



2018年第4期总64期

## 农业生物技术专题

### 本期导读

#### ▶ 前沿资讯

1. 中科院神经所在世界上首次获得基因敲入的食蟹猴
2. BioWorks在美国上市新生物杀菌剂PreFence™

#### ▶ 学术文献

1. 最大的早期分化的被子植物家族主要通过以产卵为目的蝇类来授粉使早期被子植物大部分存活了下来
2. 青藏高原冻土层与活动层不同的微生物群落
3. 拟南芥中昼夜周期规律抑制茉莉酸诱导叶片衰老

中国农业科学院农业信息研究所

联系人：邹婉侬

联系电话：010-82109850

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

2018年1月22日

## ▶ 前沿资讯

### 1. 中科院神经所在世界上首次获得基因敲入的食蟹猴

**简介:** 中科院神经科学研究所、脑科学与智能技术卓越创新中心、神经科学国家重点实验室杨辉研究组与苏州非人灵长类研究平台孙强团队合作,利用了一种以同源臂介导的末端接合(HMEJ)为基础的基因敲入策略,在世界上首次获得了基因敲入的食蟹猴。1月12日,这一重要研究成果以题为《运用 CRISPR/Cas9 编辑技术获得基因敲入食蟹猴》在线发表于《细胞研究》期刊。由于基因修饰猴模型可以用于模拟人类疾病症状,因此它可以作为研究人类疾病机制和推进临床治疗的工具。然而,由于普通猴具有繁殖周期长(5-6年一代),幼仔数量少(每胎一只)以及基因编辑效率低等特点,导致构建靶向基因编辑猴具有很大的困难和挑战性。最近的一些研究表明,CRISPR/Cas9系统可以用于构建基因敲除猴。然而,与基因敲除相反,由于种种原因例如效率低,到目前为止仍然还没有基因成功敲入猴的报道。

**来源:** 科学网

**发布日期:**2018-01-13

**全文链接:**

<http://news.sciencenet.cn/htmlnews/2018/1/399874.shtm>

### 2. BioWorks launches PreFence™ biofungicide (BioWorks在美国上市新生物杀菌剂PreFence™ )

**简介:** 美国生物农药公司拜沃(BioWorks)近日在美国上市一款新生物杀菌剂PreFence™,有效防治系列真菌病害:由链格孢菌和立枯丝核菌等引起的猝倒病;由镰孢菌、疫病菌和腐霉菌引起的枯萎病和根部病害。另外,PreFence也能用于抑制由灰霉菌引起的灰霉病。PreFence的活性成分是一种从泥炭藓中分离出的链霉菌K61菌株的菌丝和孢子,剂型为可湿性粉剂,主要通过滴灌、喷灌、添加至生长基质中和种子处理等方式使用。PreFence能够与公司 RootShield PLUS+ 和 CEASE/MilStop 产品协同使用,与许多农化品兼容,并对使用者和环境安全。

**来源:** 世界农化网

**发布日期:**2018-01-10

**全文链接:**

<http://news.agropages.com/News/NewsDetail—25027.htm>

## ▶ 学术文献

### 1. The largest early-diverging angiosperm family is mostly pollinated by ovipositing insects and so are most surviving lineages of early angiosperms (最大的早期分化的被子植物家族主要通过以产卵为目的的蝇类来授粉使早期被子植物大部分存活了下来)

**简介:** Insect pollination in basal angiosperms is assumed to mostly involve 'generalized' insects looking for food, but direct observations of ANITA grade (283 species) pollinators are sparse. We present new data for numerous Schisandraceae, the largest ANITA family,

from fieldwork, nocturnal filming, electron microscopy, barcoding and molecular clocks to infer pollinator/plant interactions over multiple years at sites throughout China to test the extent of pollinator specificity. Schisandraceae are pollinated by nocturnal gall midges that lay eggs in the flowers and whose larvae then feed on floral exudates. At least three Schisandraceae have shifted to beetle pollination. Pollination by a single midge species predominates, but one species was pollinated by different species at three locations and one by two at the same location. Based on molecular clocks, gall midges and Schisandraceae may have interacted since at least the Early Miocene. Combining these findings with a review of all published ANITA pollination data shows that ovipositing flies are the most common pollinators of living representatives of the ANITA grade. Compared to food reward-based pollination, oviposition-based systems are less wasteful of plant gametes because (i) none are eaten and (ii) female insects with herbivorous larvae reliably visit conspecific flowers.

来源: Biological Sciences期刊

发布日期:2018-01-03

全文链接:

<http://agri.ckcest.cn/ass/b2c708eb-f3d2-43ff-b90d-5db68d806c4a.pdf>

## **2. Distinct microbial communities in the active and permafrost layers on the Tibetan Plateau (青藏高原冻土层与活动层不同的微生物群落)**

简介: Permafrost represents an important understudied genetic resource. Soil microorganisms play important roles in regulating biogeochemical cycles and maintaining ecosystem function. However, our knowledge of patterns and drivers of permafrost microbial communities is limited over broad geographic scales. Using high-throughput Illumina sequencing, this study compared soil bacterial, archaeal and fungal communities between the active and permafrost layers on the Tibetan Plateau. Our results indicated that microbial alpha diversity was significantly higher in the active layer than in the permafrost layer with the exception of fungal ShannonWiener index and Simpson's diversity index, and microbial community structures were significantly different between the two layers. Our results also revealed that environmental factors such as soil fertility (soil organic carbon, dissolved organic carbon and total nitrogen contents) were the primary drivers of the beta diversity of bacterial, archaeal and fungal communities in the active layer. In contrast, environmental variables such as the mean annual precipitation and total phosphorus played dominant roles in driving the microbial beta diversity in the permafrost layer. Spatial distance was important for predicting the bacterial and archaeal beta diversity in both the active and permafrost layers, but not for fungal communities. Collectively, these results demonstrated different driving factors of microbial beta diversity between the active layer and permafrost layer, implying that the drivers of the microbial beta diversity observed in the active layer cannot be used to predict the biogeographic patterns of the microbial beta diversity in the permafrost layer.

来源: Molecular Ecology期刊

发布日期:2017-11-18

全文链接:

<http://agri.ckcest.cn/ass/1e265474-ac8d-49ec-93d2-827c85710b2a.pdf>

### 3. Circadian Evening Complex represses Jasmonate-induced leaf senescence in Arabidopsis (拟南芥中昼夜周期规律抑制茉莉酸诱导叶片衰老)

**简介:** Plants initiate leaf senescence to reallocate energy and nutrients from the aging to developing tissues for optimizing growth fitness and reproduction at the end of growing season or under stress. Jasmonate (JA), a lipid-derived phytohormone, is known as an important endogenous signal in inducing leaf senescence. However, whether and how circadian clock gates JA signaling to induce leaf senescence in plants remains elusive. In this study, we show that the Evening Complex (EC), a core component of circadian oscillator, negatively regulates leaf senescence in *Arabidopsis thaliana*. Transcriptomic profiling analysis reveals that EC is closely involved in JA signaling and response, consistent with accelerated leaf senescence unanimously displayed by EC mutants upon JA induction. We found that EC directly binds the promoter of MYC2, which encodes a key activator of JA-induced leaf senescence, and represses its expression. Genetic analysis further demonstrated that the accelerated JA-induced leaf senescence in EC mutants is abrogated by *myc2 myc3 myc4* triple mutation. Collectively, these results reveal a critical molecular mechanism illustrating how the core component of circadian clock gates JA signaling to regulate leaf senescence.

**来源:** Molecular Plant 期刊

**发布日期:** 2018-01-03

**全文链接:**

<http://agri.ckcest.cn/ass/768c1047-d4d4-49eb-b23b-754b2af6037c.pdf>