUS C* (*FLC*) copy number variation that delays flowering in cultivated lineages. Concurrently, epigenomic profiling uncovers a global increase in DNA methylation during domestication, with morphotype-specific methylation divergence regulating leaf and stem development, alongside shared loci enriched for stress adaptation. Mechanistically, domestication-linked methylation shifts remodel chromatin accessibility and 3D looping architecture to modulate both proximal and distal gene expression. By bridging structural genomic rearrangements with high-resolution epigenetic dynamics, this work establishes a unified framework for crop domestication studies. These integrated pangenome-epigenome resources will accelerate trait mapping, functional genomics, and precision breeding for climate-resilient, high-yielding lettuce and related crops.

SIBAS Regulates Tomato Fruit Growth and Quality Formation via ABA Accumulation and Target Gene Activation

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Abstract

Tomato (*Solanum lycopersicum* L.) is one of the most economically valuable vegetable crops worldwide, but its flavor has been on the decline in recent years, which has become a key constraint to the improvement of tomato quality. To create tomato varieties with excellent flavor, more favorable genetic variations are urgently needed; therefore, we constructed a genome-wide CRISPR-Cas9 transcription factor mutant library, obtained approximately 1500 mutant lines, and conducted systematic screening based on fruit shape, color, and Brix value. Among these mutants, the loss-of-function mutant *165* showed significantly reduced fruit size and soluble solid content, and further identification revealed that the causal gene was *SIBAS*. Subcellular localization and transcriptional activity assays confirmed that *SIBAS* is a nuclear-localized transcription factor with transactivation capacity, and KEGG enrichment and molecular assays showed that *SIBAS* directly binds and activates a series of downstream genes regulated by ABA, including those involved in ABA biosynthesis (*SINCE5*), sugar transport and metabolism (*SISUT1*, *SISUT4*, *SISBPASE*), and cell growth (*SIEXPA5*, *SICyclinD2*, *SILBD40*). Specifically, *SIBAS* promotes ABA biosynthesis through *SINCE5*, and the accumulated ABA in specific periods and tissues further reinforces the transcriptional activation of these target genes, forming a feed-forward regulatory loop that effectively promotes fruit expansion and sugar accumulation. Importantly, field trials confirmed that *SIBAS*-edited materials exhibit stably improved fruit size and sugar content without detectable trade-offs in plant growth, photosynthesis, or seed development. Collectively, this study not only provides a new genetic resource for flavor-improved tomato breeding but also clarifies the key role of *SIBAS*-mediated ABA accumulation in specific periods and tissues in regulating tomato fruit growth and sugar accumulation, laying a theoretical foundation for precision molecular breeding of tomato.

Cellular Biological Mechanisms of Postharvest Texture Deterioration in Loquat Fruit and Development of Preservation Technologies

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Abstract

Fruit texture is a core quality index determining fruit sensory evaluation. Loquat is a model material for studying lignification in fleshy fruits. Loquat fruit undergoes postharvest texture deterioration mainly manifested as lignification, which hinders industry development. Fruit texture changes are closely associated with the temporal and microscale spatial dynamics of cell wall components, such as cellulose, lignin and pectin. Addressing postharvest texture deterioration, our team has proposed various cell labeling strategies and imaging techniques and developed cell image analysis algorithms to investigate the distribution and deposition dynamics of cell wall components in the multicellular space of loquat, thereby elucidating cellular biological mechanisms of fruit lignification. Combining stimulated Raman scattering and confocal Raman microspectroscopy, we achieved multi-component synchronous imaging and spatial analysis of loquat flesh from the macroscopic to the single-cell level, and proposed the developmental mechanism of lignified cells. In addition to imaging the pre-formed lignin, the spatiotemporal deposition dynamics of newly synthesized lignin during lignification were studied using the bioorthogonal labeling strategy. Meanwhile, the cellular mechanism by which cell wall pectin participates in postharvest texture deterioration of loquat was clarified. Furthermore, we also engaged in fabricating a series of preservation materials such as composite films, nanoparticle coatings and non-contact hydrogel beads that could continuously release functional factors during fruit storage to delay the postharvest texture deterioration, and explored the cellular mechanisms of fruit lignification from the perspective of inhibition. In summary, a variety of novel microscopic imaging methods and image analysis algorithms were established, the cellular biological mechanisms of postharvest lignification in fruits were systematically clarified, and a series of preservation materials was developed, showing promising prospects for applications in postharvest preservation.

Exploration of Wild Grape Resources and Breeding of Cold-Resistant Varieties

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Abstract

Grapevine is one of the most important fruit crops worldwide. Currently, the widely cultivated grapevines (*Vitis vinifera*) in China exhibit weak cold tolerance, making it necessary to be buried in the soil to overwinter in northern China, which greatly restricts the development of grape industry. China is rich in wild grape germplasm resources, serving as a valuable gene pool for grape breeding and key materials for developing new varieties with high resistance and superior quality. Among these, wild grape germplasm such as *Vitis amurensis* exhibits strong cold hardiness. By assembling the first *V. amurensis* genome, we revealed that its dormant buds possess efficient aerobic respiration, resulting in lower sugar consumption and higher energy utilization efficiency. We also identified *PGK*, a key gene in the sugar metabolism pathway, which may contribute to the strong cold hardiness of *V. amurensis*. Using ATAC-seq and RNA-seq analyses, we identified key cold-responsive transcription factors such as VaERF057, VaPAT1, and VaAQUILO, and elucidated their regulatory mechanisms, while also discovering that the ethylene signaling pathway plays an important role in grapevine cold tolerance. Furthermore, using *V. amurensis* as a parent, we performed crossbreeding for new cold-hardy varieties. The resulting wine grape varieties ‘Beihong’ and ‘Beimei’ exhibit excellent cold hardiness and quality traits, and have been promoted in several grape production regions in China. Wines made from these varieties are well-received by consumers and have won multiple international awards. In the future, the rapid development of more elite grape varieties is expected through marker-assisted selection and gene editing technologies.

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Abstract

Peroxidase (POD), a pivotal enzyme in the plant antioxidant system, exhibits activity dynamics that are directly correlated with salt tolerance in tomato. This study, through micro-hyperspectral imaging technology combined with explainable AI, evaluates the importance of characteristic wavelengths in the Competitive Adaptive Reweighted Sampling-Least Squares Support Vector Machine (CARS-LSSVM), Competitive Adaptive Reweighted Sampling-Multiple Linear Regression (CARS-MLR), and Competitive Adaptive Reweighted Sampling-Convolutional Neural Network (CARS-CNN) models for detecting POD activity changes in tomato subcellular structures (chloroplasts, mitochondria, cytoplasm). Based on this, non-destructive detection of POD activity changes in tomato leaf subcellular structures was achieved. As results of model evaluation, good prediction performances for POD activity were obtained using CARS-LSSVM ($R_C=0.854$, $R_P=0.745$) for chloroplast, using CARS-MLR ($R_C=0.793$, $R_P=0.819$) for mitochondria, and using GARS-CNN ($R_C=0.897$, $R_P=0.794$) for cytoplasm. To clarify the prediction mechanisms of the CARS-LSSVM, CARS-MLR, and CARS-CNN models, this study applied SHapley Additive exPlanations (SHAP) to identify the most critical feature wavelengths contributing to the prediction of tomato POD activity. This provided a reliable physical explanation for the model decisions, confirming their effective integration of spectral and chemical information. Finally, a visualization map of POD activity distribution in subcellular structures was established. The results provide a method for monitoring salt stress levels in tomato plants, while also providing valuable references for high-quality cultivation practices.

Molecular regulatory mechanism of VuWRKY15-VuMYB1 in response to low-temperature synthesis of anthocyanins in *V. uliginosum*

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Abstract

The WRKY gene family plays a crucial role in plant growth, development, and abiotic stress. This study identified 76 members of the *V. uliginosum* WRKY gene family, among which *VuWRKY15*, as a nuclear localization transcription factor, can promote the biosynthesis of anthocyanins in *V. uliginosum* under both normal and low temperature conditions. Research has found that low temperature promotes the activity of *VuWRKY15* and *VuMYB1* promoters. Overexpressed *VuWRKY15* transgenic Arabidopsis showed a significant increase in anthocyanin content. *VuWRKY15* regulates anthocyanin accumulation by binding to the cis-acting element W-box (TTGACC) in the promoter sequences of *VuMYB1* and structural genes ANS, DFR, and UFGT. In addition, *VuWRKY15* interacts with *VuMYB1* to jointly regulate the expression of downstream structural genes and induce the biosynthesis of anthocyanins in *V. uliginosum*. This study elucidated the molecular mechanism of *VuWRKY15* and *VuMYB1* co regulating the biosynthesis of anthocyanins in *V. uliginosum* at low temperatures, identified the important role of *VuWRKY15* in flavonoid biosynthesis, laid the foundation for understanding the functional role of WRKY genes in *V. uliginosum*, and provided new directions for future research on plant metabolism and stress adaptation.

One-step creation of CMS lines using a *BoCENH3*-based haploid induction system in Brassica crop

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Abstract

Heterosis utilization in a large proportion of crops depends on the use of cytoplasmic male sterility (CMS) tools, requiring the development of homozygous fertile lines and CMS lines. Although doubled haploid (DH) technology has been developed for several crops to rapidly generate fertile lines, CMS lines are generally created by multiple rounds of backcrossing, which is time consuming and expensive. Here we describe a method for generating both homozygous fertile and CMS lines through in vivo paternal haploid induction (HI). We generated in-frame deletion and restored frameshift mutants of *BoCENH3* in *Brassica oleracea* using the CRISPR/Cas9 system. The mutants induced paternal haploids by outcrossing. We subsequently generated HI lines with CMS cytoplasm, which enabled the generation of homozygous CMS lines in one step. The *BoCENH3*-based HI system provides a new DH technology to accelerate breeding in Brassica and other crops.

Insights into karyotype evolution and flower color variation from the genome assembly of wallflower (*Erysimum cheiri*)

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Abstract

Wallflower (*Erysimum cheiri*) belongs to the monogeneric Erysimeae tribe of the mustard family (Brassicaceae). It is widely cultivated as an ornamental garden plant and appreciated for its diverse flower colors. However, the absence of a high-quality genome has hampered research on wallflower genome evolution and the mechanisms underlying variations in flower color. Here, we assembled a nearly gap-free telomere-to-telomere genome of *E. cheiri*. The assembled genome enabled the reconstruction of genome evolution in the genus *Erysimum* (274 species), tracing the changes from the ancestral $n = 8$ genome (in *E. cheiranthoides*) to the derived genomes with seven (in *E. nevadense*) and six (in *E. cheiri*) chromosome pairs. While the reduction from $n = 8$ to $n = 7$ was mediated by a nested chromosome fusion accompanied by inversions, the further decrease to $n = 6$ in *E. cheiri* resulted from an end-to-end translocation involving the other two non-homologous chromosomes. Compared with other Brassicaceae species, *E. cheiri* showed a notable expansion of gene families related to secondary metabolite biosynthesis. Its flower color variation was primarily determined by the biosynthesis and accumulation of carotenoids and flavonoids. We mapped the metabolic pathways for carotenoids and flavonoids, identifying the hub genes regulating their biosynthesis. This research lays an important foundation for understanding the chromosomal and genome evolution of the Erysimeae tribe and paves the way for future investigations into genetic studies and breeding applications of *E. cheiri*.

Integrating Multi-Omics and Gene Editing to Dissect Complex Traits and Create Innovative Germplasm in *Brassica napus*

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Abstract

Genomic design breeding aims to rationally combine genes and regulatory elements to achieve optimal agronomic traits. Here, using the improvement of “high leaf glucosinolate (GSL) but low seed GSL” in polyploid rapeseed (*Brassica napus*) as a model, we describe a comprehensive strategy for dissecting complex traits and creating innovative germplasm. Our approach begins with large-scale multi-omics integration. We developed BnaOmics, a pan-genome-based platform that enables joint analysis of genomes, structural variations (SVs), transcriptomes, and epigenomes across diverse rapeseed accessions. Using this, we systematically mapped SVs and their regulatory effects on gene expression, establishing extensive associations between SVs, expression quantitative trait loci (eQTLs), and agronomic traits. Focusing on GSL metabolism, we combined comparative genomics and time-course transcriptomics between high- and low-GSL varieties to identify key structural variations and homoeologous exchanges (HEs) controlling master regulators such as *BnaMYB28* and GSL transporters. Candidate genes with limited natural variation were then functionally validated and optimized via CRISPR/Cas9 gene editing, successfully uncoupling seed and leaf GSL accumulation. To overcome the genetic diversity bottleneck in natural germplasm, we further established an allotriploid-mediated introgression system that efficiently transfers beneficial genomic segments from related species, generating novel allelic combinations and expanding the design space for breeding. Collectively, this study outlines a coherent pipeline from multi-omics discovery to gene editing and diversity creation, providing a practical roadmap for genomic design breeding and the creation of innovative germplasm in polyploid crops.

Activation of a class I *KNOX* gene by transposon insertion is required for leafy head development in mustard

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Abstract

The development of leafy heads is a unique trait in vegetables, yet the mechanism remains unclear. Here, we report a chromosome-scale *de novo* assembly of a leaf heading mustard. By integrating comparative genomics with forward genetics, we identify *BjKNAT6*, a member of *class I KNOTTED-like (KNOXI)* subfamily, as a major regulator of leaf heading trait. We show that a 4,018-bp mutator transposon inserted in the promoter of *BjKNAT6* drives ectopic expression in leaves, and the insertion is exclusively present in heading varieties. Knocking out *BjKNAT6* gene completely abolishes heading phenotypes. *BjKNAT6* directly upregulates the expression of leaf abaxial-adaxial polarity-specifying genes, prominently *BOP* members, and qPCR profiling reveals other dorsiventrality genes are also misexpressed in heading versus nonheading plants. Moreover, transgenic expression of the lettuce heading gene *LsKNI*, another member of the *KNOXI* subfamily, is sufficient to induce heading phenotypes in mustard. Overall, our work suggests that activation of *KNOXI* genes and remodeling of leaf dorsiventrality are the conserved tactics to develop leafy heads across species.

Virulence mechanism and green control of *Pseudomonas syringae*

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Abstract

Pseudomonas syringae represents a major challenge to global agriculture, causing substantial crop losses and economic damage. Centered on the theme of mechanisms, precise detection, and green prevention and control, recent studies have advanced the understanding of pathogenicity in the model plant pathogen *Pseudomonas syringae*. These bacteria utilize sophisticated regulatory systems, including quorum sensing (QS) and the type III secretion system (T3SS), to coordinate host invasion and disease progression. Their regulatory networks are highly complex, and ongoing research has uncovered diverse virulence factors and previously uncharacterized regulatory pathways. In addition, RNA epigenetics has emerged as a critical layer of gene regulation in bacteria. N6-methyladenosine (m6A), a well-known mRNA modification in eukaryotes, has been identified and mapped in bacterial transcriptomes, revealing distinct distribution patterns and suggesting important roles in regulating gene expression, including virulence-associated processes. These mechanistic insights provide a foundation for the development of precise detection strategies based on molecular and epigenetic signatures of infection. Furthermore, targeting key regulatory nodes to modulate virulence gene expression or designing specific inhibitors offers promising avenues for environmentally friendly disease control. Integrating pathogenic mechanisms, advanced diagnostics, and sustainable management strategies will contribute to effective and green control of plant bacterial diseases.

Identification of Brassica germplasm resources resistant to diamondback moth

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Abstract

Brassica oleracea includes many highly nutritious and widely consumed vegetable crops, yet it is severely threatened by the diamondback moth, *Plutella xylostella* (L.), a notorious pest in agriculture. The insect-resistant traits developed by host plants over hundreds of millions of years provide one of the most promising methods for pest control, which is why we have screened germplasm for resistance to *P. xylostella*. Among 50 *B. oleracea* germplasm accessions, we identified a key variety, DM187, that caused 53% mortality in larvae and inhibited the development and reproduction of this moth species. In this study, we collected and cultivated 50 *B. oleracea* germplasm accessions and evaluated their resistance to *P. xylostella*. Among these germplasm resources, larvae feeding on DM187 caused the least leaf damage and exhibited the highest mortality rate. Moreover, DM187 significantly inhibited the larval length, larval weight, pupation rate, pupal weight, and adult egg production of surviving *P. xylostella*. Furthermore, ovarian anatomy showed that DM187 resulted in incomplete ovarian development and a reduced egg count in adult females. Our findings indicate that the *B. oleracea* germplasm DM187 significantly impairs the survival, development, and reproductive capacity of *P. xylostella*. These findings provide a theoretical basis for the identification and utilization of natural insect-resistant resources in vegetables, as well as for research on insect-resistant breeding, and offer a strategy for the effective management of pests in agricultural settings.

Modulation of the Lipase-like Immune Receptors by Mediator Controls Plant Immunity

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Abstract

The phytohormone salicylic acid (SA) is a critical endogenous defense signal and necessary for inducing local and systemic immunity, a broad-spectrum and long-lasting defense. The lipase-like protein, enhanced disease susceptibility1 (EDS1) is the key immune coreceptor for effector-triggered immunity and pathogen resistance. However, the molecular mechanism underlying EDS1-mediated signaling remain elusive. We have identified that EDS1 serves as a transcriptional coactivator, cooperating with the SA receptor NPR1 and cyclin-dependent kinase 8 (CDK8) (Chen *et al.*, 2019; 2021). Here, we show that EDS1 directly interacts with two modules of Mediator complex (MED), including the MED14 module and the dissociable CDK8 kinase module. EDS1 and MED14 synergistically regulate SA accumulation and drive transcriptional reprogramming for immune responses, whereas CDK8 functions largely in an EDS1-dependent manner to regulate plant immunity. We further demonstrated that CDK8-mediated phosphorylation of EDS1 specifically promotes its interaction with the partner Senescence Associated Gene 101 and cooperates with multiple immune-responsive transcription factors to control transcriptional resistance. Our results will show a novel mechanism of EDS1 signaling, in which the phosphorylation and assembly of transcriptional complexes activate transcriptional reprogramming during plant immunity.

A *Phytophthora infestans* RXLR effector subverts host nucleocytoplasmic transport for immune suppression

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Abstract

Potato late blight, caused by the oomycete pathogen *Phytophthora infestans*, poses a significant threat to potato production. Previously, we cloned an immune receptor R04373 from *Solanum americanum*, which specifically recognizes the *P. infestans* effector PITG_04373 but failed to confer effective resistance against *P. infestans*. To investigate how R04373-mediated immunity is compromised, we screened an RXLR effector library of *P. infestans* and identified another RXLR effector S04373, which specifically suppresses the hypersensitive response (HR) triggered by R04373/PITG_04373. S04373 inhibits ETI by targeting key components of host nuclear transport, importin α and β . Notably, S04373 also suppresses the HR mediated by *Rpi-chc1* and *R2*. Nucleocytoplasmic trafficking is a critical bidirectional process for the transport of RNA and proteins between the nucleus and cytoplasm, ensuring normal cellular functions. This study reveals that the nuclear localization of R04373 is essential for its activation. Furthermore, we observed that R04373 forms oligomers upon activation, though whether these multimers localize to the nucleus remains to be explored. These findings demonstrate that nuclear trafficking is indispensable for ETI activation and serves as a key target for pathogen effectors. Understanding the ETS mechanism will contribute to designing the plant immune system and restoring the impaired R genes.

Chemical imaging reveals diverse functions of small molecules in plant root growth and development

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Abstract

Mass spectrometry imaging, with its unique advantages of label free detection, high spatial resolution, and in situ metabolite analysis, offers a powerful tool for investigating the spatiotemporal distribution and functional relevance of small molecules within root tissues. This study employs this technology to characterize the spatial distribution patterns of novel small molecules in the meristematic and maturation zones of plant root tips. By constructing high resolution spatial distribution maps of root small molecules, we uncovered distinctive distribution patterns of tricarboxylic acid cycle (TCAC) metabolites. Integrating genetic, cell biological, molecular biological, and plant physiological approaches, we further deciphered the biological meaning of these spatial features and their underlying molecular mechanisms governing root growth and development. Notably, we identified itaconic acid as an endogenous plant metabolite for the first time. Through multi-omics platforms including transcriptomics, proteomics, and chemical proteomics, we elucidated its function and the underlying mechanism in plants. Together, these findings underscore the value of mass spectrometry imaging as a powerful research tool. When combined with multi-omics strategies, it provides strong technical support for discovering novel small molecules and addressing key biological questions.

***Phytophthora* Disrupts Plant Immunity by Manipulating Nitric Oxide Homeostasis through GSNOR Inhibition**

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Abstract

Phytophthora capsici is a devastating oomycete pathogen that causes severe diseases on diverse horticultural crops, including pepper, tomato, and cucurbits, leading to substantial yield losses worldwide. Nitric oxide (NO) is a key redox signaling molecule that coordinates plant development and immunity via S-nitrosylation-dependent protein modification. Although S-nitrosylation fine-tunes immune responses, it remains unclear whether pathogens hijack this process to suppress plant defense. Here we demonstrate that S-nitrosoglutathione reductase (GSNOR), which degrades S-nitrosoglutathione (GSNO) to maintain NO homeostasis, positively regulates tomato and pepper resistance against *P. capsici*. Active-site mutations abolish the defensive function of GSNOR. Notably, GSNOR is targeted by PcRD18, a virulence RxLR effector of *P. capsici*. PcRD18 elevates cellular NO content and global S-nitrosylation levels by both inhibiting GSNOR enzymatic activity and promoting its autophagy-mediated degradation via enhanced interaction with ATG8c. Structural analysis identifies critical interaction interfaces between PcRD18 and GSNOR; mutations at these sites in PcRD18 disrupt the interaction, thereby abolishing the effector's ability to increase NO levels, suppress the reactive oxygen species burst, and enhance pathogen virulence. Conversely, GSNOR mutations that impair PcRD18 binding generate a variant that confers enhanced resistance to *Phytophthora*. Our findings reveal a pathogen strategy that subverts NO homeostasis by effector-mediated hijacking of GSNOR, and suggest that engineering the host-pathogen interface to disrupt the GSNOR-PcRD18 interaction represents a promising approach for improving disease resistance in horticultural crops.

Intracellular theanine transport in tea plants

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Abstract

Theanine, a unique and major nitrogen storage amino acid in tea plants, is responsible for the tea umami taste and confers numerous health benefits. Despite its importance, the molecular and cellular mechanisms regulating its biosynthesis and accumulation remain poorly understood. In this study, we identified a vacuolar theanine transporter, CsVTT1 (Vacuolar Theanine Transporter 1), through integrative analyses including yeast mutant library screening, along with correlation analysis between gene expression and theanine accumulation, and homologous gene complementation. Our findings revealed that CsVTT1 expression is nitrogen-inducible and strongly correlates with theanine accumulation in tea plant roots under different nitrogen regimes. Functional characterization in both yeast and *Xenopus laevis* oocytes demonstrated that CsVTT1 facilitates theanine cytoplasmic to vacuolar transport. Genetic manipulation experiments showed that CsVTT1 overexpression significantly enhanced theanine accumulation in tea plant roots, whereas its knockdown reduced theanine levels. Notably, CsVTT1 overexpression in rice greatly increased arginine accumulation, the main nitrogen storage amino acid in non-tea plants, suggesting a conserved role for CsVTT1 in nitrogen metabolism and storage, consistent with its newly identified function in mediating theanine storage in the vacuole. Consequently, CsVTT1 emerges as a promising target for genetic strategies aimed at simultaneously enhancing tea quality and nitrogen use efficiency.

Gene flow from the European wild apple and selection shaped the domesticated apple genome

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Abstract

How selection and demography jointly shape perennial crop genomes remains unresolved. Apple domestication involved multiple wild progenitors and widespread post-domestication admixture, offering an ideal system to address this question. By integrating whole-genome sequencing of 218 accessions, transcriptomic data, and a GWAS of flowering time, we reveal that dessert and cider apples form distinct gene pools primarily derived from *M. sieversii*–*M. orientalis*, with contribution from European *M. sylvestris*. Notably, we find no evidence of a domestication bottleneck—consistent with the perennial crops. Selection scans show limited-overlapping targets: dessert apples exhibit hard sweeps at fruit quality, disease resistance, and flowering genes, whereas cider apples show more soft sweeps and balancing selection. Wild-to-crop introgression from *M. sylvestris* is extensive but heterogeneous, ranging from near-fixation tracts in hard-sweep regions to intermediate-frequency segments with soft-sweep signatures, suggesting both targeted and recurrent adaptive introgression. The lead flowering-time association on chromosome 9 maps to an introgressed regulatory region, supporting polygenic control. Cultivated apples also carry a lower deleterious load than their wild relatives. These results provide a comprehensive genomic portrait of perennial tree domestication, clarifying how selection and adaptive introgression shaped the cultivated apple genome, and identify actionable targets for breeding and conservation.

An auxin-induced transcriptional cascade CmBES1–CmSAUR66 orchestrates the ray floret development in *Chrysanthemum morifolium*

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Abstract

Sympetaly (fused petals) is a key morphological innovation that has arisen multiple times during evolution. It occurs via one of two developmental pathways: late sympetaly (from initially separate petal primordia that later fuse) or early sympetaly (directly from a shared ring-like primordium). Nevertheless, the genetic basis of corolla tube formation in early-sympetalous lineages remains largely unknown. In *Chrysanthemum morifolium*, an early-sympetalous species, ray floret corolla tube formation depends specifically on dorsal petal elongation. Through integrated genome-wide association studies and RNA-seq analyses, we identified *CmSAUR66* as a negative regulator of corolla tube fusion. Functional studies showed that *CmSAUR66* knockdown enhances corolla tube fusion by promoting dorsal petal elongation. Mechanistically, *CmSAUR66* acts by modulating the spatiotemporal expression of the dorsoventral asymmetry gene *CmCYC2c*; knocking down *CmCYC2c* in the amiR-*CmSAUR66* background rescues the fusion phenotype. We found that sustained auxin treatment promotes corolla tube fusion while suppressing *CmSAUR66* expression, and knocking down this gene alters auxin sensitivity. Importantly, we found that the auxin-induced transcription factor CmBES1 directly represses *CmSAUR66* expression. Consistent with this, transient overexpression of *CmSAUR66* in OX-*CmBES1* plants significantly rescued the fusion phenotype. Our study thus unveils the CmBES1–CmSAUR66 regulatory module as a central component of auxin-mediated sympetalous development, providing insights into the hormonal control of floral morphological evolution.

Discovery of a noncanonical quasi-circadian gene regulatory network in postharvest strawberry fruits

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Abstract

Strawberries represent a critical model for global horticulture, yet their extreme perishability imposes substantial post-harvest losses and severe fungal decay, creating an urgent need to understand fruit resilience under refrigerated storage. We report that despite the canonical circadian clock gene regulatory network (GRN) being arrhythmic, robust circadian oscillations are maintained in refrigerated postharvest strawberries. Through systematic dual-luciferase assays and network analysis, we identified a noncanonical GRN pillared by five uncharacterized transcription factors (TFs). Subsequent SELEX-seq, EMSA, and DAP-qPCR analyses demonstrated that this GRN was responsible for the circadian rhythms of downstream genes. Fruit-specific perturbation of this GRN led to enhanced susceptibility to *Botrytis cinerea*. These findings demonstrate that autonomous biological timing can emerge from topological plasticity independent of evolutionarily conserved clock genes, providing a conceptual framework to mitigate post-harvest deterioration.

Molecular Mechanism of Tomato Transcription Factors SIDof3 and SIDof8 Regulating Fruit Shelf Life by Modulating Sugar Accumulation and Ethylene Biosynthesis

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Abstract

Fruit shelf life and soluble sugar content are key traits determining tomato commercial value. But high-sugar accumulation is often accompanied by abnormal ethylene overproduction, accelerated ripening and shortened shelf life, a major bottleneck in tomato breeding. Dof transcription factors are involved in sugar metabolism and hormone signal, but their regulatory mechanism in coordinating tomato sugar accumulation, ethylene synthesis and shelf life remains unclear. Using a multi-target CRISPR/Cas9 tomato transcription factor mutant library, we screened the *SIDof3/SIDof8* double mutant 0815-105 with a 40% increase in soluble solid content (Brix) and an earlier ripening phenotype. Ethylene detection at the breaker stage (BR) showed significantly increased ethylene release rate in the double mutant, confirming the association of *SIDof3* and *SIDof8* with ethylene metabolism and shelf life. Integrating transcriptomics (RNA-Seq), metabolomics, and CRISPR/Cas9 techniques, combined with DNA affinity purification sequencing (DAP-seq) results, we clarified the synergistic regulation of *SIDof3* and *SIDof8*, and identified their key downstream target genes, including *SLACO6*, *SLACO*-like and *SIETR5* involved in the ethylene biosynthesis and signal transduction pathway, *SIGLUT8* and *SlpGlcT2* related to the sugar transport pathway, as well as *SICDPK27* and *SIPGL* participating in the sugar metabolism pathway. Meanwhile, it was confirmed that both transcription factors could bind to the CTTTTT motif to regulate the expression of these target genes. In summary, our study establishes a regulatory network linking sugar metabolism and ethylene synthesis. This work provides theoretical support and key molecular targets for the synergistic improvement of high-sugar traits and storage tolerance in tomato, and offers a valuable reference for trait improvement in other horticultural crops.

S-Nitrosylation of GSNOR and LCD integrates nitric oxide and hydrogen sulfide signaling to regulate cadmium-induced programmed cell death in tomato

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Abstract

Cadmium (Cd), a non-essential and toxic heavy metal, severely disrupts plant physiological and biochemical processes by inducing programmed cell death (PCD). Nitric oxide (NO) and hydrogen sulfide (H₂S) are key signaling molecules involved in plant stress responses, but the molecular mechanisms underlying their crosstalk in Cd-induced PCD remain elusive. Here, we demonstrated that Cd-triggered PCD is accompanied by NO bursts and protein S-nitrosylation. Proteomic analysis of S-nitrosylated proteins revealed that differential S-nitrosylation targets in Cd-induced vs. NO-alleviated PCD are enriched in carbohydrate metabolism and amino acid metabolism, with unique targets in cofactor/vitamin metabolism and lipid metabolism. Additionally, S-nitrosylation of proteins involved in porphyrin/chlorophyll metabolism and starch/sucrose metabolism contributes to Cd-induced leaf chlorosis, while *in vivo* S-nitrosylation of SEC23 (protein transport), ubiquitinyl hydrolase 1, and pathogenesis-related protein 1 was confirmed, with their expressions upregulated in Cd-induced PCD but downregulated by NO treatment (consistently observed in tomato seedlings with elevated S-nitrosylation levels). Building on this foundation, further investigation using GSNOR (S-nitrosoglutathione reductase, a key regulator of NO homeostasis) and LCD (L-cysteine desulfhydrase, a core enzyme for H₂S biosynthesis) knockout and overexpressing transgenic tomato demonstrated that both GSNOR and LCD inhibit Cd²⁺-induced PCD. GSNOR and LCD knockout plants exhibited increased Cd sensitivity and enhanced cell death compared to wild-type controls. Mechanistically, S-nitrosylation of GSNOR at Cys47 and LCD at Cys225 altered their subcellular localization, reduced their enzymatic activities, promoted Cd²⁺ uptake, and thereby accelerated PCD. Notably, S-nitrosylation attenuated the interaction between GSNOR and LCD during PCD progression. Collectively, our findings establish that NO modulates Cd-induced PCD via protein S-nitrosylation and GSNOR-LCD interactions constitute a critical regulatory node integrating NO and H₂S signaling in plant responses to Cd stress. These results provide novel insights into the molecular network underlying heavy metal-induced PCD and the regulatory roles of S-nitrosylation in NO-H₂S crosstalk.

Evolutionary analysis of ascorbate-glutathione cycle genes across green plants with lineage-specific profiling in grapevine (*Vitis vinifera* L.)

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Abstract

Ascorbate-glutathione (AsA-GSH) cycle genes are vital for plant processes like stomatal regulation, nutrient uptake, and stress responses. However, the relationships between the origin and expansion of the AsA-GSH cycle genes and the adaptive evolution of land plants are still unclear. To investigate their evolutionary origins and functional differences, we first used phylogenetic and expression analyses of 2424 AsA-GSH genes (1059 *APXs*, 364 *DHARs*, 629 *MDHARs*, and 372 *GRs*) derived from 127 green plants to investigate their evolutionary history and functional divergence in green plants. The results highlighted a strong linkage between plant AsA-GSH cycle genes and their adaptation to environmental stress. In grapevine (*Vitis vinifera*), 16 AsA-GSH genes were identified and analyzed for gene structure, motifs, *cis*-regulatory elements (CREs), and transcription factors (TFs) network. Gene expression profiling demonstrated their involvement in growth, hormonal regulation, and responses to biotic (*Plasmopara viticola* infection) and abiotic (cold, heat, salt, and drought) stresses. Functional validation showed that some of these grapevine genes, such as *VvAPX6/7/8*, *VvDHAR1*, *VvMDHAR2*, and *VvGR2*, are localized in diverse cellular compartments effectively mitigate oxidative stress through ROS scavenging. This study enhances our understanding of the evolutionary dynamics and functional diversification of AsA-GSH cycle genes in green plants, and the stress resilience in grapevine.

FlowerBase: An Integrated Multi-Omics Database for Ornamental Flowering Plants

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Abstract

Ornamental flowering plants are central to the horticultural industry and also provide important systems for studying flower color, scent, flowering time, floral organ development, and specialized metabolism. However, genomic, transcriptomic, metabolomic, phenotypic, variation, and breeding-related data for flowers remain scattered across species-specific studies and general repositories, limiting comparative analysis and trait-oriented discovery. Building on previous experience from HortDB V1.0, a broader genomic database for horticultural plants including fruits, vegetables, ornamentals, medicinal plants, beverages, and spices, FlowerBase focuses specifically on ornamental flowers and provides a more integrated platform for flower omics research. The database brings together high-quality genomes, transcriptome datasets, metabolites, phenotypes, genetic variants, and functional annotations, and incorporates tools such as gene search, BLAST, JBrowse, GO/KEGG enrichment, expression analysis, co-expression networks, SSR mining, primer design, GuideRNA design, and genomic selection breeding modules. These resources enable a continuous workflow from candidate gene identification and functional annotation to expression profiling, regulatory network construction, marker development, genome editing support, and breeding application. FlowerBase can facilitate studies of major ornamental traits such as flowering-time regulation, flower color formation, floral scent metabolism, and floral organ architecture without requiring users to manually assemble fragmented datasets. By integrating multi-layer omics resources with analytical and breeding-oriented tools, FlowerBase provides a focused infrastructure for comparative genomics, functional gene mining, and molecular design breeding in ornamental flowering plants, thereby supporting both fundamental plant science and the improvement of floricultural crops.

A drought-responsive cascade of dual regulatory mechanisms driving wax accumulation in kale

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Abstract

Cuticular wax plays an important role in drought resistance. However, the underlying regulatory mechanisms for wax accumulation remain unclear. Moreover, the regulatory networks of drought-induced wax accumulation remain largely unknown. Here, *BoMYB96* was identified as a candidate gene for wax content variation in kale (*Brassica oleracea* var. *acephala*) through whole-genome quantitative trait locus resequencing analysis. Two *BoMYB96* alleles, *BoMYB96*^{S0836} and *BoMYB96*^{6BZ}, were identified based on SNPs in the coding region. Overexpression and RNAi-mediated gene silencing analyses showed that *BoMYB96* positively regulates wax accumulation and drought tolerance. *BoMYB96* directly promoted the expression of three wax biosynthetic genes, *BoCER3*, *BoKCS1* and *BoKCR1*. *BoMYB96*^{S0836} exhibited higher transcriptional activation of the three genes than *BoMYB96*^{6BZ}. Drought-inducible *BoABF2* activated the expression of *BoMYB96*^{S0836} by directly binding to its promoter, and the positive role of *BoABF2* in wax biosynthesis was validated using CRISPR/Cas9. The E3 ubiquitin ligase *BoMIEL1* interacted with *BoMYB96* and mediated its ubiquitination and degradation. Western blot analysis showed that the protein levels of *BoMYB96*^{S0836} and *BoMIEL1* were significantly increased and decreased under drought, respectively. Overexpression of *BoMIEL1* significantly suppressed wax accumulation. This study reveals the *BoABF2*-*BoMYB96*-*BoMIEL1* regulatory cascade that affects wax accumulation and provides a new genetic resource for kale breeding to improve drought resistance.

Kiwifruit genomics and applications: recent advances, current challenges, and future prospects

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Abstract

Kiwifruit (*Actinidia* spp.) is a globally significant horticultural crop, renowned for its exceptional nutritional value and high vitamin C content. The remarkable genetic features of this genus, including a dioecious sexual system (XY/XX) and a wide range of ploidy (2x–10x), have driven substantial genomic and phenotypic diversification, thereby constituting a valuable germplasm resource for systematic breeding. Recent advances in kiwifruit genomics are transforming the field, yielding foundational insights into the evolution, domestication, breeding, and genetic basis of target agronomic traits. In this review, we highlight the key achievements in kiwifruit genome research over the past decades, chronologically spanning from the initial draft genome assembly to the recent super pan-genome construction. We further synthesize how multi-omics approaches have been leveraged for fine mapping, gene discovery, and the analysis of gene expression and metabolic pathways. Finally, we discuss future research directions and breeding strategies enabled by these genomic breakthroughs, particularly through the applications of genomic selection and gene editing in kiwifruit.

Epigenetic and Regulatory Mechanisms Underlying Purple Leaf Formation in *Prunus mume* ‘Meiren’

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Abstract

Prunus mume ‘Meiren’ is prized for its purple flowers and leaves, yet its leaf color exhibits instability during the growth and development, and the underlying mechanisms remain unclear. This study, we mechanistically integrated epigenetic (methylation and ASM), and genetic (alternative splicing and regulatory mechanism) to dissect the molecular basis of leaf color variation. During the transition of ‘Meiren’ leaves from purple to green, DNA methylation level markedly increases. This CHH methylation level is negatively correlated with the expression of anthocyanin synthase genes, suggesting that environmental factors may regulate leaf color changes by inducing CHH methylation. Furthermore, as an interspecific hybrid, the HM subgenome of ‘Meiren’ exhibits significantly higher CG methylation than the HC subgenome, leading to an inverse relationship between methylation and expression of the alleles of the key gene *PmMYB10.5*, i.e., ASM. This epigenetic imbalance between subgenomes may represent a potential cause underlying the formation of complex traits. Two alternative splicing variants (*PmMYB10.5b1* and *PmMYB10.5bP*) were identified. Transient overexpression in hairy root showed that neither mutant could activate anthocyanin synthase gene nor induce pigment accumulation. Furthermore, luciferase reporter assays revealed that the variants possessed transcriptional repressive activity. Thus, they may act as ‘inhibitory factors’ in anthocyanin regulation by competitively suppressing the function of the native *PmMYB10.5b*. In ‘Meiren’, three *PmGST* genes (*PmMGST17/21/51*) were identified as key regulators of purple leaf formation. Functional validation confirmed they promoted anthocyanin accumulation, and the upstream regulator *PmMYB10.5b* directly bound the promoters of *PmMGST21/51*. It elucidates the downstream regulatory mechanism of *PmMYB10.5*, and provides promising candidate genes for manipulating foliage color in woody plants. Collectively, our findings reveal a multi-layered regulatory network underlying the dynamic leaf color change in *P. mume* ‘Meiren’. It elucidates how the interplay between dynamic DNA methylation, ASM-driven allele-specific expression, the generation of inhibitory transcription factor variants, and MYB-GST module jointly governs leaf color phenotypes, providing novel genetic and epigenetic insights into the ornamental trait plasticity in woody plants.

An efficient fruit-derived callus functional genomics platform for *Siraitia grosvenorii*: Uncovering the SgWRKY50-SgVQ26 regulatory module controlling mogroside V biosynthesis

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Abstract

Mogroside V, the predominant sweet triterpenoid glycoside in *Siraitia grosvenorii*, is a key determinant of fruit quality and commercial value. However, molecular improvement of mogroside V content has been hindered by the limited understanding of its transcriptional regulation and the lack of an efficient functional validation platform in *S. grosvenorii*. Here, we integrated fruit developmental transcriptomes with mogroside accumulation profiles and identified SgWRKY50 as a candidate regulator closely associated with mogroside V biosynthesis. To support gene functional analysis, we established an efficient *Agrobacterium*-mediated transformation system using callus derived from 55-day-after-pollination fruit tissue. Response surface methodology optimized the transformation conditions to OD₆₀₀= 0.6, 150 µM acetosyringone, 20 min infection, and 3 d co-cultivation, achieving a transformation efficiency of approximately 59.6%. SgWRKY50 encoded a nucleus-localized and MeJA-responsive WRKY transcription factor that directly bound W-box elements in the promoters of SgSQE and SgCS, two key genes involved in mogroside biosynthesis, and activated their transcription. Moreover, SgVQ26 physically interacted with SgWRKY50 and enhanced SgWRKY50-mediated transcriptional activation. Functional analyses using transient fruit transformation and stable fruit-derived callus overexpression/VIGS demonstrated that SgWRKY50 positively regulated mogroside biosynthetic gene expression and promoted mogroside V accumulation. Together, this study establishes a fruit-derived callus functional genomics platform for *S. grosvenorii* and reveals an SgWRKY50-SgVQ26 transcriptional module that promotes mogroside V biosynthesis. These findings provide mechanistic insight into sweet triterpenoid accumulation and offer useful molecular targets for improving monk fruit quality through molecular breeding.

Key words: *Siraitia grosvenorii*; mogroside V; SgWRKY50; SgVQ26; WRKY-VQ module; fruit-derived callus; *Agrobacterium*-mediated transformation

***CsWRKY40–CsRAV1* module integrates auxin and brassinosteroid signaling to cooperatively regulate EGCG biosynthesis in tea plants (*Camellia sinensis* L.)**

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Abstract

Epigallocatechin-3-gallate (EGCG) is a key secondary metabolite of tea sensory quality and health care function. Auxin and brassinosteroid are important signaling molecules involved in regulating plant secondary metabolism, but the mechanism by which they cooperatively regulate EGCG biosynthesis in tea plants remains unclear. In this study, tea leaves were treated with exogenous indole-3-acetic acid (IAA) and 24-epibrassinolide (BR), and metabolomic together with transcriptomic analyses were used to elucidate how hormone signaling and transcription factors regulate EGCG biosynthesis in tea plants. Compared with the control, combined IAA and BR treatment increased EGCG content in tea plants by 13.25%, indicating a marked enhancement of EGCG accumulation. Additional analysis suggested that *CsSAUR* and *CsBR1* may be associated with the expression changes of *CsWRKY40* and *CsRAV1* in response to auxin and brassinosteroid signaling. The results of antisense oligonucleotide (AsODN) inhibition and molecular docking suggested that *CsWRKY40* and *CsRAV1* may coordinately regulate the expression of the target gene *CsPAL* in response to auxin and brassinosteroid signals, thereby cooperatively promoting EGCG biosynthesis in tea plants. This study proposes a regulatory framework in which the *CsWRKY40–CsRAV1* module may link auxin and brassinosteroid signaling with EGCG biosynthesis in tea plants, providing a new perspective for further investigation of the regulatory mechanisms underlying fresh leaf quality.

Study on polysaccharide accumulation and transcriptome of *Lycium barbarum* in response to salt stress

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Abstract

The total area of saline-alkali land in China is about 150 million hm². A large area of saline-alkali land has caused adverse effects on crop cultivation and ecological environment. *Lycium barbarum* has become one of the most successful species for biological improvement of saline-alkali land by virtue of its saline-alkali tolerance. As a medicinal and edible plant of Solanaceae, *Lycium barbarum* contains polysaccharides, flavonoids and other nutrients. Among them, *Lycium barbarum* polysaccharide has many effects such as anti-oxidation and anti-aging. In order to explore the accumulation and molecular mechanism of polysaccharides in *Lycium barbarum* fruit under salt stress, the fruit of 'Ningqi 10' was used as the material, and the control group (CK), low salt concentration group (1.72 g / KG, S1) and moderate salt concentration group (3.23 g / KG, S2) were set up. The antioxidant substances, polysaccharides and cell wall degradation enzyme activities of unripe fruit, turning fruit and red fruit were determined, and transcriptome analysis was carried out. The results showed that the total antioxidant capacity of *Lycium barbarum* fruit was relatively stable under salt stress during the development of *Lycium barbarum* fruit. SOD, POD and CAT mainly scavenged reactive oxygen species during the unripe fruit period. Flavonoids, betaine and carotenoids mainly played an antioxidant role during the red fruit period. At the same time, the polysaccharide content also increased significantly during the color change and red fruit period. Transcriptome analysis explained that differentially expressed genes were enriched in pathways related to polysaccharide synthesis and decomposition and stress regulation. Through WGCNA analysis and network mapping, it was found that UXS6Lb11G02056, PGSIP4Lb06G02518 and HMA5Lb04G02780 played an important role in regulating polysaccharide synthesis, which provided a new reference for the mechanism of polysaccharide accumulation under salt stress.

LvMYC2 integrates light, jasmonate, and ethylene signaling to regulate anthocyanin synthesis in 'Viviana' lily tepals

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Abstract

Anthocyanin biosynthesis is regulated by a complex interplay of environmental and hormonal signals. In this study, we identified LvMYC2, a bHLH transcription factor (TF), as a core regulator that integrates light, jasmonic acid (JA), and ethylene (ET) signaling to control anthocyanin accumulation in 'Viviana' lily tepals. We found that JA and ET act synergistically to enhance pigmentation, and that LvMYC2 expression is induced by all three signals. Functional analyses demonstrated that LvMYC2 targets the core TFs of each pathway—LvBBX24 (light), LvERF113 (ET), and LvMYB5 (JA/light)—by directly binding to their promoters to activate their expression. Furthermore, LvMYC2 physically interacts with LvMYB5 to form a complex that strongly activates the transcription of the structural gene LvANS, leading to enhanced anthocyanin production. Additionally, we identified LvPIF3 as an inhibitor that negatively regulates anthocyanin synthesis by repressing LvMYC2 transcription in response to light. Our results reveal a regulatory network in which LvMYC2 serves as a hub coordinating multiple signaling pathways to regulate anthocyanin biosynthesis, providing new insights into the molecular mechanisms underlying anthocyanin synthesis in lilies and offers valuable theoretical foundations for improving horticultural traits such as cut flower quality and postharvest performance.

Exogenous Indole-3-Acetic Acid and trans-Zeatin Riboside Synergistically Induced *CsHD-ZIP35* and *CsMYB125* to Promote Biosynthesis of Epigallocatechin Gallate in Tea Plants (*Camellia sinensis*)

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Abstract

As the most abundant catechin in *Camellia sinensis*, epigallocatechin gallate (EGCG) is closely related to the nutritional quality and health value of tea, and clarifying its biosynthesis regulatory network is crucial for directional improvement of tea quality. However, the regulatory mechanism by which plant hormones regulate EGCG biosynthesis in tea plants remains incompletely understood. This study was intended to explore the regulatory effects of the synergistic interaction between indole-3-acetic acid (IAA) and trans-zeatin riboside (tZR) on EGCG biosynthesis in young tea shoots. The results demonstrated that exogenous IAA-tZR treatment significantly increased the EGCG content in young tea shoots by 12.79% compared to the control. Integrated metabolomic and transcriptomic analyses, together with antisense oligodeoxynucleotide (AsODN)-mediated gene silencing, revealed that the auxin signal factor *CsARF5* and the cytokinin signal factor *CsB-ARR1* act as key synergistic regulators of the two hormone pathways. TFs *CsHD-ZIP35* and *CsMYB125* are the synergistic sites of two hormone signal factors, and *CsSCPL25* is an important downstream structural gene targeted by these transcription factors. Collectively, exogenous IAA-tZR treatment promoted the biosynthesis of EGCG in tea shoots by regulating the expression of *CsSCPL25* through *CsHD-ZIP35* and *CsMYB125*. This study provides new insights into the synergistic regulation of auxin and cytokinin signaling pathways on EGCG biosynthesis in tea plants.

Taurine Accumulation and Transcriptome Analysis in *Lycium barbarum* L. Fruits under Alkaline Stress

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Abstract

To investigate the effects of alkaline stress on osmotic adjustment and taurine metabolism in goji berry fruits, 'Ningqi 10' was treated with CK (pH 8.54), mild (T1, pH 9.48), and severe (T2, pH 10.35) alkaline stress, with three replicates. Samples were collected at young, turning-color, and red fruit stages. Osmotic regulators (proline, soluble protein, glycine betaine) and taurine metabolism indicators (precursors, intermediates, key enzyme activities) were measured. Red fruit samples were subjected to transcriptome sequencing followed by GO, KEGG, and WGCNA analyses to identify key candidate genes for taurine metabolism. Alkaline stress significantly induced the accumulation of proline, soluble protein, soluble sugar, and glycine betaine across the three stages, and activated taurine metabolism, as shown by increased precursors (e.g., cysteine), intermediates (e.g., hypotaurine), and key enzyme activities (e.g., CSAD). Transcriptome analysis identified numerous DEGs in red fruits, which were significantly enriched in pathways related to taurine and hypotaurine metabolism, osmotic adjustment, amino acid metabolism, and stress signal transduction. WGCNA identified modules (e.g., ME_{pink}) correlated with taurine-related traits and screened out candidate genes including *APK3* Lb08G00334, *YUC8* Lb02G02589, *GAD2* Lb09G00587. Alkaline stress induced the accumulation of osmotic regulators and activated taurine metabolism in goji berry fruits. Transcriptome and WGCNA analyses revealed key candidate genes, providing important insights into the molecular mechanisms of alkaline tolerance in goji berry and the potential role of taurine in plant stress resistance.

Genome-wide identification of WRKY transcription factors in *Siraitia grosvenorii* reveals SgWRKY11 as a positive regulator of jasmonate-mediated cold tolerance

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Abstract

Cold stress severely restricts the growth, cultivation range, and product quality of *Siraitia grosvenorii*, yet the molecular mechanism of its cold adaptation remains poorly understood. In this study, we performed a genome-wide identification of the WRKY transcription factor family in *S. grosvenorii* and identified 59 *SgWRKY* genes. Integrated clustering of cold-responsive *WRKY* expression with jasmonic acid (JA) dynamics highlighted *SgWRKY11* as a candidate regulator associated with JA accumulation under cold stress. *SgWRKY11* encoded a typical WRKY transcription factor with transcriptional activation activity and nuclear localization, and its expression as well as promoter activity were induced by both cold and methyl jasmonate (MeJA). Functional analyses showed that overexpression of *SgWRKY11* enhanced cold tolerance in *S. grosvenorii* fruit-derived calli and heterologous *Arabidopsis thaliana*, whereas silencing of *SgWRKY11* reduced cold tolerance in *S. grosvenorii* calli. These phenotypes were accompanied by coordinated changes in JA content, antioxidant enzyme activities, proline accumulation, membrane damage, and expression of JA biosynthetic genes. Mechanistically, yeast one-hybrid, electrophoretic mobility shift assay, and dual-luciferase assays demonstrated that *SgWRKY11* directly binds to and activates the promoters of *SgLOX17*, *SgAOS3*, and *SgOPR3-2*, thereby promoting JA biosynthesis. In addition, *SgWRKY11* physically interacted with *SgVQ23* and enhanced the expression of *SgLOX17*, *SgAOS3*, and *SgOPR3-2*, suggesting the involvement of a WRKY-VQ regulatory module in cold adaptation. Together, these findings identify *SgWRKY11* as a positive regulator of JA-mediated cold tolerance in *S. grosvenorii* and provide candidate molecular targets for the genetic improvement of cold-tolerant *S. grosvenorii* cultivars.

Key words: *Siraitia grosvenorii*; Cold stress; WRKY transcription factor; jasmonic acid; WRKY-VQ interaction

Mechanism of melatonin alleviating chilling injury via regulating ethylene metabolism in Hami melon fruit

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Abstract

Low-temperature storage is an important method to prolong the storage life of Hami melon fruit. However, Xizhoumi 25 Hami melon is a cold-sensitive cultivar, and long-term storage at inappropriate low temperatures easily induces chilling injury and reduces its commercial value. Therefore, it is crucial to explore natural, efficient and eco-friendly chemical preservatives. Previous studies showed that treatment with 100 mmol/L melatonin (MT) could markedly reduce the incidence and index of chilling injury in Hami melon. MT decreased the contents of methionine (Met) and S-adenosylmethionine (SAM), the precursors of ethylene biosynthesis, inhibited the activities of 1-aminocyclopropane-1-carboxylate synthase (ACS) and 1,1-aminocyclopropane-1-carboxylate oxidase (ACO), and lowered 1-aminocyclopropane-1-carboxylate (ACC) content. Further verification revealed that MT down-regulated the expression of *CmACS2*. These results indicate that the imbalance of ethylene metabolism is a major cause of chilling injury in Hami melon. As a key rate-limiting gene in the ethylene biosynthesis pathway, the transcription level of *ACS2* is precisely regulated by upstream transcription factors RAP2-12 and bHLH128. This study elucidates the physiological mechanism of MT in alleviating chilling injury via regulating ethylene metabolism, and provides a novel theoretical basis for enriching postharvest physiology and developing effective strategies to mitigate chilling injury of Hami melon.

Study on Texture Deterioration Mechanism of Ningxia Wolfberry Fruit under Low-temperature Storage with Different Preservatives

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Abstract

Lycium barbarum L., a medicinal and edible fruit tree with high economic value, is characteristic of Northwest China. However, due to vigorous respiratory metabolism and a high moisture content, postharvest goji berries are highly susceptible to deterioration during low-temperature storage, including browning, softening, weight loss, and decay, which severely limit their shelf life and commercial distribution. To explore green and efficient preservation technologies, this study systematically investigated the regulatory effects and molecular mechanisms of 1-MCP, melatonin, and metformin on fruit quality deterioration using 'Ningqi 5' and 'Ningqi 7' as experimental materials stored at 4°C. Physiological parameters, including color, texture, weight loss, decay incidence, as well as the contents of polysaccharides, flavonoids, ascorbic acid, and cell wall components, were measured. Combined with transcriptome sequencing and qRT-PCR validation, the results showed that all three exogenous treatments exhibited significantly better preservation effects than the control group ($P < 0.05$), with distinct treatment-specific advantages. During the early storage period (0–8 d), 1-MCP showed the most significant effect; melatonin demonstrated the best comprehensive performance in maintaining overall fruit storage quality; metformin effectively delayed cell wall degradation and suppressed the increase in related enzyme activities, achieving the highest comprehensive evaluation score by membership function analysis. qRT-PCR further confirmed that the expression levels of key candidate genes (LbACO3, LbPME2.1, LbACS5) and a transcription factor (LbWRKY72) were significantly lower in all treatment groups compared to the control group. This study elucidates the differential preservation advantages and regulatory mechanisms of the three preservatives, providing a theoretical basis for the precise application of green preservation technologies for goji berries during low-temperature storage.

Integrated physiological and transcriptomic analyses revealed a new strategy for wax gourd (*Benincasa hispida*) to cope with nitrogen deficiency and excess

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Abstract

Nitrogen (N) is the major growth-limiting nutrient for wax gourd (*Benincasa hispida*), yet the physiological and molecular bases of its response to N availability remain poorly understood. A field experiment was conducted with three N levels: N deficiency (0 kg N hm⁻², N0), agronomically optimal N (300 kg N hm⁻², N300), and N excess (500 kg N hm⁻², N500). Relative to N300, marketable yield decreased by 54.30% and 11.63% under N0 and N500. The contents of soluble protein, soluble sugar, titratable acid, and vitamin C were also reduced. The enzyme activity, chlorophyll content, photosynthetic N-use efficiency (PNUE), and N accumulation at all growth stages followed the trend N300 > N500 > N0. Under N0 and N500, the fractions of structural N (N_{str}) and proteinaceous storage N (N_{p-store}) increased (17.46–27.88% and 13.61–18.44%). Wax gourd activates corresponding metabolic adaptation mechanisms under different N levels. Under both N deficiency and excess conditions, genes related to nitrogen metabolism, amino acid synthesis, antioxidant systems, and phenylpropanoid biosynthesis are upregulated, enhancing metabolic activity and stress resistance. Particularly under N deficiency, genes associated with photosynthesis, porphyrin metabolism, the Calvin cycle, and abscisic acid (ABA) hormone signaling pathways are also activated, helping maintain energy conversion and carbon assimilation, as well as regulating stomatal movement, thereby improving plant adaptability in low-N environments. Collectively, these results reveal the physiological and molecular mechanisms of wax gourd under N stress, providing important insights for the scientific and efficient application of N fertilizer as well as the improvement of wax gourd yield and quality.

Epigenetic Regulation of Histone Acetylation by *Pichia caribbica* Against Blackhead Disease in Korla Fragrant Pear

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Abstract

Korla fragrant pear is a characteristic fruit in Xinjiang with unique flavor and high nutritional value. However, postharvest rot caused by *Alternaria alternata* leads to a loss rate of over 20%, which severely hinders the sustainable development of the Korla fragrant pear industry in Xinjiang. It is therefore urgent to develop green, efficient and targeted strategies for disease control. Previous studies revealed that *Pichia caribbica* at the concentration of 1×10^8 cell mL⁻¹ could remarkably reduce the lesion diameter of blackhead disease and inhibit disease expansion during the 6-month storage period, showing better efficacy than the concentrations of 1×10^7 cell mL⁻¹ and 1×10^9 cell mL⁻¹. Combined analyses of chromatin immunoprecipitation sequencing (ChIP-seq) for histone acetylation modification and RNA sequencing (RNA-seq) were performed on pear fruits at the peak disease stage (120 days). The results indicated that the enrichment of differential H3K27ac peaks was significantly higher in the *P. caribbica*-treated group than in the control group. Transcription factors *PybZIP* and *Pyzf-HD*, as well as three core defense genes including *PyHHT1*, *PySMXL 7-like* and *PyCORYNE*, were distinctly enriched and highly expressed in treated fruits. The differentially regulated metabolic pathways were mainly associated with phenylalanine metabolism and membrane lipid metabolism, and further verification confirmed that the phenylpropanoid pathway and phosphatidylinositol signaling pathway were markedly up-regulated throughout storage. Additionally, glycan degradation, biosynthesis of cutin, suberin and wax, carotenoid biosynthesis and nitrogen metabolism also play vital roles in the epigenetic regulation of pear resistance against blackhead disease. This study elucidates the biocontrol mechanism of *P. caribbica* against postharvest blackhead disease of Korla fragrant pear from the perspective of epigenetic modification, providing a scientific basis for improving the theory of postharvest fruit immunity and developing targeted epigenetic control technologies for postharvest diseases of Korla fragrant pear.

Molecular mechanism of *PpGST3* response to salicylic acid regulating sand pear (*Pyrus pyrifolia*) fruit senescence

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Abstract

Postharvest fruit quality is governed by hormonal signaling and redox homeostasis, which collectively regulate senescence. Salicylic acid (SA) effectively delays fruit senescence. Glutathione S-transferases (GSTs) are also implicated in senescence regulation, but their functions remain unclear in sand pear. Here, a novel *GST* gene, *PpGST3*, was identified from transcriptomic analysis, which was downregulated by SA during sand pear senescence. *PpGST3* is localized to the cytoplasm, and its overexpression in sand pear fruits and calli accelerated softening, oxidative damage, and cell wall degradation by suppressing antioxidant enzyme activities. In contrast, silencing delayed senescence and reduced oxidative stress. SA treatment further alleviated senescence by maintaining antioxidant capacity and lowering malondialdehyde levels. *PpGST3* physically interacted with the SA-responsive transcription factor *PpTGA2.1-L* to form a functional complex. Promoter analyses revealed that ethylene-responsive factors (ERFs) activated *PpGST3* transcription, while *PpTGA2.1-L* acted as a repressor, indicating SA-ethylene crosstalk. Collectively, these results indicate that *PpGST3* acts as a positive regulator of fruit senescence, whereas SA antagonizes this pathway, thereby delaying post-harvest deterioration and extending fruit shelf life.

Upregulation of Three NAC Genes in Cucumber Grafted on Figleaf Gourd Contributes to Enhanced Resistance Against FOC Infection

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Abstract

Cucumber Fusarium wilt, which is induced by the soil-borne pathogen *Fusarium oxysporum* f. sp. *Cucumerinum* (FOC), represents a highly destructive disease. Cucumber seedling grafted onto figleaf gourd (*Cucurbita ficifolia* Bouché) rootstock (CFC) demonstrated better resistance to FOC. However, the molecular mechanism underlying this enhanced disease resistance capability is largely unknown. To elucidate this, we performed transcriptome, small RNA, and degradome sequencing for leaves from CFC and self-grafted cucumbers (SGC) as controls, with and without FOC infections, respectively. Our results indicated that three NAC genes, all predicted as targets of csa-miR164, were significantly up-regulated in CFC after FOC infection. Co-transformation assay in *Nicotiana benthamiana* confirmed that csa-miR164f directly inhibits NAC2, and transient overexpression of NAC2 in cucumber enhanced resistance to FOC, supporting its positive role in defense. Therefore, our results suggest that three NACs, upregulated in CFC, as an alternative pathway, enhance the reactive oxygen species burst and hypersensitive response, which further elevates the resistance to FOC infection. These results provide new insights into the molecular basis for improved FOC resistance in CFC.

Genome-wide association study in a lettuce core collection from 811 accessions reveals genetic loci for anthocyanin accumulation and cultivar development

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Abstract

Lettuce (*Lactuca sativa*) is a globally cultivated leafy vegetable with leafy morphology critically influencing consumer preference and market value. Despite the agronomic importance of leaf traits, the genetic basis underlying their diversity remains poorly characterized. To address this, we resequenced 811 accessions collected from major lettuce production areas as well as the relative wild species, and developed a publicly accessible core collection of 268 accessions that captures 99.4% of the total genetic variation. Phenotypic evaluation of 16 leaf morphological traits across two growing seasons identified significant correlations, including negative associations between plant width and anthocyanin content, and positive correlations between apical margin incision and multiple traits. Population structure analysis revealed frequent introgression events from looseleaf type into domesticated varieties (butterhead, crisphead, romaine, and stemlettuce), highlighting dynamic gene flow during breeding. Genome-wide association studies (GWAS) pinpointed 13 robust quantitative trait loci (QTLs) and candidate genes regulating leaf morphology, including a validated anthocyanin biosynthesis regulator (ANS). Notably, we pinpointed the causal gene genotypes responsible for leaf anthocyanin coloration. Leveraging these findings, we successfully aggregated favorable alleles through genomic design breeding to develop a novel high-anthocyanin variety binfen5 with desirable leaf morphology. This integrative approach demonstrates the value of core germplasms and genomic tools for accelerating lettuce improvement.

The Bra1K array: an efficient and versatile 1K liquid-phase SNP chip for genetics and breeding in Chinese cabbage

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Abstract

The development of cost-effective and efficient genotyping platforms is essential for advancing genetics and breeding in Chinese cabbage (*Brassica rapa* L. ssp. *pekinensis*). Here, we present the Bra1K array, a liquid-phase SNP chip based on Genotyping by Target Sequencing (GBTS), comprising 1002 expertly selected probes. The array incorporates markers linked to key agronomic traits, including the flowering-related gene *BrFLC1*, clubroot-resistant genes *Crr5* and *CRs*, Turnip mosaic virus resistance gene *retr02*, and orange heading gene *BrCRTISO1*, enabling effective foreground selection. We validated the array's utility through comprehensive applications: Phylogenetic analysis of 173 accessions revealed a clear population structure consistent with morphological diversity, and the construction of two high-density genetic maps (384 and 262 markers, respectively) enabled the precise localization of the *Br-drp1* gene for dark yellow petals on chromosome A09 and the *BrYLL1* gene for yellow leaves on chromosome A06. Furthermore, in a marker-assisted backcrossing program, the Bra1K array facilitated the rapid introgression of the *Crr5* gene into the elite line Y578-2. After only two backcross cycles and one generation of selfing, we obtained homozygous, clubroot-resistant introgression lines with over 97% recovery of the recurrent parent genome. The Bra1K array is a robust, practical, and highly efficient genotyping solution that seamlessly integrates genetic exploration with molecular breeding in *B. rapa*. The Bra1K array, a novel 1K liquid-phase SNP chip developed using Genotyping by Target Sequencing (GBTS), serves as a versatile and efficient platform for genetic research and molecular breeding in *Brassica rapa*.

Extracellular Sensing of the *Colletotrichum fructicola* Elicitor CfCorE1 by Pear PbrPGIP1 Orchestrates a Molecular Booster Effect to Enhance Immunity

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Abstract

Pear anthracnose, caused by *Colletotrichum fructicola*, constitutes a major constraint to global pear production. Elucidating how plant perceives this fungus is critical for effective disease control. Extracellular immunity is considered as a critical frontline against phytopathogens, where plant polygalacturonase-inhibiting proteins (PGIPs) traditionally function by counteracting microbial polygalacturonases (PGs). However, whether PGIPs possess sensory functions for direct pathogen monitoring beyond passive inhibition remains a fundamental question in crop biotechnology. Here, we deciphered a sophisticated immune surveillance mechanism mediated by PbrPGIP1. We identified CfCorE1, a conserved fungal elicitor, as a direct ligand for PbrPGIP1. Mechanistically, PbrPGIP1 orchestrates a dual-functional defense: it not only inhibits fungal polygalacturonases (CfPGs) but also directly perceives CfCorE1 to trigger immunity. CRISPR/Cas9-mediated mutagenesis confirmed that PbrPGIP1 is indispensable for pathogen perception and resistance. Structural analyses revealed that four key residues are critical for this interaction. Remarkably, CfCorE1 binding exerts a synergistic booster effect, allosterically enhancing the inhibitory capacity of PbrPGIP1 against fungal PGs. Beyond pear, exogenous application of CfCorE1 confers broad-spectrum resistance across diverse crops. Our findings redefine the paradigm of apoplastic immunity and offer a high-efficiency molecular strategy for sustainable disease management in horticultural crops.

Regulation of MYB transcription factors in kiwifruit cold stress tolerance

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Abstract

Due to the high sensitivity of kiwifruit to cold stress, a major bottleneck faced by kiwifruit industry is to improve the cold resistance of kiwifruit. MYB transcription factors play an important role in plant cold stress response and tolerance regulation, but the regulation of MYB transcription factors in kiwifruit cold stress tolerance is still unclear. Here, our study revealed that the *AcREL1-AcMYB78-AcCBFs/AcRAP2.1* molecular module regulates the cold stress tolerance of *Actinidia chinensis*. We also elucidated that the *AaSIZ1-AaMYB31s-AaKCSs* module mediates the cold stress tolerance of *Actinidia arguta* through regulating wax synthesis. These studies explored the regulatory role of MYB transcription factors in different pathways of kiwifruit cold stress tolerance, as well as their post-translational regulatory mechanisms.

The CsMYC2.1-CsNOMT Module Drives Sakuranetin-Mediated Anthracnose Resistance in Tea Plants

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Abstract

Anthracnose, caused by *Colletotrichum* species, poses a significant threat to global tea (*Camellia sinensis*) production, yet its inducible resistance mechanisms remain largely uncharacterized. Through integrated transcriptomic and metabolomic analyses of the anthracnose-resistant cultivar ‘Zijuan’ and the susceptible cultivar ‘Longjing43’, we identified sakuranetin as a key phytoalexin in tea plants and elucidated a complete jasmonic acid (JA)-mediated defense pathway. Our functional characterization revealed that CsNOMT (Cha09g008790), a naringenin 7-O-methyltransferase, catalyzes sakuranetin biosynthesis with high substrate specificity. Following infection with *Colletotrichum camelliae*, sakuranetin accumulated exclusively in resistant cultivars, exhibiting superior antifungal activity compared to major tea catechins. Functional validation demonstrated that overexpression of CsNOMT enhanced both sakuranetin accumulation and disease resistance, while gene silencing compromised both traits. Mechanistically, we established that the JA-responsive transcription factor CsMYC2.1 directly activates *CsNOMT* transcription via G-box binding, establishing a novel JA-CsMYC2.1-CsNOMT-sakuranetin defense axis that distinguishes resistant from susceptible tea cultivars. This study represents the first comprehensive characterization of inducible phytoalexin-mediated immunity in tea, providing immediate applications for sustainable tea production. CsNOMT serves as a valuable functional marker for resistance breeding, while sakuranetin emerges as a promising natural biopesticide to reduce reliance on synthetic fungicides.

Climate change affects the suitability of Chinese cherry (*Prunus pseudocerasus* Lindl.) in China

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Abstract

The rapid development of *Prunus pseudocerasus* related industry has increasingly contributed to rural vitalization in China. This study employed a biomod2 ensemble model, utilizing environmental and species occurrence data from 151 *P. pseudocerasus* germplasm wild/local samples, to predict potential geographical distribution, suitability changes, climate dependence, and ecological niche dynamics. The optimized maximum entropy (MaxEnt) model yielded the most accurate predictions. The climate variables with the greatest impact on suitability were precipitation of warmest quarter and mean diurnal temperature range. The total potential suitable area for *P. pseudocerasus* was approximately 2.78×10^6 km², increasing with CO₂ concentration. The highly suitable area was primarily concentrated in basin terrains, plateaus, and plains of Sichuan Province. The current centroid in Lichuan exhibited gradual latitudinal and longitudinal movement. The predicted (2090s) ecological niche trends of *P. pseudocerasus* varied under different pathways and periods, with higher CO₂ concentration associated with lower niche overlap. The CO₂ emission concentration in the SSP246 scenario emerged as the most suitable climate model. Climate change is driving both the expansion of geographical distribution and the contraction of overlapping geographical distribution areas of *P. pseudocerasus*. These findings provide a theoretical basis for wild resource conservation, site selection for production, and introduction of allopatry for *P. pseudocerasus*.

Fe³⁺-Mediated Blue Pigment Formation via Collaborative Regulation of Iron Homeostasis by Multigenes: A New Strategy to Blue Flower Breeding

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Abstract

Blue flowers are the dream of ornamental plant breeders. Many important flowers cannot display a blue color because of the lack of delphinidin glycosides. Currently, blue flowers have been developed by using transgenic technologies to reconstruct the delphinidin biosynthesis pathway. Obviously, this strategy is time-consuming and laborious, and has not achieved significant results in some plants. The bright blue coloration of cornflower (*Centaurea cyanus*) is attributed to a supramolecular pigment formed via metal ion chelation with accumulated cyanidin (Cy) and co-pigments. Elucidating this mechanism will facilitate the molecular breeding of cyanidin-based blue flowers. In vitro blue pigment reconstruction experiments identified that Fe³⁺ is the primary metal ion enabling the blue transformation of Cy. Genomic analysis identified eleven *VIT/VTLs* and four *CcFers* genes in cornflower genome. Expression profiling revealed an inverse expression relationship between *CcVIT1a* and *CcFers* across various tissues. *CcVIT1a* is specifically and highly expressed in blue-colored ray florets. Subcellular localization and yeast mutant complementation assay showed that *CcVIT1a* is located on the tonoplast, whereas the *CcFers* resided in plastids. Virus-induced gene silencing of *CcVIT1a* caused a color shift from blue to violet. The expression of *CcFer1a* was significantly upregulated, while the other three *CcFers* were downregulated. These results indicate that *CcVIT1a* and *CcFers* collaboratively regulate intracellular iron homeostasis. Transient overexpression of *CcVIT1a* in the chrysanthemum CB (Cy-determined blue) sample ‘Dante purple’ induced a color transition from red-purple to violet, accompanied by the downregulation of both *CmVIT* and *CmFer1*. The transient overexpression of both *CmZIP4b* and *CcVIT1a* in chrysanthemum ‘Wandaifengguang’ induced petal cells to turn blue. This study elucidates the cooperative roles of *VIT1*, *Fer*, and iron ion-related genes in regulating intracellular iron partitioning. Collectively, our findings provide novel molecular insights and a potential strategy for breeding blue flowers through the manipulation of anthocyanin and iron metabolism.

Post-phenomics: Toward Autonomous Agricultural Systems

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Abstract

The past decades have witnessed the emergence of plant phenomics as a powerful discipline dedicated to the large-scale study of phenotypes in relation to genetic and environmental variables. By employing high-throughput imaging and sensor technologies, phenomics has enabled precise, non-destructive, continuous, and real-time measurement of growth, development, and stress responses at scale. However, the exponential growth of phenomic data, coupled with the need to understand complex plant systems as networks, necessitates a transition to post-phenomics. The post-phenomics paradigm, often enhanced by AI-driven analytics, seeks to unravel the dynamic, systems-level interactions that underlie plant behavior, paving the way for smart crop development and precision cultivation in the face of climate change. Here, we introduce an integrated knowledge base architecture tailored for the post-phenomics era. It features modularity and scalability, semantic integration, AI-driven insight generation, digital twins and feedback loops, and open, collaborative framework. We demonstrate its utility through a case study involving systems biology–level dissection of water relation traits in legumes.

Application of *Oryza sativa* secretory small protein 1 (OsSSP1) in controlling tomato gray mold disease

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Abstract

Gray mold disease caused by *Botrytis cinerea* severely restricts the development of the tomato industry in China. Previous studies in our laboratory demonstrated that the rice secretory protein OsSSP1 (*Oryza sativa* secretory small protein 1) enhances rice resistance against rice blast. However, the functional research of OsSSP1 in tomato remains unexplored. In this study, plate antifungal assays confirmed that OsSSP1 exerted no direct inhibitory effect on *B. cinerea*. Nevertheless, exogenous application of OsSSP1 significantly reduced the lesion area, disease index and biomass of *B. cinerea* in tomato leaves, promoted reactive oxygen species (ROS) burst, and thereby improved tomato resistance to gray mold. OsSSP1 activated plant immunity by triggering the jasmonic acid (JA) signaling pathway. At 24 h after OsSSP1 treatment, the expression levels of key genes involved in JA biosynthesis (*SILOX1*, *SLAOC*) and critical signal transduction factors (*SICO1*, *SLMYC2*) were markedly upregulated. Compared with the untreated control, application of the JA inhibitor suppressed the expression of JA pathway-related genes and increased leaf lesion area. After OsSSP1 complementation, the transcript levels of JA signaling genes and the lesion area were restored to levels comparable to the untreated group. In conclusion, OsSSP1 possesses promising application potential for the green prevention and control of tomato gray mold, providing a theoretical foundation for the establishment of environment-friendly disease management system.

Genomic integration of tomato chlorosis virus with less virulent tobacco rattle virus facilitates the direct infection on tomato

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Abstract

Tomato chlorosis virus (ToCV) threatens tomato production resulting in a huge loss of yield. An efficient inoculation system of ToCV can accelerate the isolation and utilization of tomato resistant genetic resources. However, no infectious clones of ToCV can directly infect tomato plants. In this study, we cloned the full-length ToCV genome including RNA1 and RNA2 molecules, and integrated their corresponding DNA fragments into less virulent tobacco rattle virus-based pTRV2GW vector, respectively. Agrobacterium suspensions carrying pTRV1, pTRV2GW-RNA1 and pTRV2GW-RNA2 plasmids were mixed equally as the ToCV infectious clones and introduced into tomato cotyledons via the needleless syringe. RT-PCR analysis detects the existence of RNA1 ORF3 and RNA2 ORF10 after the infection, and ToCV capsid protein can also be detected by western blot. Transmission electron microscopy reveals the viral aggregates of ToCV in infected leaves. Plants with the successful infection display typical disease symptoms including stunted growth, yellow leaves, increased anthocyanin accumulation on the abaxial side, reduced photosynthetic and antioxidant capacities, decreased fruit size and impaired fruit maturation. The ToCV infectious clones are applied in susceptible tomato cultivars and resistant wild species, and susceptible cultivars but not resistant species show typical disease symptoms. Western blot detects fewer viral accumulations in resistant species than susceptible cultivars. Taken together, integration of ToCV genome with less virulent TRV enables the direct infection of tomato by ToCV, which not only accelerates the resistant tomato breeding against ToCV infection, but also creates a feasible strategy to establish highly efficient viral infectious clones in other systems.

Melatonin: A key regulator in plant tolerance to organic and inorganic pollutants

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Abstract

Environmental contamination with organic and inorganic pollutants poses a serious threat to horticultural crop production and food safety. Heavy metals such as cadmium (Cd), chromium (Cr), and iron (Fe), along with organic pollutants like bisphenol A (BPA) and pesticide residues, disrupt plant metabolism, impair growth, and compromise yield quality. Melatonin, a multifunctional signaling molecule, has emerged as a potent regulator of plant defense against such toxic pollutants. Recent studies have revealed that melatonin enhances phytochelatin synthesis, regulates nutrient and sulfur metabolism, and inhibits the translocation of pollutants, thereby mitigating heavy metal toxicity. Its role in upregulating anthocyanin biosynthesis and antioxidant enzymes further contributes to chromium and iron stress tolerance, respectively. In the context of organic pollutants, melatonin modulates xenobiotic metabolism through glutathione-dependent detoxification pathways, thereby reducing pollutant uptake and residue accumulation in edible tissues. It also activates *RESPIRATORY BURST HOMOLOG (RBOH)*-mediated reactive oxygen species signaling, which primes downstream detoxification responses, thereby reducing pesticide residues. Notably, melatonin biosynthesis is upregulated under stress, including pollutant exposure, and transcription factors such as HsfA1a have been shown to enhance melatonin production, conferring resilience to Cd stress in tomato plants. Exogenous melatonin application improves photosynthetic efficiency, plant growth, and overall plant productivity under pollutant stress. This synthesis underlines melatonin's integrative role in alleviating phytotoxicity induced by both organic and inorganic pollutants and highlights its potential as a sustainable tool for enhancing crop tolerance and food safety in polluted environments.

New insights into the evolution and local adaptation of the genus *Castanea* in east Asia

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Abstract

Chestnut plants (*Castanea*) are important nut fruit trees worldwide. However, little is known regarding the genetic relationship and evolutionary history of different species within the genus. How modern chestnut plants have developed local adaptation to various climates remains a mystery. The genomic data showed that *C. henryi* first diverged in the Oligocene ~31.56 million years ago, followed by *C. mollissima*, and the divergence between *C. seguinii* and *C. crenata* occurred in the mid-Miocene. Over the last 5 million years, the population of chestnut plants has continued to decline. A combination of selective sweep and environmental association studies was applied to investigate the genomic basis of chestnut adaptation to different climates. Twenty-two candidate genes were associated with temperature and precipitation. We also revealed the molecular mechanism by which *CmTOEI* interacts with *CmZFP8* and *CmGIS3* to promote the formation of non-glandular trichomes for adaptation to low temperature and high altitudes. We found a significant expansion of *CER1* genes in Chinese chestnut (*C. mollissima*) and verified the *CmERF48* regulation of *CmCER1.6* adaptation to drought environments. These results shed light on the East Asian chestnut plants as a monophyletic group that had completed interspecific differentiation in the Miocene, and provided candidate genes for future studies on adaptation to climate change in nut trees.

Identification of *Malus sieversii* ABA receptor PYL8 interacting proteome using Y2H-seq

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Abstract

The seed dormancy of *Malus sieversii* belongs to the comprehensive type of dormancy, abscisic acid (ABA) is one of the important hormones to lift the seed dormancy. The ABA receptor pyrabactin resistance-like (PYL) protein is involved in seed germination and various stress responses. Fourteen *MsPYL* genes were evaluated in the genome of *Malus sieversii*. Phylogenetic analyses demonstrated that *MsPYL* proteins can be divided into three groups. The promoter regions of *MsPYL* genes contain cis-acting elements associated with expression induction by abiotic stresses such as abscisic acid, drought, and low temperature. *Arabidopsis* transgenic lines overexpressing *MsPYL8* exhibited a markedly reduced germination rate, an extended growth period, and a reduction in the biomass of the aboveground parts compared to the wild type. Additionally, we found that *MsPYL8* interacted with 30 proteins, including low-temperature-induced 65 kDa protein-like (LTI) and late embryogenesis abundant (LEA). The results demonstrated that *PYL8* binds to ABA during seed germination, inhibits the dephosphorylation activity of protein phosphatases type 2C (PP2C), and activates the transmission of sucrose non-fermenting-1- related protein kinases 2s (SnRK2s) to abscisic acid insensitive 5 (ABI5) signaling, thereby activating the expression of ABA-responsive genes to regulate ABA signal transduction. The screening and validation of *PYL8* interaction with LTI, and LTI interaction with ABI5, provides a foundation for further elucidation of the mechanism of *PYL* gene involvement in *Malus sieversii* seed dormancy lifting under the regulation of the ABA signaling pathway.

CsMLP19 Promotes *Candidatus Liberibacter asiaticus* Proliferation in Citrus

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Abstract

Huanglongbing (HLB), a destructive disease caused by the phloem-restricted bacterium *Candidatus Liberibacter asiaticus* (CLas), seriously threatens global citrus production. Major latex proteins (MLPs) are plant-specific ligand-binding proteins that regulate plant growth, development, and biotic stress resistance. Here, we systematically characterized the citrus MLP gene family and explored the function of CsMLP19 in CLas infection. In total, 24 CsMLP members were identified from the sweet orange (*Citrus sinensis*) genome, all encoding proteins with a conserved Gly-rich loop motif and molecular weights of 14.08–22.76 kDa. *CsMLP19* was significantly upregulated in CLas-infected leaves of both Jincheng (*C. sinensis*) and Ziyang Xiangcheng (*C. junos*), with the highest expression in roots. Its expression was markedly suppressed by salicylic acid, methyl jasmonate, and abscisic acid. Subcellular localization assays localized CsMLP19 to the nucleus and cytoplasm. *Rhizobium rhizogenes*-mediated transformation generated *CsMLP19*-overexpressing and silenced *C. junos* hairy roots. *CsMLP19* overexpression doubled CLas titers, while gene silencing reduced pathogen abundance to 20.03% of control levels. Y2H and BiFC assays verified the specific physical interaction between CsMLP19 and transcription factor CsWRKY41, with both proteins co-localized in the nucleus and cytoplasm. This study demonstrates that CsMLP19 functions as a negative regulator of citrus HLB resistance, providing novel insights into the molecular mechanism underlying citrus-CLas interaction.

***Plasmopara viticola* effector PvRxLR24 interferes grapevine stomatal immunity by targeting VvOST1(a central regulator for ABA signaling)**

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Abstract

Numerous pathogens invade plants through stomata, and plants, on the other hands, could close the stomata after sensing the pathogens PAMPs. Subsequently, pathogens could overcome this plant immune response with their phytotoxins and effectors. A previous study showed that *Plasmopara viticola*, a strictly obligate biotrophic oomycete, could inhibit the *Vitis vinifera* stomatal closure to promote infection. However, the underlying mechanism stimulating the stomata movement is still poorly understood. Here we found that an effector from *P. viticola*, PvRxLR24, could directly inhibit the kinase activity of OPEN STOMATA 1 (OST1) which is a central regulator for ABA signaling and stomatal closure, and subsequently abolish the activation of slow-type anion channel SLAC1, leading to the “stomatal lock” open. Our study demonstrates that OST1 is the direct target of pathogen effectors, and shed light a new mechanism by which pathogens could manipulate the plant ABA signaling pathways to influence stomatal movement for successful invasion.

Discovery and characterization of a novel small peptide in the grapevines

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Abstract:

The significant immune divergence observed among different plants can be attributed to the independent evolution of core signaling modules. As plant-secreted small peptides, SERINE-RICH ENDOGENOUS PEPTIDES (SCOOPs) regulate plant immunity and help plants defend against the pathogens. Previous studies have shown that PROSCOOPs are exclusive to the plant order Brassicales, and MALE DISCOVERER 1-INTERACTING RECEPTOR-LIKE KINASE 2 (MIK2) is a Brassicales-specific, conserved SCOOPs receptor. Here, we discovered the presence of SCOOPs-MIK2 pairs in various grapevines, and found that grapevine SCOOPs could activate both the grapevine and Arabidopsis immune responses. Moreover, the grapevine SCOOPs-triggered Arabidopsis immune responses were abolished in the *Arabidopsis* MIK2 mutant (*Atmik2-1*), and the AtMIK2 homologues in grapevines could also recognize SCOOPs. Collectively, our findings demonstrate that the SCOOPs-MIK2 pair is not confined to the plant order Brassicales, underscoring the diverse evolutionary patterns of SCOOPs-MIK2 pairs in both grapevine and Brassicales. These insights have significant implications for the development of broad-spectrum, peptide-based disease resistance strategies.

Postharvest Treatments of Potential 2,4-D Surrogates Improve Storage Performance and Flavor Quality in ‘Eureka’ Lemon Fruits

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Abstract

An issue of common concern in lemon production is finding a safe and efficient alternative to 2,4-dichlorophenoxyacetic acid (2,4-D). In this study, ‘Eureka’ lemon fruits were treated with three concentrations (1, 2 and 3) of fluroxypyr-meptyl (FME), a combination of fluroxypyr-meptyl and fluroxypyr (FLFM), 2,4-dichlorophenoxypropionic acid (2,4-DP), and 2-methyl-4-chlorophenoxyacetic acid (MCPA). Water and 2,4-D served as controls. We measured the storage performance indicators of fruit, such as weight loss rate and decay rate, and shelf-life quality parameters, such as juice yield, flavor compounds and pesticide residues. During storage, weight loss was significantly higher in water than under all other treatments. Weight loss rates under FME2 and 2,4-DP3 were significantly lower than under 2,4-D. Decay rates in FLFM1, 2,4-DP2, and the FME series were significantly lower than in 2,4-D and water, whereas those in 2,4-DP1 and the MCPA series were significantly higher than in 2,4-D at 200 days after treatment. Regarding shelf-life performance, juice yield in water (65.14%) and 2,4-D (68.26%) was significantly lower than under most other treatments. The highest juice yield was observed in FME2 (77.84%). Treatments 2,4-DP1, 2,4-DP2, and FME2 were superior to 2,4-D and water in maintaining total soluble solids, titratable acid, and vitamin C contents, while other treatments showed no negative effects on internal quality. Fruits under MCPA2, 2,4-DP3, 2,4-DP2, and FME2 maintained better flavor compound profiles than those in water. Notably, MCPA2 resulted in significantly higher levels of terpenes and aldehydes; FME2 effectively maintained linalool, and α -terpineol; and 2,4-DP3 performed well in maintaining D-limonene, sesquiterpenes, and alcohols compared with other treatments. All treated fruits complied with GB 2763-2026 and meet the EU standard limits for citrus. Overall, FME2 treatment resulted in the best storage performance and quality, followed by 2,4-DP3, indicating that these treatments may serve as effective postharvest alternatives for lemon preservation.

Evidence of Regulating Effect of Nitrogen Level on Ultramicrostructure and Mapping Elements of Tomato (*Lycopersicon esculentum* Mill.) Anther cell under Heat Stress

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Abstract

Write your abstract here. The abstract should be one paragraph of 300 words or less using 12pt Times New Roman font without figures or tables.

Studying the effects of different nitrogen supply levels on the ultrastructural characteristics of tomato anther cells under high temperature stress during the flowering and fruiting stages is of great significance. This study conducted an artificial control experiment on the effects of different nitrogen supply levels on tomato anther development under high temperature stress and normal temperature treatment. TEM combined with EDX analysis technology was used to characterize the ultrastructure and constituent elements of tomato anther cells, and systematically investigate the effects and regulatory mechanisms of nitrogen on tomato flowering and anther development under high temperature stress. The research results indicate that high temperature stress causes developmental abnormalities such as swelling or abnormal degradation of tomato anther tapetum cells, abnormal pollen grains, and a sudden decrease in the number of normal pollen grains, leading to pollen abortion. Appropriate nitrogen levels can regulate the changes in the ultrastructure and elemental distribution of anther cells under high temperature stress. Low nitrogen SHTN2 (1.3 g/plant) treatment can alleviate the adverse effects of high temperature stress on various structural parameters of anthers and promote pollen grain formation. Curvature K can be used as an indicator of the effect of nitrogen levels on the production of sporogenous cells in anthers, and both low nitrogen and high nitrogen treatments inhibit the production of sporogenous cells; The X-ray energy spectrum analysis of the elements in the callus like secretion of tomato anthers showed that under high temperature stress, the content of N, P, and Cl elements in the degradation secretion of callus decreased with the increase of nitrogen application rate. The nitrogen level did not participate in regulating the nitrogen metabolism behavior of the tapetum cells.

Source-sink coordination of carbohydrate, hormonal, and redox dynamics drives dormancy release in grapevine with divergent chilling requirements

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Abstract

Budbreak timing in grapevine is determined by chilling accumulation, yet the physiological mechanisms underlying cultivar-specific variation remain poorly understood. In this study, 44 grape cultivars were classified into three groups with contrasting chilling requirements (low-, medium-, and high-CR) based on budbreak dynamics across six chilling gradients (0-1000 h). Carbohydrate metabolism, phytohormone dynamics, and redox signaling were profiled in cane and bud tissues of seven representative cultivars, and their relationships with budbreak rates were examined using correlation analysis and principal component analysis (PCA). HCR cultivars exhibited significantly higher initial starch content in buds (11.3 mg/g) and a pronounced transient ABA surge (~4.5-fold at 400 h). In contrast, LCR cultivars showed earlier starch-to-sugar conversion and rapid ABA decline in canes, and a more rapid GA/ABA ratio elevation in buds. The normalized GA/ABA ratio in HCR buds increased from 0.3 to 2.2 only at 800-1000 h, coinciding with their late budbreak onset. MCR and HCR buds displayed synchronized H₂O₂ and CAT peaks at 600 h and 800 h, respectively, temporally consistent with their chilling fulfillment, while LCR buds maintained comparatively stable redox dynamics. Correlation and PCA analyses further confirmed that carbohydrate composition is the primary physiological axis differentiating CR groups in canes, while hormonal balance drives bud differentiation. Collectively, these findings support a unified source-to-sink model in which chilling-induced sugar mobilization and stress signal decline in canes coordinate hormonal reprogramming and redox activation in buds to determine cultivar-specific dormancy release timing, offering a physiological framework for predicting grapevine phenology and guiding climate-resilient cultivar selection.

Construction of the first high-density genetic linkage map and the identification of QTLs and key candidate genes associated with fruit size for Chinese cherry [*Cerasus pseudocerasus* (Lindl.) G.Don]

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Abstract

Fruit size is a crucial fruit quality trait for Chinese cherry [*Cerasus pseudocerasus* (Lindl.) G.Don]. Herein, we constructed the first single nucleotide polymorphism (SNP)-based high-density genetic linkage map for Chinese cherry by applying specific locus amplified fragment sequencing to 200 progenies selected from an F1 segregating population derived from two Chinese cherry landraces. Fruit size-related quantitative trait loci (QTLs) and QTLs co-located by multiple traits (multi-trait QTL clusters, muQTLs) were identified based on phenotypic data for two years. We discovered key candidate genes within muQTLs through transcriptomic analyses of fruits from crucial developmental stages, SNP detection and RT-qPCR validation. Integrated linkage map was constructed using SNPs, comprising eight linkage groups with a total length of cM and a resolution of 0.41 cM. A total of 107 QTLs were identified for five fruit size-related traits and subsequently merged into 49 non-redundant QTLs. Twelve non-redundant loci were consistently detected across two years, including nine high-confidence loci with logarithm of odds (LOD) scores of 3.01–4.72 and phenotypic variation explained (PVE) of 6.69%–10.30%. Furthermore, ten muQTLs were co-located by three or four traits. Within muQTLs, 23 fruit size-related candidate genes identified by transcriptomic analysis were predominantly enriched in phytohormone-related biosynthesis, metabolism and signal transduction (e.g., *IAA*), cell expansion and proliferation (e.g., *RLF*), and cell wall metabolism (e.g., *NAC*), among which seven candidates were further validated to exert putative crucial functions in governing fruit size via RT-qPCR. This study provides helpful support for genetic improvement by molecular breeding in Chinese cherry.

Mechanisms of Grape Berry Softening: From Cell Wall Integrity to Pectin Demethylation

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Abstract

Fruit softening directly impacts storage life, transportability, and consumer acceptance. However, the mechanisms by which grape berry softening remain unclear. Here, we investigated the regulatory roles of auxin on berry cell wall degradation and pectin modification during grape softening. During berry development, both fruit firmness and auxin content peaked at 4–6 weeks after full blooming and then decreased. Exogenous NAA treatment inhibited softening by delaying pectin, cellulose, and hemicellulose degradation, thereby maintaining cell wall integrity. WGCNA identified VvLBD13, which interacts with VvARF19, as a key gene in auxin-mediated softening delay. Overexpression of VvLBD13 accelerated hemicellulose degradation by activating VvXTH10 and VvEXPLA1, leading to rapid softening after veraison. Pectin play very important roles during grape berry softening. Therefore, we revealed further that pectin methylesterase (PME) activity increased during the rapid softening phase of the extra-soft flesh variety, accelerating pectin demethylation. VvPME19 was highly expressed and positively correlated with PME activity. Notably, VvPMEI8 was identified as a specific inhibitor that interacts with VvPME19 both in vivo and in vitro. Overexpression of VvPMEI8 blocked pectin demethylation and reversed the rapid softening induced by VvPME19. Our findings demonstrate that auxin signaling, through the VvLBD13-mediated pathway, and the fine-tuning of the VvPMEI8-VvPME19 module coordinately regulate grape berry softening by maintaining cell wall integrity and controlling pectin demethylation. This study provides novel insights into the regulatory mechanisms underlying fruit softening.

Disruption of Chlorophyll Metabolism and Photosynthetic Efficiency in Winter Jujube (*Ziziphus jujuba*) Induced by *Apolygus lucorum* Infestation

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Abstract

Apolygus lucorum, a cosmopolitan Hemiptera insect, poses a significant threat to *Ziziphus jujuba* (jujube), causing symptoms such as mottled chlorosis. However, the mechanisms through which *A. lucorum* affects chlorophyll biosynthesis and degradation remain unclear. This study investigates the effects of *A. lucorum* infestation on chlorophyll metabolism and photosynthetic performance in winter jujube leaves. Results revealed a substantial reduction in chlorophyll *a* and *b* content, which was strongly correlated with decreases in key photosynthetic parameters, such as the Photochemical Performance Index (PI_{ABS}) and electron transport efficiency ($\psi(E_0)$). Infestation downregulated genes critical for chlorophyll biosynthesis, such as *HEMA*, *HEMB*, and *chlG*, leading to a bottleneck in chlorophyll production. Concurrently, chlorophyll degradation pathways were upregulated, with genes like *PAO* and *RCCR* driving increased chlorophyll catabolism. This imbalance between reduced synthesis and accelerated degradation exacerbated chlorophyll loss, impairing photosynthetic capacity. Furthermore, the application of exogenous H₂O₂ intensified chlorophyll degradation, particularly in *A. lucorum*-infested leaves. The accelerated degradation of chlorophyll, coupled with reduced light-harvesting efficiency, contributed to oxidative stress and further impaired the photosynthetic machinery, despite an increase in antioxidant enzyme activity. These findings underline the critical role of chlorophyll metabolism in maintaining photosynthetic efficiency in winter jujube under *A. lucorum* infestation. It underscores the need for targeted strategies to protect chlorophyll synthesis and limit its degradation in order to mitigate the detrimental effects of *A. lucorum*-induced stress.

Enhanced Soft Rot Resistance in Chicory via 5' uORF Editing Mediated Sesquiterpene Accumulation

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Abstract

Chicory (*Cichorium intybus* L.) is a globally recognized medicinal and edible vegetable with pharmacological, economic and ecological value, yet its industrial cultivation is constrained by soft rot disease, which causes irreversible plant mortality and renders postharvest forced bud balls completely unmarketable. Comparative multi-omics analyses of our disease-resistant germplasm and susceptible commercial varieties revealed that differential genes are enriched in apoplastic regions, terpenoid biosynthesis and other pathways. Sesquiterpene lactones are characteristic bitter compounds with anti-inflammatory, hepatoprotective, and uric acid-lowering activities that emerged as pivotal defense-associated metabolites. To precisely harness this metabolic pathway without altering protein-coding sequences, we identified multiple upstream open reading frames (uORFs) in the 5'UTR of the terpenoid-related gene *CiGASh* and demonstrated that site mutation of these uORFs effectively modulates downstream translational efficiency while preserving native gene function. We further established stable tissue culture and agrobacterium-mediated genetic transformation systems for chicory, successfully obtaining *CiGASh*-overexpression seedlings with significantly enhanced resistance to *Botrytis cinerea*. Employing the cut–dip–budding delivery system and precision editing systems in chicory to functionally validate these regulatory elements. Additionally, sucrose density gradient ultracentrifugation coupled with transmission electron microscopy revealed intracellular vesicles enriched with bioactive sesquiterpenes lactones, suggesting a novel vesicle-mediated transport and storage mechanism for functional terpenoids. This integrated strategy, bridging uORF-mediated translational control with multi-omics-guided target selection, provides a robust theoretical and technical framework for improving soft rot resistance and nutritional quality in chicory, while offering novel insights into vesicle trafficking of plant specialized metabolites for sustainable agriculture, functional food development, and industrial applications.

Sucrose transporter PpsSWEET10 promotes sugar accumulation in Chinese cherry fruits

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Abstract

Sugar accumulation directly determines key fruit quality. Therefore, elucidating its patterns and underlying molecular mechanisms is crucial for genetic improvement and molecular breeding of fruit quality. Rosaceae fruit crops, characterized by diverse fruit types and flavors, provide excellent models for such research. Recently, significant progress has been made in characterizing sugar profile (composition and content) and sugar accumulation patterns of mature Rosaceae fruits. Nevertheless, existing research on sugar accumulation mechanism in Rosaceae fruit crops has predominantly focused on sorbitol, fructose and glucose, with relatively less attention given to sucrose. So far, these efforts have remained beyond full elucidation of the mechanisms underlying such diverse sugar accumulation patterns across Rosaceae fruit crops. Here, a comprehensive investigation was conducted on sugar profiles and dynamics in fruits of Chinese cherry (*Prunus pseudocerasus* Lindl.) across genotypes representing broad sugar variation in fruit, which revealed a fructose- and glucose-dominated accumulation pattern with comparatively minor sucrose. Comparative transcriptomics identified 79 sugar accumulation-related differentially expressed genes. Of these, *PpsSWEET10* showed the most pronounced differential expression within and between high- and low-sugar accessions and was discovered as the key regulator by co-expression network analysis, correlation studies, and RT-qPCR validation. Further functional analyses confirmed its essential role as a plasma membrane-localized sucrose-specific transporter that promotes sugar accumulation by specifically transporting sucrose from fruit apoplast into cytosol. Integrating these findings, a model of sugar accumulation dependent on sucrose transporter PpsSWEET10 has been first established, shedding light on the sugar accumulation mechanism in fruit crops.

Chinese cherry CpCDKB2;2 negatively regulates fruit size by modulating cell division

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Abstract

Fruit size is a key agronomic trait in horticultural crops, determined primarily by cell division and cell expansion during early developmental stages. Chinese cherry [*Cerasus pseudocerasus* (Lindl.) G.Don] generally produces small fruits, which severely limits its commercial value. Cyclin-dependent kinases (CDKs) are central regulators of the cell cycle; however, the functions of specific CDK members in fruit development remain largely unexplored in Rosaceae species. In this study, we investigated the B2-type CDK gene *CpCDKB2;2* and its regulatory role in fruit size in Chinese cherry. Expression profiling revealed that *CpCDKB2;2* is highly expressed during the early rapid growth phase of fruit development, and its transcript level is negatively correlated with final fruit size. Functional validation demonstrated that transient overexpression of *CpCDKB2;2* in Chinese cherry fruits significantly inhibited fruit enlargement and cell division, whereas virus-induced gene silencing (VIGS) promoted fruit expansion. Stable heterologous overexpression of *CpCDKB2;2* in tomato similarly resulted in smaller fruits and reduced cell proliferation, confirming that this function is conserved across species. Hormone metabolomics analysis showed that *CpCDKB2;2* overexpression decreased the levels of growth-promoting hormones (e.g., cytokinins and auxin) while increasing the level of jasmonic acid. Molecular interaction assays further revealed that the *CpCDKB2;2* protein specifically interacts with the D-type cyclins *CpCYCD2* and *CpCYCD3;2*. Collectively, our findings elucidate that *CpCDKB2;2* acts as a conserved negative regulator of fruit size by forming CDK–CYCD complexes and modulating hormonal homeostasis to suppress cell division. These results provide new molecular targets and a theoretical basis for the genetic improvement of fruit size in Chinese cherry.

Integrated multi-omics analysis dissects fruit quality traits and establishes a robust genomic selection platform in Chinese cherry (*Prunus pseudocerasus* Lindl.)

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Abstract

Chinese cherry (*Prunus pseudocerasus* Lindl.) is a valuable tetraploid fruit crop, yet its genetic improvement is hindered by a long juvenile phase and limited genomic breeding resources. Here, we developed an integrated genomics strategy to dissect fruit quality variation and enable genomic selection in Chinese cherry. Whole-genome resequencing of 399 F₁ individuals, combined with GWAS, transcriptome profiling and variant-effect annotation, uncovered a metabolism-associated cell expansion mechanism contributing to fruit enlargement. 44,384 high-confidence biallelic SNPs were used for GWAS and GS model evaluation. This analysis prioritized inositol oxygenase 2 (PpseMIOX2), PpseNAC75 and trehalose-6-phosphate phosphatase J (PpseTPPJ) as candidate regulators. Functional validation through transient overexpression, RNAi suppression and histological analysis further demonstrated that PpseMIOX2 promotes fruit enlargement by enhancing pericarp and mesocarp cell expansion. We further established a genomic prediction framework for fruit quality traits by comparing 13 statistical and machine-learning models. In this tetraploid breeding population, linear models, particularly BayesA and ridge regression, outperformed multilayer perceptron and convolutional neural network models. Prediction accuracy saturated when approximately 5,000 informative SNPs were used. We designed PpseCapture6K, a 6,279-SNP liquid-phase capture panel that achieved over 98% concordance with whole-genome resequencing. This work reveals a candidate molecular route for fruit enlargement and provides the first practical genomic selection toolkit to accelerate Chinese cherry breeding.

Multi-locus genome-wide association study reveals key genes regulating sugar accumulation in carrot (*Daucus carota* L.)

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Abstract

Carrot (*Daucus carota* L.) taproots are rich in soluble sugars, and the accumulation directly determines flavor and commercial value. However, the genetic mechanisms underlying sugar accumulation remain largely unknown. In this study, 162 carrot germplasm were subjected to whole-genome resequencing and widely targeted metabolome profiling. Subsequently, sucrose content was used as the phenotypic trait, and genome-wide significant SNPs were employed for mGWAS, leading to the identification of three candidate genes (*DcSDT1*, *DcSDT2*, and *DcSDT3*) significantly associated with sucrose accumulation. Quantitative real-time PCR (qRT-PCR) analysis revealed that *DcSDT3* was significantly upregulated in high-sugar samples, approximately 2-fold higher than in low-sugar samples, whereas *DcSDT1* and *DcSDT2* showed no significant changes. Subcellular localization indicated that *DcSDT1* was localized to the plasma membrane and nucleus, while *DcSDT2* and *DcSDT3* were localized to the plasma membrane, suggesting their potential roles in sugar accumulation through sucrose transmembrane transport or signal transduction. This study provides insights into the molecular mechanisms of sugar accumulation in carrot and offers potential targets for marker-assisted selection of high-sugar carrot varieties.

SRF2-INP2-INP1 executor complex controls pollen aperture formation

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Abstract

Pollen apertures are specialized sites on the pollen surface that receive little to no exine deposition, forming distinct structures important for pollen function. Aperture number, shape, and positions vary widely across species, resulting in diverse, species-specific patterns that make apertures fascinating from both cell-biological and evolutionary perspectives. Apertures have become a useful model for studying how cells develop distinct plasma membrane (PM) domains. During pollen development, regions of the PM where apertures will form recruit specific factors and become protected from exine deposition. However, the molecular mechanisms underlying this process and the identities of the associated aperture factors remain poorly understood. Previous studies identified two *Arabidopsis* proteins, INAPERTURATE POLLEN 1 (INP1) and the non-paralogous INP2, as essential for aperture formation and showed that they form a species-specific protein complex proposed to localize to the extracellular surface of the aperture PM domains. In this study, we identified STRUBBELIG RECEPTOR FAMILY 2 (SRF2), a receptor-like pseudokinase that spans the PM, as another factor required for aperture formation in *Arabidopsis*. SRF2 shares key features with INP1 and INP2, including mutant phenotype, expression pattern, localization to aperture PM domains, genetic interactions, and evolutionary trends. We present evidence that the extracellular domain of SRF2 interacts with INP2, and that the three proteins form a complex essential for executing the aperture formation program.

Identifying *CpSPL2a* as a Potential Regulator of Fruit Size in Chinese cherry by Genome-wide Identification of the *SPL* Gene Family and Functional Assays on Developing Fruits

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Abstract

Fruit size is one of the most important fruit quality traits for Chinese cherry [*Cerasus pseudocerasus* (Lindl.) G.Don]. Recent increasing studies have demonstrated the important roles of SQUAMOSA promoter binding protein-like (*SPL*) transcription factors in regulating key fruit traits, including size, yet the systematic identification of *SPL* genes and their potential functions in fruit size remain limited in Chinese cherry. In this study, we comprehensively identified and characterized the genome-wide *SPL* family genes in Chinese cherry genome (*CpSPLs*), and based on transcriptomic data generated from the fruits collected at five crucial developmental stages of large-fruited landrace ‘HF’ and small-fruited landrace ‘PJHH’, fruit size-related candidate genes were selected to validate their expression patterns by RT-qPCR in ‘HF’, ‘PJHH’, and their six F1 individuals across the five key developmental stages. Meantime, the key *CpSPL* gene was screened out to carry out functional verification via transient transformation assays in both ‘HF’ and ‘PJHH’ fruits. A total of 21 *CpSPL* members were identified and divided into eight phylogenetic clades, with 15 genes clustered into four clades that harbored previously reported fruit/seed size-related *SPL* homologs. Furthermore, transcriptomic data revealed diverse expression patterns among *CpSPL* genes. Integrating phylogeny and expression patterns of *CpSPL* genes, nine candidates were subject to RT-qPCR analyses, which pinpointed *CpSPL2a* as the key candidate related to fruit size. Finally, transient overexpression and virus-Induced gene silencing (VIGS) assays collectively revealed that *CpSPL2a* positively modulated cherry fruit size, with the *CpSPL2a*-overexpressed fruits showing increases of 12.79%-20.70%, 1.98%-7.96%, 5.60%-8.89% and 6.05%-6.09% in fruit weight, fruit longitudinal diameter, fruit transverse diameter, and fruit lateral diameter, respectively, and *CpSPL2a*-silenced fruits exhibiting decreases of 6.00%-21.93%, 1.63-6.29%, 3.32%-5.85% and 0.23%-5.95% in these traits. Our study provides new gene materials and molecular evidence for genetic improvement in cherry fruit size.

Auxin Response Factor CpARF4 Participates in Fruit Abscission by Negatively Regulating Cell Wall Degradation-Related Genes in the Pedicel Abscission Zones of Chinese Cherry

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Abstract

With the frequent occurrence of adverse weather in recent years, massive fruit abscission during fruit development has become an increasingly prominent industrial challenge for Chinese cherry [*Cerasus pseudocerasus* (Lindl.) G.Don]. Accordingly, it is of great importance to investigate the molecular regulatory network underlying fruit abscission. Previous studies have revealed that fruit abscission is closely associated with decreased auxin levels in the pedicel abscission zone, and identified the candidate auxin response factor CpARF4 involved in regulating fruit abscission. However, its specific regulatory mode remains unclear. This study aims to elucidate the molecular mechanism by which the CpARF4 transcription factor mediates auxin signaling to regulate fruit abscission in Chinese cherry. Exogenous auxin treatment effectively alleviated fruit abscission. Through qRT-PCR analysis, CpARF4 was confirmed as a core negative regulator of this process; its transient silencing significantly accelerated cell wall degradation and fruit abscission, whereas its overexpression produced the opposite effect. Heterologous transformation in tomato further confirmed the conserved function of CpARF4 in inhibiting organ abscission. By integrating transcriptome sequencing and promoter cis-element analysis, four cell wall degradation-related target genes, namely *CpPME2*, *CpPME7*, *CpEXLB1b* and *CpXTH23*, were screened out. Both in vivo and in vitro assays demonstrated that CpARF4 directly binds to and represses the promoters of these genes, thereby suppressing cell wall breakdown in abscission zones. In summary, this study elucidates the key molecular mechanism by which CpARF4, as an auxin response factor, negatively regulates fruit abscission in Chinese cherry through directly modulating cell wall degradation, providing theoretical support and important gene resources for mitigating fruit abscission during fruit development in Chinese cherry.

Targeted Phytohormone Metabolomics Profiling Provides Insights Into the Regulatory Mechanisms Underlying Fruit Size Formation and Massive Fruit Abscission in Growing Chinese Cherry Fruits

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Abstract

Chinese cherry [*Cerasus pseudocerasus* (Lindl.) G.Don], native to China, is an economically important fruit crop characterized small fruits with an average single fruit weight of 2–4 g. Previous studies have shown that the extent of massive fruit abscission during fruit development varies drastically across different germplasms, and those with higher average single fruit weights tend to suffer from more severe fruit abscission in growing. Nevertheless, the endogenous phytohormone-mediated regulatory mechanisms governing fruit size formation and excessive fruit abscission during the fruit growth remain poorly understood. To elucidate dynamic metabolic patterns of phytohormones in three fruits tissues and further shed light on the hormone regulatory networks underlying fruit size formation and severe fruit abscission in growing, we selected three Chinese cherry genotypes with divergent fruit size and abscission characteristics in this study, and conducted large-scale targeted phytohormone metabolomics focusing on auxin and its derivatives. A total of 86 hormone metabolites were identified across the embryo, flesh, and pedicel in five developmental stages of Chinese cherry fruits, in which ten auxin metabolites were ubiquitously expressed in all tissues across all developmental stages of three Chinese cherry genotypes. In the embryo as the source-side supply tissue, auxin metabolism exhibited a dynamic developmental pattern characterized by biosynthesis, storage and conjugation-mediated inactivation, and was significantly associated with multiple hormone modules. During the stages of pre-fruit core hardening and fruit core hardening, auxin precursor input and IAA biosynthesis represented important metabolic nodes in the flesh that contributed to fruit size formation, accompanied by the response of SA–JA–GA–CK related modules. In the pedicel, genotypes with different abscission rates showed distinct metabolic partitioning: the high-abscission genotype displayed a high-oxidation and low-active-auxin metabolic state, whereas the low-abscission genotype did not exhibit a strong oxidative pathway. This study reveals the endogenous hormone metabolic mechanisms underlying fruit size formation and abscission during the dynamic development of Chinese cherry, and provides targeted clues for subsequent candidate gene mining and functional module identification.

Auxin biosynthetic key gene *CpYUC10B* in embryo involved in large-fruited Chinese cherry mass abscission during the core-hardening process

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Abstract

Chinese cherry [*Cerasus pseudocerasus* (Lindl.) G.Don] is an economically important Rosaceae fruit crop in China. Massive fruit abscission during core-hardening process in majority of large-fruited Chinese cherry landraces leads to a catastrophic yield loss, hindering the development of Chinese cherry industry. Herein, we conducted systematic physiological analyses and comprehensively characterized the dynamic changes of auxin-centered phytohormones during fruit development for four Chinese cherry individuals showing different degrees of fruit abscission. These analyses, along with exogenous IAA rescue, confirmed the endogenous hormone imbalance resulting from the reduction of IAA contents in embryo as the primary trigger for young fruit abscission. Transcriptomic analyses showed divergent expression patterns of IAA synthesis- and transported-related genes at two crucial fruit developmental stages within and among embryo, pedicel, and flesh. Weighted gene co-expression network analysis prioritized rate-limiting *YUCCA* flavin monooxygenase encoding gene *CpYUC10B*. Transient overexpression of *CpYUC10B* increased IAA contents and transmembrane transport protein *CpPIN1* expression in embryo, pedicel, and flesh, and suppressed cell wall hydrolases in pedicel, consequently reducing fruit abscission. In contrast, VIGS-mediated silencing produced opposite effects. Our results will provide a valuable theoretical foundation and practical reference for enhancing yield stability and offer new gene for breeding large-fruited Chinese cherries by genetic improvement.

Auxin biosynthetic key gene *CpYUC10B* in embryo involved in large-fruited Chinese cherry mass abscission during the core-hardening process

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Abstract

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Gap-less, haplotype-resolved genome assemblies of two *Hippophae rhamnoides* subspecies and integrative analysis of their oil biosynthesis mechanism

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Abstract

Seabuckthorn (*Hippophae rhamnoides*) is a perennial woody oil crop and horticultural species from the Elaeagnaceae family with high nutritional and economic importance. However, the presence of numerous gaps and unplaced contig sequences poses significant challenges, potentially impacting downstream data analysis and functional research. We assembled gap-less, haplotype-resolved genomes of two representative seabuckthorn subspecies *H. r.* subsp. *mongolica* which is characterized by large fruits, high yield, high oil content, and sparse thorns; and *H. r.* subsp. *sinensis*, which exhibits strong stress resistance, rapid growth, and high Vc content. The haplotype resolved assemblies for *H. r.* subsp. *mongolica* and *H. r.* subsp. *sinensis* were 2.33 Gb and 2.09 Gb, respectively, with contig N50 values of 97 Mb and 81 Mb. Structure variations analysis showed that non-syntenic or unaligned regions accounted for 28.3% to 48.4% of each query genome, highlighting substantial haplotype-specific variation, interspecies divergence, and the expansion of repetitive or structurally complex genomic regions. Furthermore, we present a chromosome-level genome assembly of 'Gaoyou No.1' with a final size of 1.27 Gb and a scaffold N50 size of 99.72 Mb. 14 298 SVs were characterized in 'Gaoyou No.1' compared with reference genome. Through whole-transcriptome analysis, 49 and 55 enzymatic genes involved in the fatty acid and triacylglycerol biosynthesis pathways were identified, respectively. Among these, 21 genes harbored SVs. Further, 90 lncRNA-mRNA pairs, 88 miRNA-mRNA pairs, and 42 lncRNA-miRNA-mRNA regulatory modules were predicted. We propose that these SVs and regulatory modules play important roles in enhancing sea buckthorn seed oil yield and quality, offering potential targets for genetic improvement. In summary, these resources not only provide a high resolution view of genome architecture and gene content, but also offer mechanistic insights into the species-specific accumulation of seed oil. Together, they form a foundational platform for evolutionary studies and targeted breeding in seabuckthorn.

Integrated circRNA–miRNA–mRNA Network Reveals Key Regulators of Oil and Bioactive Compound Biosynthesis in Sea Buckthorn

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Abstract

Sea buckthorn (*Hippophae rhamnoides* L.) is an important woody oil crop valued for its fruits and seeds, which are rich in oil as well as diverse bioactive compounds with high nutritional and medicinal value. The accumulation of oil and other bioactive compounds differs markedly among tissues and developmental stages, suggesting the involvement of complex regulatory mechanisms. Although miRNA-mediated regulation of oil biosynthesis has been reported in sea buckthorn, the integrated circRNA–miRNA–mRNA regulatory network underlying the biosynthesis of oil and other bioactive compounds remains largely unexplored. Using previously generated transcriptome, small RNA, and circRNA sequencing datasets from pulp and seed tissues of the high-oil sea buckthorn cultivar ‘Rgao’ at four developmental stages, we performed an integrated analysis of circRNA, miRNA, and mRNA expression profiles and constructed a comprehensive circRNA–miRNA–mRNA competing endogenous RNA (ceRNA) regulatory network. Seven regulatory modules comprising nine circRNAs, eight miRNAs, and nine target mRNAs were identified. These target genes were involved in lipid biosynthesis (LPCAT and LPAT), fatty acid biosynthesis (KAS II, FAD2/6, and FAD3/7/8), sterol biosynthesis (CAS1 and SMT1), and vitamin C and vitamin E biosynthesis (GME1 and HPT1). Notably, circ_0006478 and circ_0007072 converged on the regulation of GME1 through miR319a and miR159b-3p, respectively. Moreover, miR275 simultaneously targeted LPAT and KAS II while being regulated by circ_0014910 and circ_0011383, suggesting coordinated regulation of fatty acid and lipid biosynthesis. These findings provide the first comprehensive circRNA–miRNA–mRNA regulatory network associated with lipid and bioactive compound biosynthesis in sea buckthorn and offer valuable candidate regulators for elucidating the molecular mechanisms underlying fruit quality formation and molecular breeding.

CvNLP2 responds to nitrate and induces the expression of *CvCRY1a* to promote *Chrysanthemum vestitum* flowering under short-day conditions

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Abstract

Nitrogen (N) is an important nutrient for plants that can affect various developmental processes, including flowering. However, the mechanism by which nitrogen regulates flowering remains unclear. *Chrysanthemum vestitum* is a typical short-day plant that has been shown to flower early in response to both short-day (SD) conditions and optimal nitrate concentrations. Here, we revealed that a member of the transcription factor NIN-like protein (NLP) in *C. vestitum*, *CvNLP2*, was highly expressed under low nitrate conditions. The flowering of *CvNLP2* overexpression (OE) lines of *C. vestitum* was significantly advanced, especially under optimal nitrate conditions, where the phenotype was more pronounced. Transgenic plants with silenced *CvNLP2* exhibited delayed flowering. Based on transcriptome analysis, it was found that the expression of *CRYPTOCHROME1* (*CvCRY1*) and other flowering genes was significantly up-regulated in OE-*CvNLP2* lines. Protein-DNA binding assays showed that *CvNLP2* directly bound to the *CvCRY1a* promoter to activate *CvCRY1a* expression. Overexpression of *CvCRY1a* promotes early flowering, while RNAi-*CvCRY1a* lines exhibit a delayed or slightly delayed flowering phenotype, with one line showing a significant delay. Moreover, the flowering of OE-*CvCRY1a* lines was advanced under different nitrate conditions compared with RNAi-*CvCRY1a* lines. In conclusion, this study defined a synergistic mechanism through which nitrate, acting as either a nutrient or a signal, regulates flowering in conjunction with short-day signals. This discovery provides new insights into the mechanism by which plants flower through the regulation of the photoperiod pathway under different nitrate conditions.

Effects of different preservatives on the postharvest storage effect of golden autumn sugar oranges

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Abstract

In this experiment, the fruit of early-maturing citrus variety Golden Autumn Sugar Tangerines were taken as the material, and different combinations of preservation treatments were set up to analyze the decay rate, weight loss rate and internal quality of the fruit at 0、 10 and 30 days after picking, in order to screen out the best combination of treatments suitable for the post-harvest storage of the fruit. The results showed that after 30 days of postharvest treatment, compared with the control group, the chemical fungicide hydrogen peroxide at 0.5 g/L had the best effect, and the decay rate and weight loss rate of Golden Autumn Sugar Tangerines were significantly reduced, the content of soluble solids was slightly increased, and the titratable acid and vitamin C content were both significantly lower than that of the control group ($P<0.05$). The food additives of 0.4 g/L sodium dehydroacetate, 20 mM hydrogen peroxide, and glacial acetic acid with a mass fraction of 0.10% had a better effect on the treatment, which was consistent with the effect of hydrogen peroxide treatment on the fruits, and had a better freshness preservation effect, with glacial acetic acid treatment being the best. The above four treatment reagents are all green and safe preservation materials, with the development potential of new preservation agents.

Foliar selenium reprograms root metabolism and rhizosphere microbiome to immobilize cadmium in cell walls and reduce bioavailability in water spinach

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Abstract

Cadmium (Cd) pollution in soil severely threatens the safe production of leafy vegetables and human health. Selenium (Se) can effectively restrict heavy metal uptake in crops. This study used water spinach (*Ipomoea aquatica* Forsk.) to investigate the effects of foliar-applied sodium selenite (Na₂SeO₃) and selenium nanoparticles (SeNPs) on plant growth, photosynthesis, antioxidant systems, Cd translocation, and rhizosphere microenvironment under Cd stress. Results showed that 2 mg/L Se presented the optimal mitigation effect. Compared with the Cd-only treatment, both Se forms significantly increased plant height by 80.00% and 72.38%, total chlorophyll by 40.39% and 38.97%, enhanced antioxidant enzyme activities and AsA-GSH levels, and reduced oxidative damage. Foliar Se also decreased shoot Cd content by 56.63% and 47.10%, translocation factor by 22.27% and 21.94%, while increasing Cd retention in cell walls. In the rhizosphere, Se reduced available Cd by 25.26% and 20.31% via converting acid-soluble Cd into stable fractions. Furthermore, Se reshaped rhizosphere metabolite profiles and recruited specific beneficial bacteria, improving soil enzyme activities and accelerating carbon and nitrogen cycling. In conclusion, foliar 2 mg/L Na₂SeO₃ or SeNPs synergistically alleviate Cd stress in water spinach by enhancing antioxidation, immobilizing Cd in cell walls, reducing Cd bioavailability, and optimizing rhizosphere microecology, providing a reliable technical basis for safe vegetable production in Cd-contaminated farmland.



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