



2019年第10期总10期

## 设施园艺专题

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2019年5月6日

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## ▶ 前沿资讯

### 1. 研究揭示植物再生的伤口信号转导机制

**简介:** 强大的再生能力是植物适应严酷环境所必需的生存技能之一。受伤离体的枝条或叶片掉落在湿润的土壤表面后,能够在伤口处快速再生不定根,继而生存下去。“受伤”是引发再生的原因,但伤口信号如何控制再生,目前知之甚少。近日,中国科学院分子植物科学卓越创新中心/植物生理生态研究所研究员徐麟团队联合南通大学、美国佐治亚大学、中科院上海有机化学研究所等机构,揭示了植物再生的伤口信号转导机制,相关研究结果4月22日发表于《自然-植物》。

**来源:** 科学网

**发布日期:**2019-04-25

**全文链接:**

<http://news.sciencenet.cn/htmlnews/2019/4/425674.shtm>

### 2. 2019首届全国农业科技成果转化大会举行

**简介:** 高叶酸玉米,可以冷水冲泡的茶粉,无人植保机,纤维长度质量媲美美棉澳棉的国产CCIA棉花成衣&hellip;&hellip;农业“黑科技”一起来开大会了。4月25日,由中国农业科学院和成都市人民政府主办,全国农业科技成果转移服务中心、国家种业科技成果产权交易中心等机构承办的2019首届全国农业科技成果转化大会暨第七届成都国际都市现代农业博览会,中国乳业创新发展大会暨第十七届中国国际奶业展览会在成都拉开帷幕。

**来源:** 科学网

**发布日期:**2019-04-25

**全文链接:**

<http://news.sciencenet.cn/htmlnews/2019/4/425677.shtm>

### 3. 2019中国农业展望大会在京召开

**简介:** 4月20日,2019中国农业展望大会在北京开幕,农业农村部市场预警专家委员会发布了《中国农业展望报告(2019-2028)》。

**来源:** 农业农村部新闻办公室

**发布日期:**2019-04-20

**全文链接:**

[http://www.moa.gov.cn/xw/tpxw/201904/t20190420\\_6212076.htm](http://www.moa.gov.cn/xw/tpxw/201904/t20190420_6212076.htm)

## ▶ 学术文献

### 1. AtEDT1/HDG11 regulates stomatal density and water use efficiency via ERECTA and E2Fa (AT EDT1/HDG11通过ERECTA和E2Fa调节气孔密度和水分利用效率)

**简介:** Improvement of crop drought resistance and water use efficiency (WUE) has been a

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major endeavor in agriculture. Arabidopsis ENHANCED DROUGHT TOLERANCE1/HOMEODOMAIN GLABROUS11 (AtEDT1/HDG11), a homeodomain-START transcription factor we previously identified from enhanced drought tolerance1 mutant (edt1), has been demonstrated to significantly improve drought tolerance and WUE in multiple plant species when constitutively overexpressed. Here, we report the genetic evidence suggesting a genetic pathway, which consists of EDT1/HDG11, ERECTA, and E2Fa loci, and regulates WUE by modulating stomatal density. AtEDT1/HDG11 transcriptionally activates ERECTA by binding to HD cis-elements in the ERECTA promoter. ERECTA in turn depends on E2Fa to modulate the expression of cell cycle-related genes. This modulation affects the transition from mitosis to endocycle, leading to increased ploidy levels in leaf cells, and therefore increased cell size and decreased stomatal density. Our results suggest a possible EDT1/HDG11-ERECTA-E2Fa genetic pathway that reduces stomatal density by increasing cell size and provide a new avenue to improve WUE of crops.

来源: New Phytologist

发布日期: 2019-04-23

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6B/Csgk0FzDxqeAWrjiAAv6TDUC5ik562.pdf>

## **2 . The H3K27me3 demethylase REF6 promotes leaf senescence through directly activating major senescence regulatory and functional genes in Arabidopsis (H3K27me3去甲基化酶REF6通过直接激活拟南芥中的主要衰老调节和功能基因从而促进叶片衰老)**

简介: The roles of histone demethylation in the regulation of plant flowering, disease resistance, rhythmic response, and seed germination have been elucidated recently; however, how histone demethylation affects leaf senescence remains largely unclear. In this study, we exploited yeast one-hybrid (Y1H) to screen for the upstream regulators of NONYELLOWING1 (NYE1), and identified RELATIVE OF EARLY FLOWERING6 (REF6), a histone H3 lysine 27 tri-methylation (H3K27me3) demethylase, as a putative binding protein of NYE1 promoter. By in vivo and in vitro analyses, we demonstrated that REF6 directly binds to the motif CTCGYTY in NYE1/2 promoters through its zinc finger domain and positively regulates their expression. Loss-of-function of REF6 delayed chlorophyll (Chl) degradation, whereas overexpression of REF6 accelerated Chl degradation. Subsequently, we revealed that REF6 positively regulates the general senescence process by directly up-regulating ETHYLENE INSENSITIVE 2 (EIN2), ORESARA1 (ORE1), NAC-LIKE, ACTIVATED BY AP3/PI (NAP), PYRUVATE ORTHOPHOSPHATE DIKINASE (PPDK), PHYTOALEXIN DEFICIENT 4 (PAD4), LIPOXYGENASE 1 (LOX1), NAC DOMAIN CONTAINING PROTEIN 3 (AtNAC3), and NAC TRANSCRIPTION FACTOR-LIKE 9 (NTL9), the key regulatory and functional genes predominantly involved in the regulation of developmental leaf senescence. Importantly, loss-of-function of REF6 increased H3K27me3 levels at all the target Senescence associated genes (SAGs). We therefore conclusively demonstrate that H3K27me3 methylation represents an epigenetic mechanism prohibiting the premature transcriptional activation of

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key developmentally up-regulated senescence regulatory as well as functional genes in Arabidopsis.

来源: PLoS Genetics

发布日期: 2019-04-14

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6B/Csgk0FzDxNCAHzRDAD3AiwR0h7M086.pdf>