



2017年第4期总12期

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## ▶ 前沿资讯

### 1. 中国农科院发布十三五规划：欲四年建成世界一流

**简介：**1月9日，中国农业科学院在京召开新闻发布会，公布了《中国农业科学院“十三五”科学技术发展规划》（以下简称《规划》）。中国农业科学院党组书记陈萌山向《中国科学报》记者表示，根据《规划》，中国农科院将在2020年初步建成世界一流农业科研院所。中国农科院副院长万建民介绍，《规划》明确了农业科学中心建设的部署，形成以“世界级农业科学中心”和“国家级农业科学技术中心”建设为核心内容的规划实施布局，统筹优化配置各类项目资源，推动科研管理机制创新。

**来源：**基因农业网

**全文链接：**

<http://www.agrogene.cn/info-3676.shtml>

### 2. 河南成立一家国际性小麦玉米科研平台

**简介：**日前，由河南农业大学和国际玉米小麦改良中心（CIMMYT）合作共建的“CIMMYT-中国（河南）小麦玉米联合研究中心”宣告成立，河南农业大学校长、中国工程院院士张改平和CIMMYT所长马丁·柯洛浦夫博士分别代表双方在共建协议上签字，该中心的成立和合作协议的正式签署，是对2016年8月17日双方合作备忘录相关内容的进一步落实和提升。

**来源：**科学网

**全文链接：**

<http://news.sciencenet.cn/htmlnews/2017/1/365517.shtm>

## ▶ 学术文献

### 1. Characterization of a dynamic metabolon producing the defense compound dhurrin in sorghum (对于高粱中的一种防御化合物蜀黍氰甙的特征描述)

**简介：**Metabolic highways may be orchestrated by the assembly of sequential enzymes into protein complexes, or metabolons, to facilitate efficient channeling of intermediates and to prevent undesired metabolic cross-talk while maintaining metabolic flexibility. Here we report the isolation of the dynamic metabolon that catalyzes the formation of the cyanogenic glucoside dhurrin, a defense compound produced in sorghum plants. The metabolon was reconstituted in liposomes, which demonstrated the importance of membrane surface charge and the presence of the glucosyltransferase for metabolic channeling. We used in planta fluorescence lifetime imaging microscopy and fluorescence correlation spectroscopy to study functional and structural characteristics of the metabolon. Understanding the regulation of biosynthetic metabolons offers opportunities to optimize synthetic biology approaches for efficient production of high-value products in heterologous hosts.

**来源：**science

**全文链接：**

<http://agri.ckcest.cn/ass/NK007-20170123005.pdf>

## 2. Comparison of synandrium structure and development in three species from the Myristicaceae (肉豆蔻科三种代表种的合生雄蕊柱发育及结构的对比)

简介: Species of Myristicaceae have diverse morphology and structure of their synandria, making them an interesting group for androecium evolution research. To clarify the morphology, structure, and origin of the synandrium, scanning electron microscopy and histology were performed on staminate flowers of *Horsfieldia pandurifolia* H.H.Hu, *H. tetratepala* C.Y.Wu & W.T.Wang, and *Myristica fragrans* Houtt. at different developmental stages. A whorl of stamen primordia was rapidly initiated around the margin of the floral apex in groups of two in *H. pandurifolia* and groups of three in *M. fragrans*. Each stamen primordium grew longitudinally, producing a pair of anther lobes and four microsporangia, accompanying one vascular bundle in *H. pandurifolia* and *M. fragrans*. In *H. tetratepala*, three stamen primordia groups were formed, and each group with several anthers was supported by one vascular bundle, indicating a secondary increase of stamen. Three types of synandrium origin were observed: in *M. fragrans*, the central sterile column tissues originated from the elongate receptacle; in *H. pandurifolia* and *H. tetratepala* they were derived from a combination of floral meristem and fused connectives, and a combination of receptacular tissue and stamen groups. The diverse origins of the central sterile column suggest that the synandrium develops differently and independently in different genera and species of Myristicaceae.

来源: 基因农业网

全文链接:

<http://agri.ckcest.cn/ass/NK007-20170123002.pdf>

## 3. Arabidopsis thaliana GH3.5 acyl acid amido synthetase mediates metabolic crosstalk in auxin and salicylic acid homeostasis (GH3.5 酰基氨基酸合成酶调节拟南芥代谢过程中生长素和水杨酸的平衡)

简介: In *Arabidopsis thaliana*, the acyl acid amido synthetase Gretchen Hagen 3.5 (AtGH3.5) conjugates both indole-3-acetic acid (IAA) and salicylic acid (SA) to modulate auxin and pathogen response pathways. To understand the molecular basis for the activity of AtGH3.5, we determined the X-ray crystal structure of the enzyme in complex with IAA and AMP. Biochemical analysis demonstrates that the substrate preference of AtGH3.5 is wider than originally described and includes the natural auxin phenylacetic acid (PAA) and the potential SA precursor benzoic acid (BA). Residues that determine IAA versus BA substrate preference were identified. The dual functionality of AtGH3.5 is unique to this enzyme although multiple IAA-conjugating GH3 proteins share nearly identical acyl acid binding sites. In planta analysis of IAA, PAA, SA, and BA and their respective aspartyl conjugates were determined in wild-type and overexpressing lines of *A. thaliana*. This study suggests that AtGH3.5 conjugates auxins (i.e., IAA and PAA) and benzoates (i.e., SA and BA) to mediate crosstalk between different metabolic pathways, broadening the potential roles for GH3 acyl acid amido synthetases in plants.

来源: PNAS

全文链接:

<http://agri.ckcest.cn/ass/NK007-20170123004.pdf>