

Genomic evidence for evolutionary history and local adaptation of two endemic apricots: *Prunus hongpingensis* and *P. zhengheensis*

原文链接: <https://doi.org/10.1093/hr/uhad215>

微信导读: [Hortic Res](#) | [华中农大解析两种南方特有杏基因组并揭示其进化历史过程](#)

Development of virus-induced genome editing methods in Solanaceous crops

原文链接: <https://doi.org/10.1093/hr/uhad233>

茄科作物中病毒诱导基因组编辑方法的开发

Genetic architecture and genomic prediction of plant height-related traits in chrysanthemum

原文链接: <https://doi.org/10.1093/hr/uhad236>

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Integrated proteomic analysis reveals interactions between phosphorylation and ubiquitination in rose response to *Botrytis* infection

原文链接: <https://doi.org/10.1093/hr/uhad238>

蛋白质组学分析揭示了玫瑰对灰霉菌感染反应中磷酸化和泛素化之间的相互作用

Two transcription factors, AcREM14 and AcC3H1, enhance the resistance of kiwifruit *Actinidiachinensis* var. *chinensis* to *Pseudomonas syringae* pv. *Actinidiae*

原文链接: <https://doi.org/10.1093/hr/uhad242>

转录因子 AcREM14 和 AcC3H1 增强中华猕猴桃对丁香假单胞菌的抗性

Genome-wide association analysis identifies a candidate gene controlling seed size and yield in *Xanthoceras sorbifolium* Bunge

原文链接: <https://doi.org/10.1093/hr/uhad243>

全基因组关联分析鉴定了一个调控文冠果种子大小及产量的候选基因

The haplotype-resolved telomere-to-telomere carnation (*Dianthus caryophyllus*) genome reveals the correlation between genome architecture and gene expression

原文链接: <https://doi.org/10.1093/hr/uhad244>

T2T 基因组揭示了康乃馨基因组结构和基因表达之间的相关性

MODMS: a multi-omics database for facilitating biological studies on alfalfa (*Medicago sativa* L.)

原文链接: <https://doi.org/10.1093/hr/uhad245>

微信导读: [Hortic Res](#) | [兰州大学刘志鹏团队构建紫花苜蓿多组学数据库 MODMS](#)

A putative E3 ubiquitin ligase substrate receptor degrades transcription factor SmNAC to enhance bacterial wilt resistance in eggplant

原文链接: <https://doi.org/10.1093/hr/uhad246>

一种假定的 E3 泛素连接酶底物受体降解转录因子 SmNAC 来增强茄子的青枯病抗性

Construction of a high-density genetic map for yardlong bean and identification of ANT1 as a regulator of anthocyanin biosynthesis

原文链接: <https://doi.org/10.1093/hr/uhad247>

微信导读: [Hortic Res](#) | [江苏省农业科学院揭示长豇豆鲜荚花青素合成的分子机制](#)

Signalling mechanisms and agricultural applications of (Z)-3-hexenyl butyrate-mediated stomatal closure

原文链接: <https://doi.org/10.1093/hr/uhad248>

(Z)-3-己烯基丁酸介导的气孔关闭的信号传导机制及其农业应用

Vacuolar proteomic analysis reveals tonoplast transporters for accumulation of citric acid and sugar in citrus fruit

原文链接: <https://doi.org/10.1093/hr/uhad249>

微信导读: [Hortic Res](#) | [华中农大果树栽培团队建立柑橘果实液泡蛋白组并发掘糖酸积累紧密关联液泡膜蛋白](#)

Efficient and heritable A-to-K base editing in rice and tomato

原文链接: <https://doi.org/10.1093/hr/uhad250>

微信导读: [Hortic Res](#) | [朱健康院士团队优化碱基编辑工具实现水稻和番茄高效可遗传的 A 到 K 碱基编辑](#)

The *Botrytis cinerea* effector BcXYG1 suppress immunity in *Fragaria vesca* by targeting FvBPL4 and FvACD11

原文链接: <https://doi.org/10.1093/hr/uhad251>

灰霉菌分泌蛋白 BcXYG1 通过靶向 FvBPL4 和 FvACD11 抑制森林草莓的免疫

Phased gap-free genome assembly of octoploid cultivated strawberry illustrates the genetic and epigenetic divergence among subgenomes

原文链接: <https://doi.org/10.1093/hr/uhad252>

八倍体栽培草莓的无间隙基因组组装揭示了草莓亚基因组之间的遗传和表观遗传差异

Nitrogen-potassium balance improves leaf photosynthetic capacity by regulating leaf nitrogen allocation in apple

原文链接: <https://doi.org/10.1093/hr/uhad253>

微信导读: [Hortic Res](#) | [山东农业大学姜远茂团队揭示氮钾平衡调控叶片氮分配提高苹果叶片光合能力的机制](#)

A LIWRKY33-LIHSFA4-LICAT2 module confers resistance to *Botrytis cinerea* in lily

原文链接: <https://doi.org/10.1093/hr/uhad254>

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Populus cathayana genome and population resequencing provide insights into its evolution and adaptation

原文链接: <https://doi.org/10.1093/hr/uhad255>

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A highly diversified NLR cluster in melon contains homologs that confer powdery mildew and aphid resistance

原文链接: <https://doi.org/10.1093/hr/uhad256>

甜瓜中一个高度多样化的 NLR 基因簇包含赋予其白粉病和蚜虫抗性的同源基因

A telomere-to-telomere reference genome of ficus (*Ficus hispida*) provides new insights into sex-determination

原文链接: <https://doi.org/10.1093/hr/uhad257>

微信导读: [Hortic Res](#) | [中国农科院深圳农业基因组研究所发表首个榕属植物 T2T 基因组](#)

Multi-omics landscape to decrypt the distinct flavonoid biosynthesis of *Scutellaria baicalensis* across multiple tissues

原文链接: <https://doi.org/10.1093/hr/uhad258>

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A biosynthetic network for protoberberine production in *Coptis chinensis*

原文链接: <https://doi.org/10.1093/hr/uhad259>

黄连中的原小檗碱生物合成网络

Telomere-to-telomere and gap-free genome assembly of a susceptible grapevine species (Thompson Seedless) to facilitate grape functional genomics

原文链接: <https://doi.org/10.1093/hr/uhad260>

微信导读: [Hortic Res | 西北农林科技大学组装感病葡萄汤普森无核 T2T 基因组](#)

A Ca²⁺ sensor BraCBL1.2 involves in BraCRa-mediated clubroot resistance in Chinese cabbage

原文链接: <https://doi.org/10.1093/hr/uhad261>

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Tracking organelle activities through efficient and stable root genetic transformation system in woody plants

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Comprehensive dissection of variation and accumulation of free amino acids in tea accessions

原文链接: <https://doi.org/10.1093/hr/uhad263>

茶树游离氨基酸变异与积累的综合剖析

Genome variation and LTR-RT analyses of an ancient peach landrace reveal mechanism of blood flesh fruit color formation and fruit maturity date advancement

原文链接: <https://doi.org/10.1093/hr/uhad265>

一份古老的桃地方品种基因组变异及 LTR 类型转座子分析揭示了红肉形成及果实提前成熟的机制

An Efficient Protoplast-based Genome Editing protocol for *Vitis* species

原文链接: <https://doi.org/10.1093/hr/uhad266>

一种高效的基于原生质体的葡萄属物种基因组编辑程序

A metabolomics study in citrus provides insight into bioactive phenylpropanoid metabolism

原文链接: <https://doi.org/10.1093/hr/uhad267>

柑橘的代谢组学研究提供了生物活性苯丙烷代谢的见解

Phased genomics reveals hidden somatic mutations and provides insight into fruit development in sweet orange

原文链接: <https://doi.org/10.1093/hr/uhad268>

基因组学揭示了甜橙中隐藏的体细胞突变为果实发育提供了见解

A chromosome-level genome assembly of *Agave hybrid* NO.11648 provides insights into the CAM photosynthesis

原文链接: <https://doi.org/10.1093/hr/uhad269>

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Genomic analysis of fruit size and shape traits in apple: unveiling candidate genes through GWAS analysis

原文链接: <https://doi.org/10.1093/hr/uhad270>

苹果果实大小和形状形状的基因组分析：通过 GWAS 分析发掘候选基因

Strawberry soluble solids QTL with inverse effects on yield

原文链接: <https://doi.org/10.1093/hr/uhad271>

草莓可溶性固形物对产量具有反作用的 QTL

A QTL of eggplant shapes the rhizosphere bacterial community, co-responsible for resistance to bacterial wilt

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DataColor: unveiling biological data relationships through distinctive color mapping

原文链接: <https://doi.org/10.1093/hr/uhad273>

DataColor: 通过独特的颜色映射揭示生物数据关系

Insights into the Superrosids phylogeny and flavonoid synthesis from the telomere-to-telomere gap-free genome assembly of *Penthorum chinense* Pursh

原文链接: <https://doi.org/10.1093/hr/uhad274>

扯根菜 T2T 基因组揭示其超微结构系统发育和黄酮类化合物合成机制

Gibberellins involved in fruit ripening and softening by mediating multiple hormonal signals in tomato

原文链接: <https://doi.org/10.1093/hr/uhad275>

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ABA-CsABI5-CsCalS11 module upregulates Callose deposition of citrus infected with *Candidatus Liberibacter asiaticus*

原文链接: <https://doi.org/10.1093/hr/uhad276>

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Integration of metabolomics and transcriptomics reveals the regulation mechanism of the phenylpropanoid biosynthesis pathway in insect resistance traits in *Solanum habrochaites*

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A 49-bp deletion of *PmAP2L* results in a double flower phenotype in *Prunus mume*

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RNA virus-mediated gene editing for tomato trait breeding

原文链接: <https://doi.org/10.1093/hr/uhad279>

RNA 病毒介导的基因编辑用于番茄性状育种

Lskipk Lsatpase double mutants are necessary and sufficient for the compact plant architecture of butterhead lettuce

原文链接: <https://doi.org/10.1093/hr/uhad280>

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Deciphering the intricate hierarchical gene regulatory network: unraveling multi-level regulation and modifications driving secondary cell wall formation

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复杂层次化调控网络解读: 次生细胞壁形成的多层次调控与修饰的揭密

mRNA-miRNA analyses reveal the involvement of *CsbHLH1* and miR1446 in the regulation of caffeine biosynthesis in *Camellia sinensis*

原文链接: <https://doi.org/10.1093/hr/uhad282>

mRNA-miRNA 分析揭示 *CsbHLH1* 和 miR1446 参与茶树咖啡因生物合成的调控

Dissecting the complex genetic basis of pre- and post-harvest traits in *Vitis vinifera L.* using genome-wide association studies

原文链接: <https://doi.org/10.1093/hr/uhad283>

全基因组关联研究解析葡萄采前和采后性状的复杂遗传基础

Exploring N⁶-methyladenosine (m⁶A) modification in tree species: opportunities and challenges

原文链接: <https://doi.org/10.1093/hr/uhad284>

探索 N⁶-甲基腺苷 (m⁶A) 在树种中的修饰: 机遇与挑战

AlliumDB: A central portal for comparative and functional genomics in *Allium*

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微信导读: [Hortic Res](#) | 青岛农业大学园艺学院研究团队发布葱属比较和功能基因组学数据库

NYUS.2: an automated machine learning prediction model for the large-scale real-time simulation of grapevine freezing tolerance in North America

原文链接: <https://doi.org/10.1093/hr/uhad286>

NYUS.2: 北美葡萄耐冻性大规模实时模拟的自动机器学习预测模型

IAA-miR164a-NAC100L1 module mediates symbiotic incompatibility of cucumber/pumpkin grafted seedlings through regulating callose deposition

原文链接: <https://doi.org/10.1093/hr/uhad287>

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MdSnRK1.1 interacts with MdGLK1 to regulate abscisic acid-mediated chlorophyll accumulation in apple

原文链接: <https://doi.org/10.1093/hr/uhad288>

微信导读: [Hortic Res](#) | 山东农业大学由春香/王小非教授团队揭示 MdSnRK1 调控苹果叶绿素积累的分子机制

Transgressive segregation, hopeful monsters, and phenotypic selection drove rapid genetic gains and breakthroughs in predictive breeding for quantitative resistance to *Macrophomina* in strawberry

原文链接: <https://doi.org/10.1093/hr/uhad289>

超亲分离以及表型选择驱动在草莓对大丽轮枝菌的抗性研究的快速遗传增益和定量预测育种中取得突破

Tissue culture-free transformation of traditional Chinese medicinal plants with root suckering capability

原文链接: <https://doi.org/10.1093/hr/uhad290>

无需组织培养的传统中药植物基于根蘖的转化方法

MicroRNA396 negatively regulates shoot regeneration in tomato

原文链接: <https://doi.org/10.1093/hr/uhad291>

MicroRNA396 负调控番茄芽再生

Advanced metabolic engineering strategies for increasing artemisinin yield in *Artemisia annua* L.

原文链接: <https://doi.org/10.1093/hr/uhad292>

提高黄花蒿青蒿素产量的先进代谢工程策略

miR156b-targeted *VvSBP8/13* functions downstream of the abscisic acid signal to regulate anthocyanins biosynthesis in grapevine fruit under drought

原文链接: <https://doi.org/10.1093/hr/uhad293>

微信导读: [Hortic Res | 西北农林科技大学揭示葡萄 miR156b 靶向 *VvSBP8/13* 参与干旱诱导花色苷积累分子机制](#)

Exploring large-scale gene coexpression networks in peach (*Prunus persica* L.): A new tool for predicting gene function

原文链接: <https://doi.org/10.1093/hr/uhad294>

桃大规模基因共表达网络的探索: 预测基因功能的新工具

CsMLO8/11 are required for full susceptibility of cucumber stem to powdery mildew and interact with CsCRK2 and CsRbohD

原文链接: <https://doi.org/10.1093/hr/uhad295>

CsMLO8/11 是黄瓜茎对白粉菌完全感病所必需的, 并与 CsCRK2 和 CsRbohD 相互作用

Haplotype-resolved genome assembly of *Corydalis yanhusuo*, a traditional Chinese medicine with unusual telomere motif

原文链接: <https://doi.org/10.1093/hr/uhad296>

端粒基序异常的传统中药延胡索药材的单倍型解析基因组组装

RtNAC055 promotes drought tolerance via a stomatal closure pathway linked to methyl jasmonate/hydrogen peroxide signaling in *Reaumuria trigyna*

原文链接: <https://doi.org/10.1093/hr/uhae001>

RtNAC055 通过与茉莉酸甲酯/过氧化氢信号相关的气孔关闭途径促进长叶红砂的耐旱性

Phenotyping, genetics and ‘-omics’ approaches to unravel and introgress enhanced resistance against apple scab (*Venturia inaequalis*) in apple cultivars (*Malus × domestica*)

原文链接: <https://doi.org/10.1093/hr/uhae002>

表型、遗传学和组学联合分析的解析和应用以增强苹果对斑点病的抗性

A natural mutation in the promoter of the aconitase gene *ZjACO3* influences fruit citric acid content in jujube

原文链接: <https://doi.org/10.1093/hr/uhae003>

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Cuticular wax biosynthesis in blueberries (*Vaccinium corymbosum* L.): Transcript and metabolite changes during ripening and storage affect key fruit quality traits

原文链接: <https://doi.org/10.1093/hr/uhae004>

蓝莓表皮蜡的生物合成：成熟和贮藏过程中转录和代谢产物的变化影响果实的主要品质性状

The lemon genome and DNA methylome unveil epigenetic regulation of citric acid biosynthesis during fruit development

原文链接: <https://doi.org/10.1093/hr/uhae005>

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Chloroplast C-to-U editing, regulated by a PPR protein BoYgl-2, is important for chlorophyll biosynthesis in cabbage

原文链接: <https://doi.org/10.1093/hr/uhae006>

微信导读: [Hortic Res](#) | 中国农科院蔬菜花卉所张扬勇团队揭示甘蓝 PPR 蛋白 BoYgl-2 调控叶绿体 RNA C-U 编辑新机制

EasyDAM_V4: Guided-GAN-based cross-species data labeling for fruit detection with significant shape difference

原文链接: <https://doi.org/10.1093/hr/uhae007>

EasyDAM_V4: 基于 GAN 的引导跨物种数据标记以进行具有显著形状差异的水果检测

Genome and GWAS analysis identified genes significantly related to phenotypic state of *Rhododendron* bark

原文链接: <https://doi.org/10.1093/hr/uhae008>

基因组和 GWAS 分析鉴定了与杜鹃树皮表型状态显著相关的基因

Leaf variegation caused by plastome structural variation: an example from *Dianella tasmanica*

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DNA methylome analysis reveals novel insights into active hypomethylated regulatory mechanisms of temperature-dependent flower opening in *Osmanthus fragrans*

原文链接: <https://doi.org/10.1093/hr/uhae010>

DNA 甲基化组分析揭示了桂花温度依赖的花开放主动低甲基化调控机制的新见解

Towards the completion of Koch's postulates for the citrus huanglongbing bacterium, *Candidatus Liberibacter asiaticus*

原文链接: <https://doi.org/10.1093/hr/uhae011>

柑橘黄龙病科赫假说的完善

CsMYB73 negatively regulates theanine accumulation mediated by *CsGGT2* and *CsGGT4* in tea shoots (*Camellia sinensis*)

原文链接: <https://doi.org/10.1093/hr/uhae012>

微信导读: [Hortic Res](#) | 安徽农业大学宛晓春团队揭示 CsMYB73 负调控茶树新梢茶氨酸积累的新机制

Flowering genes identification, network analysis and database construction for 837 plants

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A comprehensive overview of omics-based approaches to enhance biotic and abiotic stress tolerance in sweet potato

原文链接: <https://doi.org/10.1093/hr/uhae014>

基于组学以提高甘薯生物和非生物胁迫耐受性的方法

The cellular and molecular basis of the spur development in *Impatiens uliginosa*

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Enhanced photosynthetic efficiency by nitrogen-doped carbon dots via plastoquinone-involved electron transfer in plants

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BL-Hi-C reveals the 3D genome structure of *Brassica* crops with high sensitivity

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Leguminous green manure intercropping changes the soil microbial community and increases soil nutrients and key quality components of tea leaves

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豆科绿肥间作改变了土壤微生物群落，增加了土壤养分和茶叶关键品质成分

Insights into the functional role of tomato *TM6* as transcriptional regulator of flower development

原文链接: <https://doi.org/10.1093/hr/uhae019>

番茄 *TM6* 作为花发育转录调控因子的功能作用

Genetic regulation of volatile production in two melon introgression line collections with contrasting ripening behavior

原文链接: <https://doi.org/10.1093/hr/uhae020>

两个甜瓜渐渗品系挥发性物质产量的遗传调控

Efficient targeted mutagenesis in tetraploid *Pogostemon cablin* by the CRISPR/Cas9-mediated genomic editing system

原文链接: <https://doi.org/10.1093/hr/uhae021>

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A haplotype-resolved gap-free genome assembly provides novel insight into monoterpenoid diversification in *Mentha suaveolens* ‘Variegata’

原文链接: <https://doi.org/10.1093/hr/uhae022>

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PMAT: an efficient plant mitogenome assembly toolkit using low coverage HiFi sequencing data

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CRISPR/Cas9 revolutionizes *Macleaya cordata* breeding: a leap in sanguinarine biosynthesis

原文链接: <https://doi.org/10.1093/hr/uhae024>

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Diploid wax apple (*Syzygium samarangense*) genome identified NAC genes regulating fruit development

原文链接: <https://doi.org/10.1093/hr/uhae025>

二倍体莲雾基因组鉴定调节果实发育的 NAC 基因

5-Aminolevulinic acid improves cold resistance through regulation of SIMYB4/SIMYB88-SIGSTU43 module to scavenge reactive oxygen species in tomato

原文链接: <https://doi.org/10.1093/hr/uhae026>

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Allele-specific DNA methylation and gene expression during shoot organogenesis in tissue culture of hybrid poplar

原文链接: <https://doi.org/10.1093/hr/uhae027>

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SIWRKY80-mediated jasmonic acid pathway positively regulates tomato resistance to saline-alkali stress by enhancing spermidine content and stabilizing Na⁺/K⁺ homeostasis

原文链接: <https://doi.org/10.1093/hr/uhae028>

SIWRKY80 介导的 JA 通路通过提高亚精胺含量和稳定 Na⁺/K⁺ 稳态，正向调节番茄对盐碱胁迫的抗性

Apple E3 ligase MdPUB23 mediates ubiquitin-dependent degradation of MdABI5 to delay ABA-triggered leaf senescence

原文链接: <https://doi.org/10.1093/hr/uhae029>

苹果 E3 连接酶 MdPUB23 介导 MdABI5 的泛素化降解以延缓 ABA 引发的叶片衰老

Two large inversions seriously suppress recombination and are essential for key genotype fixation in cabbage (*Brassica oleracea* L. var. *capitata*)

原文链接: <https://doi.org/10.1093/hr/uhae030>

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Hypermethylation in the promoter regions of flavonoid pathway genes is associated with skin color fading during 'Daihong' apple fruit development

原文链接: <https://doi.org/10.1093/hr/uhae031>

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T2T reference genome assembly and genome-wide association study reveal the genetic basis of Chinese bayberry fruit quality

原文链接: <https://doi.org/10.1093/hr/uhae033>

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The chromosome-scale genome and population genomics reveal the adaptative evolution of *Populus pruinosa* to desertification environment

原文链接: <https://doi.org/10.1093/hr/uhae034>

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Identification and application of an exocarp-preferential promoter for genetic engineering of tomato fruit

原文链接: <https://doi.org/10.1093/hr/uhae035>

番茄果实基因工程外果皮启动子的鉴定及应用

Genome-wide identification of bHLH transcription factors and functional analysis in salt gland development of the recretohalophyte sea lavender (*Limonium bicolor*)

原文链接: <https://doi.org/10.1093/hr/uhae036>

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Identification and characterization of two P450 enzymes from *Citrus sinensis* involved in TMTT and DMNT biosyntheses and Asian citrus psyllid defense

原文链接: <https://doi.org/10.1093/hr/uhae037>

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The *Cissus quadrangularis* genome reveals its adaptive features in an arid habitat

原文链接: <https://doi.org/10.1093/hr/uhae038>

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cla-miR164-*NO APICAL MERISTEM (CINAM)* regulates the inflorescence architecture development of *Chrysanthemum lavandulifolium*

原文链接: <https://doi.org/10.1093/hr/uhae039>

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TSPO-induced degradation of the ethylene receptor RhETR3 promotes salt tolerance in rose (*Rosa hybrida*)

原文链接: <https://doi.org/10.1093/hr/uhae040>

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Plant-LncPipe: a computational pipeline providing significant improvement in plant lncRNA identification

原文链接: <https://doi.org/10.1093/hr/uhae041>

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Characterization of *O*-methyltransferases in the biosynthesis of phenylphenalenone phytoalexins based on the telomere-to-telomere gapless genome of *Musella lasiocarpa*

原文链接: <https://doi.org/10.1093/hr/uhae042>

基于 T2T 基因组筛选地涌金莲苯萘酮植保素生物合成途径中的 O-甲基转移酶

Transcriptional regulation of flavonol biosynthesis in plants

原文链接: <https://doi.org/10.1093/hr/uhae043>

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LaMYC7, a positive regulator of linalool and caryophyllene biosynthesis, confers plant resistance to *Pseudomonas syringae*

原文链接: <https://doi.org/10.1093/hr/uhae044>

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Engineered dsRNA – protein nanoparticles for effective systemic gene silencing in plants

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Emerging roles and mechanisms of lncRNAs in fruit and vegetables

原文链接: <https://doi.org/10.1093/hr/uhae046>

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The Smi-miR858a-SmMYB module regulates tanshinone and phenolic acid biosynthesis in *Salvia miltiorrhiza*

原文链接: <https://doi.org/10.1093/hr/uhae047>

Smi-miR858a-SmMYB 模块调节丹参中丹参酮和酚酸的生物合成

Diversity of flavour characteristics of table grapes and their contributing volatile compounds analysed by the solvent-assisted flavour evaporation method

原文链接: <https://doi.org/10.1093/hr/uhae048>

采用溶剂辅助风味蒸发法分析食用葡萄风味特征及其挥发性成分的多样性

Defensive alteration of root exudate composition by grafting *Prunus* sp. onto resistant rootstock contributes to reducing crown gall disease

原文链接: <https://doi.org/10.1093/hr/uhae049>

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A mutation in the brassinosteroid biosynthesis gene *CpDWF5* disrupts vegetative and reproductive development and salt stress response in squash (*Cucurbita pepo*)

原文链接: <https://doi.org/10.1093/hr/uhae050>

油菜素内酯生物合成基因 *CpDWF5* 突变破坏了西葫芦营养生长和生殖发育以及盐胁迫响应

MdARF3 switches the lateral root elongation to regulate dwarfing in apple plants

原文链接: <https://doi.org/10.1093/hr/uhae051>

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PsmiR159b-*PsMYB65* module functions in the resumption of bud growth after endodormancy by affecting the cell cycle in tree peony

原文链接: <https://doi.org/10.1093/hr/uhae052>

PsmiR159b-*PsMYB65* 模块通过影响牡丹细胞周期，在内休眠后的芽生长恢复中发挥作用

Banana MabHLH28 positively regulates the expression of softening-related genes to mediate fruit ripening independently or via cooperating with MaWRKY49/111

原文链接: <https://doi.org/10.1093/hr/uhae053>

香蕉 MabHLH28 通过独立或协同 MaWRKY49/111 正调控软化相关基因表达来介导果实成熟

Auxin regulates bulbil initiation by mediating sucrose metabolism in *Lilium lancifolium*

原文链接: <https://doi.org/10.1093/hr/uhae054>

生长素介导卷丹百合蔗糖代谢调控球茎发育

A natural variation in *SISCaBP8* promoter contributes to the loss of saline-alkaline tolerance during tomato improvement

原文链接: <https://doi.org/10.1093/hr/uhae055>

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Genome-wide methylation, transcriptome and characteristic metabolites reveal the balance between diosgenin and brassinosteroids in *Dioscorea zingiberensis*

原文链接: <https://doi.org/10.1093/hr/uhae056>

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Pumpkin CmoDREB2A enhances salt tolerance of grafted cucumber through interaction with CmoNAC1 to regulate H₂O₂ and ABA signaling and K⁺/Na⁺ homeostasis

原文链接: <https://doi.org/10.1093/hr/uhae057>

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RNA sequencing analysis reveals *PgbHLH28* as the key regulator in response to methyl jasmonate-induced saponin accumulation in *Platycodon grandiflorus*

原文链接: <https://doi.org/10.1093/hr/uhae058>

RNA 测序分析表明 *PgbHLH28* 是响应茉莉酸甲酯诱导桔梗皂苷积累的关键调控因子

Transcriptomic analyses to summarize gene expression patterns that occur during leaf initiation of Chinese cabbage

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转录组学分析总结大白菜叶片发育过程中的基因表达模式

Dissection of the spatial dynamics of biosynthesis, transport, and turnover of major amino acids in tea plants (*Camellia sinensis*)

原文链接: <https://doi.org/10.1093/hr/uhae060>

茶树主要氨基酸生物合成、运输和周转的空间动态解析

Phosphorylation of birch BpNAC90 improves the activation of gene expression to confer drought tolerance

原文链接: <https://doi.org/10.1093/hr/uhae061>

桦树 BpNAC90 磷酸化提高基因表达的激活从而赋予其耐旱性

RNA-seq-based comparative transcriptome analysis reveals the role of *CsPrx73* in waterlogging-triggered adventitious root formation in cucumber

原文链接: <https://doi.org/10.1093/hr/uhae062>

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Chromosome-scale reference genome of broccoli (*Brassica oleracea* var. *italica* Plenck) provides insights into glucosinolate biosynthesis

原文链接: <https://doi.org/10.1093/hr/uhae063>

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Chromosome-scale genome, together with transcriptome and metabolome, provided insights into the evolution and anthocyanin biosynthesis of *Rubus rosaefolius* Sm. (Rosaceae)

原文链接: <https://doi.org/10.1093/hr/uhae064>

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Ethylene-responsive VviERF003 modulates glycosylated monoterpene synthesis by upregulating *VviGT14* in grapes

原文链接: <https://doi.org/10.1093/hr/uhae065>

乙烯响应的 VviERF003 通过上调葡萄中的 *VviGT14* 调节糖基化单萜的合成

CaSTH2 disables CaWRKY40 from activating pepper thermotolerance and immunity against *Ralstonia solanacearum* via physical interaction

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Harnessing the power of microbes: Enhancing soybean growth in an acidic soil through AMF inoculation rather than P-fertilization

原文链接: <https://doi.org/10.1093/hr/uhae067>

利用微生物的力量: 通过接种 AMF 而不是施磷肥以促进大豆在酸性土壤中的生长

Multi-omics analysis reveals key regulatory defense pathways and genes involved in salt tolerance of rose plants

原文链接: <https://doi.org/10.1093/hr/uhae068>

多组学分析揭示了玫瑰耐盐性的关键调控防御途径和相关基因

MAPK20-mediated ATG6 phosphorylation is critical for pollen development in *Solanum lycopersicum* L.

原文链接: <https://doi.org/10.1093/hr/uhae069>

MAPK20 介导的 ATG6 磷酸化对番茄花粉发育至关重要

Genome-wide variants and optimal allelic combinations for citric acid in tomato

原文链接: <https://doi.org/10.1093/hr/uhae070>

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Haplotype-resolved T2T reference genomes for wild and domesticated accessions shed new insights into the domestication of jujube

原文链接: <https://doi.org/10.1093/hr/uhae071>

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MdbZIP44 - MdcPRF2-like - *Md α-GP2* regulate starch and sugar metabolism in apple under nitrogen supply

原文链接: <https://doi.org/10.1093/hr/uhae072>

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Integrated proteomic, transcriptomic, and metabolomic profiling reveals that the gibberellin - abscisic acid hub runs flower development in the Chinese orchid *Cymbidium sinense*

原文链接: <https://doi.org/10.1093/hr/uhae073>

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CsEXL3 regulate mechanical harvest-related droopy leaves under the transcriptional activation of CsBES1.2 in tea plant

原文链接: <https://doi.org/10.1093/hr/uhae074>

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euAP2a, a key gene that regulates flowering time in peach (*Prunus persica*) by modulating thermo-responsive transcription programming

原文链接: <https://doi.org/10.1093/hr/uhae076>

euAP2a 通过调节热响应转录程序调节桃开花时间的关键基因

Coping with alpine habitats: genomic insights into the adaptation strategies of *Triplostegia glandulifera* (Caprifoliaceae)

原文链接: <https://doi.org/10.1093/hr/uhae077>

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Extracellular perception of multiple novel core effectors from the broad host-range pear anthracnose pathogen *Colletotrichum fructicola* in the nonhost *Nicotiana benthamiana*

原文链接: <https://doi.org/10.1093/hr/uhae078>

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Chromosome-level genome assemblies of *Musa ornata* and *Musa velutina* provide insights into pericarp dehiscence and anthocyanin biosynthesis in banana

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Diploid genome assembly of the Malbec grapevine cultivar enables haplotype-aware analysis of transcriptomic differences underlying clonal phenotypic variation

原文链接: <https://doi.org/10.1093/hr/uhae080>

马尔贝克葡萄品种的基因组能够实现基于单倍型的转录组差异分析

Calmodulin-like protein MdCML15 interacts with MdBT2 to modulate iron homeostasis in apple

原文链接: <https://doi.org/10.1093/hr/uhae081>

钙调素样蛋白 MdCML15 与 MdBT2 互作调节苹果内铁稳态

Exploring salt tolerance mechanisms using machine learning for transcriptomic insights: case study in *Spartina alterniflora*

原文链接: <https://doi.org/10.1093/hr/uhae082>

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VvWRKY5 positively regulates wounding-induced anthocyanin accumulation in grape by interplaying with VvMYBA1 and promoting jasmonic acid biosynthesis

原文链接: <https://doi.org/10.1093/hr/uhae083>

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Genome-wide transcriptome analysis reveals key regulatory networks and genes involved in the determination of seed hardness in vegetable soybean

原文链接: <https://doi.org/10.1093/hr/uhae084>

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The *CsmiR397a-CsLAC17* module regulates lignin biosynthesis to balance the tenderness and gray blight resistance in young tea shoots

原文链接: <https://doi.org/10.1093/hr/uhae085>

CsmiR397a-CsLAC17 模块调节木质素生物合成，以平衡茶树嫩梢的嫩度和灰霉病抗性

Interaction among homeodomain transcription factors mediates ethylene biosynthesis during pear fruit ripening

原文链接: <https://doi.org/10.1093/hr/uhae086>

同源异型域转录因子之间的相互作用介导梨果实成熟过程中乙烯的生物合成

Identification of allelic relationship and translocation region among chromosomal translocation lines that leads to less-seed watermelon

原文链接: <https://doi.org/10.1093/hr/uhae087>

导致少籽西瓜染色体易位系等位基因关系和易位区的鉴定

Nuclear Factor Y-A3b binds to the *SINGLE FLOWER TRUSS* promoter and regulates flowering time in tomato

原文链接: <https://doi.org/10.1093/hr/uhae088>

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The high-quality genome of *Grona styracifolia* uncover the genomic mechanism of high level of schaftoside, a promising drug candidate for treatment of COVID-19

原文链接: <https://doi.org/10.1093/hr/uhae089>

微信导读: [广金钱草多组学研究揭示治疗 COVID-19 候选药物夏佛塔昔的生物合成机制](#)

Pyrus betulaefolia ERF3 interacts with HsfC1a to coordinately regulate aquaporin *PIP1;4* and *NCED4* for drought tolerance

原文链接: <https://doi.org/10.1093/hr/uhae090>

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Cytochemical localization and synthesis mechanism of the glucomannan in pseudobulbs of *Bletilla striata* Reichb. f.

原文链接: <https://doi.org/10.1093/hr/uhae092>

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Multi-omic dissection of the cold resistance traits of white water lily

原文链接: <https://doi.org/10.1093/hr/uhae093>

多组学分析揭示白睡莲抗寒性状

Adaptive regulation of miRNAs/milRNAs in tissue-specific interaction between apple and *Valsa mali*

原文链接: <https://doi.org/10.1093/hr/uhae094>

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Integrative analysis of the methylome and transcriptome of tomato fruit (*Solanum lycopersicum* L.) induced by postharvest handling

原文链接: <https://doi.org/10.1093/hr/uhae095>

微信导读: [番茄果实采后处理成熟诱导的 DNA 甲基化和转录组综合分析](#)

SIGAD2 is the target of *SITHM27*, positively regulates cold tolerance by mediating anthocyanin biosynthesis in tomato

原文链接: <https://doi.org/10.1093/hr/uhae096>

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Roles of the *APETALA3-3* ortholog in the petal identity specification and morphological differentiation in *Delphinium anthriscifolium* flowers

原文链接: <https://doi.org/10.1093/hr/uhae097>

APETALA3-3 同源基因在还亮草花瓣鉴别和形态分化中的作用

Four novel *Cit7GlcTs* functional in flavonoid 7-*O*-glucoside biosynthesis are vital to flavonoid biosynthesis shunting in citrus

原文链接: <https://doi.org/10.1093/hr/uhae098>

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The critical roles of three sugar-related proteins (HXK, SnRK1, TOR) in regulating plant growth and stress responses

原文链接: <https://doi.org/10.1093/hr/uhae099>

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HortGenome Search Engine, a universal genomic search engine for horticultural crops

原文链接: <https://doi.org/10.1093/hr/uhae100>

园艺作物基因组搜索引擎: [HortGenome Search Engine](#)

Specific chromatin states and m6A modifications are associated with mRNA mobility *in planta*

原文链接: <https://doi.org/10.1093/hr/uhae101>

特定的染色质状态和 m6A 修饰与 mRNA 流动性有关

Regulatory role of *Prunus mume* DAM6 on lipid body accumulation and phytohormone metabolism in the dormant vegetative meristem

原文链接: <https://doi.org/10.1093/hr/uhae102>

DAM6 对梅花休眠营养分生组织脂质体积和植物激素代谢的调控作用

Haplotype-resolved genome of *Prunus zhengheensis* provides insight into its evolution and low temperature adaptation in apricot

原文链接: <https://doi.org/10.1093/hr/uhae103>

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BoaBZR1.1 mediates brassinosteroid-induced carotenoid biosynthesis in Chinese kale

原文链接: <https://doi.org/10.1093/hr/uhae104>

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Genomic, transcriptomic, and metabolomic analyses provide insights into the evolution and development of a medicinal plant *Saposhnikovia divaricata* (Apiaceae)

原文链接: <https://doi.org/10.1093/hr/uhae105>

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A phased genome of the highly heterozygous 'Texas' almond uncovers patterns of allele-specific expression linked to heterozygous structural variants

原文链接: <https://doi.org/10.1093/hr/uhae106>

杏仁的阶段性基因组揭示了与杂合结构变异相关的等位基因特异性表达模式

Telomere-to-telomere reference genome for *Panax ginseng* highlights the evolution of saponin biosynthesis

原文链接: <https://doi.org/10.1093/hr/uhae107>

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Efficient purging of deleterious mutations contributes to the survival of a rare conifer

原文链接: <https://doi.org/10.1093/hr/uhae108>

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Comparative population genomics reveals convergent and divergent selection in the apricot - peach - plum - mei complex

原文链接: <https://doi.org/10.1093/hr/uhae109>

比较群体基因组学揭示杏-桃-梅复合体的趋同选择和趋异选择

Heterotrimeric G α -subunit regulates flower and fruit development in CLAVATA signaling pathway in cucumber

原文链接: <https://doi.org/10.1093/hr/uhae110>

异三聚体 G α -亚基通过 CLAVATA 信号通路介导黄瓜花和果实发育

Enhancing tomato fruit antioxidant potential through hydrogen nanobubble irrigation

原文链接: <https://doi.org/10.1093/hr/uhae111>

氢纳米气泡灌溉可提高番茄果实抗氧化能力

Variation of mesophyll conductance mediated by nitrogen form is related to changes in cell wall property and chloroplast number

原文链接: <https://doi.org/10.1093/hr/uhae112>

氮形态介导的叶肉电导率变化与细胞壁特性和叶绿体数量的变化有关

Chromosome-level genome assembly and population genomics reveals crucial selection for subgynoecey development in chieh-qua

原文链接: <https://doi.org/10.1093/hr/uhae113>

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Comparative transcriptome and functional analyses provide insights into the key factors regulating shoot regeneration in highbush blueberry

原文链接: <https://doi.org/10.1093/hr/uhae114>

比较转录组和功能分析为调控高丛蓝莓芽再生调控的关键因素提供了见解

The transcription factor CpMYB62 controls the genetic network that leads to the determination of female flowers in *Cucurbita pepo*

原文链接: <https://doi.org/10.1093/hr/uhae115>

转录因子 CpMYB62 调控西葫芦雌花分化的遗传网络

AcMYB266, a key regulator of the red coloration in pineapple peel: a case of subfunctionalization in tandem duplicated genes

原文链接: <https://doi.org/10.1093/hr/uhae116>

AcMYB266, 菠萝皮红色的关键调节因子: 串联重复基因亚功能化案例

De novo assembling a high-quality genome sequence of Amur grape (*Vitis amurensis* Rupr.) gives insight into *Vitis* divergence and sex determination

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Transposable elements in Rosaceae: insights into genome evolution, expression dynamics, and syntenic gene regulation

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蔷薇科植物中的转座子: 基因组进化、表达动力学和同线基因调控的见解

A telomere-to-telomere gap-free reference genome assembly of avocado provides useful resources for identifying genes related to fatty acid biosynthesis and disease resistance

原文链接: <https://doi.org/10.1093/hr/uhae119>

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Haplotype-resolved chromosomal-level genome assembly reveals regulatory variations in mulberry fruit anthocyanin content

原文链接: <https://doi.org/10.1093/hr/uhae120>

单倍型染色体水平基因组组装揭示了桑椹花青素含量的调控变化

Plants attacked above-ground by leaf-mining flies change below-ground microbiota to enhance plant defense

原文链接: <https://doi.org/10.1093/hr/uhae121>

植物在地上受到采叶蝇的攻击会改变地下的微生物群, 以增强植物防御能力

New citizen science initiative enhances flowering onset predictions for fruit trees in Great Britain

原文链接: <https://doi.org/10.1093/hr/uhae122>

新公民科学倡议加强了对英国果树开花起始的预测

Development of ABE and AKBE base editors in watermelon

原文链接: <https://doi.org/10.1093/hr/uhae123>

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CRISPR/Cas9-mediated mutation of *FERULATE 5-HYDROXYLASE* enhances adsorption capacity of lignocellulose-based porous carbon from paper mulberry

原文链接: <https://doi.org/10.1093/hr/uhae124>

CRISPR/Cas9 介导的 *FERULATE 5*-羟化酶突变增强了构树中木质纤维素基多孔碳吸附能力

Jasmonate enhances cold acclimation in jojoba by promoting flavonol synthesis

原文链接: <https://doi.org/10.1093/hr/uhae125>

茉莉酸通过促进黄酮醇合成增强荷荷巴的冷适应性

Evolutionary conservation of receptor compensation for stem cell homeostasis in Solanaceae plants

原文链接: <https://doi.org/10.1093/hr/uhae126>

茄科植物干细胞稳态受体补偿的进化保守性

Characterization of the CsCENH3 protein and centromeric DNA profiles reveal the structures of centromeres in cucumber

原文链接: <https://doi.org/10.1093/hr/uhae127>

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Biography of *Vitis* genomics: recent advances and prospective

原文链接: <https://doi.org/10.1093/hr/uhae128>

葡萄属植物基因组学: 最新进展和展望

Evolutionarily conserved 12-oxophytodienoate reductase *trans*-lncRNA pair affects disease resistance in tea (*Camellia sinensis*) via the Jasmonic acid signaling pathway

原文链接: <https://doi.org/10.1093/hr/uhae129>

进化保守的 12-氧二烯酸还原酶反式 lncRNA 通过茉莉酸信号通路影响茶的抗病性

CRISPR/Cas9 genome editing of potato *SrDMR6-1* results in plants less affected by different stress conditions

原文链接: <https://doi.org/10.1093/hr/uhae130>

CRISPR/Cas9 编辑 *SrDMR6-1* 基因提高马铃薯受不同胁迫条件的耐受性

Genomic prediction and genome-wide association study using combined genotypic data from different genotyping systems: Application to apple fruit quality traits

原文链接: <https://doi.org/10.1093/hr/uhae131>

利用不同基因分型系统的组合基因型数据进行基因组预测和全基因组关联研究: 应用于苹果果实品质性状

Sugar import mediated by sugar transporters and cell wall invertases for seed development in *Camellia oleifera*

原文链接: <https://doi.org/10.1093/hr/uhae133>

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PE (*Prickly Eggplant*) encoding a cytokinin-activating enzyme responsible for the formation of prickles in eggplant

原文链接: <https://doi.org/10.1093/hr/uhae134>

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Metagenome-enabled models improve genomic predictive ability and identification of herbivory-limiting genes in sweetpotato

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宏基因组提高了对甘薯的基因组预测能力和草食动物限制基因的鉴定

The phosphorylation of a WD40-repeat protein negatively regulates flavonoid biosynthesis in *Camellia sinensis* under drought stress

原文链接: <https://doi.org/10.1093/hr/uhae136>

干旱胁迫下 WD40-repeat 蛋白磷酸化负调控茶树类黄酮的生物合成

Exploration of a European-centered strawberry diversity panel provides markers and candidate genes for the control of fruit quality traits

原文链接: <https://doi.org/10.1093/hr/uhae137>

以欧洲为中心的草莓多样性的探索为控制果实质量性状提供了标记和候选基因

Genetic and epigenetic signatures for improved breeding of cultivated blueberry

原文链接: <https://doi.org/10.1093/hr/uhae138>

栽培蓝莓改良育种的遗传和表观遗传特征

A CRISPR/Cas9-induced male-sterile line facilitating easy hybrid production in polyploid rapeseed (*Brassica napus*)

原文链接: <https://doi.org/10.1093/hr/uhae139>

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Integrated multi-omics investigation revealed the importance of phenylpropanoid metabolism in the defense response of *Lilium regale* Wilson to *Fusarium* wilt

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Haplotype-resolved genome assembly for tetraploid Chinese cherry (*Prunus pseudocerasus*) offers insights into fruit firmness

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JrGA20ox1- transformed rootstocks deliver drought response signals to wild-type scions in grafted walnut

原文链接: <https://doi.org/10.1093/hr/uhae143>

JrGA20ox1 能从砧木向嫁接核桃野生型接穗传递干旱响应信号

Functional data analysis-based yield modeling in year-round crop cultivation

原文链接: <https://doi.org/10.1093/hr/uhae144>

基于功能数据分析的全年作物种植产量模型

In vivo and *ex vivo* study on cell wall components as part of the network in tomato fruit during the ripening process

原文链接: <https://doi.org/10.1093/hr/uhae145>

体内和离体研究揭示细胞壁成分可作为番茄果实成熟调控网络的一部分

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

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JrPHL8-JrWRKY4-JrSTH2L module regulates resistance to *Colletotrichum gloeosporioides* in walnut

原文链接: <https://doi.org/10.1093/hr/uhae148>

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Chloroplast protein StFC-II was manipulated by a *Phytophthora* effector to enhance host susceptibility

原文链接: <https://doi.org/10.1093/hr/uhae149>

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MIKC type MADS-box transcription factor LcSVP2 is involved in dormancy regulation of the terminal buds in evergreen perennial litchi (*Litchi chinensis* Sonn.)

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Spearmint targets microtubules by (-)-carvone

原文链接: <https://doi.org/10.1093/hr/uhae151>

胡椒薄荷通过(-)-卡韦烯靶向微管

Metabolome profiling and transcriptome analysis unveiling the crucial role of magnesium transport system for magnesium homeostasis in tea plants

原文链接: <https://doi.org/10.1093/hr/uhae152>

代谢组和转录组分析揭示了镁转运系统在茶树镁稳态中的关键作用

Genomic diversity, population structure, and genome-wide association reveal genetic differentiation and trait improvements in mango

原文链接: <https://doi.org/10.1093/hr/uhae153>

基因组多样性、群体结构和全基因组关联揭示了芒果的遗传分化和性状改良

A novel tomato interspecific (*Solanum lycopersicum* var. *cerasiforme* and *Solanum pimpinellifolium*) MAGIC population facilitates trait association and candidate gene discovery in untapped exotic germplasm

原文链接: <https://doi.org/10.1093/hr/uhae154>

番茄种间 MAGIC 群体为外来种质的性状关联和候选基因鉴定奠定了基础

A simple and efficient gene functional analysis method for studying the growth and development of peach seedlings

原文链接: <https://doi.org/10.1093/hr/uhae155>

一种简单有效的研究桃幼苗生长发育的基因功能分析方法

The evolutionary significance of whole genome duplications in oil biosynthesis of oil crops

原文链接: <https://doi.org/10.1093/hr/uhae156>

全基因组复制在油料作物油脂生物合成中的进化意义

MiR319a-mediated salt stress response in poplar

原文链接: <https://doi.org/10.1093/hr/uhae157>

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Dynamic histone modification signatures coordinate developmental programs in strawberry fruit ripening

原文链接: <https://doi.org/10.1093/hr/uhae158>

动态组蛋白修饰信号协调草莓果实成熟过程中的发育程序

MdVQ17 negatively regulates apple resistance to *Glomerella* leaf spot by promoting MdWRKY17-mediated salicylic acid degradation and pectin lyase activity

原文链接: <https://doi.org/10.1093/hr/uhae159>

MdVQ17 通过促进 MdWRKY17 介导的 SA 降解和果胶裂解酶活性来负调节苹果对炭疽叶枯病的抗性

Advancing PAM-less genome editing in soybean using CRISPR-SpRY

原文链接: <https://doi.org/10.1093/hr/uhae160>

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CsMIK1 regulates inflorescence development and grain production in *Cannabis sativa* plants

原文链接: <https://doi.org/10.1093/hr/uhae161>

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Ralstonia solanacearum type III effector RipAF1 mediates plant resistance signaling by ADP-ribosylation of host FBN1

原文链接: <https://doi.org/10.1093/hr/uhae162>

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The WUSCHEL-related homeobox transcription factor *CsWOX3* negatively regulates fruit spine morphogenesis in cucumber (*Cucumis sativus* L.)

原文链接: <https://doi.org/10.1093/hr/uhae163>

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Chemical induction of DNA demethylation by 5-Azacytidine enhances tomato fruit defense against gray mold through dicer-like protein *DCL2c*

原文链接: <https://doi.org/10.1093/hr/uhae164>

微信导读: [DNA 甲基化抑制剂处理增强番茄果实对灰霉病的防御](#)

BcSRC2 interacts with BcAPX4 to increase ascorbic acid content for responding ABA signaling and drought stress in pak choi

原文链接: <https://doi.org/10.1093/hr/uhae165>

微信导读: [Hortic Res | 南京农业大学揭示 BcSRC2 与 BcAPX4 互作提高了不结球白菜 VC 含量及干旱胁迫抗性](#)

The jacktree genome and population genomics provides insights for the mechanisms of the germination obstacle and the conservation of endangered ornamental plants

原文链接: <https://doi.org/10.1093/hr/uhae166>

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Genome resequencing reveals the genetic basis of population evolution, local adaptation, and rewiring of the rhizome metabolome in *Atractylodes lancea*

原文链接: <https://doi.org/10.1093/hr/uhae167>

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The gapless genome assembly and multi-omics analyses unveil a pivotal regulatory mechanism of oil biosynthesis in the olive tree

原文链接: <https://doi.org/10.1093/hr/uhae168>

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Stem lodging Resistance-1 controls stem strength by positively regulating the biosynthesis of cell wall components in *Capsicum annuum* L.

原文链接: <https://doi.org/10.1093/hr/uhae169>

微信导读: [Hortic Res | 湖南农业大学邹学校院士团队在辣椒茎秆抗倒伏研究上取得重要进展](#)

Panax notoginseng: panoramagram of phytochemical and pharmacological properties, biosynthesis, and regulation and production of ginsenosides

原文链接: <https://doi.org/10.1093/hr/uhae170>

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Tracing the color: quantitative trait loci analysis reveals new insights into red-flesh pigmentation in apple (*Malus domestica*)

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A nested reciprocal experimental design to map the genetic architecture of transgenerational phenotypic plasticity

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Relevance and regulation of alternative splicing in plant secondary metabolism: current understanding and future directions

原文链接: <https://doi.org/10.1093/hr/uhae173>

可变剪接在植物次生代谢中的相关性和调控: 目前的认知和未来的方向

Integrated multi-omics profiling reveals a landscape of dramatic metabolic defect in *Artemisia annua*

原文链接: <https://doi.org/10.1093/hr/uhae174>

综合多组学分析揭示了黄花蒿中显著的代谢缺陷

Advances in understanding the graft healing mechanism: a review of factors and regulatory pathways

原文链接: <https://doi.org/10.1093/hr/uhae175>

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Integrated transcriptome and metabolome reveal that SISYTA modulates ROS responses driving resistance defense in *Solanum lycopersicum*

原文链接: <https://doi.org/10.1093/hr/uhae176>

微信导读: [Hortic Res](#) | [西南大学孙现超团队揭示番茄 SISYTA 通过调控病原侵染后 ROS 的合成抑制植物免疫的新机制](#)

The gap-free genome and multi-omics analysis of *Citrus reticulata* ‘Chachi’ reveal the dynamics of fruit flavonoid biosynthesis

原文链接: <https://doi.org/10.1093/hr/uhae177>

微信导读: [Hortic Res](#) | [广东省农业科学院果树研究所联合浙江农林大学在茶枝柑基因组组装及类黄酮类物质生物合成研究上取得重要进展](#)

CsPHRs-CsJAZ3 incorporates phosphate signaling and jasmonate pathway to regulate the catechins biosynthesis in *Camellia sinensis*

原文链接: <https://doi.org/10.1093/hr/uhae178>

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Magnetofected pollen gene delivery system could generate genetically modified *Cucumis sativus*

原文链接: <https://doi.org/10.1093/hr/uhae179>

利用花粉磁转染系统产生转基因黄瓜

Small molecules, enormous functions: potential approach for overcoming bottlenecks in embryogenic tissue induction and maintenance in conifers

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Haplotype-resolved genome and mapping of freezing tolerance in the wild potato *Solanum commersonii*

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Dynamic temporal transcriptome analysis reveals grape VIMYB59-*VICKX4* regulatory module controls fruit set

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SITrxh functions downstream of SIMYB86 and positively regulates nitrate stress tolerance via S-nitrosation in tomato seedling

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The gap-free genome of *Forsythia suspensa* illuminates the intricate landscape of centromeres

原文链接: <https://doi.org/10.1093/hr/uhae185>

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Siderophore interactions drive the ability of *Pseudomonas* spp. consortia to protect tomato against *Ralstonia solanacearum*

原文链接: <https://doi.org/10.1093/hr/uhae186>

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Development of super-infective ternary vector systems for enhancing the *Agrobacterium*-mediated plant transformation and genome editing efficiency

原文链接: <https://doi.org/10.1093/hr/uhae187>

构建高侵染效率三元载体系统以提高农杆菌介导的植物转化和基因组编辑效率

Restorer of fertility like 30, encoding a mitochondrion-localized pentatricopeptide repeat protein, regulates wood formation in poplar

原文链接: <https://doi.org/10.1093/hr/uhae188>

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Single-cell RNA sequencing reveals a high-resolution cell atlas of petals in *Prunus mume* at different flowering development stages

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Phospholipid production and signaling by a plant defense inducer against *Podosphaera xanthii* is genotype-dependent

原文链接: <https://doi.org/10.1093/hr/uhae190>

植物防御诱导剂对黄瓜白粉菌的磷脂产生和信号传导存在基因型依赖性

Association analysis of BSA-seq, BSR-seq, and RNA-seq reveals key genes involved in purple leaf formation in a tea population (*Camellia sinensis*)

原文链接: <https://doi.org/10.1093/hr/uhae191>

微信导读: [Hortic Res | 中国农业科学院茶叶研究所在茶树群体紫化研究中取得新进展](#)

Sorbitol mediates age-dependent changes in apple plant growth strategy through gibberellin signaling

原文链接: <https://doi.org/10.1093/hr/uhae192>

山梨醇通过赤霉素信号介导苹果植物生长策略的年龄依赖性变化

The tomato WRKY-B transcription factor modulates lateral branching by targeting *BLIND*, *PIN4*, and *IAA15*

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Genomic data provides insights into the evolutionary history and adaptive differentiation of two tetraploid strawberries

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SIDELLA interacts with SIPIF4 to regulate arbuscular mycorrhizal symbiosis and phosphate uptake in tomato

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Integrating QTL mapping and transcriptomics to decipher the genetic architecture of sterol metabolism in *Brassica napus* L

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Improvement and application of vacuum-infiltration system in tomato

原文链接: <https://doi.org/10.1093/hr/uhae197>

番茄真空渗灌系统的改进与应用

Full-length transcriptome sequencing of pepper fruit during development and construction of a transcript variation database

原文链接: <https://doi.org/10.1093/hr/uhae198>

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Fruit ripening and postharvest changes in very early - harvested tomatoes

原文链接: <https://doi.org/10.1093/hr/uhae199>

极早采收番茄的果实成熟与采后变化

Abscisic acid regulates Cl⁻ efflux via the ABI5-ZAT10-SLAH3 module in chloride-stressed *Malus hupehensis*

原文链接: <https://doi.org/10.1093/hr/uhae200>

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Chromosome-scale reference genome of an ancient landrace: unveiling the genetic basis of seed weight in the food legume crop pigeonpea (*Cajanus cajan*)

原文链接: <https://doi.org/10.1093/hr/uhae201>

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Mutation of YFT3, an isomerase in the isoprenoid biosynthetic pathway, impairs its catalytic activity and carotenoid accumulation in tomato fruit

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A genome assembly of decaploid *Houttuynia cordata* provides insights into the evolution of *Houttuynia* and the biosynthesis of alkaloids

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Is ATP a signaling regulator for postharvest chilling tolerance in fruits?

原文链接: <https://doi.org/10.1093/hr/uhae204>

ATP 是果实采后耐冷性的信号调节因子吗?

Deploying deep Solanaceae domestication and virus biotechnology knowledge to enhance food system performance and diversity,

原文链接: <https://doi.org/10.1093/hr/uhae205>

深入挖掘茄科植物驯化和病毒生物技术知识以提升食物系统的性能和多样性

Local and systemic transcriptome and spliceome reprogramming induced by the root-knot nematode *Meloidogyne incognita* in tomato

原文链接: <https://doi.org/10.1093/hr/uhae206>

番茄根结线虫诱导的局部和系统转录组和剪接组重编程

Nitrogen reduces calcium availability by promoting oxalate biosynthesis in apple leaves

原文链接: <https://doi.org/10.1093/hr/uhae208>

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Auxin response factors: important keys for understanding regulatory mechanisms of fleshy fruit development and ripening

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Transcription factors LvBBX24 and LvZIP44 coordinated anthocyanin accumulation in response to light in lily petals

原文链接: <https://doi.org/10.1093/hr/uhae211>

转录因子 LvBBX24 和 LvZIP44 协调百合花瓣中花青素苷响应光的积累

PpBBX32 and PpZAT5 modulate temperature-dependent and tissue-specific anthocyanin accumulation in peach fruit

原文链接: <https://doi.org/10.1093/hr/uhae212>

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Light stress elicits soilborne disease suppression mediated by root-secreted flavonoids in *Panax notoginseng*

原文链接: <https://doi.org/10.1093/hr/uhae213>

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Single-cell transcriptomic analysis of flowering regulation and vernalization in Chinese cabbage shoot apex

原文链接: <https://doi.org/10.1093/hr/uhae214>

大白菜茎尖开花调控和春化的单细胞转录组分析

ABIOTIC STRESS GENE 1 mediates aroma volatiles accumulation by activating MdLOX1a in apple

原文链接: <https://doi.org/10.1093/hr/uhae215>

MdASG1 通过激活苹果中的 MdLOX1a 介导香气挥发物的积累

Orphan gene *BR2* positively regulates bolting resistance through the vernalization pathway in Chinese cabbage

原文链接: <https://doi.org/10.1093/hr/uhae216>

BR2 基因通过春化途径正向调节大白菜抽薹

Visualization of metabolite distribution based on matrix-assisted laser desorption/ionization – mass spectrometry imaging of tea seedlings (*Camellia sinensis*)

原文链接: <https://doi.org/10.1093/hr/uhae218>

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CaMYB80 enhances the cold tolerance of pepper by directly targeting *CaPOAI*

原文链接: <https://doi.org/10.1093/hr/uhae219>

CaMYB80 通过直接靶向 *CaPOAI* 增强辣椒的耐寒性

Floral volatile benzenoids/phenylpropanoids: biosynthetic pathway, regulation and ecological value

原文链接: <https://doi.org/10.1093/hr/uhae220>

微信导读: [Hortic Res](#) 综述 | 北京林业大学和中国科学院植物研究所综述了苯环型/苯丙素类香气物质生物合成及调控机制研究进展

Discovery of bifunctional diterpene cyclases/synthases in bacteria supports a bacterial origin for the plant terpene synthase gene family

原文链接: <https://doi.org/10.1093/hr/uhae221>

细菌中双功能二萜环化酶/合酶的发现支持植物萜类合成酶基因家族的细菌起源

Fine mapping and identification of candidate genes associated with powdery mildew resistance in melon (*Cucumis melo* L.)

原文链接: <https://doi.org/10.1093/hr/uhae222>

甜瓜白粉病抗性候选基因的精细定位与鉴定

Fertility restorer gene *CaRf* and PepperSNP50K provide a promising breeding system for hybrid pepper

原文链接: <https://doi.org/10.1093/hr/uhae223>

育性恢复基因 *CaRf* 和 PepperSNP50K 为杂交辣椒提供了一个有前景的育种系统

HortDB V1.0: a genomic database of horticultural plants

原文链接: <https://doi.org/10.1093/hr/uhae224>

HortDB V1.0: 园艺植物基因组数据库

The art of tartness: the genetics of organic acid content in fresh fruits

原文链接: <https://doi.org/10.1093/hr/uhae225>

酸味艺术: 鲜果中有机酸含量的遗传学

Interference of skeleton photoperiod in circadian clock and photosynthetic efficiency of tea plant: in-depth analysis of mathematical model

原文链接: <https://doi.org/10.1093/hr/uhae226>

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Morphological and genetic characterization of the muscadine fruit abscission zone

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美洲圆叶葡萄果实离层区的形态和遗传特征

The transcription factor MYC2 positively regulates terpene trilactone biosynthesis through activating *GbGGPPS* expression in *Ginkgo biloba*

原文链接: <https://doi.org/10.1093/hr/uhae228>

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Ethylene in fruits: beyond ripening control

原文链接: <https://doi.org/10.1093/hr/uhae229>

果实中的乙烯: 后熟控制

Genome-wide association study identifies the genetic basis of key agronomic traits in 207 sugar beet accessions

原文链接: <https://doi.org/10.1093/hr/uhae230>

全基因组关联研究鉴定了 207 份甜菜种质中关键农艺性状的遗传基础

Salicylic acid improves chilling tolerance via CsNPR1 - CsICE1 interaction in grafted cucumbers

原文链接: <https://doi.org/10.1093/hr/uhae231>

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A small secreted protein serves as a plant-derived effector mediating symbiosis between *Populus* and *Laccaria bicolor*

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一种小分泌蛋白作为植物来源的效应因子介导杨树和双色蜡蘑之间的共生关系

Inference of the genetic basis of fruit texture in highbush blueberries using genome-wide association analyses

原文链接: <https://doi.org/10.1093/hr/uhae233>

利用全基因组关联分析推断高丛蓝莓果实质地的遗传基础

Histone deacetylase SIHDA7 impacts fruit ripening and shelf life in tomato

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CsTs, a C-type lectin receptor-like kinase, regulates the development trichome development and cuticle metabolism in cucumber (*Cucumis sativus*)

原文链接: <https://doi.org/10.1093/hr/uhae235>

CsTs, 一种 C 型凝集素类受体激酶, 调节黄瓜的毛状体发育和角质层代谢

Genotype-associated core bacteria enhance host resistance against kiwifruit bacterial canker

原文链接: <https://doi.org/10.1093/hr/uhae236>

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CGD: a multi-omics database for *Chrysanthemum* genomic and biological research

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Unveiling pepper immunity's robustness to temperature shifts: insights for empowering future crops

原文链接: <https://doi.org/10.1093/hr/uhae239>

揭示辣椒免疫对温度变化的稳健性：为未来作物赋能的见解

Potassium stimulates fruit sugar accumulation by increasing carbon flow in *Citrus sinensis*

原文链接: <https://doi.org/10.1093/hr/uhae240>

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Accumulation of dually targeted StGPT1 in chloroplasts mediated by StRFP1, an E3 ubiquitin ligase, enhances plant immunity

原文链接: <https://doi.org/10.1093/hr/uhae241>

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CsSPX3-CsPHL7-CsGSI/CsTS1 module mediated Pi-regulated negatively theanine biosynthesis in tea (*Camellia sinensis*)

原文链接: <https://doi.org/10.1093/hr/uhae242>

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Saline-alkali stress affects the accumulation of proanthocyanidins and sesquiterpenoids via the MYB5-ANR/TPS31 cascades in the rose petals

原文链接: <https://doi.org/10.1093/hr/uhae243>

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Inflorescence development in female cannabis plants is mediated by photoperiod and gibberellin

原文链接: <https://doi.org/10.1093/hr/uhae245>

大麻的花序发育受光周期和赤霉素的介导

Exploring genetic diversity, population structure, and subgenome differences in the allopolyploid *Camelina sativa*: implications for future breeding and research studies

原文链接: <https://doi.org/10.1093/hr/uhae247>

探索异源多倍体亚麻荠的遗传多样性、种群结构和亚基因组差异：对未来育种和研究的启示

A low-cost dpMIG-seq method for elucidating complex inheritance in polysomic crops: a case study in tetraploid blueberry

原文链接: <https://doi.org/10.1093/hr/uhae248>

一种低成本的 dpMIG-seq 方法用于解析多倍体作物的复杂遗传特性：以四倍体蓝莓为例

A telomere-to-telomere gap-free reference genome of *Chionanthus retusus* provides insights into the molecular mechanism underlying petal shape changes

原文链接: <https://doi.org/10.1093/hr/uhae249>

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Haplotype-resolved nonaploid genome provides insights into *in vitro* flowering in bamboos

原文链接: <https://doi.org/10.1093/hr/uhae250>

单倍型参考基因组为竹子的开花提供了解

Apple vacuolar sugar transporters regulated by MdDREB2A enhance drought resistance by promoting accumulation of soluble sugars and activating ABA signaling

原文链接: <https://doi.org/10.1093/hr/uhae251>

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De novo gene integration into regulatory networks via interaction with conserved genes in peach

原文链接: <https://doi.org/10.1093/hr/uhae252>

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TOR balances plant growth and cold tolerance by orchestrating amino acid-derived metabolism in tomato

原文链接: <https://doi.org/10.1093/hr/uhae253>

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Graft incompatibility between pepper and tomato elicits an immune response and triggers localized cell death

原文链接: <https://doi.org/10.1093/hr/uhae255>

辣椒与番茄之间的嫁接不亲和性引发免疫反应并触发局部细胞死亡

Converging functional phenotyping with systems mapping to illuminate the genotype – phenotype associations

原文链接: <https://doi.org/10.1093/hr/uhae256>

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High-resolution genetic map and SNP chip for molecular breeding in *Panax ginseng*, a tetraploid medicinal plant

原文链接: <https://doi.org/10.1093/hr/uhae257>

四倍体药用植物人参的高分辨率遗传图谱和 SNP 芯片用于分子育种

A glimpse of light on the mystery of regulating temperate fruit tree blooming time

原文链接: <https://doi.org/10.1093/hr/uhae258>

温带果树花期调控

Genome-wide mapping of main histone modifications and coordination regulation of metabolic genes under salt stress in pea (*Pisum sativum* L)

原文链接: <https://doi.org/10.1093/hr/uhae259>

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Integrated genome-wide association and transcriptomic studies reveal genetic architecture of bulb storability of plentiful garlic germplasm resources

原文链接: <https://doi.org/10.1093/hr/uhae260>

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Genome-wide screen and multi-omics analysis reveal *OGT1* participate in the biosynthesis of safflower flavonoid glycosides

原文链接: <https://doi.org/10.1093/hr/uhae261>

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Enhancing aphid resistance in horticultural crops: a breeding prospective

原文链接: <https://doi.org/10.1093/hr/uhae275>

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SISTOP1-regulated *SHAK5* expression confers Al tolerance in tomato by facilitating citrate secretion from roots

原文链接: <https://doi.org/10.1093/hr/uhae282>

微信导读: [Hortic Res | 云南农业大学杨建立/范伟团队揭示番茄抗酸铝分子调控新机制](#)

plantGIR: a genomic database of plants

原文链接: <https://doi.org/10.1093/hr/uhae342>

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