2017年第41期总49期

# 农业生物技术专题

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## 前沿资讯

### 1. 中国农业科学院西部农业研究中心在新疆昌吉成立

**简介：**新疆是农业大区，也是我国面向中亚的桥头堡，是“丝绸之路经济带”建设的核心区。新疆农业资源丰富、特色鲜明，粮食、棉花、肉类、乳品等重要农产品增长潜力巨大。多年来，新疆的“三农”工作一直备受关注。为加快新疆农业现代化进程，满足新疆农业供给侧结构性改革需求，2014年，中国农业科学院与新疆维吾尔自治区人民政府签订了《农业科技合作协议》。随着战略合作的不断深入，9月25日，中国农业科学院西部农业研究中心（以下简称西部中心）应运而生。？

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**来源：**科学网

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**全文链接:**

http://news.sciencenet.cn/htmlnews/2017/9/389484.shtm

### 2. 中国科学家首次破译牡丹基因组 三项成果世界领先

**简介：**９月２６日，洛阳农林科学院和深圳华大基因农业控股有限公司共同召开新闻发布会宣布，中国科学家在世界上首次成功破译牡丹基因组，填补了芍药科植物基因组研究空白。据深圳华大农业应用研究院院长董扬介绍，牡丹基因组的破译，在国际植物基因组研究上填补了芍药科植物基因组的空白，在牡丹研究方面具有里程碑意义。董扬说，此次破译取得了三项世界领先。首次完成了牡丹基因组精细图的绘制，使“数字化牡丹”精彩呈现。完成牡丹基因组组装大小１２．２５ＧＢ，拼接片段Ｃｏｎｔｉｇｓ　Ｎ５０＝１２８ＫＢ，基因组完整度９８％，双端比对率９８．８％，锚定染色体８５％的基因组精细图谱，实现了超大基因组三代测序技术的完美组装。

**来源：**新华社

**发布日期:**2017-09-27

**全文链接:**

http://news.xinhuanet.com/science/2017-09/27/c_136641553.htm

### 3. Genome-wide RAD sequencing data provide unprecedented resolution of the phylogeny of temperate bamboos（全基因组的RAD序列数据前所未有的解析了温带竹子的分支系统发育问题）

**简介：**温带竹子分支(the temperate bamboo clade)包括23-32属，约546种，主要分布于东亚地区（特别是喜马拉雅）和东南亚地区。科研人员利用一种简化基因组测序的方法即RAD (restriction-site-associated DNA) 测序方法，在全基因组水平开发大量的SNPs标记，对第五分支（Phyllostachys clade）及其相关支系（Shibataea, and Arundinaria clades）的系统发育关系进行了研究。基于RAD测序数据所获得的SNP矩阵，构建了目前为止竹亚科分辨率最高的一棵系统发育树，并得到8个主要的分支。结果表明，基于叶绿体片段所命名的第五分支(Phyllostachys clade)，第四(Shibataea clade)及第六分支（Arundinaria clade）均不为单系。与叶绿体片段所得到的结果不同的是，

基于RAD数据的系统发育关系与按照形态性状的传统分类结果较一致。具有细型地下茎的物种形成了两个单系分支，一支为主要分布于东亚低海拔地区的Sino-Japanese clade，另一支为特有分布于横断山-喜马拉雅高海拔地区的alpine Bashania。

**来源：**Scientific Reports期刊

**发布日期:**2017-09-14

**全文链接:**

http://agri.ckcest.cn/ass/a53950dd-4f97-4282-b2bd-79113fbcea83.pdf

## 学术文献

### 1. Genome analysis of Taraxacum kok-saghyz Rodin provides new insights into rubber biosynthesis（橡胶草的基因分析为橡胶制品的合成提供了新的见解）

**简介：**The Russian dandelion Taraxacum kok-saghyz Rodin (TKS), a member of the Composite family and a potential alternative source of natural rubber (NR) and inulin, is an ideal model system for studying rubber biosynthesis. Here we present the draft genome of TKS, the first assembled NR-producing weed plant. The draft TKS genome assembly has a length of 1.29 Gb, containing 46,731 predicted protein-coding genes and 68.56% repeats, in which the LTR-RT elements predominantly contribute to the genome enlargement. We analyzed the heterozygous regions/genes, suggesting its possible involvement in inbreeding depression. Through comparative studies between rubber-producing and non-rubber-producing plants, we found that enzymes of the mevalonate (MVA) pathway and rubber elongation might be critical for rubber biosynthesis, and several key isoforms have been isolated showing predominantly expressed in the latex, indicating their crucial functions in rubber biosynthesis. Moreover, for two important families in rubber elongation, the CPT/CPTL and REF/SRPP families, diverse evolutionary tracks have been revealed. These results provide valuable resources and new insights into the mechanism of NR biosynthesis, and facilitate the development of alternative NR producing crops.

**来源：**National Science Review

**发布日期:**2017-08-25

**全文链接:**

http://agri.ckcest.cn/ass/7f4908c2-c1ee-4543-ac2f-56eb1a22bba9.pdf

### 2. Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean（全基因组相关联的研究分析解析了大豆重要性状的遗传网络）

**简介：**Soybean (Glycine max [L.] Merr.) is one of the most important oil and protein crops. Ever-increasing soybean consumption necessitates the improvement of varieties for more efficient production. However, both correlations among different traits and genetic interactions among genes that affect a single trait pose a challenge to soybean breeding.Results.To understand the genetic networks underlying phenotypic correlations, we

collected 809 soybean accessions worldwide and phenotyped them for two years at three locations for 84 agronomic traits. Genome-wide association studies identified 245 significant genetic loci, among which 95 genetically interacted with other loci. We determined that 14 oil synthesis-related genes are responsible for fatty acid accumulation in soybean and function in line with an additive model. Network analyses demonstrated that 51 traits could be linked through the linkage disequilibrium of 115 associated loci and these links reflect phenotypic correlations. We revealed that 23 loci, including the known Dt1 E2 E1 Ln Dt2, Fan, and Fap loci, as well as 16 undefined associated loci, have pleiotropic effects on different traits.This study provides insights into the genetic correlation among complex traits and will facilitate future soybean functional studies and breeding through molecular design.

**来源：**Genome Biology期刊
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http://agri.ckcest.cn/ass/be1d5f13-8f46-49ab-9b90-4b354ce0f9a1.pdf